New Zealand Food Safety
Haumaru Kai Aotearoa

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2017

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Prepared for New Zealand Food Safety
by Isabelle Pattis, Peter Cressey, Liza Lopez, Rebekah Roos, Beverley Horn & Tanya Soboleva

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PO Box 2526
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Telephone: 0800 00 83 33
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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 2017

ESR Report FW18022

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 in New Zealand* 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.

The current report for 2017 highlights that *Campylobacter* remains our top priority foodborne pathogen of concern, 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*.

The report also highlights the occurrence of other foodborne pathogens such as the shiga-toxigenic *Escherichia coli* (STEC) from raw drinking milk, and *Yersinia* species potentially from fresh produce. While the available New Zealand information does not strongly implicate horticultural products in foodborne illness, overseas data does show a strong relationship and consequently NZFS will watch this food group closely. In addition, MPI will strengthen its research programme to identify optimal methods for detection and characterisation of *Yersinia* to facilitate robust attribution studies.

This report notes for the first time a gradual shift to molecular methodology by medical laboratories in New Zealand, and it is likely that this will have an effect on the overall numbers of notified human illnesses, and by definition of a fixed attribution factor, the numbers of estimated foodborne illnesses. However, while notified STEC infections have increased, there is no evidence that foodborne sources are increasing, and indeed other that raw drinking milk, food is not implicated in any STEC illnesses. 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.

Also highlighted in this report are changes to better represent contemporary food risk factors rather than historical or perceived factors from the international literature. For instance, the eating habits of New Zealand consumers is rapidly changing, e.g. more raw, bagged, long shelf life, chilled foods and smoothies.

Robust *Foodborne Disease in New Zealand* reports are necessary to ensure that MPI's 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 MPI will continue to improve the analysis of risk factors and develop contemporary strategies for presentation of this information for the 2018 report.

ESR
Science for Communities

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2017

Prepared for Ministry for Primary Industries under
Project MRP/17/03 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2017,
as part of an overall contract for scientific services

by

Isabelle Pattis
Peter Cressey
Liza Lopez
Rebekah Roos
Beverley Horn

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INTRODUCTION

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 MPI'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 MPI and its stakeholders.

This report for the calendar year 2017 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 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 five sets of published country-specific estimates are given in Table 1, for the USA [3], Canada [4], Australia [5, 6], England and Wales [7] and the Netherlands [8]. 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

* Note that water is not considered a food.

outbreak 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.
[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 2017 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 2017 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, b]
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
VTEC/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).
VTEC = Verotoxin-producing *Escherichia coli* STEC = Shiga toxin-producing *Escherichia coli*.
[a] International statistical classification of disease and related health problems 10th revision [12].
[b] The 11th revision of the ICD-11 is expected to be released in June 2018.

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, verotoxin- or shiga toxin-producing *Escherichia coli* (VTEC/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 notifiable diseases in the form of acute gastrointestinal illness and sequelae which are considered to result from these 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 VTEC/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 some laboratories have started to introduce changes in enteric testing methods and screening criteria. Traditional culture methods are being replaced by more sensitive polymerase chain reaction (PCR) methods that detect microbial DNA. From 22 June 2015 onwards, all community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for *Campylobacter, Shigella, Salmonella*, VTEC/STEC, *Giardia* and *Cryptosporidium*. To the best of our knowledge no changes were introduced in other laboratories during 2016. Since January 2017, laboratories servicing Southern DHB (ongoing) and Lakes DHB (January 2017 - June 2017)[*] also changed to enteric PCR panels. 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. As more laboratories are shifting to molecular methods in 2018 it needs to be determined if and how notification rates and trends are affected. Without multiple years of data, 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. A decrease in disease rate as based on culture derived methods may be masked by the increased sensitivity of the PCR methodology. The current assumption is that all laboratories will have transistioned to molecular testing methods by 2020.

Where VTEC/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 VTEC/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 in the DHBs listed above are now screened for *Giardia* spp. and *Cryptosporidium* spp. when previously only those specimens where parasite screening was requested were tested.

[*] From July 2017 onwards Lakes DHB changed their laboratory and enteric testing was again done by traditional culture methods.

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2017 in Table 4 below.

Table 4. Estimated proportion and incidence of the main foodborne diseases for 2017

	Total notified		Estimated foodborne transmission		
	Cases	Rate[b]	Cases	Proportion (%)	Rate[b]
Campylobacteriosis	6482	135.2	3771	63.8 (44.1-83.2)[c]	78.7 (54.4-102.6)[d]
Cryptosporidiosis	1192	24.9	NE	-	-
Giardiasis	1648	34.4	NE	-	-
Hepatitis A	58	1.2	NE	-	-
Listeriosis	21	0.4	17	87.8 (57.9-98.5)[c]	0.4 (0.3-0.4)[d]
Salmonellosis	1119	23.3	452	62.1 (35.2-86.4)[c]	9.4 (5.3-13.1)[d]
Shigellosis	245	5.1	NE	-	-
VTEC/STEC infection	547	11.4	147	29.9 (3.5-60.7)[c]	3.1 (0.4-6.3)[d]
Yersiniosis	918	19.2	537	63.2 (29.0-91.5)[c]	11.2 (5.1-16.2)[d]

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 exclude travel-related cases.

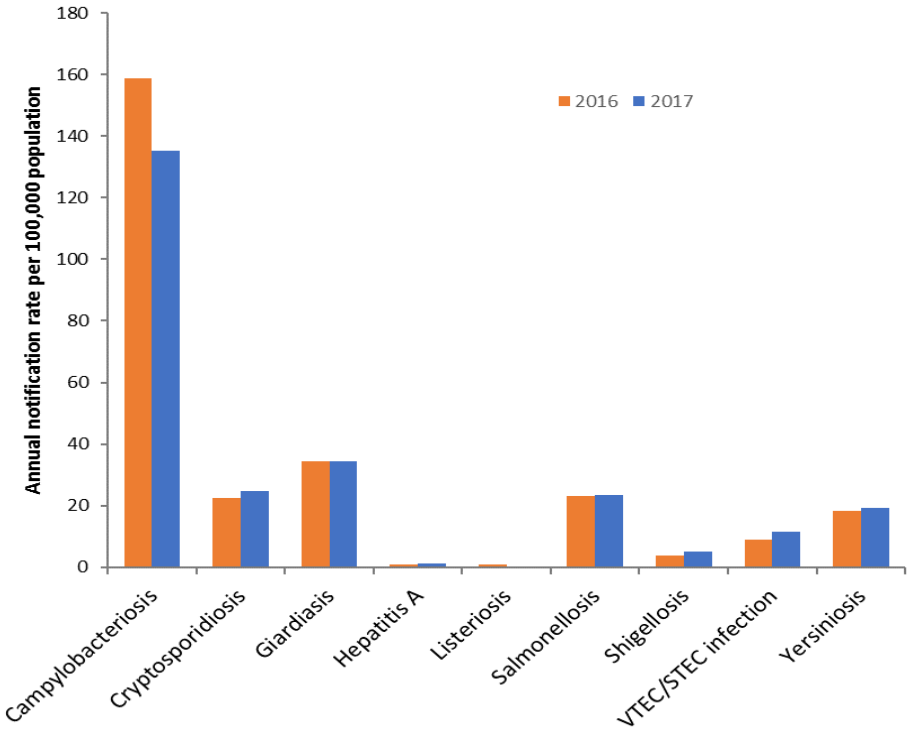
[b] Rate per 100,000, mid-year estimated population.

[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 2017 a continued increase in notification rates was apparent for shigellosis, VTEC/STEC infection, and yersiniosis compared to 2016 (Figure 1). This increase might be partially due additional laboratories changing their methodology to molecular methods.

Figure 1. Notification rates of the main foodborne diseases, 2016–2017



Reporting against targets

The performance targets for potentially foodborne diseases come under scrutiny by the Ministry for Primary Industries (MPI) on an annual basis. In 2015, 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 MPI. 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 VTEC/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 VTEC/STEC and norovirus are outside of the influence of MPI.

MPI 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 foodborne diseases are available and MPI is supporting projects to increase the quality of data. The source of the data is the *Notifiable Diseases in New Zealand Annual Report,* by ESR [13]. MPI has also 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 the Ministry of Health (MoH)*. The estimate of the foodborne proportion of campylobacteriosis determined by the expert elicitation is approximately 0.6.

From year to year, fluctuations in disease rates may occur due to modifications in clinical, laboratory and notification practices as well as changes in food exposures. These are highlighted and corrected for where possible.

* 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.

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 2017 is given in Table 5.

Table 5. Estimated proportion and incidence of foodborne campylobacteriosis for 2017

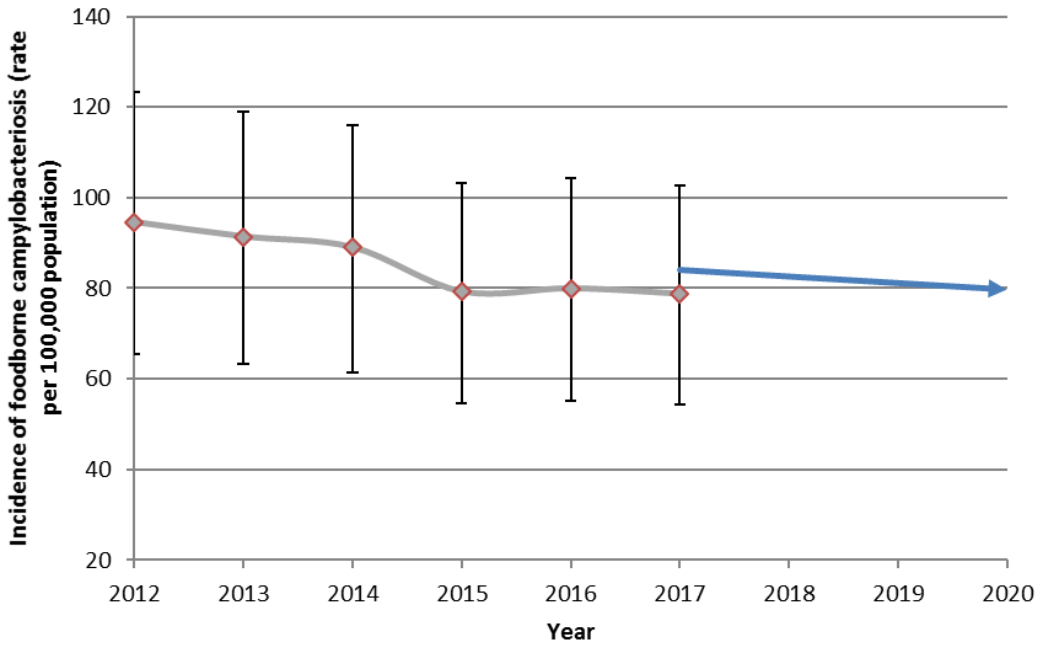
	Cases	Proportion (%)	Rate (per 100,000, mid-year estimated population)
Total notified	6482		135.2
Estimated not related to overseas travel[a]	5912	91.2	123.3
Estimated foodborne transmission	3771	63.8 (44.1-83.2)[b]	78.7 (54.4-102.6)[c]

[a] The estimated percentage of cases relating to overseas travel is 8.8%.
[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.

Presentation

The trend in relative rates (most likely estimates) compared with the 2016 to 2020 goal is shown in Figure 2. The estimated foodborne rates for 2012 to 2017 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 new target for 2017 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 2017 by data source

During 2017, no cases of *B. cereus* intoxication were 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 Ministry of Health (MoH) National Minimum Dataset (NMDS). Of the three hospital admissions recorded in 2017, two were reported with *B. cereus* intoxication as the primary diagnosis and one was reported as another relevant diagnosis.

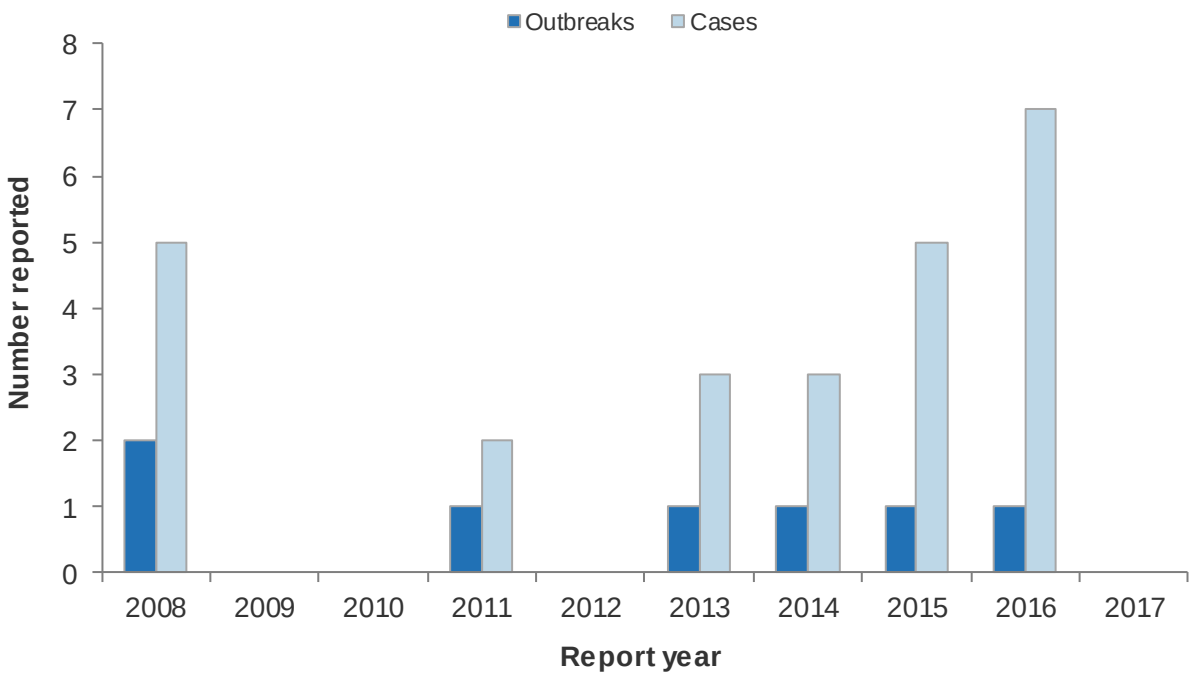
Expert consultation estimated that 97% (minimum = 90%, maximum = 100%) of *B. cereus* intoxication will be due to foodborne transmission [14]. The expert consultation also estimated that approximately 60% of the foodborne transmission would be due to consumption of rice.

Outbreaks reported as caused by *Bacillus cereus*

During 2017, no outbreaks caused by *B. cereus* intoxication were reported in EpiSurv.

Outbreaks of *B. cereus* intoxication are rare, with only seven outbreaks reported since 2008 (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, 2008−2017



Recent surveys

Nil.

Relevant New Zealand studies and publications

Papers

Farm dairy effluent was collected from four Waikato dairy farms and the bacterial species present were characterised by molecular techniques [15]. *B. cereus* was identified on all four farms, but was only identified in the summer on three farms, while on the fourth it was only identified in the winter sampling.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2017 are given in Table 6.

Table 6. Summary of surveillance data for campylobacteriosis, 2017

Parameter	Value in 2017	Source
Number of notified cases	6482	EpiSurv
Notification rate (per 100,000)	135.2	EpiSurv
Hospitalisations (% of notifications)[a]	712 (11%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	570 (8.8%)	EpiSurv
Estimated food-related cases (%)[b]	3771 (63.8%)	Expert consultation

[a] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.
[b] For estimation of food-related cases the proportions derived from expert consultation 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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017–June 2017) 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 2017 by data source

During 2017, 6482 cases (135.2 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv.

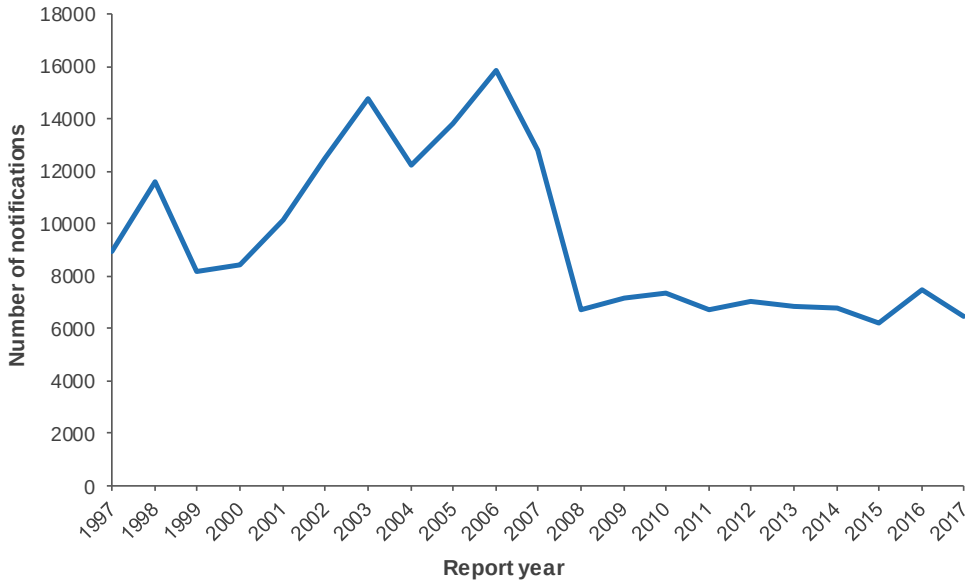
The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the MoH NMDS database. Of the 712 hospital admissions (14.9 admissions per 100,000 population) recorded in 2017, 576 were reported with campylobacteriosis as the principal diagnosis and 136 with campylobacteriosis 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

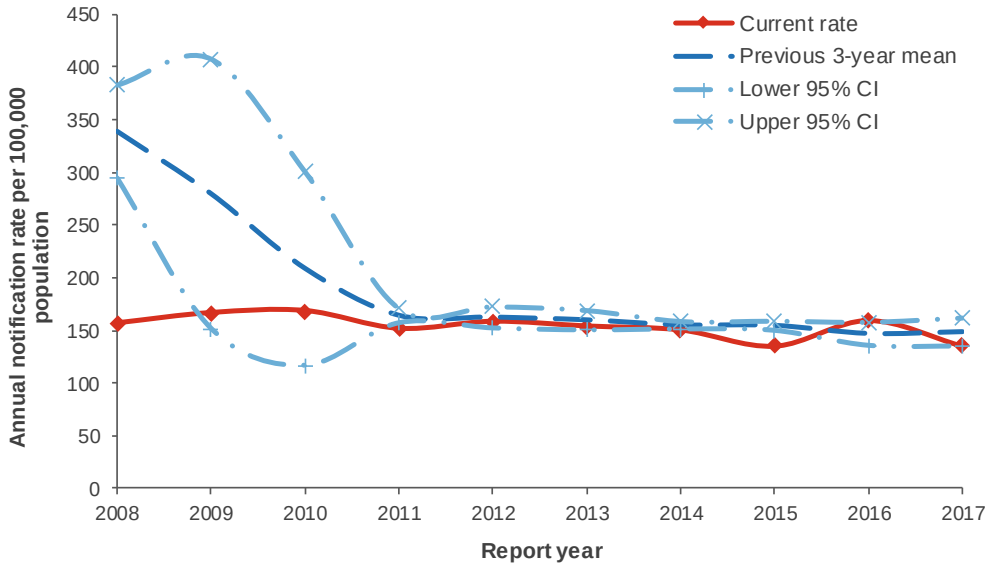
The number of campylobacteriosis notifications reported each year generally increased from 1997, up to the highest number recorded in 2006 (15,873 cases). During 2007 and 2008, there was a significant decrease in the number of cases reported (Figure 4). The number of notifications each year has remained stable from 2008 to 2017, with the exception of 2016, due to the outbreak in Hawke's Bay attributed to contaminated drinking water [16].

Figure 4. Campylobacteriosis notifications by year, 1997–2017



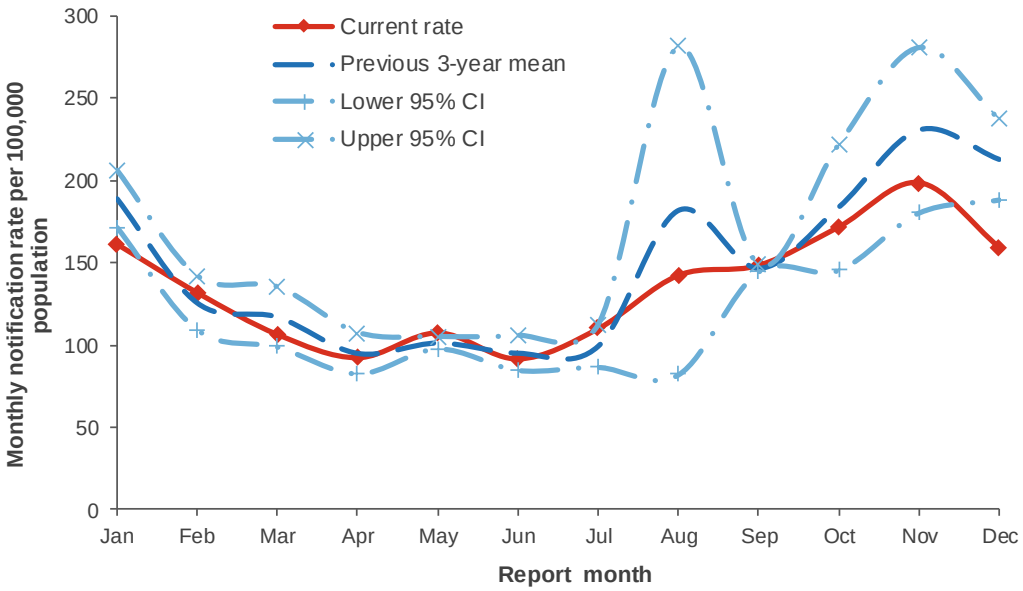
The campylobacteriosis annual rate trend (Figure 5) was very similar to the corresponding annual notification trend (Figure 4); with the notification rate remaining stable between 2008 and 2017. The notification rate was significantly higher in 2016 (158.9 cases per 100,000 population) than the previous three-year average (146.5 cases per 100,000), due to one outbreak in Hawke's Bay attributed to contaminated drinking water [16].

Figure 5. Campylobacteriosis notification rate by year, 2008–2017



The number of notified cases of campylobacteriosis per 100,000 population by month for 2017 is shown in Figure 6. The monthly number of notifications in 2017 ranged from 367 notifications (June) to 793 notifications (November). The lowest notification rates occurred between February and July in 2017. Rates by month in 2017 followed a similar pattern as seen in the three years prior to 2016 (2013–2015). The current previous three-year mean is influenced by a outbreak in Hawke's Bay in 2016 attributed to contaminated drinking water [16]. 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.

Figure 6. Campylobacteriosis monthly rate (annualised), 2017



Similar to previous years, the rate of notifications for campylobacteriosis was higher for males (151.9 notifications per 100,000 population) than for females (119.0 notifications per 100,000 population) in 2017. However, the rate of hospitalisations was similar for both genders (14.8 and 14.9 admissions per 100,000 population, respectively, Table 7).

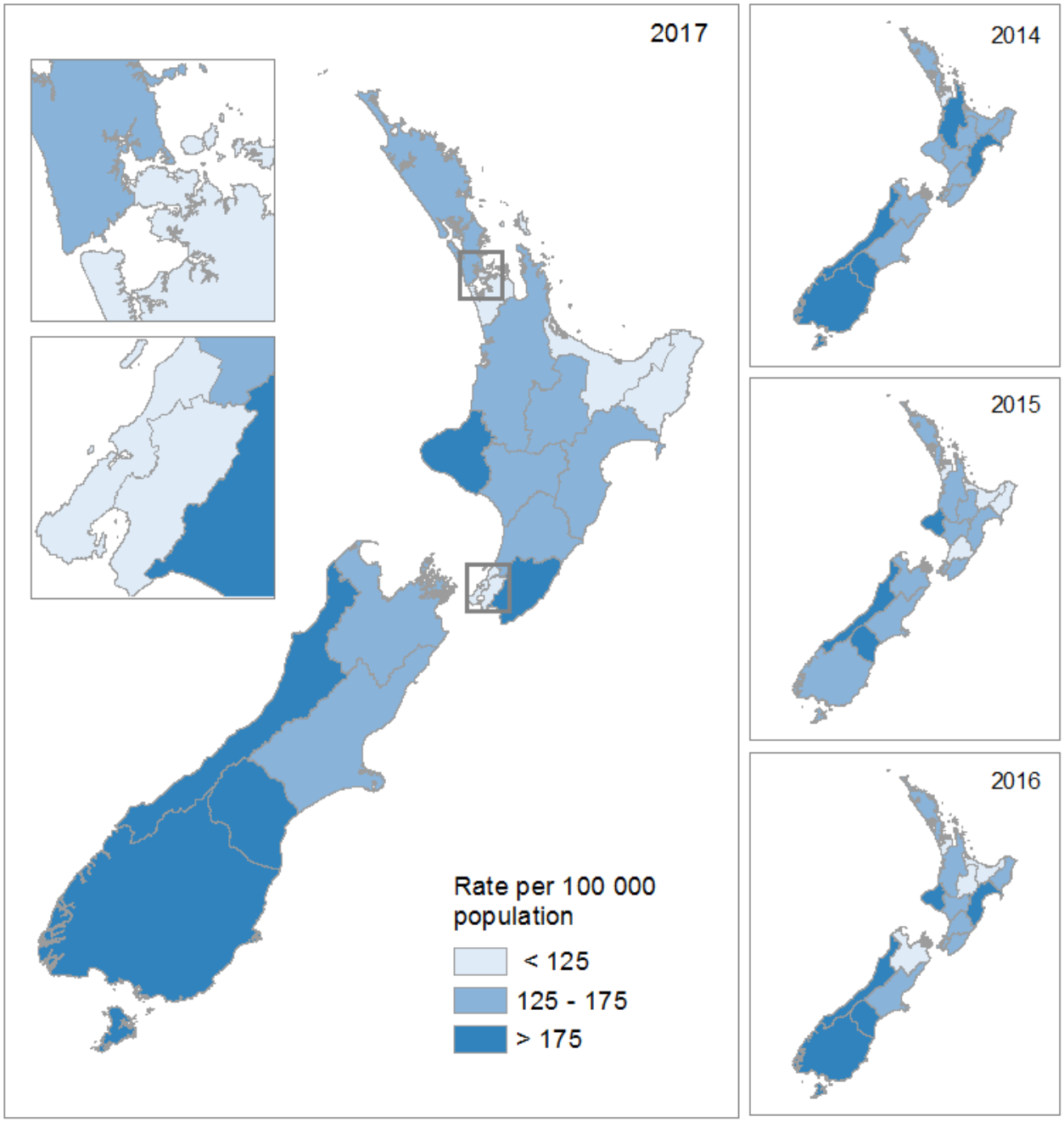
Table 7. Campylobacteriosis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3586	151.9	349	14.8
Female	2896	119.0	363	14.9
Total	**6482**	**135.2**	**712**	**14.9**

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

Campylobacteriosis rates varied throughout the country in 2017 as shown in Figure 7. In the South Island, South Canterbury DHB (246.6 per 100,000 population, 147 cases), Southern DHB (229.4 per 100,000 population, 744 cases) and West Coast DHB (187.7 per 100,000 population, 61 cases) were higher than other DHBs (range 142.5-156.7 per 100,000 population). In the North Island, Taranaki DHB (191.4 per 100,000, 226 cases) had the highest rate, followed by Wairarapa DHB (177.5 per 100,000, 79 cases). The lowest rate in New Zealand was reported for Counties-Manukau DHB (85.4 per 100,000, 467 cases). South Canterbury and West coast DHBs have consistently been in the highest quantile in the last four years.

Figure 7. Geographic distribution of campylobacteriosis notifications, 2014–2017



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). 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 2017 were reported for children aged 1 to 4 years (257.9 per 100,000 population, 633 cases) and infants aged less than 1 year (241.0 per 100,000, 146 cases). The highest hospitalisation rate was for the 70 years and over age group (43.5 admissions per 100,000 population), which was noticeably higher than any other age group (Table 8).

Table 8. Campylobacteriosis cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	146	241.0	12	19.8
1 to 4	633	257.9	33	13.4
5 to 9	320	98.1	18	5.5
10 to 14	243	80.6	17	5.6
15 to 19	380	120.1	30	9.5
20 to 29	979	136.4	97	13.5
30 to 39	682	113.5	73	12.1
40 to 49	672	108.7	56	9.1
50 to 59	856	138.3	76	12.3
60 to 69	772	154.4	88	17.6
70+	796	163.3	212	43.5
Unknown	3	-	0	1
Total	**6482**	**135.2**	**712**	**14.9**

[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 2017, 8.8% (95% CI 7.8-9.9%) 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 2017. The resultant distribution has a mean of 571 cases (95% CI 490-657).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 8.4% (95% CI 7.9-8.9%).

Outbreaks reported as caused by *Campylobacter* spp.

In 2017, four (57.1%) of the outbreaks caused by *Campylobacter* spp. and 19 (61.3%) of the associated cases were reported as foodborne (Table 9). 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 1.3% (7/531) of all enteric outbreaks and 0.3% (31/9538) of all associated cases reported in 2017.

Table 9. *Campylobacter* spp. outbreaks reported, 2017

Measure	Foodborne *Campylobacter* spp. Outbreaks	All *Campylobacter* spp. outbreaks
Outbreaks	4	7
Cases	19	31
Hospitalised cases	1	1

During 2008 to 2017, 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 outbreaks with high numbers of associated cases (51, 32 and 17).

Figure 8. Foodborne *Campylobacter* spp. outbreaks and associated cases reported by year, 2008–2017

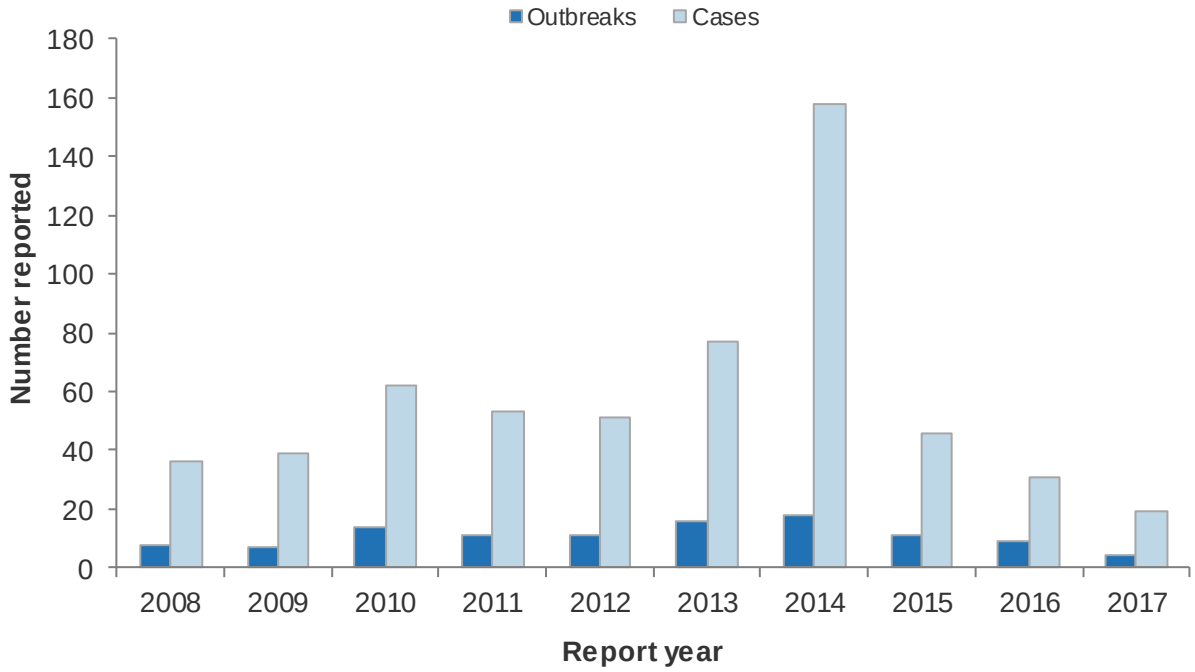


Table 10 contains details of the four foodborne outbreaks of campylobacteriosis reported in 2017. In all outbreaks with a suspected food vehicle (Table 10), the evidence for the implicated food was weak.

Table 10. Details of foodborne *Campylobacter* spp. outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Toi Te Ora	Jan	Unknown	Unknown	Unknown	1C, 2P
Regional	May	Unknown	Home	Unknown	3C, 3P
Hawke's Bay	Jun	Raw milk	Other food outlet	Other food outlet	3C
Northland	Nov	Home made bacon and egg pie	Camp	School	2C, 5P

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

In 2017, no food or clinical samples were submitted to ESR's Public Health Laboratory relating to the food-associated *Campylobacter* spp. outbreaks listed in Table 10.

Disease sequelae - Guillain-Barré syndrome

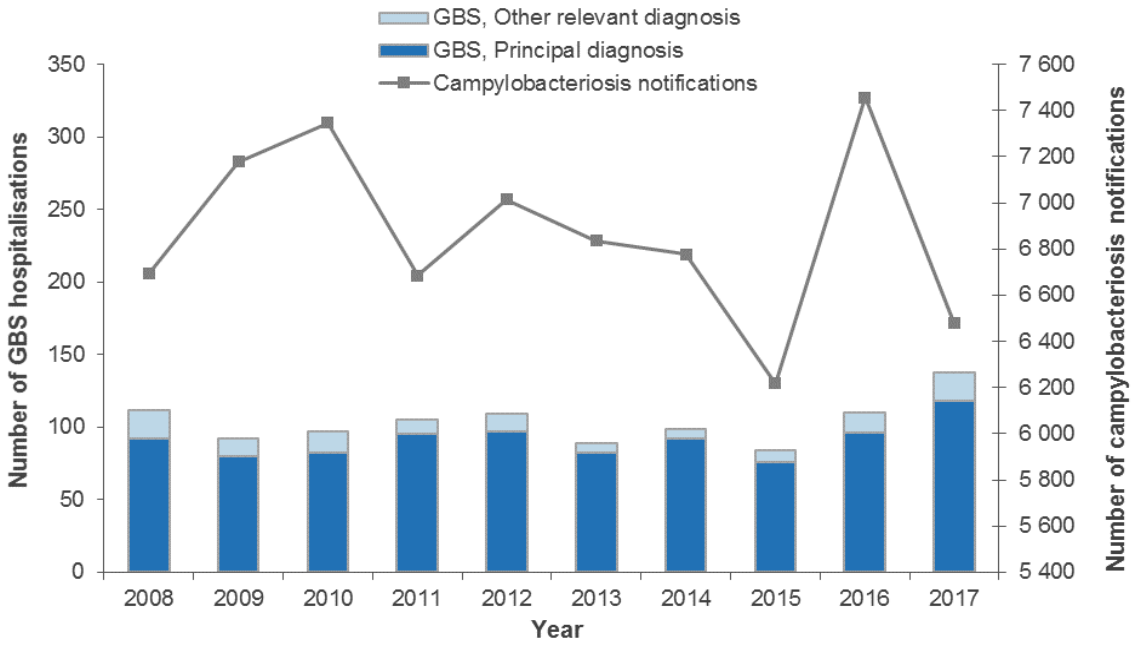
Guillain-Barré syndrome (GBS) may be preceded by an infection with *Campylobacter jejuni*. Other respiratory or intestinal illnesses and other triggers may also precede an episode of GBS.

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 2017 were considered, rather than all cases that were hospitalised in 2017. That is, if a GBS cases hospitalised in 2017 had been hospitalised with GBS in a

previous year, the 2017 admission was considered to be a readmission, rather than an incident case. There were 138 incident hospitalised cases recorded in 2017 (2.8 admissions per 100,000 population), 118 were reported with GBS as the primary diagnosis and 20 with this condition as another relevant diagnosis.

Between 2008 and 2017, the annual number of incident hospitalised cases (any diagnosis code) for GBS ranged from 84 to 138 (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, 2008–2017



In 2017, the number of incident hospitalised cases due to GBS was higher for males than for females (Table 11). This is consistent with the pattern seen for GBS in most previous years, except 2016 when case numbers for males and females were almost identical. It is also consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2017 (Table 7).

Table 11. Guillain-Barré syndrome hospitalised cases by sex, 2017

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	74	3.1
Female	64	2.6
Total	**138**	**2.8**

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

In 2017, the highest rates of incident hospitalisation for GBS were in the 60 to 69 years age group, followed by the 70 years and over age group (Table 12).

Table 12. Guillain-Barré syndrome hospitalised cases by age group, 2017

Age group (years)	Hospitalised cases	
	No.	Rate[b]
<5	5	1.6
5 to 9	6	1.8
10 to 14	1	-
15 to 19	9	2.8
20 to 29	9	1.3
30 to 39	20	3.3
40 to 49	8	1.3
50 to 59	22	3.6
60 to 69	31	6.2
70+	27	5.5
Total	**138**	**2.8**

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Campylobacter spp. were detected in faeces from farmed red deer (*Cervus elaphus, n* = 206) in Canterbury and Southland [17]. Isolation rates varied between regions, with 8.0% of samples from Canterbury positive for *Campylobacter* and 17.0% of samples from Southland. Isolates from Southland were more likely to be of *C. coli* or contain a mixture of *C. coli* and *C. jejuni* (12/20) than isolates from Canterbury (1/7).
While companion pet (dogs and cats) food is not intended for human consumption, bacterial contamination patterns can provide information on contamination in the meat-producing species included in the pet food. Raw retail pet food diets (*n* = 50) were sampled in the Palmerston North area and tested for *Campylobacter* spp. [18]. *Campyobacter* spp. were isolated from 14 (28%) samples, including *C. jejuni* (22%), *C. coli* (6%) and *C. lari* (6%). Six isolates identified as *Campylobacter* spp. by PCR, were subsequently found to be *Arcobacter butzleri*. Poultry meat-based foods were more likely to be *Campylobacter* positive than non-poultry meats.

Relevant regulatory developments

MPI updated their *Campylobacter* Risk Management Strategy for the period 2017–2020 [19]. MPI's goal is to implement a *Campylobacter* Risk Management Strategy that results in continuous reduction in the incidence of foodborne campylobacteriosis.

MPI has endorsed two Key Performance Indicators to drive improvement toward this goal:

- Key Performance Indicator 1: The number of human cases of foodborne campylobacteriosis reduced by 10% from 88.4 to 79.6 per 100,000 per head of population by the end of 2020.
- Key Performance Indicator 2: The number of broiler processing premises (standard throughput) with more than 30% of NMD carcass rinsate samples positive for *Campylobacter* reduced from three to zero by the end of 2017.

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 2017 by data source

During 2017, one case (0.02 per 100,000 population) of ciguatera fish poisoning was 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 six hospital admissions (0.1 admissions per 100,000 population) recorded in 2017, all six 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 2017, two outbreaks of ciguatera fish poisoning were reported in EpiSurv, with 31 associated cases (Table 13). 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.

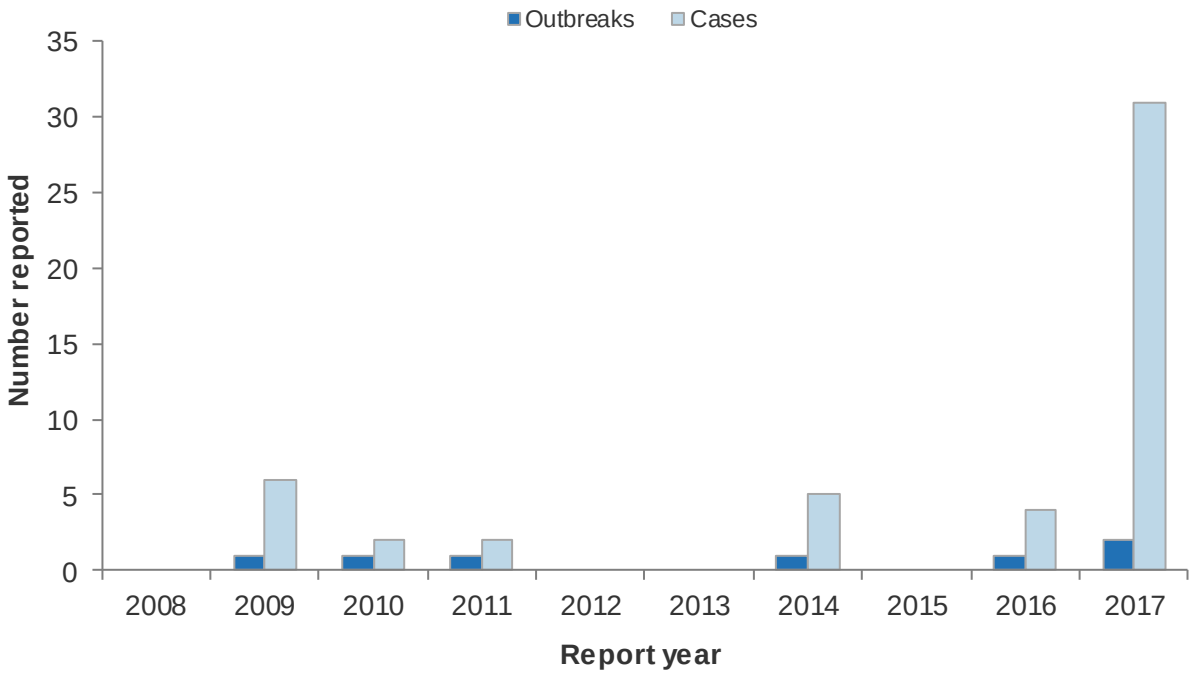
Table 13. Ciguatera fish poisoning outbreaks reported, 2017

Measure	Foodborne ciguatera fish poisoning outbreaks
Outbreaks	2
Cases	31
Hospitalised cases[a]	0

[a] Source: EpiSurv.

Over the 10-year period from 2008 to 2017, seven outbreaks of ciguatera fish poisoning were reported, with no more than two outbreaks of ciguatera fish poisoning reported in any year (Figure 10). In 2017, the number of cases associated with one outbreak was unusually high (27 cases).

Figure 10. Ciguatera fish poisoning outbreaks and associated cases reported by year, 2008–2017



The suspected vehicle was recorded for one outbreak as cooked kawakawa fish in Episurv. Raw and cooked fish samples relating to one outbreak (Auckland PHU) were submitted to ESR's Public Health Laboratory and ciguatoxin was detected (Table 14).

Table 14. Details of ciguatera fish poisoning outbreak, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Toi Te Ora	Aug	Unknown	Hotel/motel/ Restaurant/café/bakery	Overseas manufacturer	1C, 26P
Auckland	Aug	Cooked kawakawa fish	Supermarket/delicatessen	Home/Supermarket/ delicatessen	0C, 4P

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

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 2017 by data source

During 2017, no cases of *C. perfringens* intoxication were reported in EpiSurv.

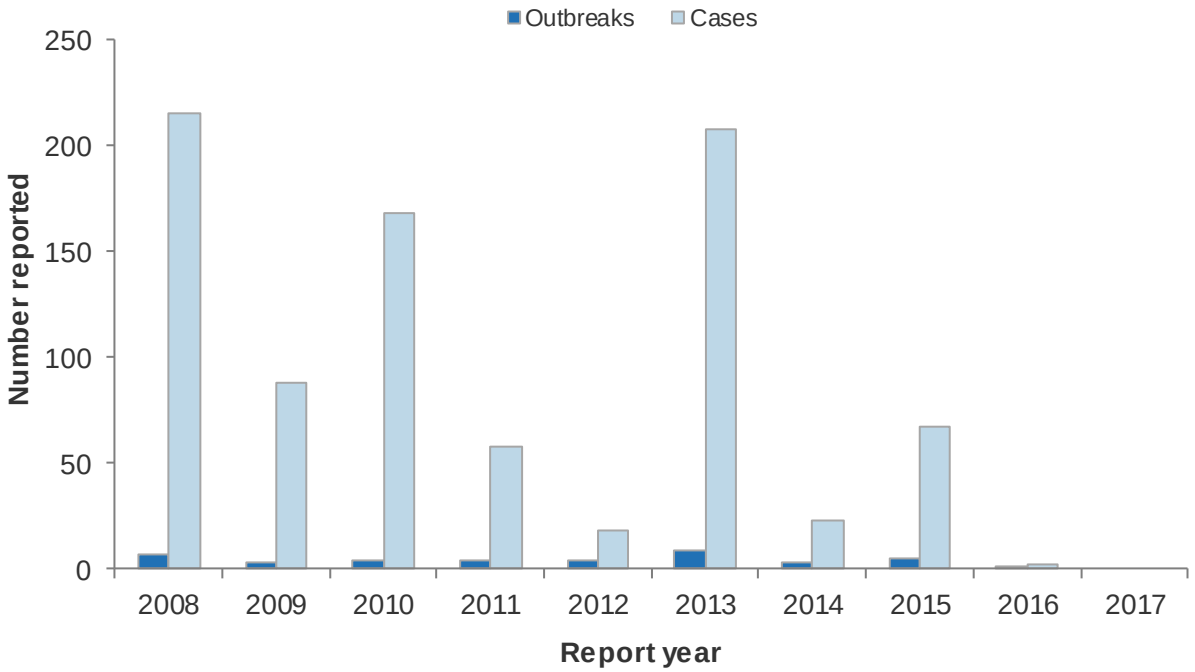
The ICD-10 code A05.2 was used to extract foodborne *C. perfringens* intoxication hospitalisation data from the MoH NMDS database. There were no hospital admissions recorded in 2017 with *C. perfringens* intoxication as a diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

There were no *C. perfringens* intoxication outbreaks reported in 2017. 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.

Between 2008 and 2017, the number of foodborne outbreaks associated with *C. perfringens* ranged from one (2016) 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 2008 (215 cases). In 2017 no outbreaks were recorded.

Figure 11. Foodborne *C. perfringens* outbreaks and associated cases reported by year, 2008–2017



Recent surveys

Nil.

Relevant New Zealand studies and publications

Papers

Farm dairy effluent was collected from four Waikato dairy farms and the bacterial species present were characterised by molecular techniques [15]. *C. perfringens* was identified on three of the four farms, but was only identified in the summer on two farms, while on the third farm it was identified in both the winter and summer samplings.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2017 are given in Table 15.

Table 15. Summary of surveillance data for cryptosporidiosis, 2017

Parameter	Value in 2017	Source
Number of notified cases	1192	EpiSurv
Notification rate (per 100,000)	24.9	EpiSurv
Hospitalisations (% of notifications)[a]	67 (5.6%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	120 (10.1%)	EpiSurv
Estimated food-related cases (%)	NE	-

NE = not estimated, no information is available on the food attributable proportion of cryptosporidiosis in New Zealand.
[a] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.

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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017) were screened by multiplex PCR for a range of pathogens, including *Cryptosporidium*. 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 for cryptosporidiosis as a decrease in disease rate may be masked by the increased sensitivity of the PCR methodology.

Cryptosporidiosis cases reported in 2017 by data source

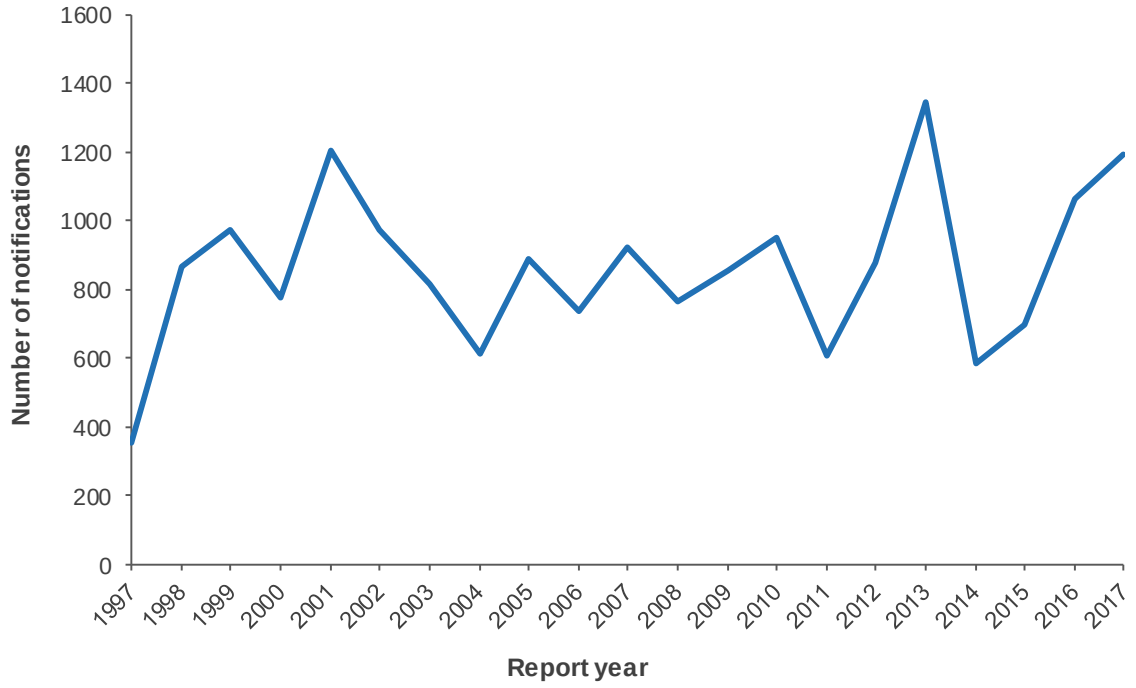
During 2017, 1192 cases (24.9 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 67 hospital admissions (1.4 admissions per 100,000 population) recorded in 2017, 46 were reported with cryptosporidiosis as the principal diagnosis and 21 with cryptosporidiosis as another relevant diagnosis.

Notifiable disease data

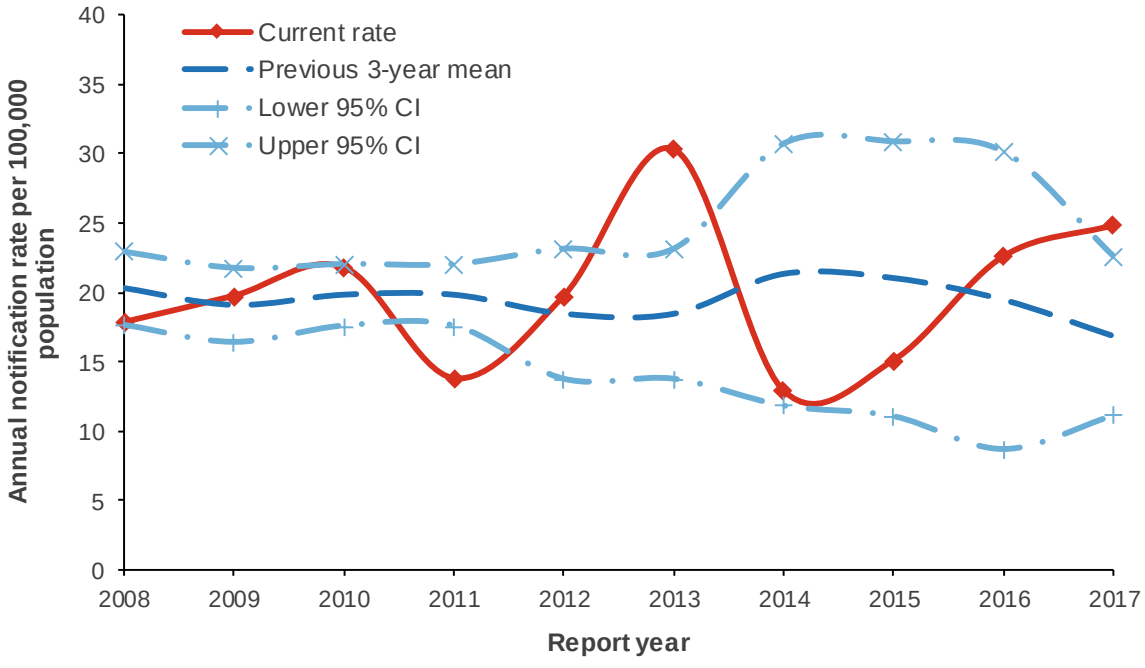
The highest recorded number of cryptosporidiosis notifications since cryptosporidiosis became a notifiable disease in 1996 was 1384 notifications in 2013 followed by 1208 notifications in 2001 and 1192 notifications in 2017. There are no clear trends regarding the number of cryptosporidiosis notifications over the 20 year time period (Figure 12).

Figure 12. Cryptosporidiosis notifications by year, 1997–2017



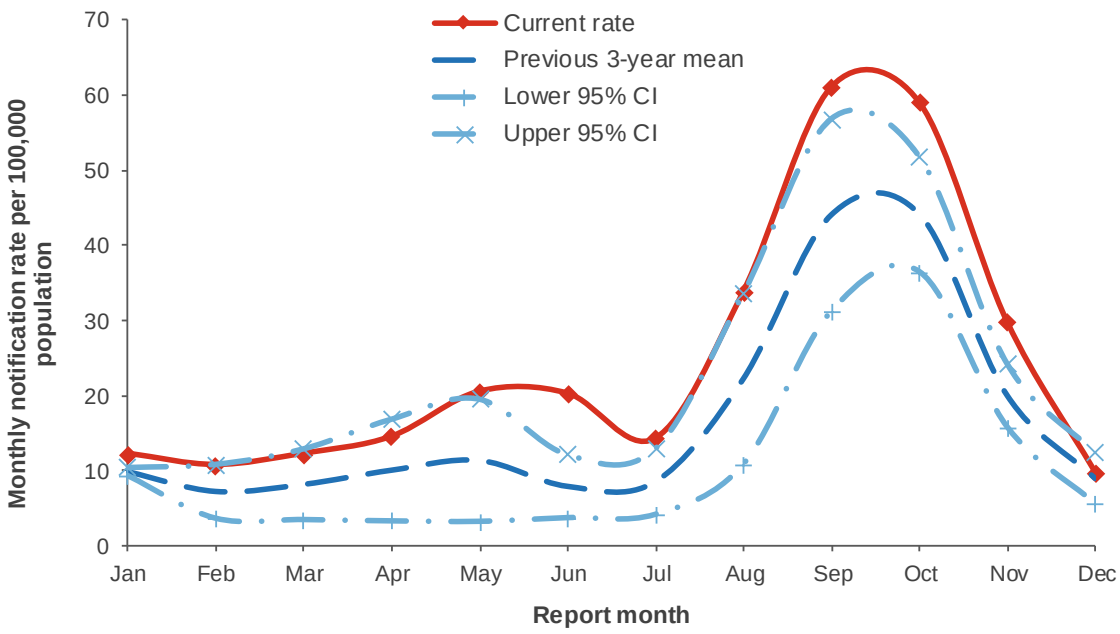
In 2017, the cryptosporidiosis notification rate was higher (24.9 cases per 100,000 population) than the previous three-year average (16.9 cases per 100,000) (Figure 13).

Figure 13. Cryptosporidiosis notification rate by year, 2008–2017



The number of notified cases of cryptosporidiosis reported per 100,000 population by month for 2017 was similar compared to the previous three years (2014–2016), but with slightly higher notification rates (Figure 14). There is a distinct seasonal pattern, with the highest number of notifications generally reported during spring each year. The monthly number of notifications in 2017 ranged from 39 notifications (December) to 244 notifications (September).

Figure 14. Cryptosporidiosis monthly rate (annualised), 2017



In 2017, the rate of notifications and hospitalisations for cryptosporidiosis was somewhat higher for females (25.9 and 1.5 per 100,000 population) compared with males (23.8 and 1.3 per 100,000 population) (Table 16).

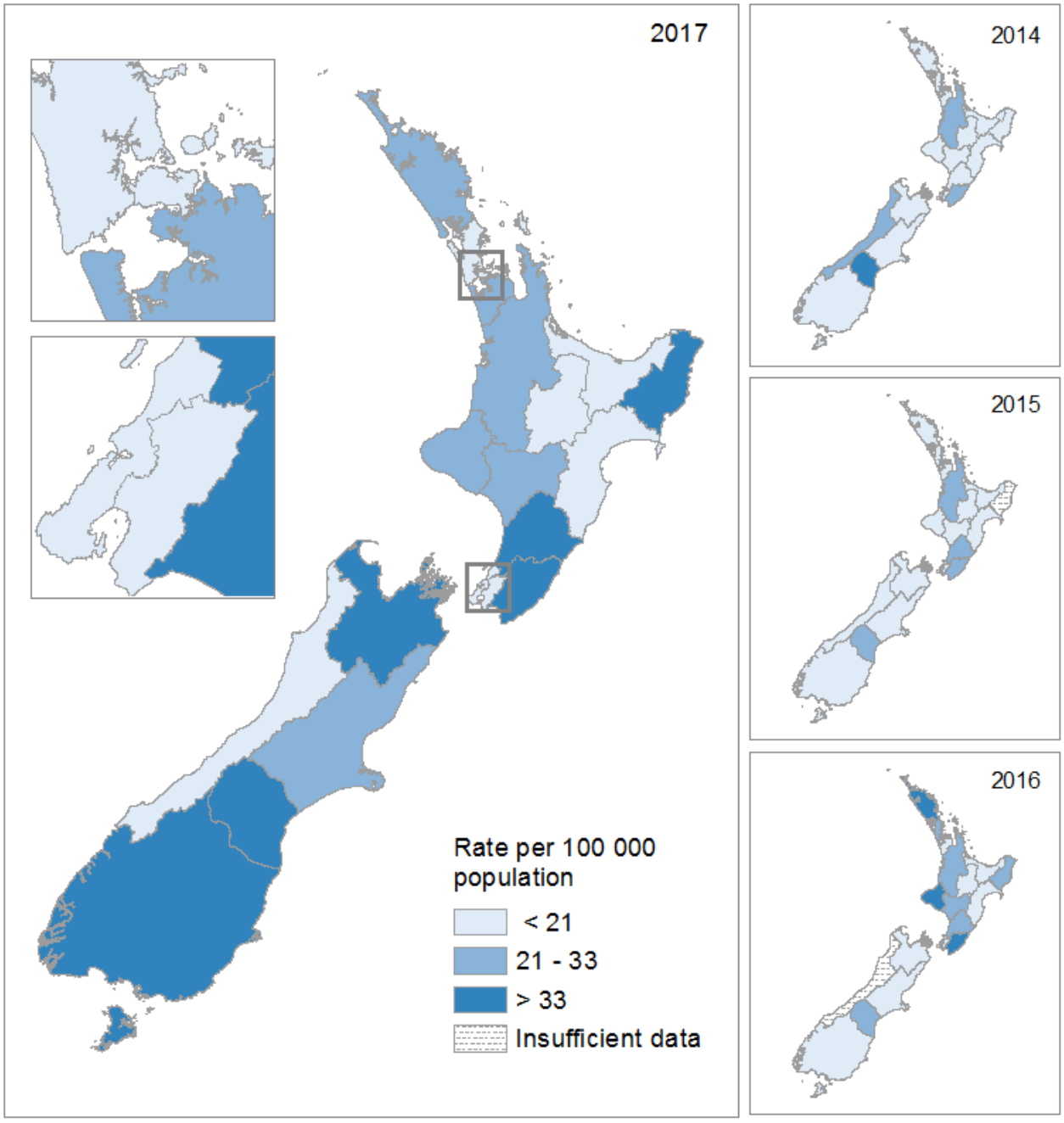
Table 16. Cryptosporidiosis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	561	23.8	31	1.3
Female	631	25.9	36	1.5
Total	**1192**	**24.9**	**67**	**1.4**

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

Cryptosporidiosis rates varied throughout the country in 2017 as shown in Figure 15. The highest rates of cryptosporidiosis were reported for the DHBs South Canterbury (62.1 per 100,000, 37 cases), Nelson Marlborough (55.8 per 100,000, 83 cases), and Tairawhiti (53.6 per 100,000, 26 cases), followed by the DHBs Southern (45.3 per 100,000, 147 cases), and Wairarapa (44.9 per 100,000, 20 cases).

Figure 15. Geographic distribution of cryptosporidiosis notifications, 2014–2017



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). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

During 2017, the highest cryptosporidiosis age-specific notification rates were for the 1 to 4 years age group (130.0 per 100,000 population, 319 cases), followed by the 5 to 9 (45.7 per 100,000, 149 cases) and the less than 1 year (33.0 per 100,000, 20 cases) age groups (Table 17). The hospitalisation rate was also highest in the 1 to 4 years age group.

Table 17. Cryptosporidiosis cases by age group, 2017

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	20	33.0	0	-
1 to 4	319	130.0	18	7.3
5 to 9	149	45.7	4	-
10 to 14	70	23.2	3	-
15 to 19	71	22.4	6	1.9
20 to 29	215	30.0	12	1.7
30 to 39	146	24.3	7	1.2
40 to 49	84	13.6	5	0.8
50 to 59	58	9.4	6	1.0
60 to 69	39	7.8	2	-
70+	21	4.3	4	-
Total	**1192**	**24.9**	**67**	**1.4**

[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 2017, where information on travel was provided, 10.1% (95% CI 8.2-12.2%) 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 2017. The resultant distribution has a mean of 120 cases (95% CI 90-154).

If data from the last four years are considered, the estimated proportion of cases travelling overseas within the incubation period of the organism was 10.5% (95% CI 9.4-11.7%).

Outbreaks reported as caused by *Cryptosporidium* spp.

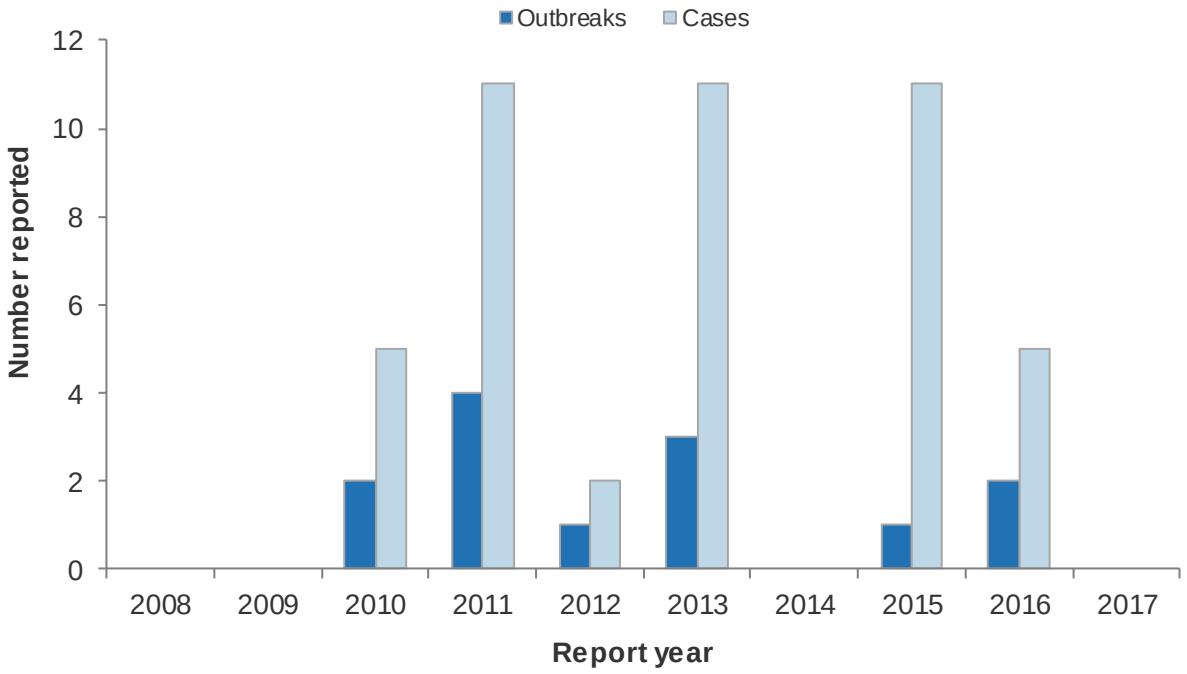
In 2017, none of the *Cryptosporidium* spp. outbreaks was reported as potentially foodborne (Table 18). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks of cryptosporidiosis accounted for 5.1% (27/531) of all enteric outbreaks and 1.9% (184/9538) of all associated cases.

Table 18. *Cryptosporidium* spp. outbreaks reported, 2017

Measure	Foodborne *Cryptosporidium* spp. outbreaks	All *Cryptosporidium* spp. outbreaks
Outbreaks	0	27
Cases	0	184
Hospitalised cases	0	3

Foodborne transmission has been rarely reported for *Cryptosporidium* spp. outbreaks, with not more than four outbreaks reported each year in the ten year-period 2008−2016. 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, 2008–2017



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2017 are given in Table 19.

Table 19. Summary of surveillance data for giardiasis, 2017

Parameter	Value in 2017	Source
Number of notified cases	1648	EpiSurv
Notification rate (per 100,000)	34.4	EpiSurv
Hospitalisations (% of notifications)[a]	69 (4.2%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	383 (23.3%)	EpiSurv
Estimated food-related cases	NE	-

NE = not estimated, no information is available on the food attributable proportion of giardiasis in New Zealand.
[a] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.

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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017–June 2017) 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 2017 by data source

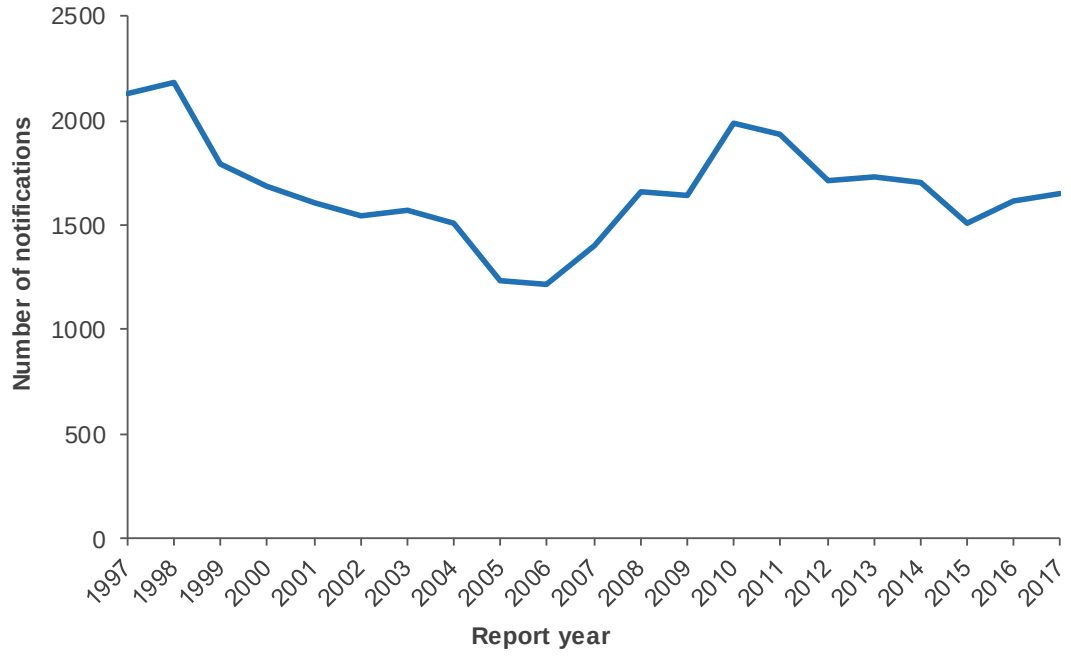
During 2017, 1648 cases (34.4 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 69 hospital admissions (1.4 admissions per 100,000 population) recorded in 2017, 37 were reported with giardiasis as the principal diagnosis and 32 with giardiasis as another relevant diagnosis.

Notifiable disease data

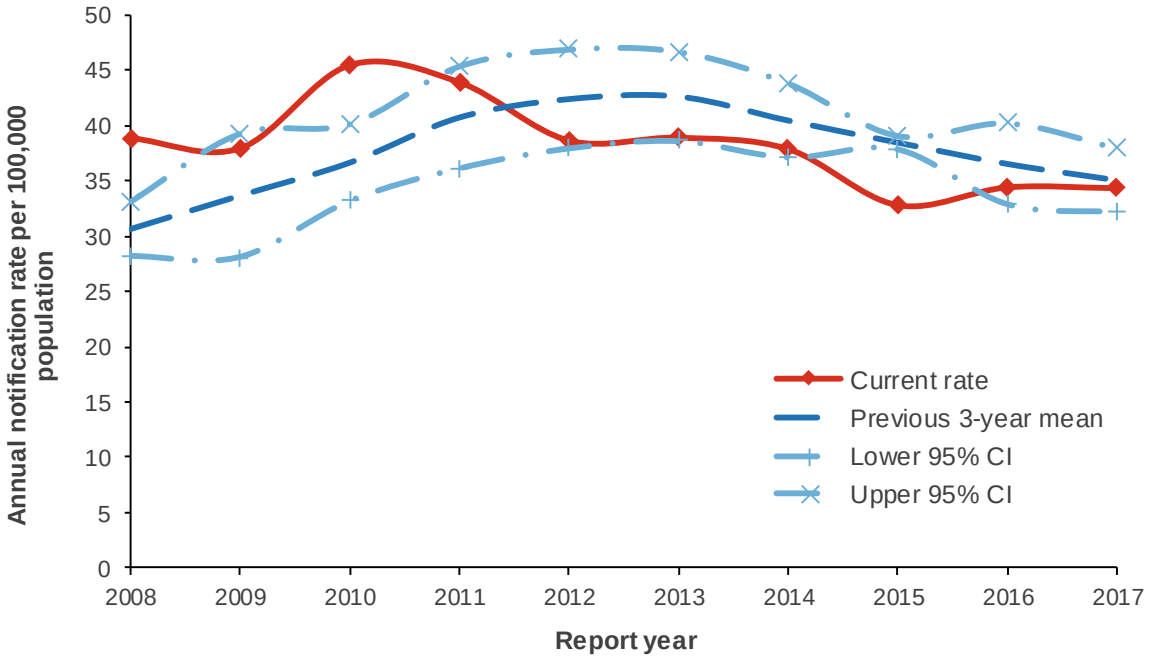
There was a steady decrease in the number of giardiasis cases reported each year from 1998 to 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 followed by decreases in the number of notifications. The highest number of notifications since 1999 was reported in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

Figure 17. Giardiasis notifications by year, 1997–2017



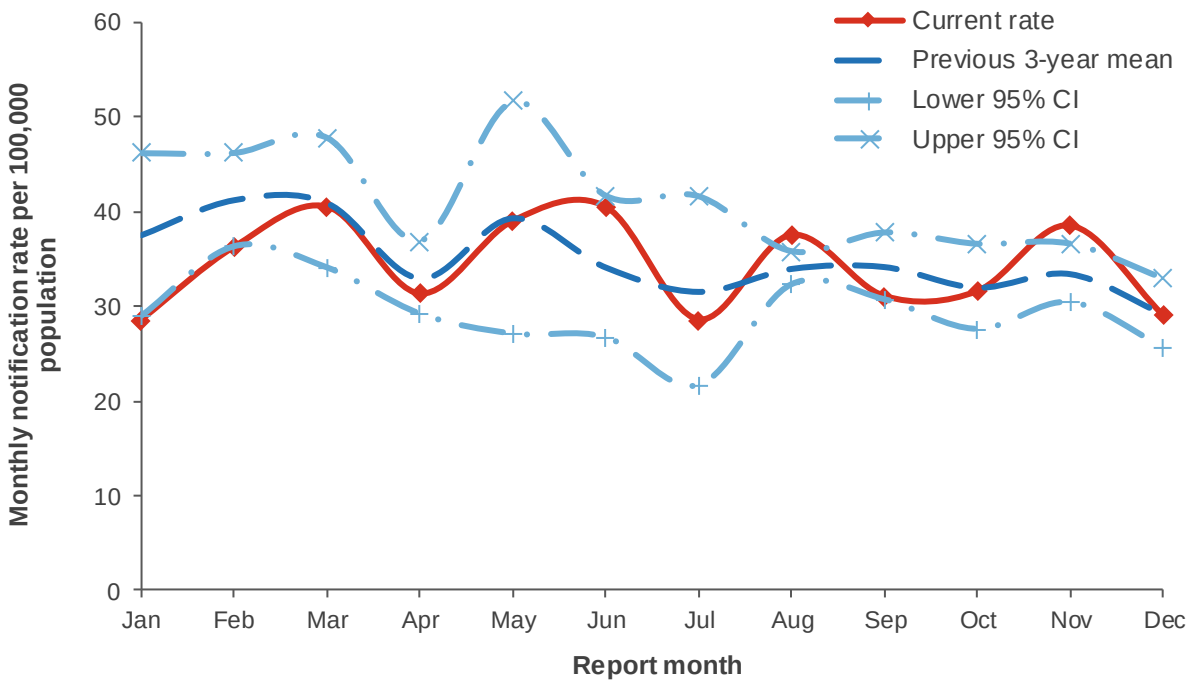
The 2017 notification rate was lower than 2010 to 2014 and similar to 2015 and 2016, maintaining the downward trend since 2010. Between 2007 and 2010 there had been a generally increasing trend (Figure 18). The notification rate in 2017 was similar (34.4 cases per 100,000 population) to the previous three-year average (35.1 cases per 100,000).

Figure 18. Giardiasis notification rate by year, 2008–2017



There was no seasonal pattern in the population rate of giardiasis notifications reported by month either historically in the previous three years (2014–2016) or in 2017 (Figure 19). The monthly number of notifications in 2017 ranged from 114 notifications (January and July) to 162 notifications (March and June).

Figure 19. Giardiasis monthly rate (annualised), 2017



In 2017 the number and rate for notifications and hospitalisations were higher for males (35.9 notifications and 1.7 hospitalisations per 100,000 population) than females (32.9 notifications and 1.2 hospitalisations per 100,000 population, Table 20).

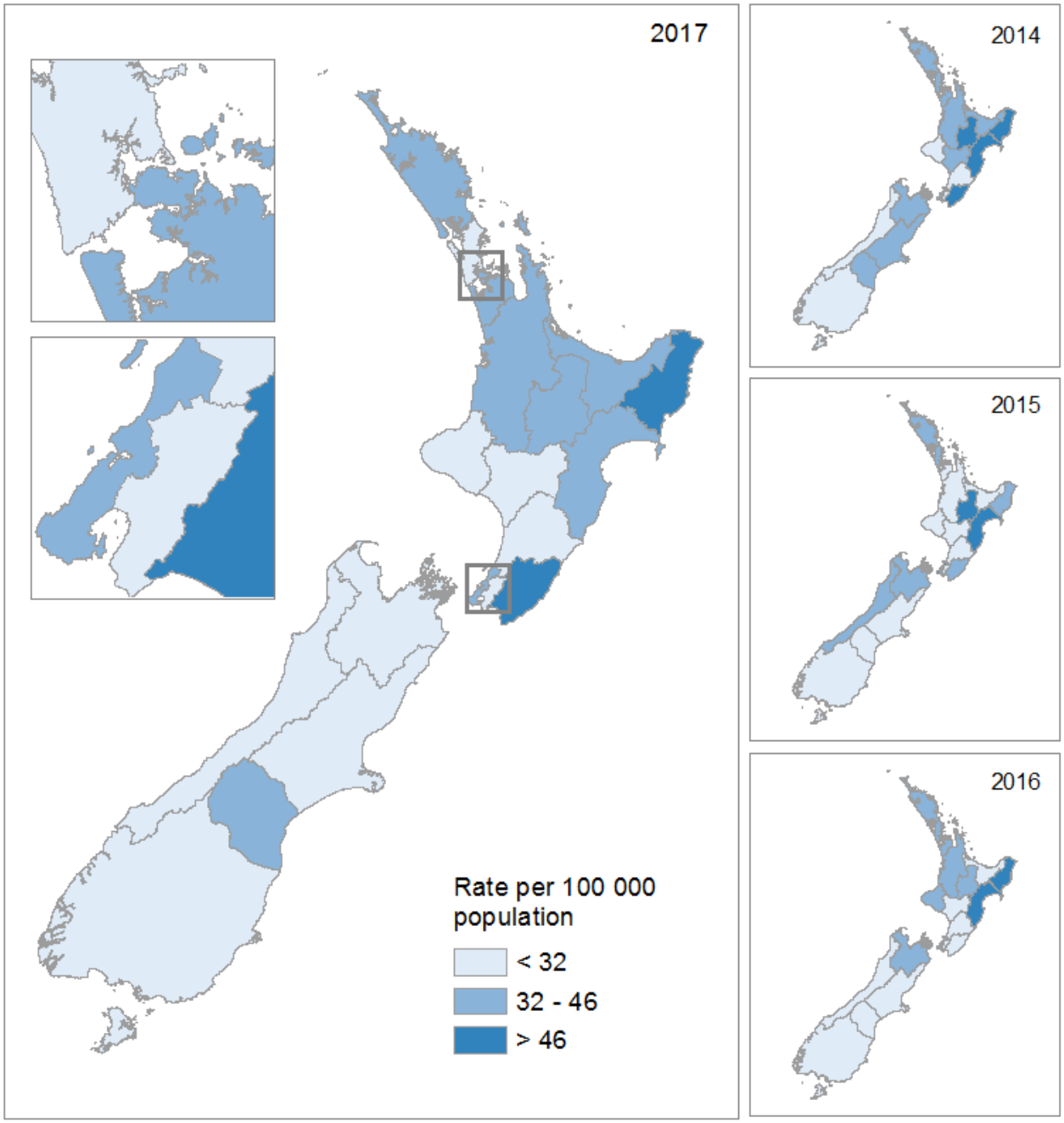
Table 20. Giardiasis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	847	35.9	41	1.7
Female	801	32.9	28	1.2
Total	**1648**	**34.4**	**69**	**1.4**

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

Giardiasis rates varied throughout the country during 2017 (Figure 20). The highest rate was reported for Tairawhiti (78.4 per 100,000 population, 38 cases), followed by Wairarapa (65.2 per 100,000, 29 cases). The lowest rates were reported for West Coast (15.4 per 100,000, 5 cases), Hutt Valley (18.3 per 100,000, 27 cases) and MidCentraly (19.3 per 100,000 population, 34 cases) DHBs.

Figure 20. Geographic distribution of giardiasis notifications, 2014–2017



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). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

In 2017, the highest notification rate was for the 1 to 4 years age group (110.0 per 100,000 population, 270 cases), followed by the 30 to 39 years age group (61.8 per 100,000, 371 cases) and the under 1 age group (36.3 per 100,000, 22 cases) (Table 21). The highest hospitalisation rate was also for the 1 to 4 years age group (4.5 per 100,000 population).

Table 21. Giardiasis cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	22	36.3	0	-
1 to 4	270	110.0	11	4.5
5 to 9	104	31.9	9	2.8
10 to 14	47	15.6	3	-
15 to 19	44	13.9	2	-
20 to 29	209	29.1	7	1.0
30 to 39	371	61.8	6	1.0
40 to 49	204	33.0	4	-
50 to 59	175	28.3	7	1.1
60 to 69	145	29.0	8	1.6
70+	57	11.7	12	2.5
Total	**1648**	**34.4**	**69**	**1.4**

[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 2017, 23.3% (95% CI 20.7–26.1%) 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 2017. The resultant distribution has a mean of 384 cases (95% CI 324–449).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 22.7% (95% CI 21.4%–24.1%).

Outbreaks reported as caused by *Giardia* spp.

In 2017, there were 24 *Giardia* spp. outbreaks reported, one of these was associated with a suspected or known foodborne source (Table 22). 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 4.5% (24/531) of all enteric outbreaks and 1.8% (170/9538) of all associated cases.

Table 22. *Giardia* spp. outbreaks reported, 2017

Measure	Foodborne *Giardia* spp. outbreaks	All *Giardia* spp. outbreaks
Outbreaks	1	24
Cases	3	170
Hospitalised cases	0	3

The highest number of foodborne *Giardia* spp. outbreaks and associated cases reported in the period from 2008 to 2017 was in 2013 (10 outbreaks and 36 associated cases). Between 2008 and 2017, between one and six foodborne *Giardia* spp. outbreaks were reported each year, with the exception of 2009 when no outbreaks were reported and 2013 (Figure 21).

Figure 21. Foodborne *Giardia* spp. outbreaks and associated cases reported by year, 2008–2017

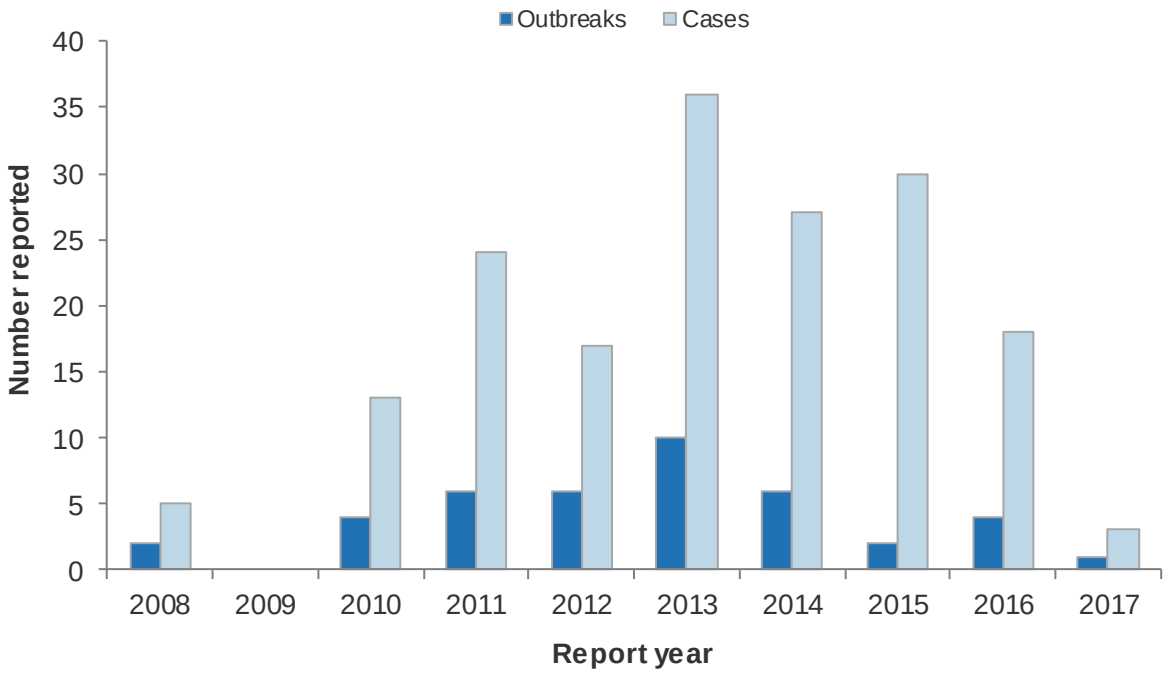


Table 23 contains details of the foodborne *Giardia* spp. outbreak reported in 2017. The suspected vehicle of infection for this outbreak was recorded as unknown in EpiSurv.

Table 23. Details of foodborne *Giardia* spp. outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Aug	Unknown	Home	Home	3C, 3P

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

In 2017, no food or clinical samples were submitted to ESR's Public Health Laboratory relating to the food-associated *Giardia* spp. outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2017 are given in Table 24.

Table 24. Summary of surveillance data for hepatitis A, 2017

Parameter	Value in 2017	Source
Number of notified cases	58	EpiSurv
Notification rate (per 100,000)	1.2	EpiSurv
Hospitalisations[b] (% of notifications)[a]	40 (69%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Travel-related cases (%)[a]	32 (55.2%)	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] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.

[b] Hospitalisations with acute hepatitis A as the principal diagnosis.

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 2017 by data source

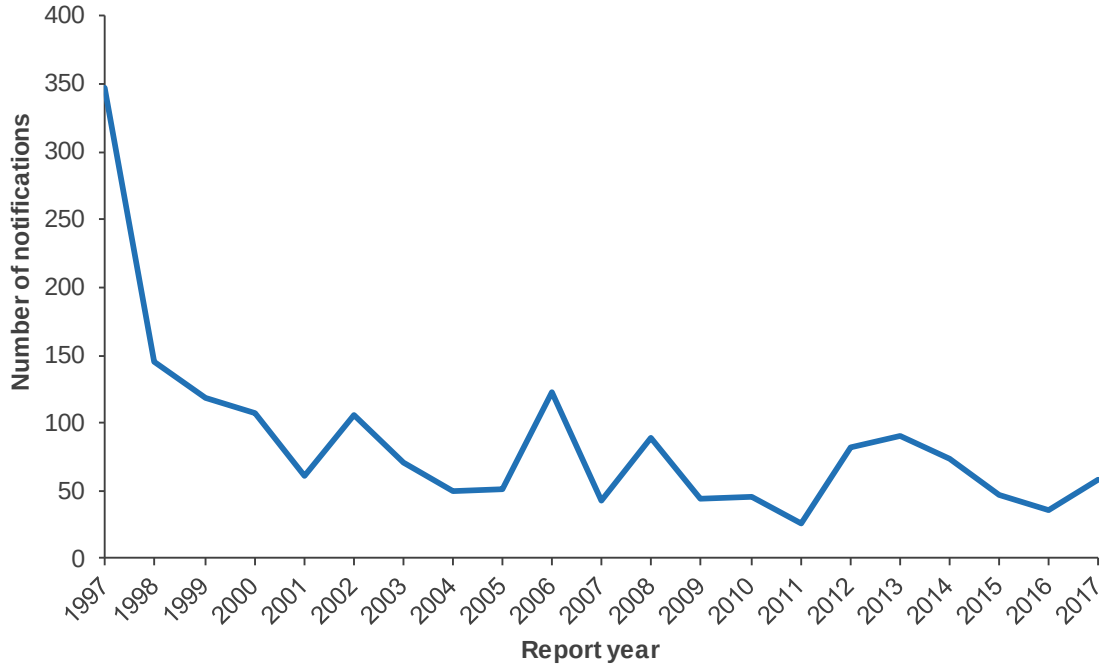
During 2017, 58 cases (1.2 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv.

The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the MoH NMDS database. Of the 81 hospital admissions (1.7 admissions per 100,000 population) recorded in 2017, 40 were reported with acute hepatitis A as the principal diagnosis and 41 with acute hepatitis A as another relevant diagnosis.

Notifiable disease data

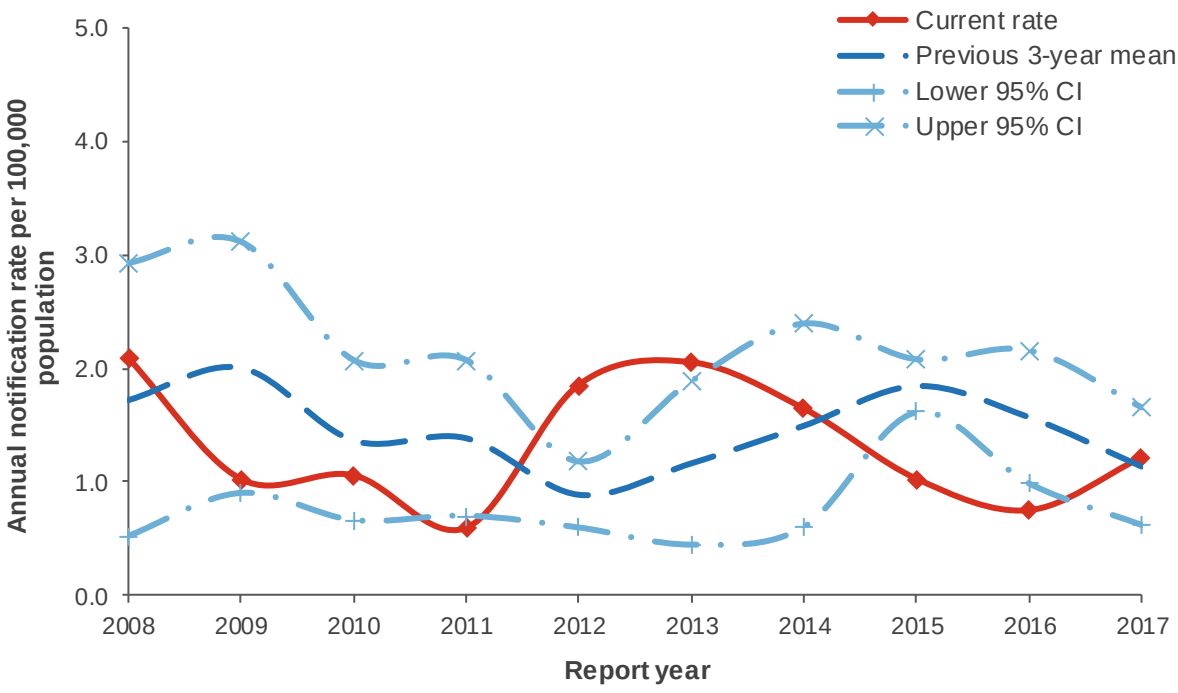
Between 2001 and 2017, the annual number of notifications has remained in the range of 26 (2011) to 123 (2006), having decreased from 347 in 1997 (Figure 22).

Figure 22. Hepatitis A notifications by year, 1997–2017



Hepatitis A notification rates have varied throughout the 10-year period 2008–2017 in the range of 0.6 to 2.1 per 100,000 population (Figure 23). In 2017, the notification rate was slightly higher (1.2 cases per 100,000 population) than the previous three-year average (1.1 cases per 100,000).

Figure 23. Hepatitis A notification rate by year, 2008–2018



In 2017, hepatitis A notifications were the same for males and females, whereas hospital admissions were slightly higher for females than for males (0.9 and 0.7 hospitalisations per 100,000 population, respectively) (Table 25).

Table 25. Hepatitis A cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	29	1.2	17	0.7
Female	29	1.2	23	0.9
Total	**58**	**1.2**	**40**	0.8

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

In 2017, the highest notification rate was reported for the less than 20 years and the 20 to 39 years age groups (1.8 per 100,000, 23 and 24 cases, respectively) with lower rates for the 40 to 59 years and over 60 years age groups (0.5 per 100,000, respectively). Hospitalisation rates were highest for the 20 to 39 years age group (Table 26).

Table 26. Hepatitis A cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<20	23	1.8	10	0.8
20 to 39	24	1.8	21	1.6
40 to 59	6	0.5	4	0.3
60+	5	0.5	5	0.5
Total	**58**	**1.2**	**40**	**0.8**

[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 2017, all 58 hepatitis A cases provided information on overseas travel, and 55.2% (95% CI 41.5–68.3%) 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 57.8% (95% CI 50.9–64.6%).

Outbreaks reported as caused by hepatitis A virus

In 2017, there were five outbreaks with 20 associated caused by hepatitis A virus. Two of these outbreaks 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% (5/531) of all enteric outbreaks and 0.2% (20/9538) of all associated cases.

Table 27. Hepatitis A outbreaks reported, 2017

Measure	Foodborne hepatitis A outbreaks	All hepatitis A outbreaks
Outbreaks	2	5
Cases	8	20
Hospitalised cases	1	3

Foodborne hepatitis A outbreaks are rare with only five outbreaks reported in the period 2008 to 2017 (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, 2008–2017

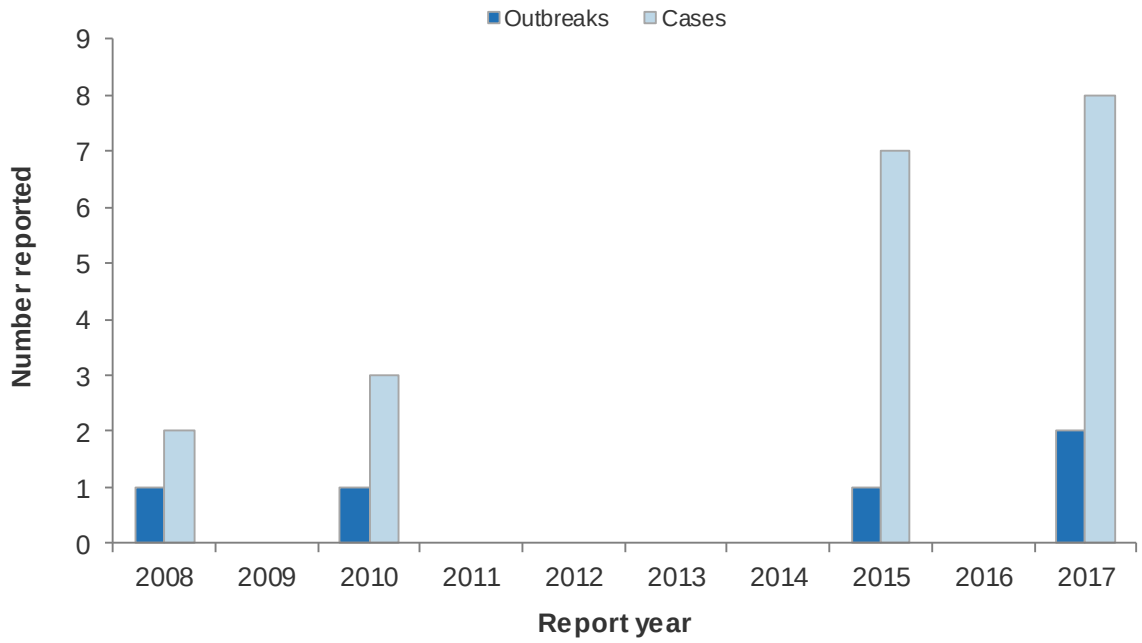


Table 28 contains details of the two foodborne hepatitis A outbreaks reported in 2017. The suspected vehicle of infection were cucumbers for one outbreak and unknown for the other outbreak. The level of evidence for suspected foods was recorded as weak. Food samples (raw oysters and mussels) were submitted to ESR's Enteric, Environmental and Food Virology Laboratory relating to the hepatitis A virus outbreak in Auckland in February. No hepatitis A virus was detected in the bivalve molluscan shellfish samples submitted for analysis.

Table 28. Details of the foodborne hepatitis A virus outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Feb	Telegraph cucumbers, raw oysters, mussles	Supermarket/delicatessen/Other setting	Unknown	6C, 0P
Auckland	Oct	Unknown	Home	Home	2C,0P

PHU: Public Health Unit, C: confirmed, P: probable

During 2017 it was possible to test for hepatitis A virus in the following foods: bivalve molluscan shellfish, soft berry fruit and leafy salads.

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. The data relates to individual cases and includes all outbreaks where specimens were submitted to ESR for genotyping. The data includes those which are not associated with foodborne transmission. In 2017, hepatitis A virus I.A was the most commonly identified genotype, similar to 2016.

Table 29. Hepatitis A subtypes identified by the Enteric, Environmental and Food Virology Laboratory, 2016–2017

Hepatitis A virus genotypes	2016	2017
I.A	16	20
III.A	1	4
I.B	0	1
Unable to genotype	0	2
Negative	6	4
Total	**23**	**31**

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 2017 by data source

Nine cases of histamine (scombroid) fish poisoning were reported in EpiSurv during 2017 (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. Of the eight hospital admissions (0.2 admissions per 100,000 population) recorded in 2017, seven were reported with scombroid fish poisoning as the principal diagnosis and one as another relevant diagnosis.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

Two histamine (scombroid) fish poisoning outbreaks were reported in 2017 involving seven associated cases, three 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, 2017

Measure	Foodborne histamine fish poisoning outbreaks	All histamine fish poisoning outbreaks
Outbreaks	2	2
Cases	7	7
Hospitalised cases	3	3

Between 2008 and 2017 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 number of outbreaks was reported in 2010 (4 outbreaks, 13 cases). 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, 2008–2017

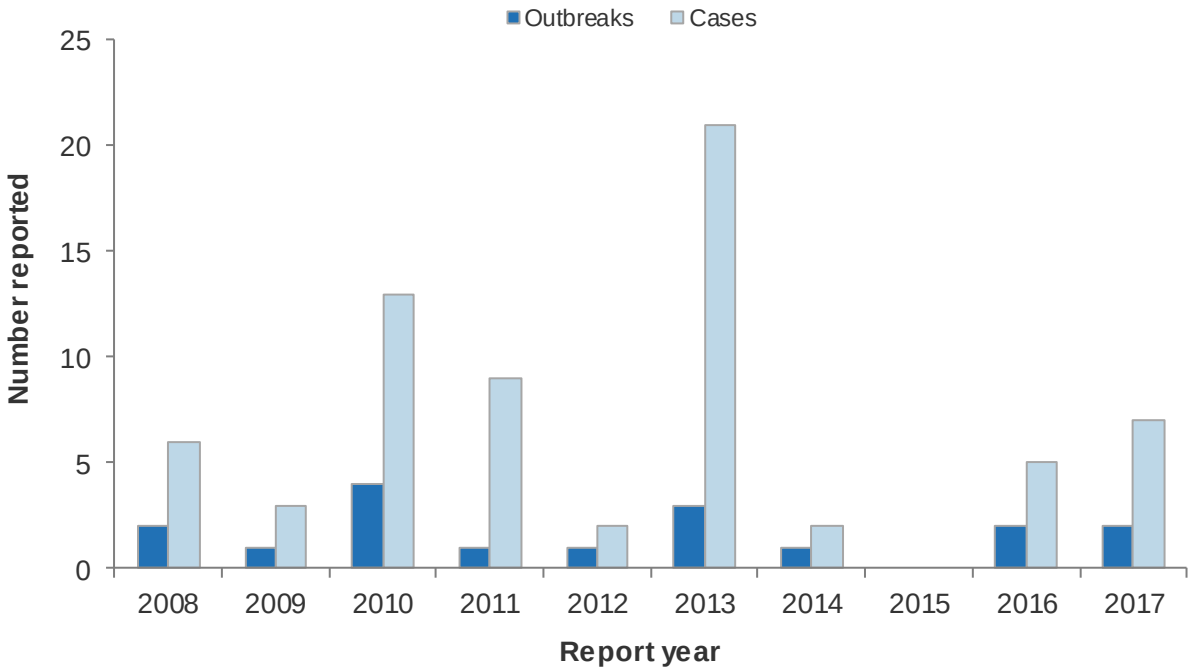


Table 31 contains details of the two foodborne histamine fish poisoning outbreaks reported in 2017. For both outbreaks the evidence for foodborne transmission was listed as weak in EpiSurv.

Table 31. Details of foodborne histamine fish poisoning outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Toi Te Ora	Jan	Fish cakes made with tuna	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 1P
Auckland	May	Fish	Hostel/boarding house	Caterers	2C, 3P

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

In 2017, no samples related to the two histamine fish poisoning outbreaks were submitted to ESR's Public Health Laboratory.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2017 are given in Table 32.

Table 32. Summary of surveillance data for listeriosis, 2017

Parameter	Value in 2017	Source
Number of notified cases[a]	21	EpiSurv
Notification rate (per 100,000)	0.4	EpiSurv
Hospitalisations [b]	18 (85.7%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Travel-related cases (%)[b]	1 (5.6%)	EpiSurv
Estimated food-related cases (%)[c]	17 (87.8%)	Expert consultation

[a] Includes non-perinatal (20) and perinatal cases (1).
[b] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.
[c] For estimation of food-related cases the proportions derived from expert consultation 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	A case occurring in an infant from seven days before birth until seven days after birth.

Listeriosis cases reported in 2017 by data source

During 2017, 21 cases (0.4 per 100,000 population) of listeriosis were reported in EpiSurv, of which one was perinatal.

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 18 hospital admissions (0.4 admissions per 100,000 population) recorded in 2017, six were reported with listeriosis as the principal diagnosis and 12 with listeriosis as another relevant diagnosis.

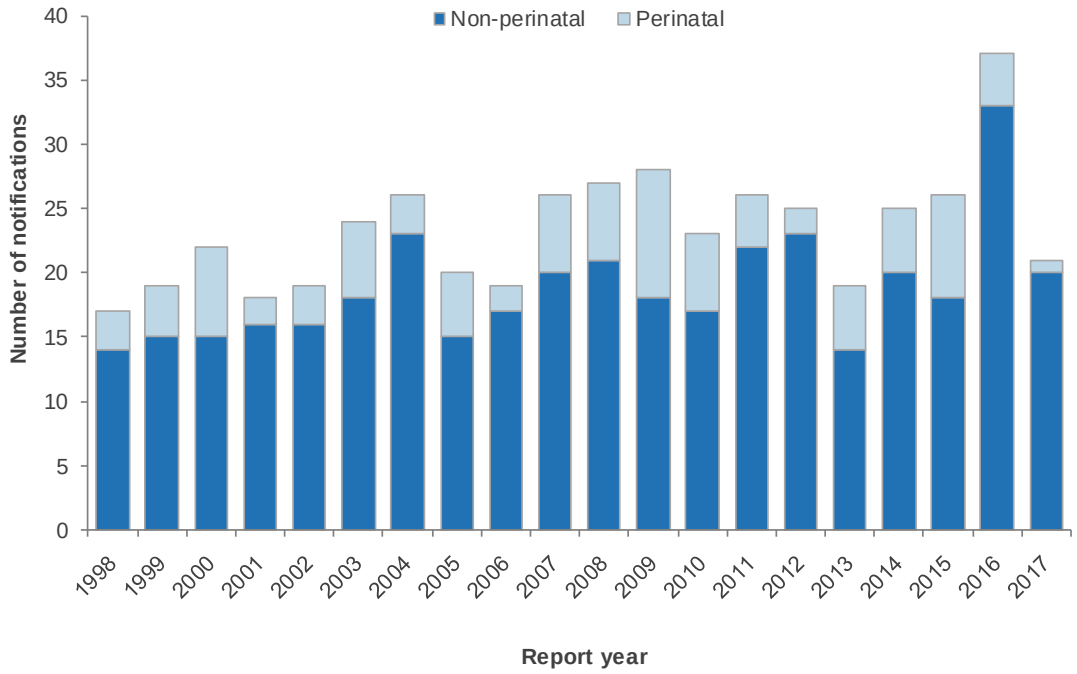
No resulting deaths were recorded in EpiSurv in 2017.

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 2017, the annual number of listeriosis notifications has fluctuated between 17 (1998) and 28 (2009) (Figure 26). In 2016, the total number of notifications (36) was higher compared to the other years, with four notifications reported as perinatal. 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, 1998–2017



In 2017, the rate and number of notifications for listeriosis was similar for females (0.4 per 100,000 population, 10 cases) and males (0.5 per 100,000, 11 cases). The number and rate of hospitalisations were also similar for females and males (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 perinatal case.

Table 33. Listeriosis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	11	0.5	8	0.4
Female	10	0.4	10	0.4
Total	**21**	**0.4**	**18**	**0.3**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

In 2017, rates for listeriosis were highest in the 60 years and over age group for both the notifications (1.5 per 100,000 population, 15 cases) and hospitalisations (1.0 per 100,000, 10 admissions) (Table 34).

Table 34. Listeriosis cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<20	1	-	2	-
20 to 39	1	-	1	-
40 to 59	4	-	5	0.4
60+	15	1.5	10	1.0
Total	**21**	**0.4**	**18**	**0.4**

[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 2017. 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 20 isolates of *L. monocytogenes* during 2017.

Table 35 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2013 and 2017. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of seven to 16 isolates over the period 2013 to 2017.

Table 35. *L. monocytogenes* serotypes identified by the Special Bacteriology Laboratory, 2013–2017

Serotype	2013		2014		2015		2016		2017	
	No.	%	No.	%	No.	%	No.	%	No.	%
O1/2	12	63.2	12	42.9	12	63.2	12	42.9	13	65
O4	7	36.8	16	57.1	7	36.8	16	57.1	7	35
Total	**19**		**28**		**19**		**28**		**20**	

Recent surveys

Listeria prevalence in was determined in ready-to-eat (RTE) meat processing areas and meat products at four small dual-operator and retail butcheries [20]. *L. monocytogenes* was isolated from 20.6% (33/160) of samples across the four butcheries, which included 18.2% (4/22) of RTE meat products, 7.0% (5/71) of food contact surfaces and 35.8% (24/67) of non-food contact surface samples (commonly, floor and drain areas). Additional *Listeria* spp. (*L. welshimeri* and *L. innocua*) were identified in 8.8% (14/160) of samples.

Pulsed-field gel electrophoresis (PFGE) was used to type all *L. monocytogenes* isolates obtained during the study, and seven PFGE pulsotypes were observed amongst the isolates. Pulsotypes identified at later sampling rounds were typically the same or a subset of those identified at the initial round of sampling, which could indicate a persistence of resident *L. monocytogenes* reservoirs rather than sporadic introduction events.

Relevant New Zealand studies and publications

Journal papers

Strains of *L. monocytogenes* (*n* = 12) were collected from five mussel processing facilities and were characterised as either persistent or sporadic [21]. Persistent strains were more likely to form biofilms, exhibit greater recovery after incubation on dry surfaces and be heat resistant. However, no genetic clustering or persistent or sporadic strains were found.

A survey collected 1485 samples (five samples of each of 297 lots) of ready-to-eat (RTE) meat products in original manufacturer packaging from 32 New Zealand producers [22]. When adjusted for market share and regulatory regime, the survey results suggest a national prevalence of *L. monocytogenes* in retail RTE red meats of 3.0% (1.9–4.1%: 2.5–97.5th percentile range). Enumeration of *L. monocytogenes* in individual samples from positive lots gave results below the countable range (<50 CFU/g) in 82 out of 95 samples. Thirteen samples were found to contain between 50 and 500 CFU/g *L. monocytogenes,* but all of these samples were manufactured by one operator. Pulsed field gel electrophoresis (PFGE) typing of all of the *L. monocytogenes* strains obtained from the survey identified 12 different pulsotypes. Different pulsotypes were often identified in samples from the same operator sampled on separate occasions. A total of 46 lots (15.5%) contained *Listeria* spp. (including *L. monocytogenes*).

Relevant regulatory developments

During 2017, MPI published further guidance documents to support control of *L. monocytogenes* in the food industry. The documents published in 2017 were:

- Part 1: *Listeria* management and glossary (update) [23]
- Part 2: Good operating practices (update) [24]
- Part 3: Monitoring activities (update) [25]
- Part 4: Corrective actions [26]
- How to use: *Listeria* in ready-to-eat foods training resource [27]
- Risk Management Programme Template for Dual Operator Butchers. Attachment U – *Listeria* management procedures for wholesale butchers who sell ready-to-eat animal products [28]
- How to use Attachment U [29].

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 2017 by data source

During 2017, 68 cases (1.4 per 100,000 population) of norovirus infection with no associated deaths were reported in EpiSurv. It should be noted that not every case of norovirus infection is notifiable; only those that are part of a common source outbreak or from a person in a high risk category. In 2017 there were 6517 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 478 hospital admissions (10.0 admissions per 100,000 population) recorded in 2017, 201 were reported with norovirus infection as the principal diagnosis and 277 with norovirus infection as another relevant diagnosis. Of the 478 hospital admissions, 223 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. 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 2017, 17 (6.5%) of the 261 norovirus outbreaks and 308 (4.7%) of the 6517 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 49.2% (261/531) of all enteric outbreaks and 68.3% (6517/9538) of all outbreak-associated cases reported in 2017.

Table 36. Norovirus outbreaks reported, 2017

Measure	Foodborne norovirus infection outbreaks	All norovirus infection outbreaks
Outbreaks	17	261
Cases	308	6517
Hospitalised cases	0	91

Between 2008 and 2017 the annual number of foodborne norovirus outbreaks reported each year ranged from 17 (2013 and 2015) to 30 (2009) (Figure 27). The total number of cases associated with these outbreaks each year ranged from 177 (2013) to 618 cases (2008).

Figure 27. Foodborne norovirus outbreaks and associated cases reported by year, 2008–2017

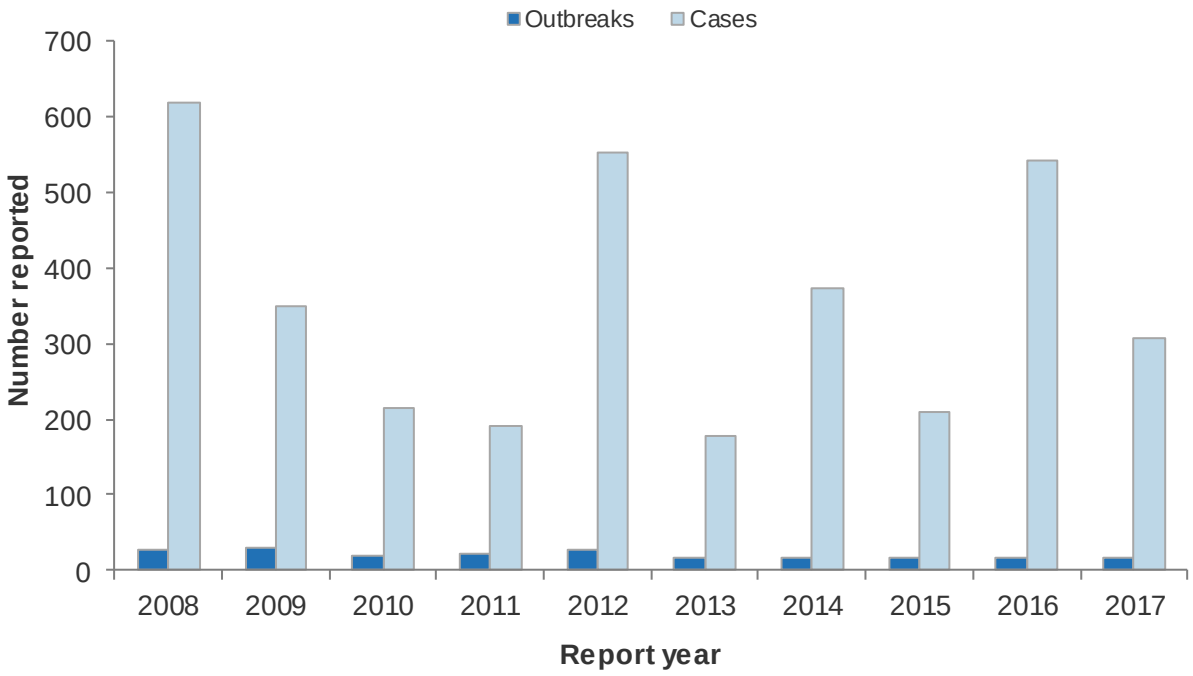


Table 37 contains details of the 17 foodborne norovirus outbreaks reported in 2017. A suspected food vehicle was not identified in 11 of these outbreaks. The level of evidence for suspected foods was recorded as strong for three outbreaks (Auckland in January and September, MidCentral in March).

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory in 2017, faecal specimens relating to 14 of the 17 foodborne outbreaks (Table 37) were received for norovirus testing. Of these, norovirus was detected in faecal samples from 13 foodborne outbreaks.

During 2017 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, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Jan	Oysters[a]	Restaurant/cafe/bakery/ Other food outlet	Other food outlet	6C, 3P
Auckland	Jan	Oysters[a]	Home	Home	0C, 2P
Auckland	Feb	Raw oysters[a]	Other food outlet	Unknown	2C, 0P
MidCentral	Mar	Various food items (mixed club sandwiches, savouries)	School	Restaurant/cafe/bakery	3C, 23P
MidCentral	Jun	Unknown	School	School	1C, 96P
C and PH	Jun	Unknown	Fast food restaurant	Takeaway	0C, 4P
Auckland	Jul	Unknown	Long term care facility	Long term care facility	5C, 18P
Auckland	Sep	Seafood dish with raw oysters	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 8P
Hawke's Bay	Sep	Unknown	Caterers	Caterers	30C, 0P
C and PH	Oct	Unknown	Long term care facility/ Restaurant/café/bakery	Long term care facility/ Restaurant/café/bakery	54C, 0P
Hawke's Bay	Oct	Filled wraps	Other setting	Restaurant/cafe/bakery	5C, 0P
Auckland	Oct	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 2P
Regional	Oct	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 2P
Auckland	Dec	Unknown	Other institution	Other institution	0C, 14P
Auckland	Dec	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 0P
C and PH	Dec	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	4C, 0P
Auckland	Dec	Unknown	Home	Home	4C, 10P

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

[a] All three outbreaks were related to the consumption of oysters sourced from the same harvesting area.

Table 38 shows the number of hospitalised cases and total cases by genotype for the 17 foodborne norovirus outbreaks reported during 2017. The outbreaks are due to a variety of genotypes, with no genotypes being noticeably more prevalent than the others. The highest number of total cases was related to one outbreak at a school due to GII.15 (97 cases).

Table 38. Norovirus genotypes reported in foodborne outbreaks, 2017

Norovirus genotype	Outbreaks	Total cases	Hospitalised cases
GII.P16/GII.2	3	21	0
GI.3	3	39	0
GI.Pb/GI.6	2	35	0
GII.4 Sydney 2012	2	28	0
GII.P16/GII.4	2	16	0
GII.15	1	97	0
Not determined	4	72	0
Total	**17**	**308**	**0**

Norovirus types commonly reported

Norovirus genotyping data from ESR's Norovirus Reference Laboratory are shown in Table 39. The data relates to outbreaks not individual cases and includes all outbreaks, including those which are not associated with foodborne transmission.

In 2017, norovirus genogroup II (GII) was identified in 186/239 (77.8%) outbreaks. In the previous four years GII was identified in between 70.1% (2013) and 90.8% (2015) of outbreaks. In 2017, genogroup I (GI) was identified in 51/239 (21.3%) outbreaks. The norovirus genotype was determined for 99.6% (238/239) of ESR laboratory-confirmed norovirus outbreaks. As in previous years, GII.4 was the predominant norovirus genotype identified (129/238, 54.2% of outbreaks).

Table 39. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2013–2017

Norovirus genotypes	2013	2014	2015	2016	2017
Genogroup I	**45**	**51**	**13**	**29**	**51**
GI untyped	-	1	-	1	0
GI.1	1	-	-	2	2
GI.2	1	12	7	3	0
GI.3	12	17	2	15	29
GI.4	23	-	-	-	1
GI.5	1	1	2	-	1
GI.6	4	10	2	6	15
GI.7	1	1	-	-	1
GI.8	-	-	-	-	2
GI.9	2	9	-	2	0
Genogroup II	**110**	**253**	**167**	**159**	**186**
GII untyped	-	4	5	1	1
GII.1	-	-	-	-	-
GII.2	13	2	14	1	2
GII.3	-	1	2	-	-
GII.4	55	203	90	84	129
GII.5	1	-	-	-	-
GII.6	4	22	19	2	14
GII.7	18	6	2	6	1
GII.8	-	1	1	-	2
GII.13	-	-	-	-	2
GII.15	-	-	-	-	1
GII.17	-	2	6	-	5
GII.20	-	1	-	-	0
GII.P12/GII.3	2	-	18	19	2
GII.P16/GII.2	-	-	-	27	18
GII.P16/GII.13	9	2	-	-	3
Other GII recombinants	8	9	10	19	6
Mixed GI and GII	**2**	**8**	**4**	**-**	**2**
Total outbreaks	**157**	**312**	**184**	**188**	**239**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

In 2017 the analysis of the complete capsid sequences of emerging norovirus GII.17 Kawasaki 308 from 13 countries, including New Zealand, was published. It was demonstrated that the viruses had originated from a single haplotype since the initial emergence in China in late 2014. The authors postulate a global spread of the sublineage SL2 [30].

Relevant regulatory developments

Nil.

Salmonellosis

Summary data for salmonellosis in 2017 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, 2017

Parameter	Value in 2017	Source
Number of notified cases	1119	EpiSurv
Notification rate (per 100,000)	23.3	EpiSurv
Hospitalisations (% of notifications)[a]	214 (19.1%)	MoH NMDS, EpiSurv
Deaths	1	EpiSurv
Estimated travel-related cases (%)[a]	391 (35.0%)	EpiSurv
Estimated food-related cases (%)[b]	452 (62.1%)	Expert consultation

[a] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.
[b] For estimation of food-related cases the proportions derived from expert consultation 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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017–June 2017) 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 2017 by data source

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

During 2017, 1119 cases (23.3 per 100,000 population) of salmonellosis and one resulting death were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 1216 cases infected with non-typhoidal *Salmonella* spp. (25.3 cases per 100,000) on the basis of clinical isolates received.

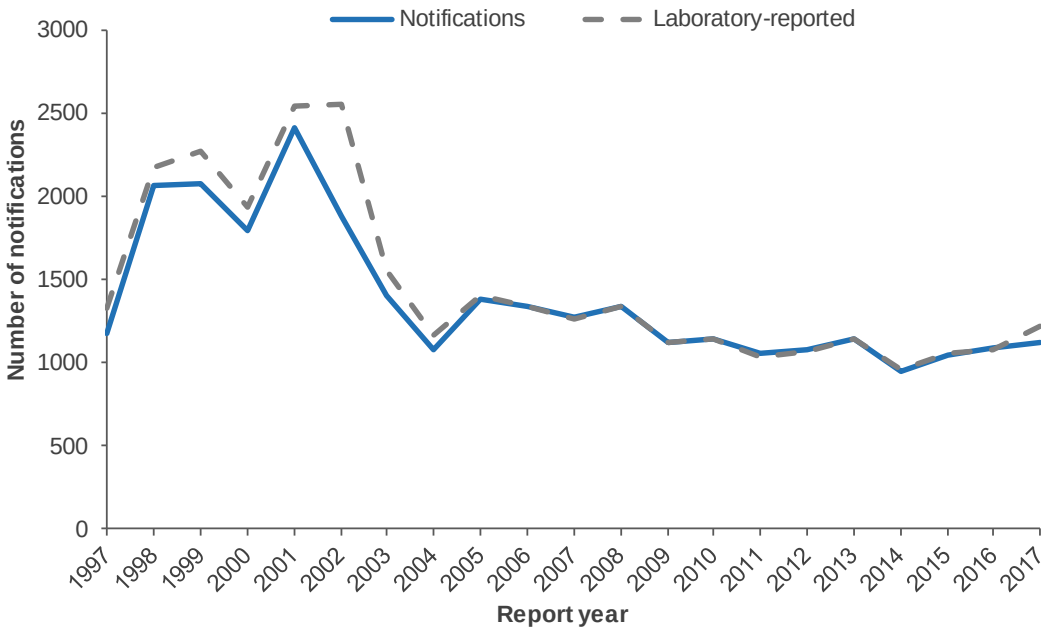
The ICD-10 code A02 was used to extract salmonellosis hospitalisation data from the MoH NMDS database. Of the 214 hospital admissions (4.5 admissions per 100,000 population) recorded in 2017, 174 were reported with salmonellosis as the principal diagnosis and 40 with salmonellosis as another relevant 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

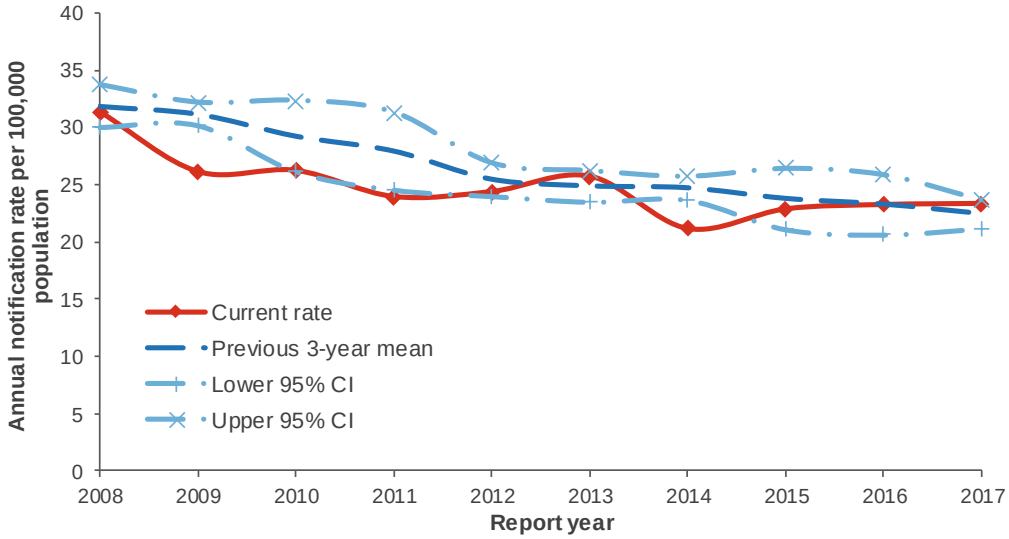
Following a generally increasing trend of salmonellosis notifications from 1997 to 2001 there was a sharp fall in notifications between 2001 and 2004. The notifications have continued to decline since 2005 but at a much slower rate. The lowest number of notifications was reported in 2014 (955 cases) (Figure 28).

Figure 28. Salmonellosis notifications and laboratory-reported cases by year, 1997–2017



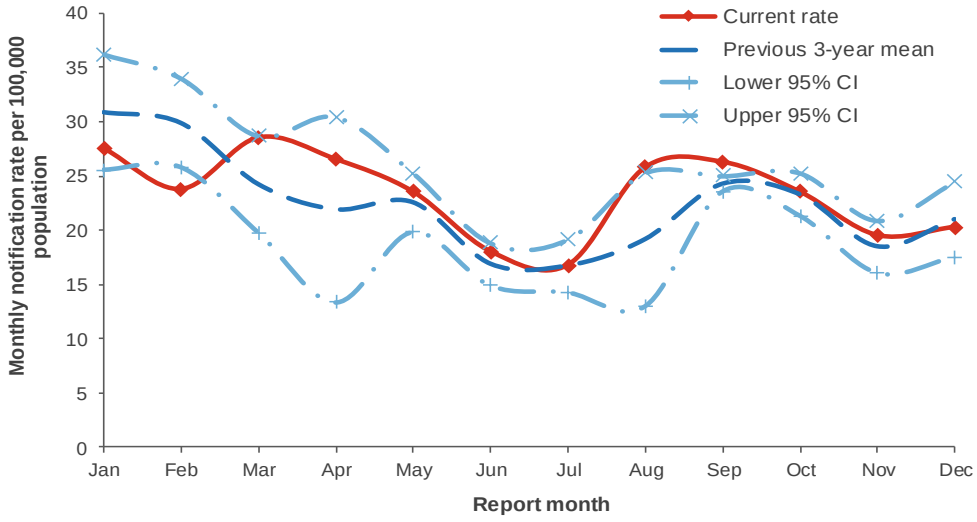
In 2017, the salmonellosis notification rate was lower than in the years 2010 to 2013 and similar to 2015 and 2016 (Figure 29). The notification rate in 2017 was slightly higher (23.3 cases per 100,000 population) than the previous three-year average (22.4 cases per 100,000).

Figure 29. Salmonellosis notification rate by year, 2008–2017



The number of notified cases of salmonellosis per 100,000 population by month for 2017 is shown in Figure 30. The overall trend for 2017 was similar to the previous three-year mean with higher rates during summer and early autumn months and lowest rates during the winter months (June and July). The monthly number of notifications in 2017 ranged from 67 notifications (July) to 114 notifications (March).

Figure 30. Salmonellosis monthly rate (annualised), 2017



In 2017, the number and rate of notifications were higher for males than for females. Hospitalisation rates were similar for both genders (Table 41). In 2016 notification rates were similar for both genders, however hospitalisation rates were higher for males.

Table 41. Salmonellosis cases by sex, 2017

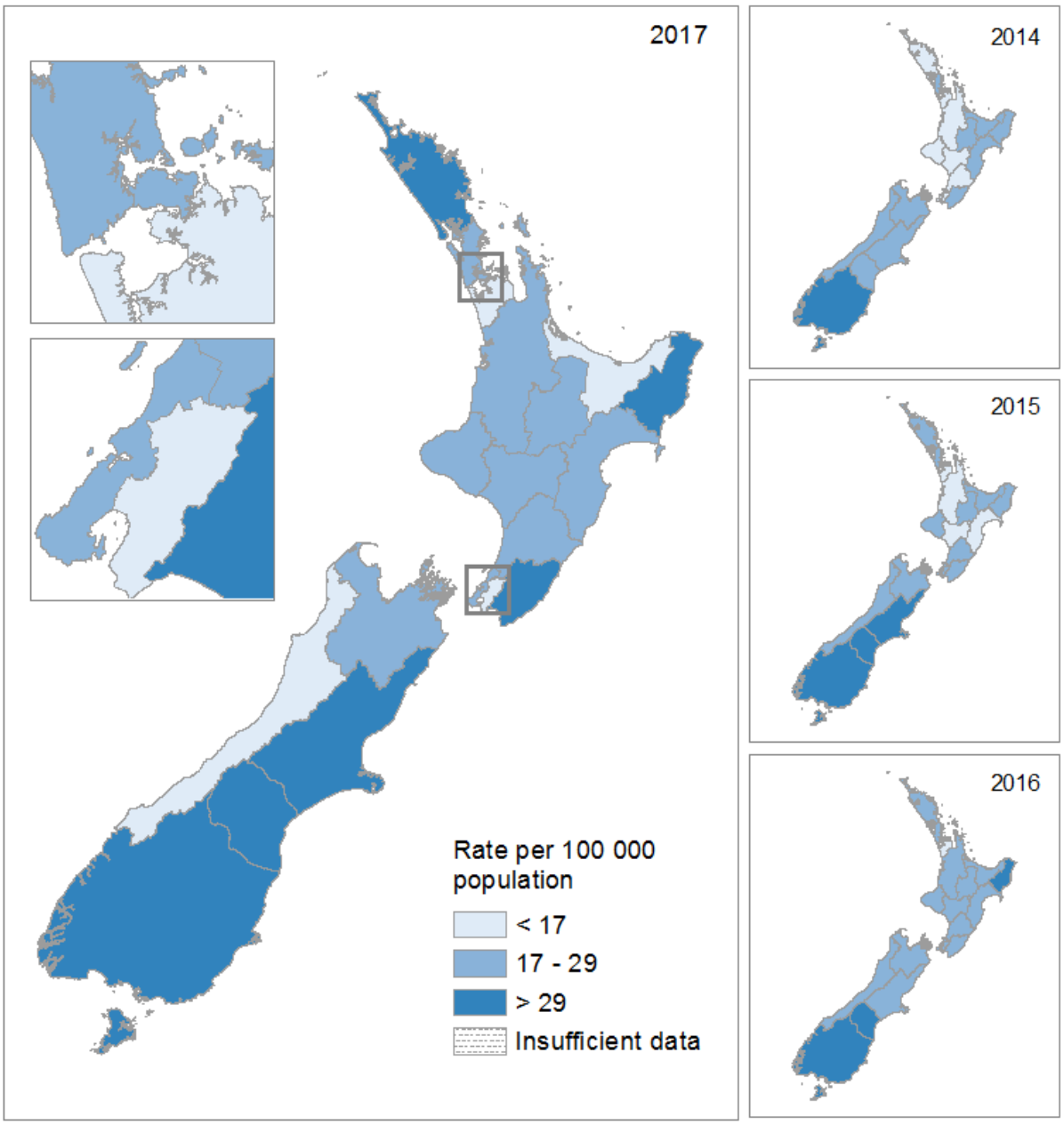
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	597	25.3	104	4.4
Female	521	21.4	110	4.5
Unknown	1	-	0	-
Total	**1119**	**23.3**	**214**	**4.5**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

In 2017, rates of salmonellosis varied throughout the country as illustrated in Figure 31. The highest salmonellosis notification rate was for Tairawhiti DHB (45.4 per 100,000, 22 cases), followed by South Canterbury DHB (36.9 per 100,000 population, 22 cases), Canterbury DHB (36.3 per 100,000 population, 200 cases), Northland DHB (33.6 per 100,000, 59 cases) and Southern DHB (30.8 per 100,000, 100 cases). Southern DHB had consistently high salmonellosis notification rates between 2014 and 2017 compared to the rest of the country.

Figure 31. Geographic distribution of salmonellosis notifications, 2014–2017



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). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

In 2017, notification rates and hospitalisation rates of salmonellosis were highest for infants aged less than 1 year (113.9 cases and 31.4 admissions per 100,000 population) and children aged 1 to 4 years (65.6 cases and 9.4 admissions per 100,000 population) when compared to other age groups (Table 42).

Table 42. Salmonellosis cases by age group, 2017

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	69	113.9	19	31.4
1 to 4	161	65.6	23	9.4
5 to 9	53	16.2	6	1.8
10 to 14	42	13.9	3	1.0
15 to 19	54	17.1	8	2.5
20 to 29	165	23.0	28	3.9
30 to 39	119	19.8	20	3.3
40 to 49	106	17.1	23	3.7
50 to 59	156	25.2	25	4.0
60 to 69	115	23.0	25	5.0
70+	79	16.2	34	7.0
Total	**1119**	**23.3**	**214**	**4.5**

[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 2017, 35.0% (95% CI 32.0–38.2%) 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 2017. The resultant distribution has a mean of 392 cases (95% CI 337–451).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 32.8% (95% CI 31.2–34.4%).

Outbreaks reported as caused by *Salmonella*

In 2017, there were 13 *Salmonella* outbreaks reported, of which four (30.8%) 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, 2017

Measure	Foodborne *Salmonella* spp. outbreaks	All *Salmonella* spp. outbreaks
Outbreaks	4	13
Cases	15	40
Hospitalised cases	5	6

The number of foodborne *Salmonella* outbreaks reported between 2008 and 2017 ranged from three (2015) to 12 (2016) (Figure 32). The total number of cases associated with the outbreaks has varied over the same period with peaks in 2008 (121 cases) and 2012 (104 cases).

Figure 32. Foodborne *Salmonella* outbreaks and associated cases reported by year, 2008–2017

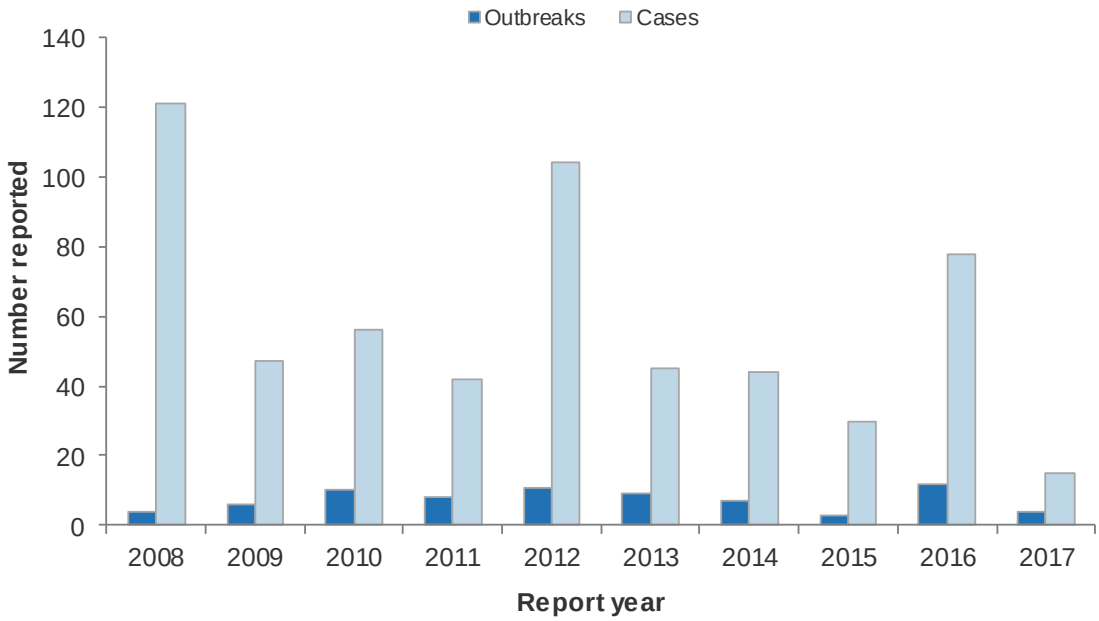


Table 44 contains details of the four foodborne *Salmonella* outbreaks reported in 2017. For all outbreaks the evidence linking the outbreak to a suspected food vehicle was weak. No samples relating to the outbreaks of salmonellosis in Table 44 were submitted to ESR's Public Health Laboratory.

Table 44. Details of foodborne *Salmonella* outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Waikato	Mar	Raw eggs, chicken, untreated water	Marae	Marae	4C, 1P
Waikato	May	Unknown	Community, church, sports gathering	Community, church, sports gathering	3C, 2P
Auckland	Sep	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 2P
Auckland	Oct	Unknown	Home	Home	2C, 0P

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

Salmonella types commonly reported

Human isolates

Isolates from 1103 cases infected with non-typhoidal *Salmonella* were typed by the ESR Enteric Reference Laboratory during 2017. Of these cases, 429 (38.9%) 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 2017, of which *S.* Typhimurium phage type 56 variant (prior to 2012 known as RDNC-May 06 (115 cases)), *S.* Typhimurium phage type 101 (65 cases) and *S.* Enteritidis phage type 11 (55 cases) were

most commonly detected. The most common of the other serotypes were *S.* Brandenburg (54 cases) and *S.* Bovismorbificans (52 cases). *Salmonella* serotypes showing an increase in 2017 compared with 2016 included: *S.* Typhimurium phage type 56 variant, *S.* Typhimurium phage type 101 and *S.* Brandenburg.

Table 45. *Salmonella* case serotypes and subtypes identified by the Enteric Reference Laboratory, 2013–2017

Serotype[a]	2013	2014	2015	2016	2017
***S.* Typhimurium**	**481**	**392**	**447**	**389**	**429**
1	30	22	38	34	22
9	13	17	27	42	14
12a	15	20	18	6	7
56 variant[b]	122	72	96	64	115
101	26	41	56	47	65
135	48	35	64	30	34
156	17	9	27	12	4
160	69	27	9	6	5
Other or unknown	141	149	112	148	163
***S.* Enteritidis**	**137**	**116**	**110**	**114**	**151**
1b	14	5	4	8	7
11[c]	27	39	45	46	55
Other or unknown	96	72	61	60	89
Other serotypes	**523**	**450**	**496**	**570**	**523**
S. Agona	11	15	12	18	16
S. Bovismorbificans	8	4	23	39	52
S. Brandenburg	52	35	52	67	54
S. Infantis	70	56	52	14	18
S. Mississippi	20	21	16	21	15
S. Montevideo	11	7	3	2	2
S. Saintpaul	43	26	37	35	27
S. Stanley	31	34	25	60	39
S. Thompson	16	5	32	13	12
S. Virchow	15	5	16	10	7
S. Weltevreden	28	31	18	18	21
S. enterica (I) ser. 4,[5],12 : i : -	27	27	22	23	28
Other or unknown	191	184	188	250	232
Total	**1141**	**958**	**1053**	**1073**	**1103**

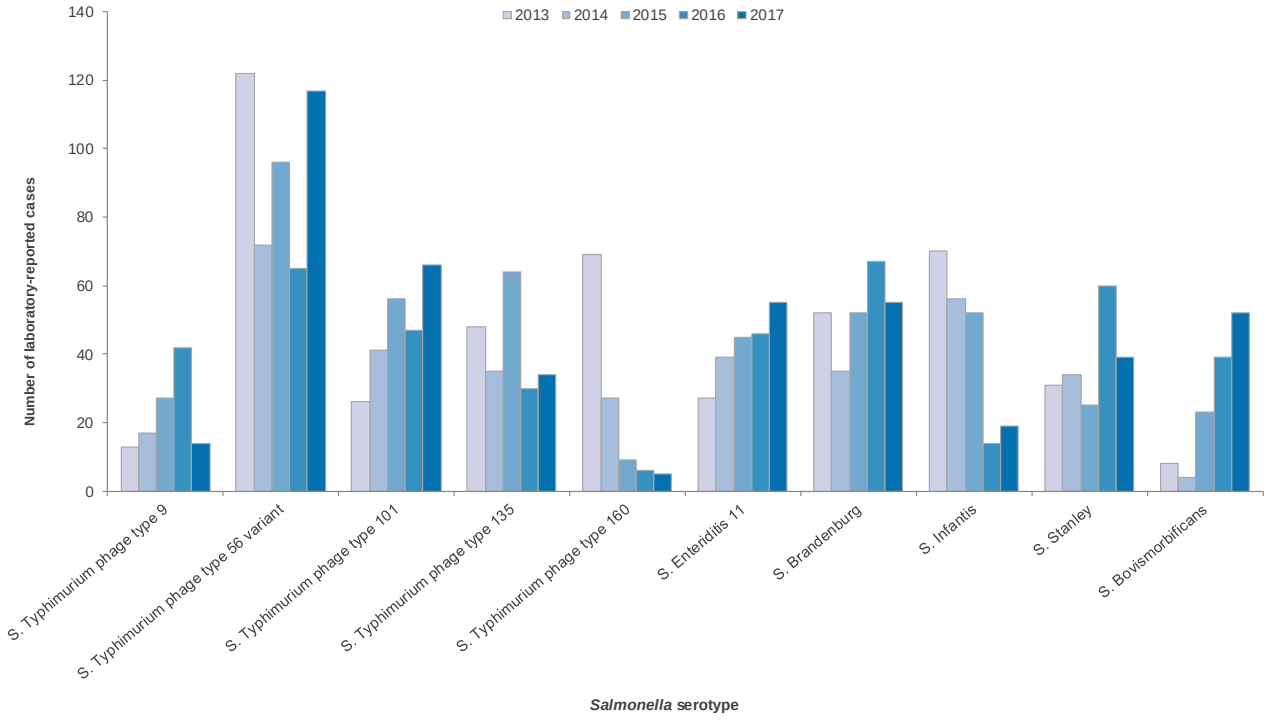
[a] Excludes *S.* Paratyphi and *S.* Typhi.

[b] Prior to 2013, *S.* Typhimurium phage type 56 variant was known as *S.* Typhimurium RDNC-May 06.

[c] Prior to 2012, *S.* Enteritidis phage type 11 was known as a 9a. Further typing was performed on isolates previously confirmed as *S.* Enteritidis phage type 9a, however, typing results revealed that some isolates previously reported as *S.* Enteritidis phage type 9a were phage type 11.

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 2013 and 2017, with numbers remaining high relative to the other serotypes shown. *S.* Typhimurium phage type 160 has continued with a decreasing trend with only five cases of that serotype in 2017. An increased number of cases were serotyped as *S*. Bovismorbificans in 2017 compared to the previous four years.

Figure 33. Number of laboratory-reported cases for selected *Salmonella* serotypes by year, 2013–2017



Non-human isolates

A total of 972 non-human *Salmonella* isolates were typed by the Enteric Reference Laboratory during 2017. *S.* Typhimurium and *S.* Bovismorbificans were the most commonly isolated serotypes in non-human samples in 2017. *Salmonella* Typhimurium phage type 56 variant (prior to 2012 known as RDNC-May 06 (59 isolates)) and *S.* Typhimurium phage type 101 (92 isolates) were the most commonly detected phage types. The most common of the other serotypes were *S.* Bovismorbificans and *S.* Brandenburg with 292 and 137 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, 2013–2017

Serotype	2013	2014	2015	2016	2017	Major sources, 2017
S. Typhimurium	**358**	**220**	**258**	**249**	**372**	
1	26	13	16	14	19	Bovine (16)
9	39	9	9	12	20	Bovine (13), ovine (6)
12a	12	12	19	1	8	Bovine (8)
56 variant[a]	79	38	56	43	59	Bovine (19), feline (15), equine (8)
101	57	48	32	45	92	Bovine (80)
108/170	8	10	3	21	34	Bovine (27)
135	15	12	18	10	11	Bovine (9)
RDNC	32	16	41	31	42	Bovine (37)
Unknown or other	98	72	67	93	87	
Other serotypes	**609**	**509**	**379**	**435**	**600**	
S. Agona	42	17	22	10	17	Bovine (12)
S. Anatum	28	23	6	9	12	Meat/bone meal (8), bovine (3)
S. Bovismorbificans	14	13	71	135	292	Bovine (269)
S. Brandenburg	197	129	102	127	137	Bovine (97), ovine (25), canine (6)
S. Hindmarsh	56	77	49	48	27	Ovine (22), bovine (5),
S. Infantis	67	27	14	20	26	Meat/bone meal (13), bovine (7)
S. Mbandaka	26	20	10	6	9	Bovine (4), meat/bone meal (3)
S. Saintpaul	22	22	12	9	12	Bovine (4), reptile (3)
S. Senftenberg	12	19	15	4	9	Bovine (5)
Other or unknown serotypes	145	162	78	67	48	
Total	**967**	**729**	**637**	**684**	**972**	

[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.

Outbreak types

Table 47 shows the number of hospitalised cases and total cases by subtype for the four foodborne *Salmonella* outbreaks reported during 2017. A *Salmonella* subtype was determined for all of the foodborne *Salmonella* outbreaks in 2017. A total of five cases associated with foodborne salmonellosis outbreaks were hospitalised in 2017.

Table 47. *Salmonella* subtypes reported in foodborne outbreaks, 2017

Pathogen and subtype	Outbreaks	Total cases	Hospitalised cases
S. Enteritidis phage type 11	2	10	4
S. Typhimurium phage type 56 variant	1	3	0
S. Typhimurium phage type 1	1	2	1
Total	**4**	**15**	**5**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A survey collected 1485 samples (5 samples of each of 297 lots) of ready-to-eat (RTE) meat products in original manufacturer packaging from 32 New Zealand producers [22]. None of the samples was found to contain *Salmonella* spp.

Relevant regulatory developments

Nil.

Sapovirus infection

Case definition

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

Sapovirus infection cases reported in 2017 by data source

In 2017, three individual cases of sapovirus infection were reported in EpiSurv (0.06 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 2017, 15 sapovirus outbreaks were reported in EpiSurv with 233 associated cases and no deaths. None of the outbreaks was reported to be foodborne (Table 48). 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 48. Sapovirus outbreaks reported, 2017

Measure	Foodborne sapovirus outbreaks	All sapovirus outbreaks
Outbreaks	0	15
Cases	0	233
Hospitalised cases	0	0

None of the outbreaks was listed as potentially foodborne. In the last five years there have been between zero and three foodborne outbreaks notified each year.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2017 are given in Table 49.

Table 49. Summary of surveillance data for shigellosis, 2017

Parameter	Value in 2017	Source
Number of notified cases	245	EpiSurv
Notification rate (per 100,000)	5.1	EpiSurv
Hospitalisations (% of notifications)[a]	46 (18.8%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	139 (57.0%)	EpiSurv
Estimated food-related cases (%)	NE	-

NE = not estimated, no information is available on the food attributable proportion of shigellosis in New Zealand.
[a] Percentage of the number of notified cases. Cases hospitalised may not be notified on EpiSurv.

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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017–June 2017) 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 unclear at this stage how laboratory changes have affected the notification rates for shigellosis as a decrease in disease rate may be masked by the increased sensitivity of the PCR methodology.

Shigellosis cases reported in 2017 by data source

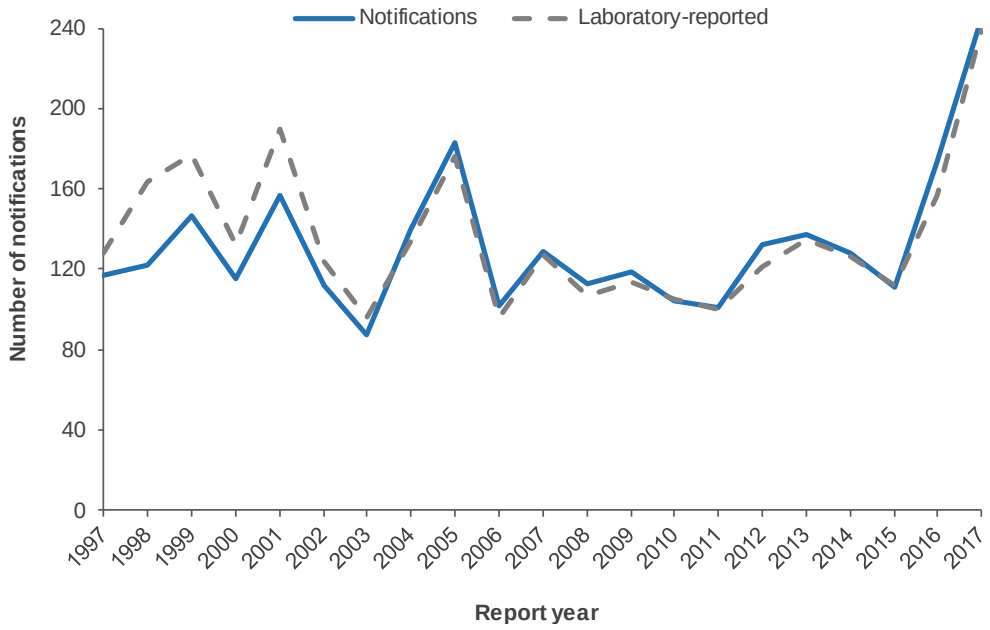
During 2017, 245 cases (5.1 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 239 cases (4.9 per 100,000 population) infected with *Shigella* in 2017.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 46 hospital admissions (one admission per 100,000 population) recorded in 2017, 34 were reported with shigellosis as the principal diagnosis and 12 with shigellosis as another relevant diagnosis.

Notifiable disease data

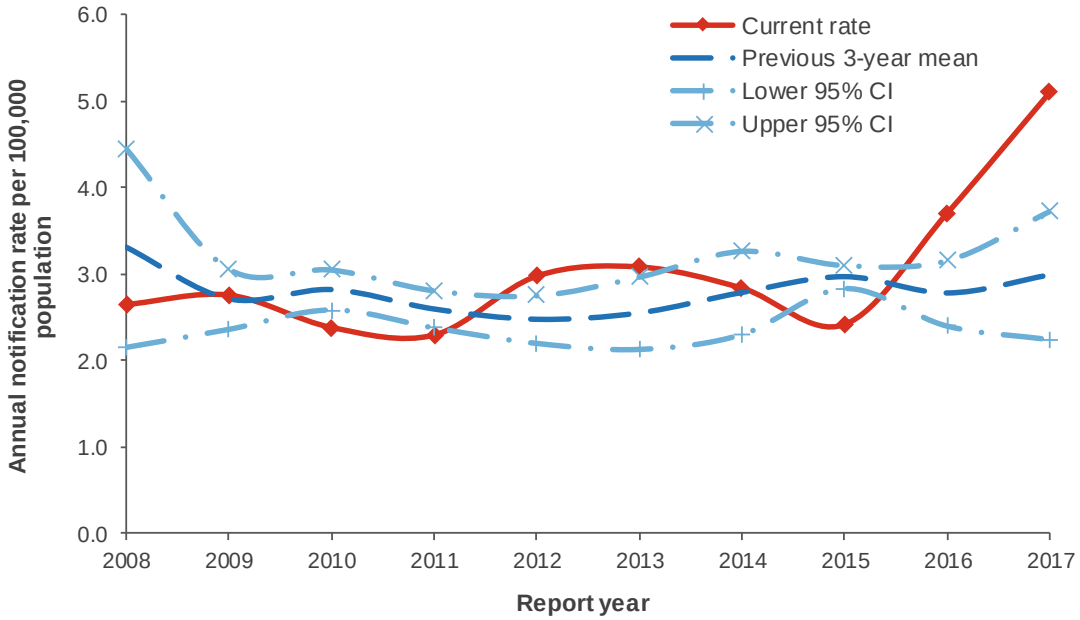
The number of notifications and laboratory reported cases of shigellosis was variable from year to year with the highest number of notifications in 2017 (245), followed by the the second and third highest number of notifications in 2005 (183 cases) and in 2016 (174 cases). Between 2006 and 2015 the number of notifications has been in the range of 101 to 137 cases (Figure 34).

Figure 34. Shigellosis notifications and laboratory-reported cases by year, 1997–2017



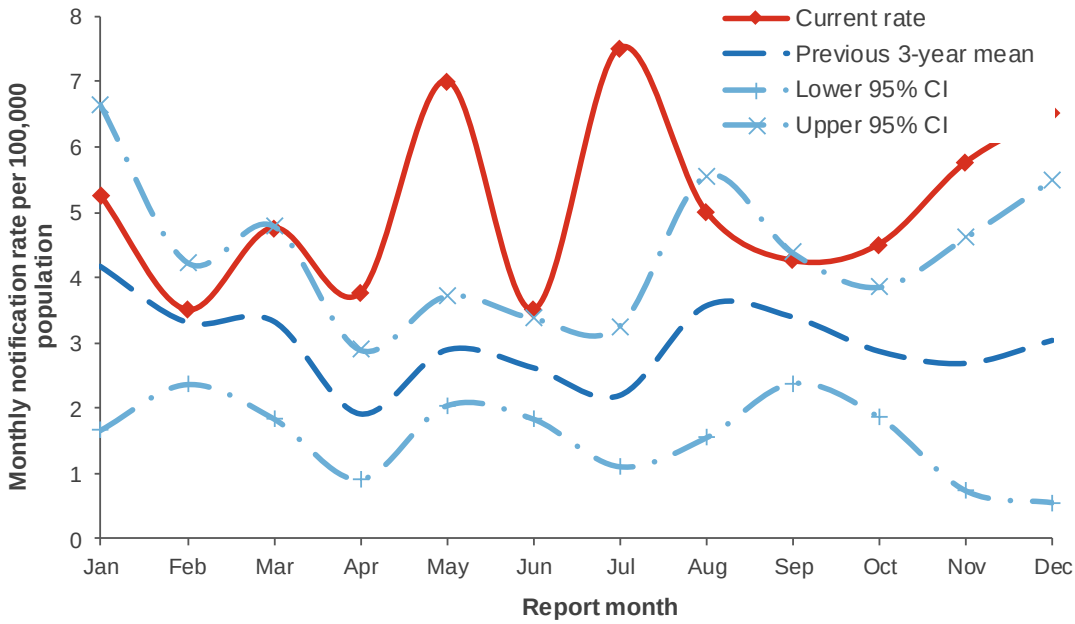
Between 2007 and 2015, the shigellosis notification rate has consistently been in the range of 2.3 to 3.1 notifications per 100,000 population (Figure 35), with an increase in 2016 (3.7 per 100,000 population) and a further increase noted in 2017 (5.1 per 100,000 population). The notification rate in 2017 was higher than the previous three-year average (3.0 cases per 100,000).

Figure 35. Shigellosis notification rate by year, 2008–2017



The number of notified cases of shigellosis per 100,000 population by month for 2017 is shown in Figure 36. In 2017, the shigellosis notification rate was generally higher than the previous three-year mean for the month, with two pronounced peaks in May and July. The number of notifications per month was small, ranging from 14 in February and June to 30 in July.

Figure 36. Shigellosis monthly rate (annualised), 2017



In 2017, the rates for notification and hospitalisation were higher for males (5.7 and 1.2 per 100,000 population, respectively) compared to females (4.5 and 0.7 per 100,000, respectively) (Table 50).

Table 50. Shigellosis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	135	5.7	28	1.2
Female	110	4.5	18	0.7
Total	**245**	**5.1**	**46**	**1.0**

[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 (11.4 per 100,000 population, 28 cases). The number of hospitalisations was low in all age groups, ranging from 0 to 7 hospitalisations across all age groups (Table 51).

Table 51. Shigellosis cases by age group, 2017

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	1	-	1	
1 to 4	28	11.4	7	2.9
5 to 9	13	4.0	6	1.8
10 to 14	4	-	0	
15 to 19	15	4.7	0	
20 to 29	46	6.4	4	-
30 to 39	32	5.3	3	-
40 to 49	31	5.0	5	0.8
50 to 59	33	5.3	6	1.0
60 to 69	22	4.4	7	1.4
70+	20	4.1	7	1.4
Total	**245**	**5.1**	**46**	**1.0**

[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 2017, 56.8% (95% CI 50.2–63.3%) 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 2017. The resultant distribution has a mean of 139 cases (95% CI 108–174).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 58.8% (95% CI 54.8–62.6%).

Outbreaks reported as caused by *Shigella* spp.

In 2017, there were eight *Shigella* spp. outbreaks reported and three of these were reported to be foodborne (Table 52). 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 were five hospitalisations due to a foodborne *Shigella* spp. associated outbreak.

Table 52. *Shigella* spp. outbreaks reported, 2017

Measure	Foodborne *Shigella* spp. outbreaks	All *Shigella* spp. outbreaks
Outbreaks	3	8
Cases	17	32
Hospitalised cases	5	7

The number of foodborne shigellosis outbreaks has ranged between zero and five outbreaks each year in the ten year period 2008–2017, with between two and 39 associated cases (Figure 37).

Figure 37. Foodborne *Shigella* spp. outbreaks and associated cases reported by year, 2008–2017

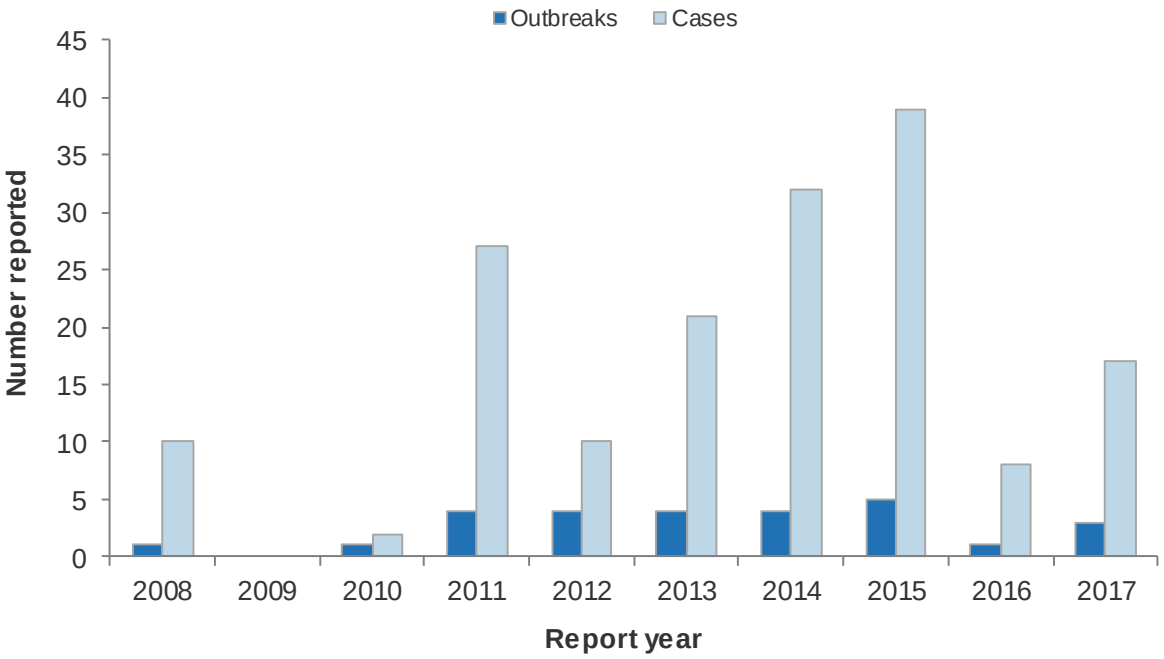


Table 53 contains details of the foodborne *Shigella* spp. outbreaks reported in 2017. The evidence linking these outbreaks to specific foods or food in general was weak.

Table 53. Details of foodborne *Shigella* spp. outbreaks, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Toi Te Ora	Jun	Unknown	Hotel/motel	Unknown	1C, 5P
Auckland	Jul	Unknown	Other setting	Overseas manufacturer	1C, 3P
Auckland	Dec	Raw fish/shellfish imported from Tonga	Unknown	Unknown	7C, 0P

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

No clinical or food samples relating to the three *Shigella* spp. outbreaks listed in Table 53 were submitted to ESR's Public Health Laboratory.

Shigella types commonly reported

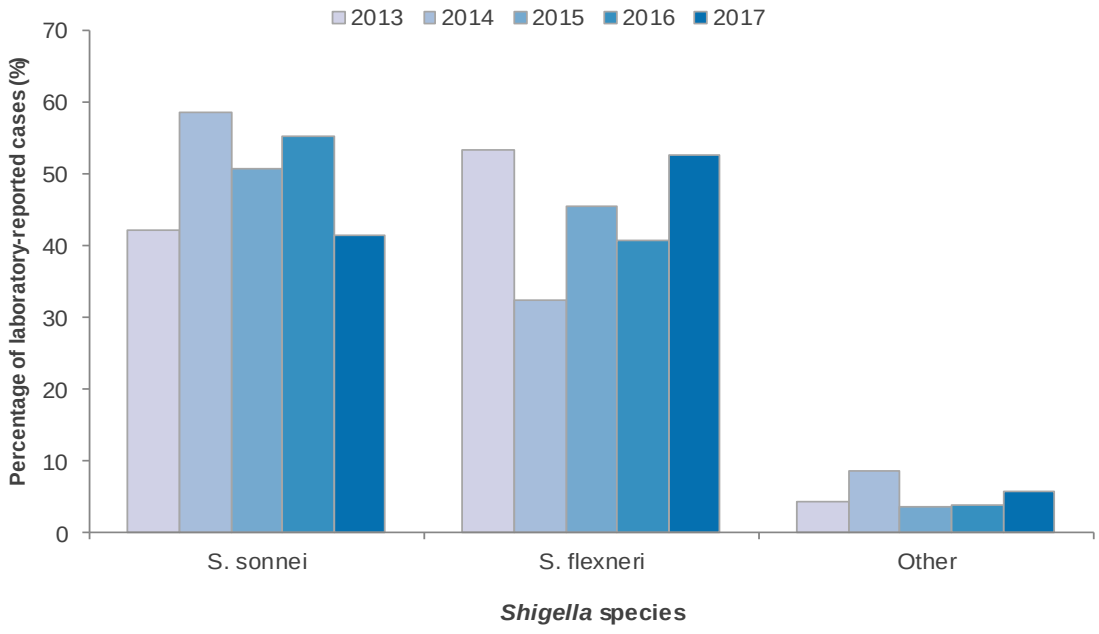
In 2017, the Enteric Reference Laboratory at ESR reported 239 types from cases infected with *Shigella* spp.. *S. sonnei* and *S. flexneri* were the species most often identified. Of these, *S. sonnei* biotype g was most common in 2017 (Table 54).

Table 54. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2013–2017

Species	2013	2014	2015	2016	2017
S. sonnei	**57**	**74**	**57**	**87**	**99**
biotype a	35	32	20	31	30
biotype f	1	6	0	1	1
biotype g	21	36	37	55	68
S. flexneri	**72**	**41**	**51**	**64**	**126**
1	6	7	8	21	42
2a	12	11	14	18	18
2b	2	6	6	4	7
3a	10	4	7	1	5
Other	42	13	16	20	57
Other	**6**	**11**	**4**	**6**	**14**
S. boydii	5	9	4	3	13
S. dysenteriae	1	1	0	2	1
Shigella species not identified	0	1	0	1	0
Total	**135**	**126**	**112**	**157**	**239**

The percentage of shigellosis cases infected with *S. sonnei* in 2017 (41%) was slightly below the range of values observed between 2013 and 2016 (between 42% and 59%). The percentage of shigellosis cases with *S. flexneri* in 2017 (53%) was within the range of values observed between 2013 and 2016 (between 33% and 53%) (Figure 38).

Figure 38. Percentage of laboratory-reported cases by *Shigella* species and year, 2013–2017



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 2017 by data source

During 2017, 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. There were five hospital admissions recorded in 2017 with *S. aureus* intoxication recorded as the principal diagnosis, all of which were female.

Outbreaks reported as caused by *Staphylococcus aureus*

In 2017, two foodborne *S. aureus* outbreaks were reported with 12 associated cases (Table 55). 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 55. *S. aureus* outbreaks reported, 2017

Measure	Foodborne *S. aureus* outbreaks	All *S. aureus* outbreaks
Outbreaks	2	2
Cases	12	12
Hospitalised cases	0	0

The number of foodborne outbreaks associated with *S. aureus* reported each year between 2008 and 2017 ranged from zero to two (Figure 39). No *S. aureus* outbreaks were reported in EpiSurv in three of the last ten years.

Figure 39. Foodborne *S. aureus* outbreaks and associated cases reported by year, 2008–2017

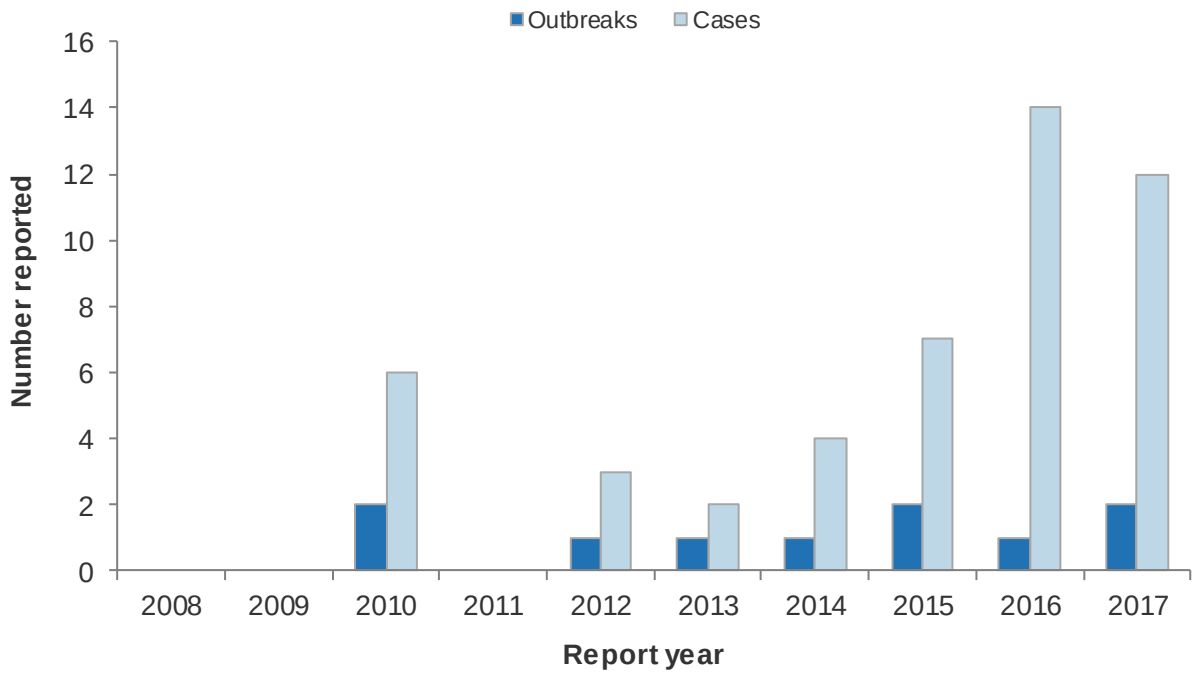


Table 56 contains details of the two foodborne *S. aureus* outbreaks reported in 2017. The evidence linking these outbreaks to specific food vehicles was weak.

Table 56. Details of foodborne *S. aureus* outbreak, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Taranaki	Sep	Unknown	Childcare centre	Childcare centre	1C, 6P
Regional	Dec	Chicken sandwich	Supermarket/delicatessen	Supermarket/delicatessen	0C, 5P

PHU: Public Health Unit, Regional: Regional Public Health, Taranaki: Taranaki Health Protection Unit, C: confirmed, P: probable.

In 2017, samples relating to both outbreaks were submitted to ESR's Public Health Laboratory, listed in Table 56. *S. aureus* and staphylococcus enterotoxin were detected in faecal samples relating to one outbreak (Taranaki). *S. aureus* and staphylococcus enterotoxin were detected in food samples and *S. aureus* was detected in faecal samples relating to the second outbreak (Regional).

Recent surveys

Nil.

Relevant New Zealand studies and publications

Papers

A survey collected 1485 samples (five samples of each of 297 lots) of ready-to-eat (RTE) meat products in original manufacturer packaging from 32 New Zealand producers [22]. None of the samples was found to contain unacceptable levels of coagulase-positive staphylococci.

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 2017

During 2017, five cases (0.1 per 100,000 population) of toxic shellfish poisoning and no resulting deaths were reported in EpiSurv. One case was reported with neurologic shellfish poisoning and the poisoning type was not specified for four cases.

All five cases were adults aged between 20 and 49 years and had eaten recreationally collected seafood. Three cases were male and two were female. Cases were reported from Northland (4 cases) and Bay of Plenty (1 case) DHBs. Three cases were from the European or Other ethnic group and two cases were of Māori ethnicity. In EpiSurv, one case (20.0%) was 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 four hospital admissions (0.08 admissions per 100,000 population) were reported in 2017, all were reported with 'other fish and shellfish poisoning' as the primary diagnosis. Note that this ICD-10 code includes shellfish and other fish. It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified.

Outbreaks reported as caused by toxic shellfish poisoning

In 2017, 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.

In the period 2011 to 2015 there were two outbreaks due to toxic shellfish poisoning: One outbreak in 2012 with 29 cases and one outbreak in 2014 with 13 cases.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

During 2017, MPI release two guidance documents related to marine biotoxins:

- Guide for the validation and approval of new marine biotoxin test methods (update) [31], and
- Guide for the release of fish or fish product detained or recalled for marine biotoxin reasons [32].

VTEC/STEC infection

Summary data for VTEC/STEC infection in 2017 are given in Table 57.

Table 57. Summary of surveillance data for VTEC/STEC infection, 2017

Parameter	Value in 2017	Source
Number of notified cases	547	EpiSurv
Notification rate (per 100,000)	11.4	EpiSurv
Hospitalisations (% of notifications)[a]	20 (3.7%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	55 (10.1%)	EpiSurv
Estimated food-related cases (%)[b]	147 (29.9%)	Expert consultation

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

[b] For estimation of food-related cases the proportions derived from expert consultation exclude travel-related cases. The expert elicitation derived separate estimates of the foodborne proportion for O157 VTEC/STEC and non-O157 VTEC/STEC. The estimate for O157 VTEC/STEC, the dominant serotype, has been used to estimate the number of food-related cases.

Case definition

Clinical description: Diarrhoea resulting from infection with VTEC/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 VTEC/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 VTEC/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 VTEC/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" [33].

While it is likely that this simplified terminology may gain credence, the New Zealand *Schedule of notifiable diseases* lists the disease caused by these organisms as "Verotoxin-producing or Shiga toxin-producing *Escherichia coli*" [34]. At this stage, the current report will maintain terminology that aligns with the New Zealand schedule.

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 (since June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017–June 2017) were screened by multiplex PCR for a range of pathogens, including VTEC/STEC. Prior to the change in methodology only faecal samples with blood, or those from under 5-year-olds were tested for VTEC/STEC infection. For the Auckland and Northland areas these changes have resulted in an increased notification rate for VTEC/STEC.

VTEC/STEC infection cases reported in 2017 by data source

During 2017, 547 cases (11.4 per 100,000 population) of VTEC/STEC infection and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 528 cases (11.0 per 100,000) infected with VTEC/STEC in 2017.

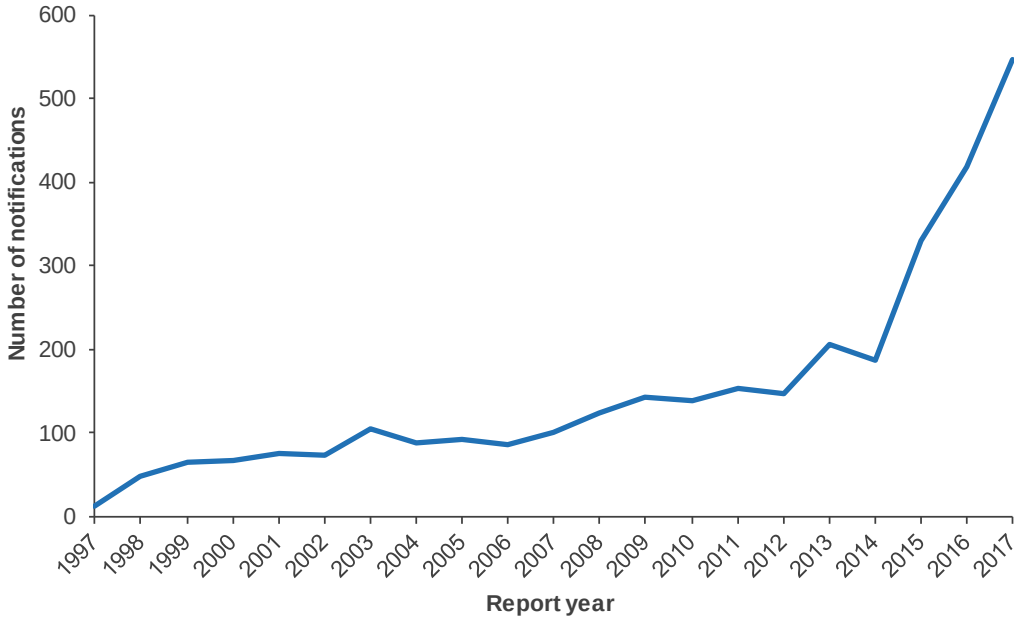
The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E*. *coli* infection hospitalisation data from the MoH NMDS database. Of the 20 hospital admissions (0.4 admissions per 100,000 population) recorded in 2017, 11 were reported with enterohaemorrhagic *E*. *coli* infection as the principal diagnosis and nine 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 VTEC/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 VTEC/STEC transmission was due to red meat, irrespective of serotype.

Notifiable disease data

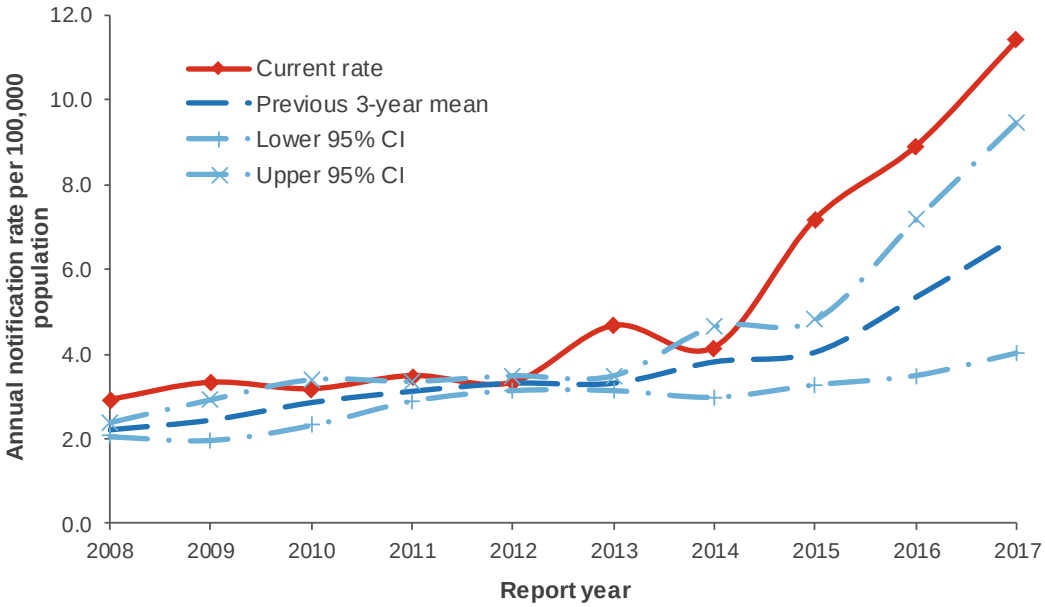
In 2015, there was a large increase in VTEC/STEC notifications compared to previous years with a further increase in 2016 and 2017 (Figure 46 and Figure 47).

Figure 40. VTEC/STEC infection notifications by year, 1997–2017



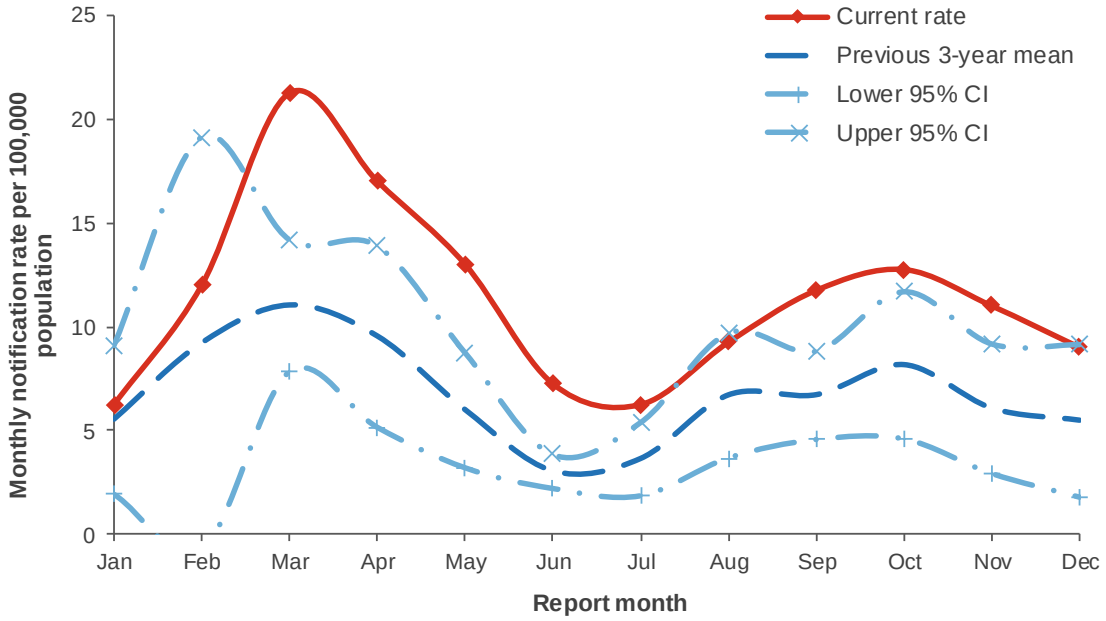
Between 2008 and 2014, the notification rate of VTEC/STEC infection has been in the range of 2.9 to 4.6 notifications per 100,000 population (Figure 41), with increasing rates noted in 2015, 2016 and 2017 (7.2, 8.9 and 11.4, respectively, per 100,000 population). The notification rate in 2017 was much higher than the previous three-year average (6.7 cases per 100,000).

Figure 41. VTEC/STEC infection notification rate by year, 2008–2017



The number of notified cases of VTEC/STEC infection per 100,000 population by month for 2017 are shown in Figure 42. The 2017 the trend in monthly notification rates was generally similar to recent years (2014-2016) with a small increase in spring, and a high peak from February to April.

Figure 42. VTEC/STEC infection monthly rate (annualised), 2017



In 2017 notification rates were similar for females and males (11.8 and 11.1 notifications per 100,000 population, respectively), however, hospitalisation rates were higher for females (0.6 admissions per 100,000) compared to males (0.3 admissions per 100,000) (Table 58).

Table 58. VTEC/STEC infection cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	261	11.1	6	0.3
Female	286	11.8	14	0.6
Total	**547**	**11.4**	**20**	**0.4**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

In 2017, the VTEC/STEC infection notification rate was highest for the less than 1 year age group (59.4 per 100,000 population, 36 cases) and the 1 to 4 years age group (48.9 per 100,000, 120 cases). Notification rates for the under five year olds were more than three times the rates for any other age group. The number of hospitalisations ranged between zero and six for each of the age groups (Table 59).

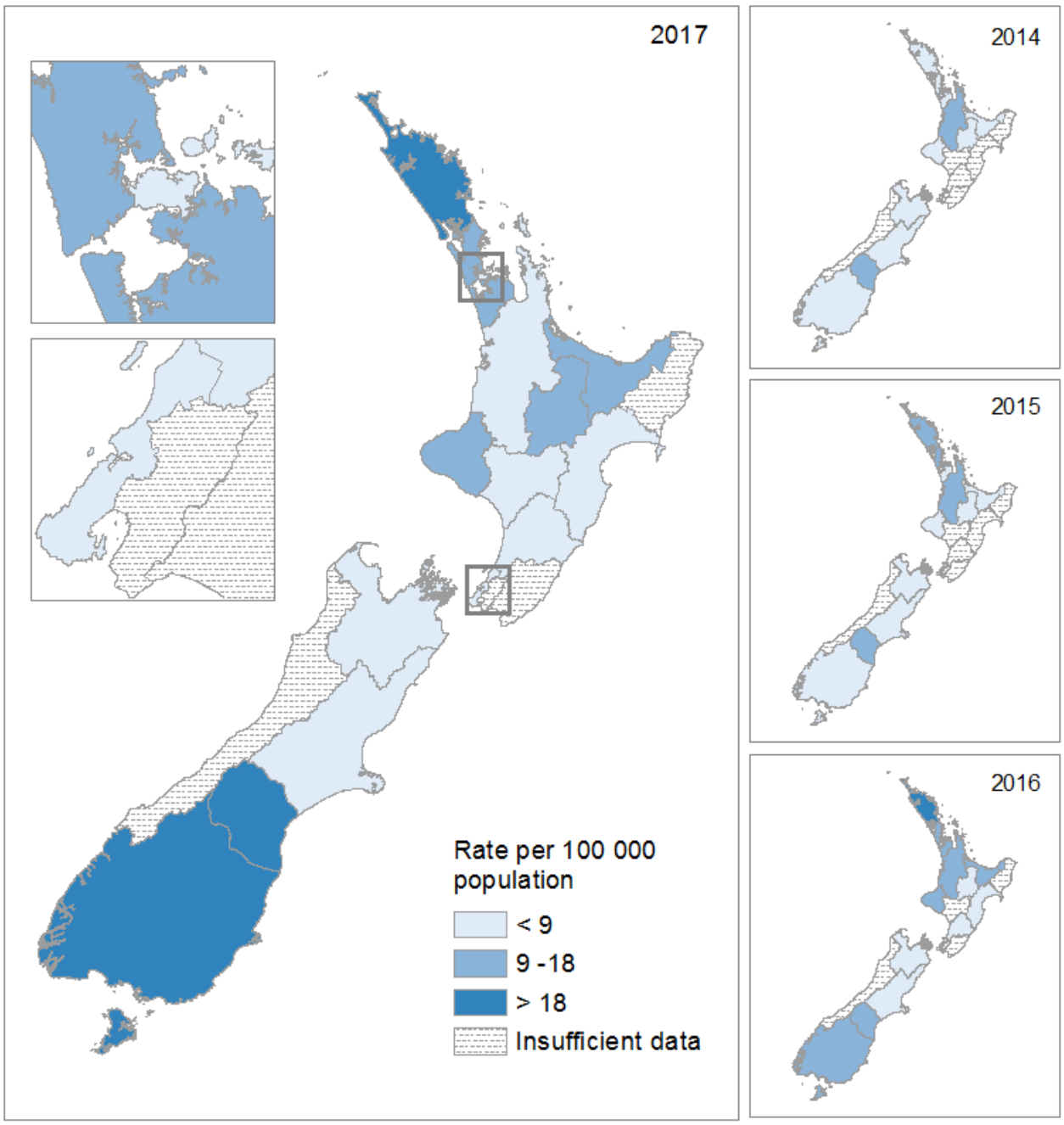
Table 59. VTEC/STEC infection cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	36	59.4	0	-
1 to 4	120	48.9	6	2.4
5 to 9	31	9.5	2	-
10 to 14	28	9.3	0	-
15 to 19	23	7.3	0	-
20 to 29	59	8.2	1	-
30 to 39	44	7.3	2	-
40 to 49	36	5.8	1	-
50 to 59	47	7.6	1	-
60 to 69	48	9.6	2	-
70+	75	15.4	5	1.0
Total	**547**	**11.4**	**20**	**0.4**

[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 VTEC/STEC infection varied throughout the country as illustrated in Figure 43. In 2017, the highest rates of VTEC/STEC infection were reported for the DHBs Southern (41.9 per 100,000, 136 cases) and Northland (40.5 per 100,000, 71 cases), followed by South Canterbury DHB (18.5 per 100,000, 11 cases) and Waitemata DHB (12.9 per 100,000, 78 cases). The high rates reported for Southern and Northland DHBs may be due to the more sensitive assays used (refer to Figure 43 footnote). Note that rates were not calculated for four DHBs where there were insufficient (less than five) cases notified in 2017.

Figure 43. Geographic distribution of VTEC/STEC infection notifications, 2014–2017



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). 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 2017, 10.1% (95% CI 7.6–13.0%) had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all VTEC/STEC infection cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of VTEC/STEC infection in 2017. The resultant distribution has a mean of 55 cases (95% CI 36–77%).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 9.0% (95% CI 7.5–10.7%).

Outbreaks reported as caused by VTEC/STEC

Of the 11 outbreaks (197 cases) of VTEC/STEC infection during 2017, one outbreak was classed as foodborne (Table 60). 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 60. VTEC/STEC outbreaks reported, 2017

Measure	Foodborne VTEC/STEC outbreaks	All VTEC/STEC outbreaks
Outbreaks	1	11
Cases	157	197
Hospitalised cases	0	3

The number of foodborne VTEC/STEC outbreaks reported between 2008 and 2017 ranged from one to four (2014), with no outbreaks reported for four of the ten years (Figure 44). The total number of cases associated with the outbreaks has varied over the same period with peaks in 2008 (14 cases) and 2014 (15 cases). In 2017, one outbreak involved 157 cases, which was a higher number of cases than has been previously seen in New Zealand for foodborne VTEC/STEC outbreaks.

Figure 44. Foodborne VTEC/STEC outbreaks and associated cases reported by year, 2008–2017

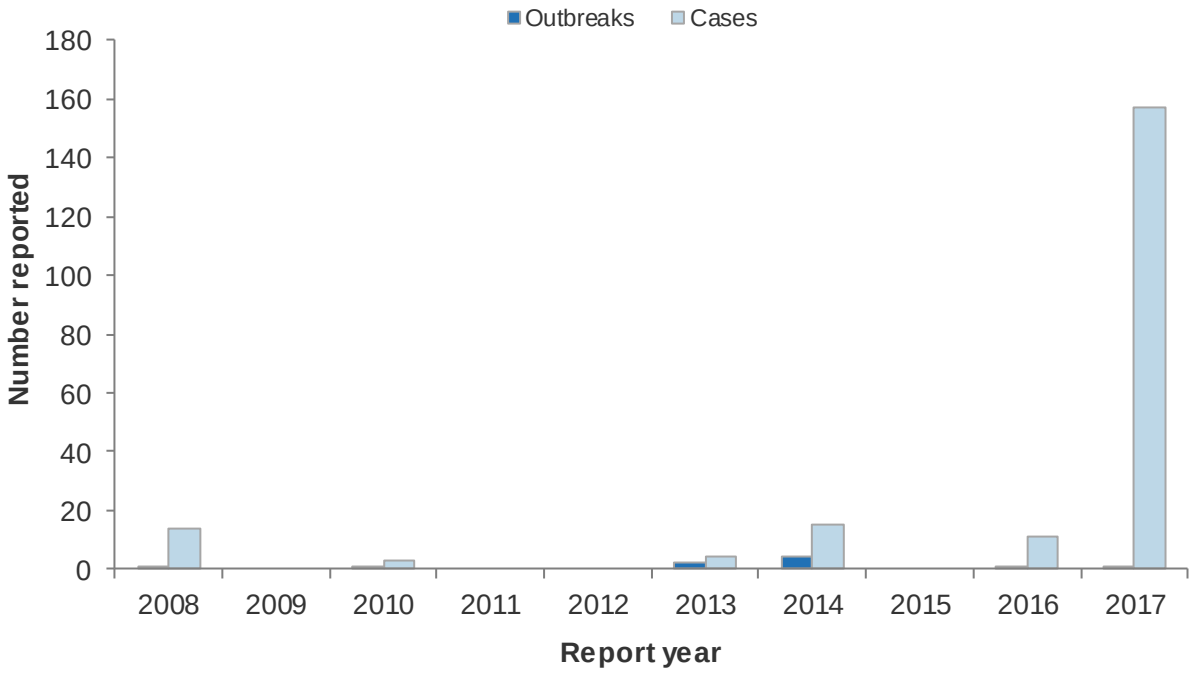


Table 61 contains details of the foodborne VTEC/STEC outbreak reported in 2017. The suspected food vehicle is unknown.

Table 61. Details of foodborne VTEC/STEC outbreaks reported, 2017

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Feb	Unknown	Cruise ship, airline, tour bus, train	Cruise ship	2C, 155P

PHU: Public Health Unit, C: confirmed, P: probable.

In 2017, faecal samples were submitted to ESR's Public Health Laboratory relating to the food-associated VTEC/STEC outbreak listed in Table 61 (Auckland). Atypical EPEC was isolated from the associated faecal samples.

VTEC/STEC types commonly reported

A total of 528 cases infected with VTEC/STEC were reported by the ESR Enteric Reference Laboratory in 2017. Of these, 196 (37.1%) isolates were identified as *E. coli* O157:H7, 226 (42.8%) as non-O157 and for 106 (20.1%) isolates the serotype was not identified.

Of the 332 non-O157 isolates, 44 were typed as O26:H11, 22 as ONT:H2 and 10 as O146:H21 (Table 62). The percentage of non-O157 VTEC/STEC cases in 2015 was higher than 2013 and 2014 probably due to the changes in laboratory methods and the screening of all faecal samples submitted to an Auckland laboratory (Figure 45). The further increase in the percentage of non-O157 case isolates in 2016 (from 29.4% in 2015 to 36.9% in 2016) may be due to a full year of applying the new approach in Auckland compared to half a year in 2015. In 2017, 42.8% of isolates were non-O157 VTEC/STEC.

Figure 45. Percentage of *E. coli* O157 and non-O157 laboratory-reported cases by year, 2013–2017

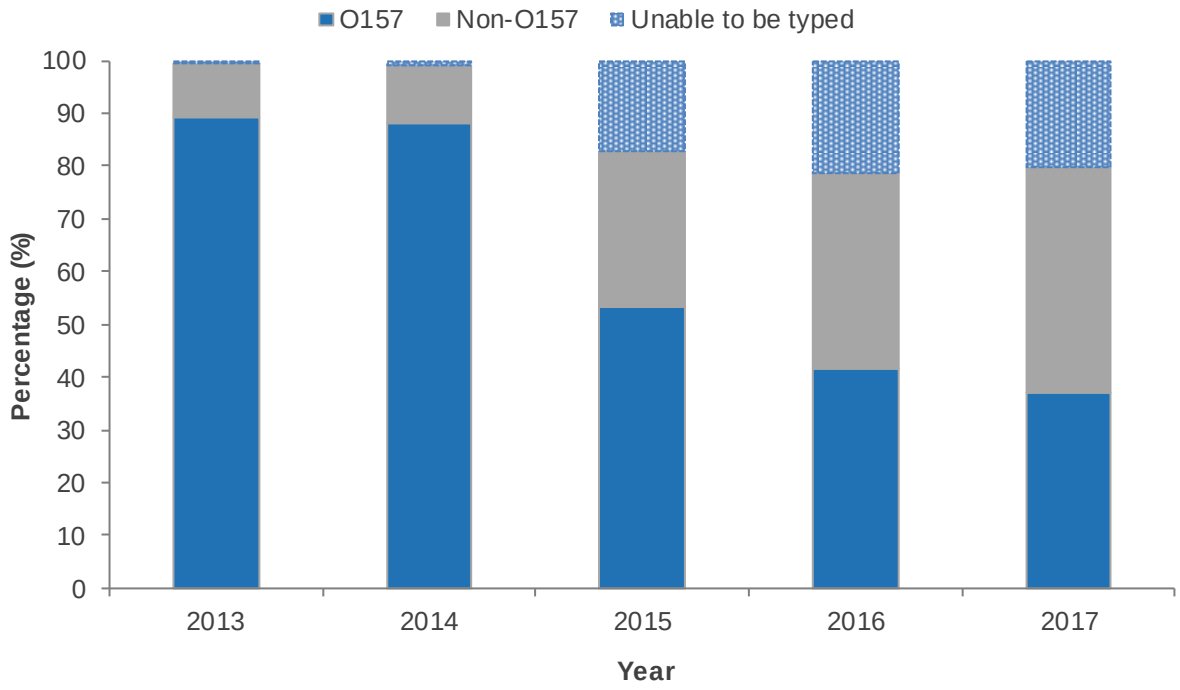


Table 62. VTEC/STEC subtypes identified by the Enteric Reference Laboratory, 2013–2017

Serotype	2013	2014	2015	2016	2017
O157	**192**	**170**	**183**	**205**	**196**
O157:H7	192	170	183	205	196
Non-O157	**22**	**21**	**101**	**181**	**226**
O103:H2	-	-	2	2	3
O128:H2	1	-	4	25	6
O128:HNM	-	-	-	5	1
O145:H2	-	-	-	3	1
O146:H21	-	1	2	4	13
O146:HNM	-	-	-	-	3
O165:HNM	-	-	-	-	3
O153:HNT	-	-	-	-	2
O176:HNM	-	3	10	2	4
O186:HNM	-	-	-	-	4
O26:H11	1	1	14	46	44
O26:HNM	-	-	-	5	4
O38:H26	1	2	5	10	7
O5:HNM	-	-	-	4	1
O64:H20	-	-	-	3	2
O84:HNM	-	-	-	-	6
O91:HNM	-	-	5	2	2
ONT:H2	1	1	9	3	22
ONT:H21	-	-	-	-	4
ONT:H26	-	-	-	-	4
ONT:H7	-	-	-	3	7
ONT:HNM	1	2	10	6	9
ONT:HNT	-	-	-	-	4
ORough:H2	-	-	-	6	4
ORough:HNM	1	-	3	2	8
Other types[a]	14	11	25	42	61
Unable to be typed	**1**	**2**	**59**	**105**	**106**
Total	**215**	**193**	**343**	**491**	**528**

[a] Cases not listed in table, single cases unless indicated otherwise. NM: Non-Motile, NT: Non-Typable

2013: O84:HNM, O84:HNT, O116:H11, O121:H19 (two cases), O121:HNT, O123:HMN, O145:H34, O156:H25, O163:H19, O177:HNM, O179:H8, O182:HNM, ORough:H2

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

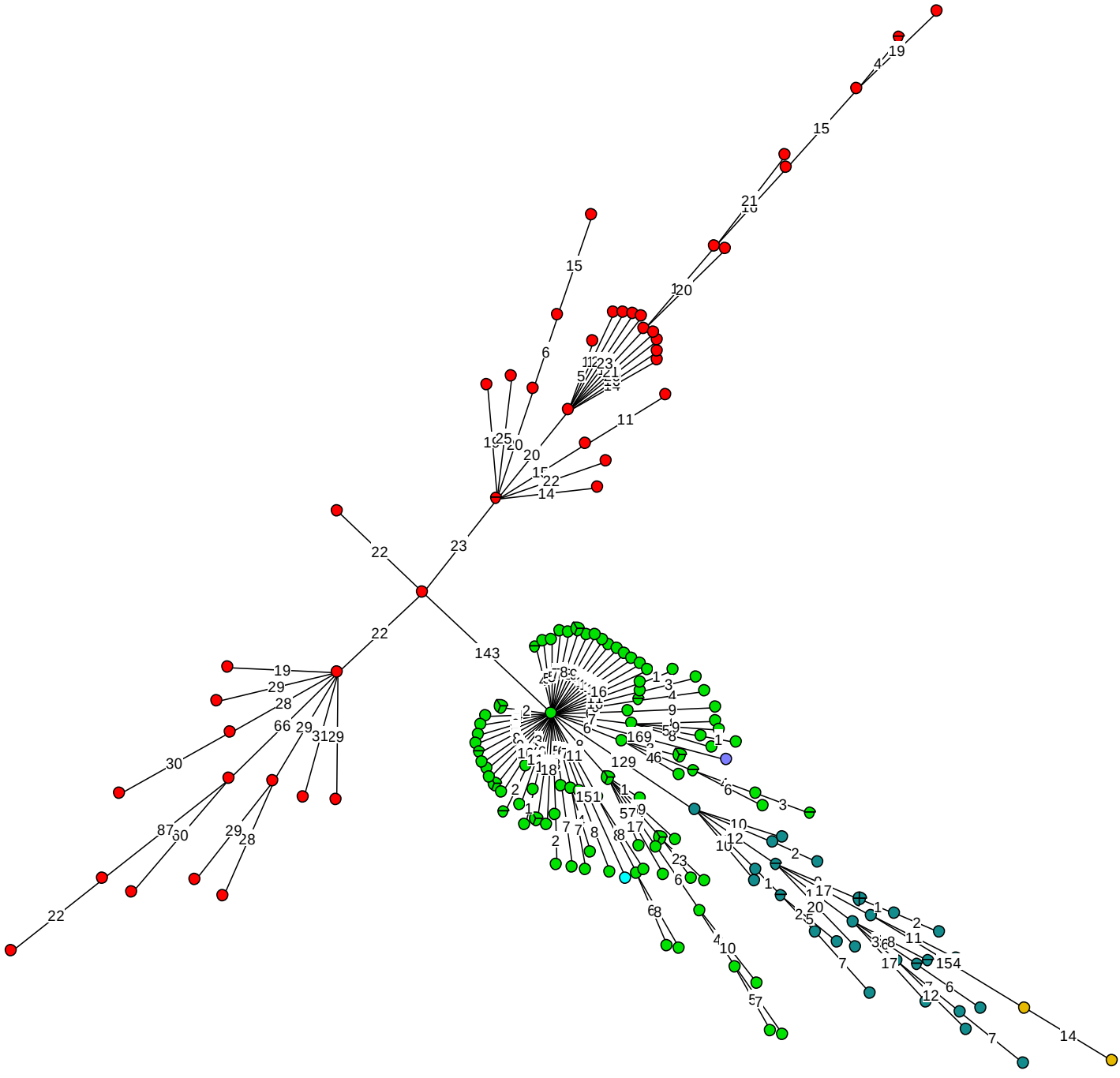
2015: O38:HNM, O55:HNT, O8:H28, O80:HNM, O84:H2, O91:H21, O112:H8, O128:HNM, O130:H11, O145:HNM, O149:H18, O163:H19, O174:H8, O174:HNM, O177:HNM, O178:H7, O179:H8, O183:H18, O186:H10, ONT:H26, ONT:H49, ONT:HNT, ORough:H16, ORough:H2, ORough:H7

2016: O38:HNM, O55:H12, O63:H6, O65:H2, O75:H7, O76:H19 (two cases), O76:H20, O8:HNM, O90:H2, O81:H6, O84:HNM (two cases), O91:H21 (two cases), O95:H16, O96:H5, O101:H2, O101:HNM, O103:H25, O104:H7, O111:HNM, O113:H4, O130:H11 (2 cases), O146:H8, O149:H2, O15:H2, O162:H7, O172:HNM, O174:HNM, O178:H7, O182:HNM, O183:H18 (3 cases), O183:HNM, ONT:H10, ONT:H13, ONT:H14, ONT:H21, ONT:H28, ONT:H5, ONT:HNT (two cases), ORough:H21, ORough:H7

2017: O103:H25, O107:H7, O111:HNM (two cases), O113:H21 (two cases), O117:H7, O123:H2, O128:H2, O128:HNM, O128:HNT, O130:H11, O130:H23, O145:HNM, O146:H11, O146:HNT, O148:H21, O15:H14, O15:H21, O156:H19, O174:H8, 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, O5:HNM, 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, ONT:NHM, ORough:H25, ORough:HNT

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 using the Enterobase core wgMLST scheme. Consistent with previous PFGE analysis there is a wide diversity of genotypes present, with many of the isolates quite distinct from any other. There are, however, a number of small clusters of indistinguishable isolates.

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



Note: Each circle is a different genotype of *E. coli* O157, with indistinguishable isolates indicated by divisions within each circle (in the diagram above there are a maximum of three indistinguishable isolates). Numbers on branches are the number of loci differences. Colours show group separation with >75 allele differences between groups.

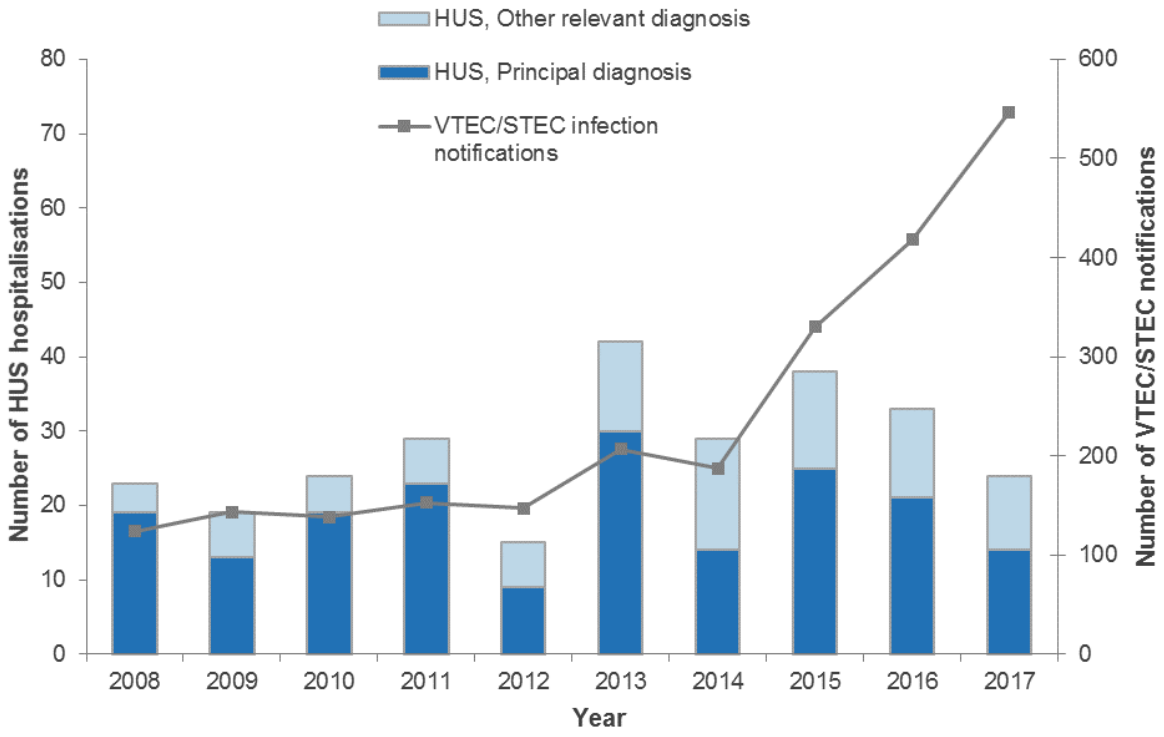
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from a VTEC/STEC infection. HUS is usually preceded by a VTEC/STEC infection [35]. While most HUS cases are associated with *E. coli* O157 infections, non-O157 genotypes differ markedly in their virulence with respect to HUS causation [36].

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 2017 year were considered, rather than all cases that were hospitalised in that year. That is, if a HUS cases hospitalised in 2017 had been hospitalised with HUS in a previous year, the 2017 admission was considered to be a readmission, rather than an incident case. Of the 24 incident hospital admissions recorded in 2017 (0.5 per 100,000 population), 14 were reported with HUS as the primary diagnosis and 10 with HUS as another relevant diagnosis.

Between 2008 and 2017, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 42 (Figure 47). In 2017, the number of incident hospitalised cases decreased to 24 from 33 in 2016 and 38 in 2015. This decrease corresponded with an increase in the number of VTEC/STEC notifications (Figure 46).

Figure 47. Haemolytic-uraemic syndrome (HUS) hospitalised cases, 2008–2017



In 2017, the number of male incident hospitalised cases due to HUS was greater than the number of female cases (Table 63). This is a reversal of the pattern seen in 2016, when more females were hospitalised with HUS than males.

Table 63. Haemolytic uraemic syndrome hospitalised cases by sex, 2017

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	14	0.6
Female	10	0.4
Total	**24**	**0.5**

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

In 2017, the highest age-specific rates of incident hospitalised cases due to HUS were in the less than 5 years age group (Table 64). The age distribution of incident hospitalised HUS cases in 2017 was notable for the small number of cases in the older age categories. This was similar to the patterns seen in 2016, however in 2015 10 of 38 incident cases were 60 years or older.

Table 64. Haemolytic uraemic syndrome hospitalised cases by age group, 2017

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
<5	12	3.9
5 to 9	1	-
10 to 14	2	-
15 to 19	0	-
20 to 29	2	-
30 to 39	0	-
40 to 49	2	-
50 to 59	3	-
60 to 69	0	-
70+	2	-
Total	**24**	**0.5**

[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 2017, 12 cases of HUS were reported to the NZPSU, including one recurrent HUS case, of which 10 had a diarrhoeal prodrome. The median age of cases was 2.1 years. Eight of the 10 cases had *E. coli* O157:H7 isolated from their stools. Seven of the 10 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

During 2017, nine New Zealand laboratories submitted a total of 135 meat enrichment broths to the Enteric Reference Laboratory (ERL) for confirmation [37]. These broths included 134 from adult cow carcasses and one from a bobby calf. This year the origin of the broths was spread disproportionately across the country with 32% of the samples being submitted by primary laboratories located in the South Island. The number of meat enrichment samples where “no Super 6 STEC” was recovered increased from 72% last year to 76% (71/93) this season.

Relevant New Zealand studies and publications

Journal papers

The prevalence and spatial distribution of VTEC/STEC serogroups O26, O103, O111 and O145 in calves in New Zealand was examined [38]. Serogroup O26 was most commonly detected (134/299 samples), followed by O103 (68/299) and O145 (47/299). O111 was not detected. Farms positive for O26, O103 and O145 were present in three important dairy regions of the North Island.

Relevant regulatory developments

During 2017, MPI released two guidance documents related to the manufacture of uncooked, comminuted, fermented meat (UCFM) and the control of VTEC/STEC in this product type:

- Production of uncooked fermented salami (UCFM) [39], and
- Complying with the Uncooked Comminuted Fermented Meat (UCFM) Standard [40].

Yersiniosis

Summary data for yersiniosis in 2017 are given in Table 65.

Table 65. Summary of surveillance data for yersiniosis, 2017

Parameter	Value in 2017	Source
Number of notified cases	918	EpiSurv
Notification rate (per 100,000)	19.2	EpiSurv
Hospitalisations (% of notifications)[a]	87 (9.5%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	67 (7.4%)	EpiSurv
Estimated food-related cases (%)[b]	537 (63.2%)	Expert consultation

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

Yersiniosis cases reported in 2017 by data source

During 2017, 918 cases (19.2 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv.

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 87 hospital admissions (1.8 admissions per 100,000 population) recorded in 2017, 53 were reported with yersiniosis as the principal diagnosis and 34 with yersiniosis as another relevant diagnosis.

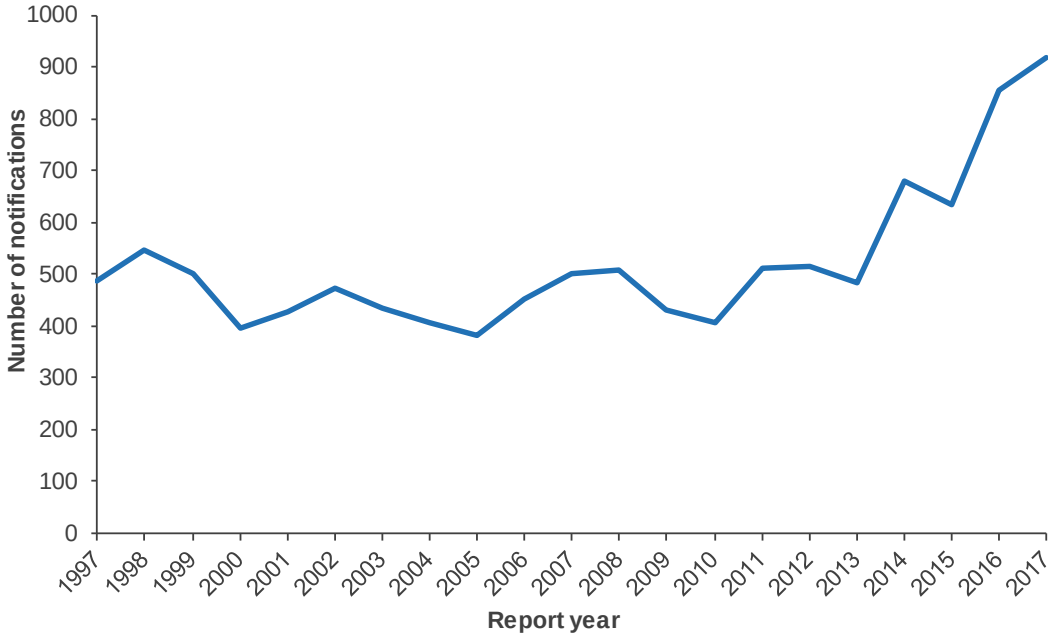
It has been estimated by expert consultation that 63.2% (95th percentile credible interval: 29.0% to 91.5%) of yersiniosis incidence is due to foodborne transmission. Approximately 70% of foodborne transmission was estimated to be due to consumption of pork.

[*] 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].

Notifiable disease data

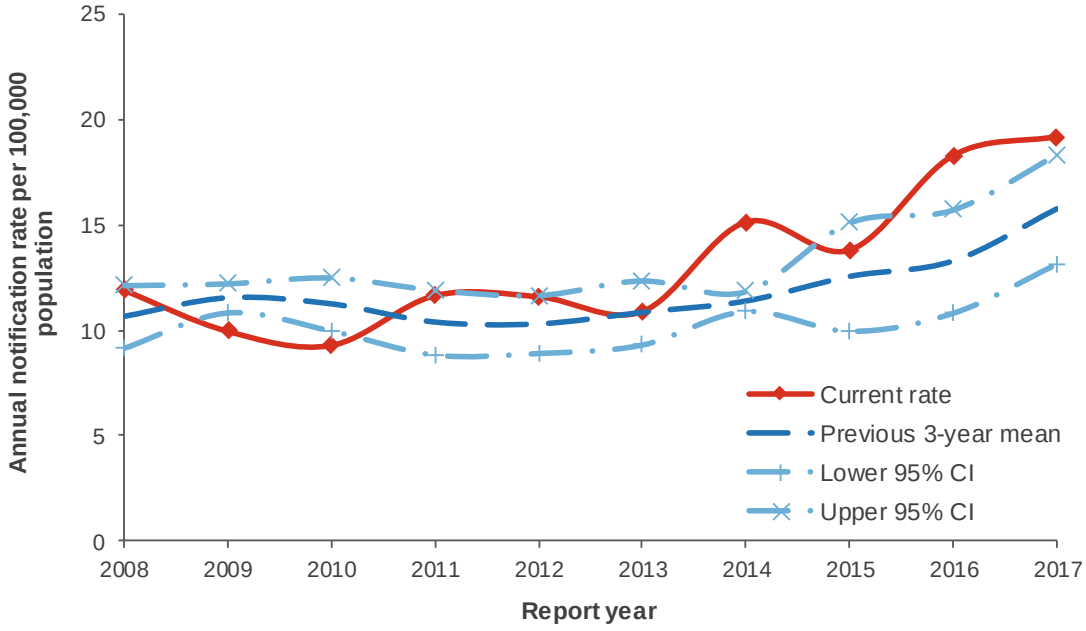
Yersiniosis became notifiable in 1996. Between 1998 and 2013 the annual number of notifications reported ranged between 383 and 546. Since 2013, higher numbers of notifications have been recorded, with the highest number of notifications reported in 2017 (918) (Figure 48).

Figure 48. Yersiniosis notifications by year, 1997–2017



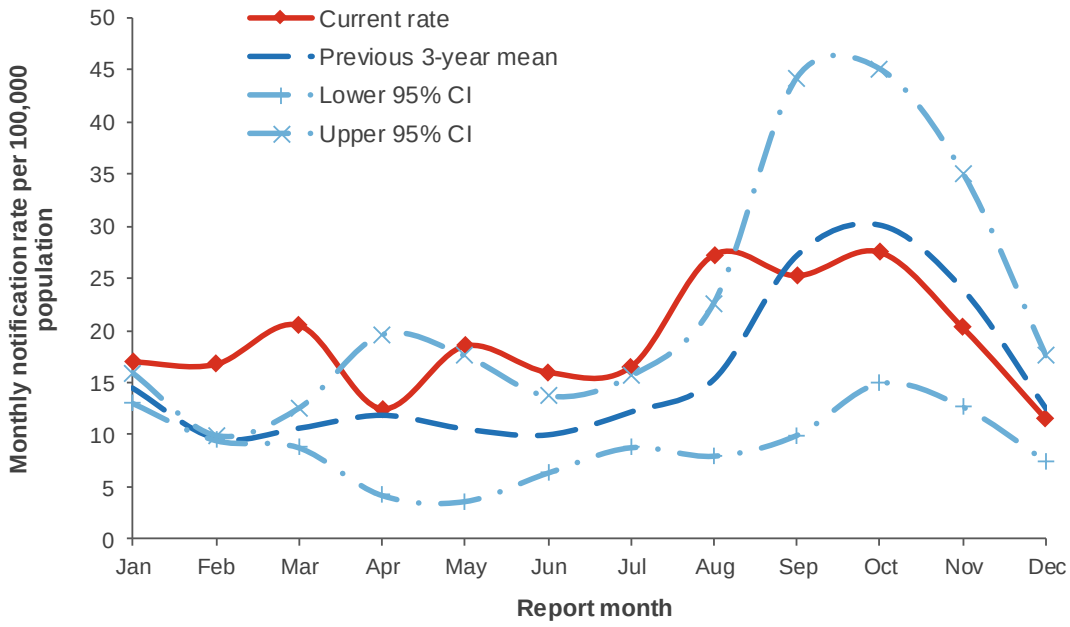
The yersiniosis annual notification rate remained stable between 2008 and 2013 (ranging from 9.3 to 11.9 per 100,000) and increased steadily since then (Figure 49). In 2017, the rate has increased to 19.2 per 100,000 population. The notification rate in 2017 was higher than the previous three-year average (15.7 cases per 100,000).

Figure 49. Yersiniosis notification rate by year, 2008–2017



The number of notified cases of yersiniosis per 100,000 population by month for 2017 is shown in Figure 50. In 2017, no seasonal trend in monthly notification rate was apparent, apart from slightly higher rates in spring (August to October). In previous years (2014–2016) increased rates were observed in October and November. The monthly number of notifications in 2017 ranged from 46 notifications (December) to 110 notifications (October).

Figure 50. Yersiniosis monthly rate (annualised), 2017



In 2017, the yersiniosis notification and hospitalisation rates were similar for males and females (Table 66). In 2016, the notification and hospitalisation rates were slightly higher for females than for males.

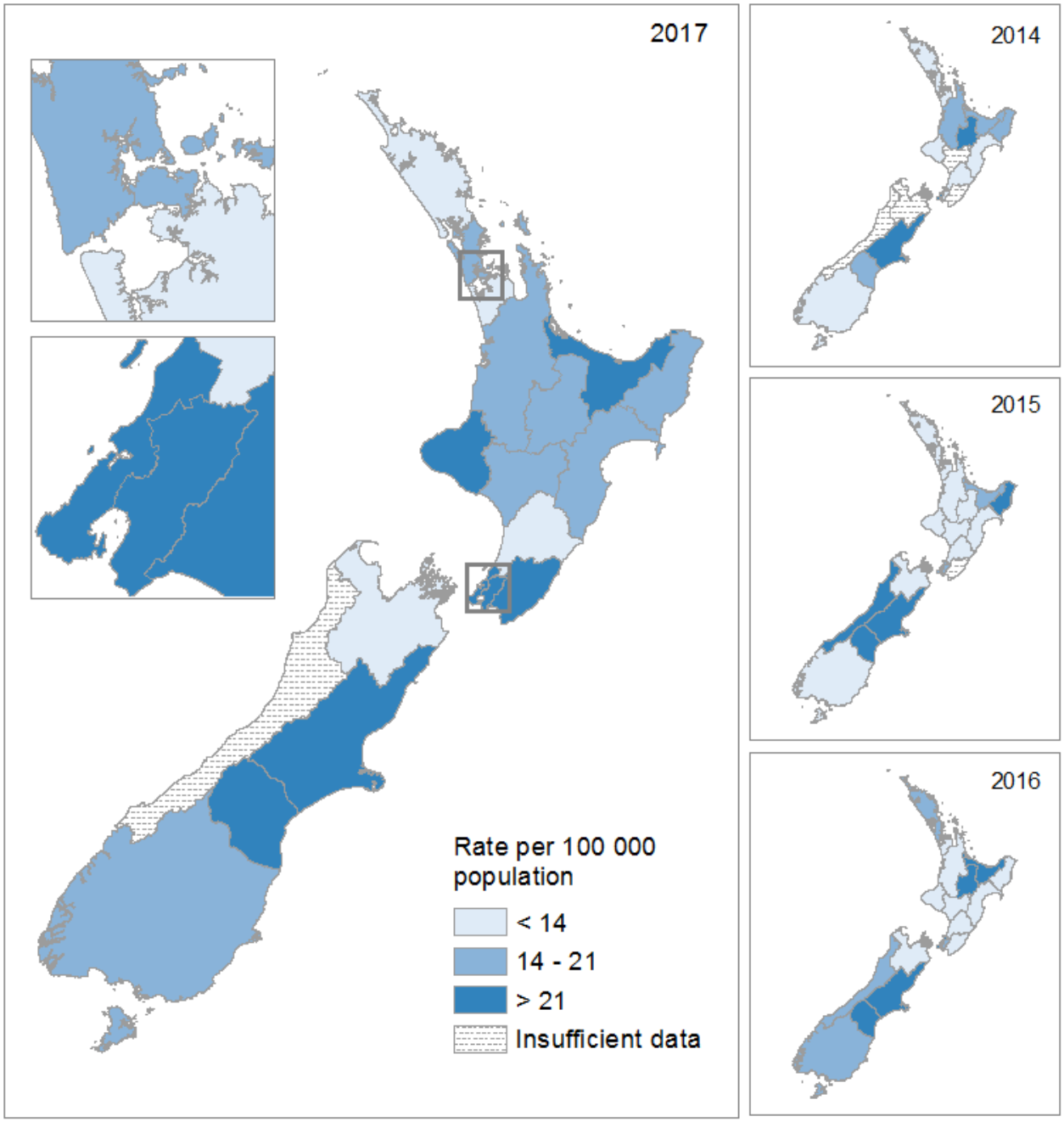
Table 66. Yersiniosis cases by sex, 2017

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	468	19.8	41	1.7
Female	450	18.5	46	1.9
Total	**918**	**19.2**	**87**	**1.8**

[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 2017, the highest rates were reported for the DHBs Wairarapa (33.7 per 100,000 population, 15 cases), Canterbury (28.5 per 100,000 population, 157 cases) and South Canterbury (28.5 per 100,000, 17 cases), Capital & Coast (26.9 per 100,000 population, 84 cases), and Hutt Valley (25.7 per 100,000 population, 38 cases). Canterbury DHB had consistently high yersiniosis notification rates between 2014 and 2017 compared to the rest of the country. Note that rates were not calculated for one DHB where there were insufficient (less than five) cases notified in 2017.

Figure 51. Geographic distribution of yersiniosis notifications, 2014–2017



In 2017, the highest yersiniosis notification rates were for the less than 1 year (102.4 per 100,000 population, 62 cases) and 1 to 4 years (57.5 per 100,000, 141 cases) age groups. The less than 1 year-age group presented with a higher rate compared to 2016 (77.0 per 100,000 population, 46 cases). Notification rates for the under five year olds were more than twice the rates for any other age group (Table 67). The highest hospitalisation rate was reported for the under 1 year age group (24.8 per 100,000 population, 15 cases).

Table 67. Yersiniosis cases by age group, 2017

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	62	102.4	15	24.8
1 to 4	141	57.5	5	2.0
5 to 9	33	10.1	1	-
10 to 14	38	12.6	3	-
15 to 19	32	10.1	3	-
20 to 29	118	16.4	7	1.0
30 to 39	103	17.1	6	1.0
40 to 49	96	15.5	9	1.5
50 to 59	111	17.9	7	1.1
60 to 69	102	20.4	13	2.6
70+	82	16.8	18	3.7
Total	**918**	**19.2**	**87**	**1.8**

[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 2017, 7.4% (95% CI 5.4–10.0%) 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 2017. The resultant distribution has a mean of 68 cases (95% CI 44–97%).

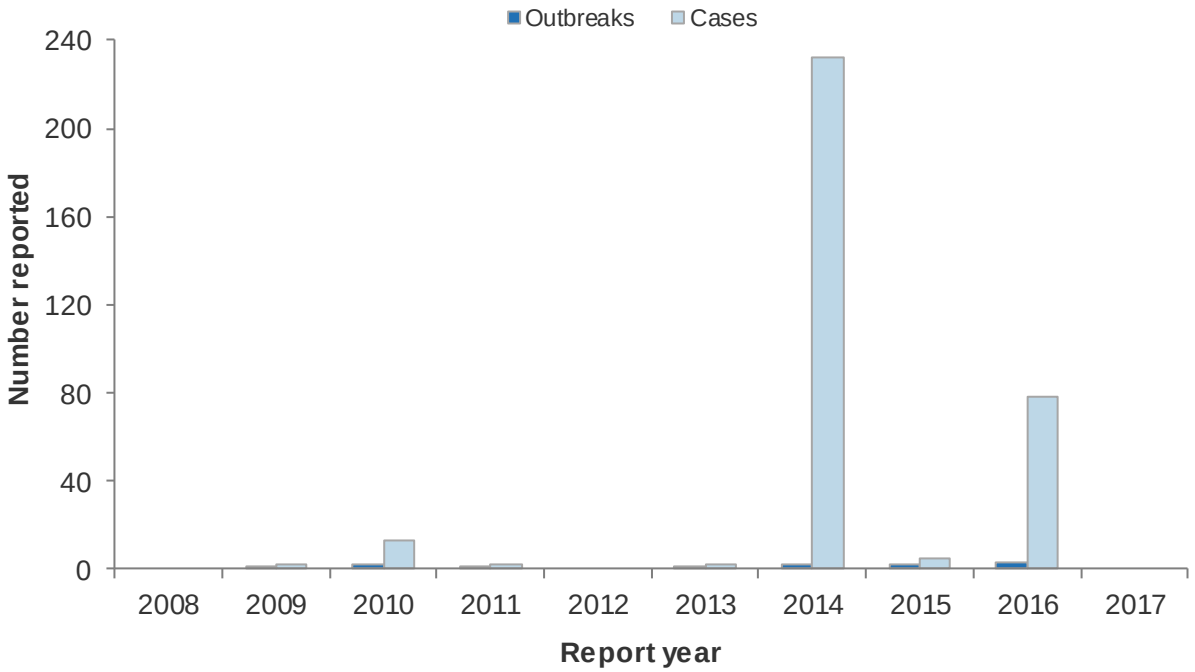
If data from the last four years are considered, the estimated proportion of cases travelling overseas within the incubation period of the organism was 8.4% (95% CI 7.2–9.8%).

Outbreaks reported as caused by *Yersinia* spp.

During 2017, there were no *Yersinia* spp. outbreaks reported 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.

Between 2008 and 2017 very few foodborne *Yersinia* spp. outbreaks were reported in EpiSurv (two 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, 2007–2017



Yersinia types commonly reported

In 2017, clinical laboratories submitted 919 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 90.8% of these isolates. The remaining 84 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. Between 2013 and 2017, 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. An increase in the percentage of cases being reported with *Y. enterocolitica* biotypes 2/3 and a decrease in the percentage of reported cases with *Y. enterocolitica* biotype 4 was observed in the years 2013 to 2017.

These numbers need to be interpreted with some caution as

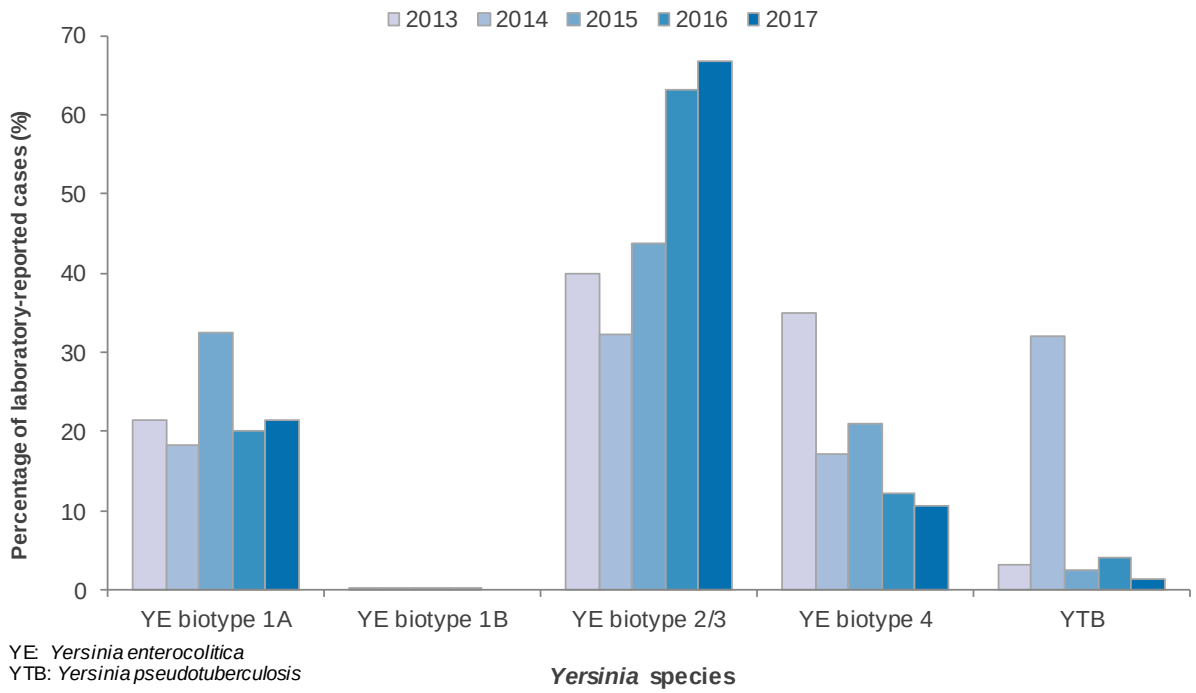
a) not all clinical laboratories forward isolates to ERL for confirmation and biotyping,
b) the number of isolates forwarded for confirmation and typing, as a percentage of all notifications, has changed during this period and
c) successful isolation and identification of *Yersinia* spp. is influenced by the methods used by laboratories.

Table 68. Notifiable *Yersinia* spp. identified by the Enteric Reference Laboratory, 2013–2017

Species	2013	2014	2015	2016	2017
Yersinia enterocolitica	**405**	**384**	**521**	**748**	**822**
biotype 1A	90	103	173	157	178
biotype 1B	1	1	1	1	0
biotype 2/3[a]	167	182	232	493	556
biotype 4	146	97	111	96	88
biotype not identified	1	1	4	1	0
Yersinia pseudotuberculosis	**13**	**181**	**13**	**32**	**12**
Total	**418**	**565**	**534**	**780**	**834**

[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 [41]. 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, 2013–2017



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Yersinia spp. were detected in composite faecal samples from farmed red deer (*Cervus elaphus, n* = 42) in Canterbury and Southland [17]. Five of the composites were positive for *Y. enterocolitica* and one was positive for *Y. pseudotuberculosis*.

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 2017, 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, risk factors are not reported.

Further information about notifiable diseases can be found in the *Notifiable Diseases in New Zealand: Annual Report 2017 [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 2017 [42].

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

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.

MPI project reports and other publications

MPI 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 MPI 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 MPI are the experts in this area and the regulatory developments summarised in this report were confirmed with MPI.

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 22 February 2018. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 16 April 2018. 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 2017 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2018, the New Zealand population was estimated to be 4,793,150. The mid-year population estimate for 2013 used in the analysis of trends was updated in the 2014 report, following the release of the 2013 census data. This report uses 4,442,100 for the 2013 mid-year population estimate, compared to 4,471,040 used in 2013 report. 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 (2014−2016).

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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, 2016–2017

Disease	2016		2017		Change [b,c]
	Cases	Rates	Cases	Rates	
Campylobacteriosis	7456	158.9	6482	135.2	←
Cryptosporidiosis	1062	22.6	1192	24.9	➔
Gastroenteritis[a]	513	10.9	325	6.8	←
Giardiasis	1616	34.4	1648	34.4	→
Hepatitis A	35	0.7	58	1.2	➔
Listeriosis	36	0.8	21	0.4	←
Salmonellosis	1091	23.2	1119	23.3	→
Shigellosis	174	3.7	245	5.1	➔
VTEC/STEC infection	418	8.9	547	11.4	➔
Yersiniosis	858	18.3	918	19.2	→

[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, 1997–2017

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

Disease	ICD 10 Codes	2015		2016		2017	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	574	117	608	124	576	136
Cryptosporidiosis	A07.2	22	9	39	11	46	21
Giardiasis	A07.1	34	21	29	22	37	32
Hepatitis A	B15	27	39	19	65	40	41
Listeriosis	A32	19	14	21	22	6	12
Salmonellosis	A02	148	33	159	53	174	40
Shigellosis	A03	10	10	21	10	34	12
VTEC/STEC infection	A04.3	14	6	10	6	11	9
Yersiniosis	A04.6	38	24	41	26	53	34

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, 2017

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	526	74.1	141	48.0	346	62.8	63	117.7	5035	158.1	6482	135.2
Cryptosporidiosis	137	19.3	46	15.6	47	8.5	12	22.4	897	28.2	1192	24.9
Gastroenteritis[c]	36	5.1	10	3.4	23	4.2	2	-	228	7.2	325	6.8
Giardiasis	130	18.3	28	9.5	98	17.8	33	61.7	1278	40.1	1648	34.4
Hepatitis A	12	1.7	20	6.8	12	2.2	1	-	11	0.3	58	1.2
Listeriosis	5	0.7	3	-	1	-	0	-	11	0.3	21	0.4
Salmonellosis	111	15.6	49	16.7	91	16.5	13	24.3	825	25.9	1119	23.3
Shigellosis	14	2.0	79	26.9	24	4.4	5	9.3	118	3.7	245	5.4
VTEC/STEC infection	70	9.9	17	5.8	28	5.1	12	22.4	400	12.6	547	11.4
Yersiniosis	101	14.2	33	11.2	164	29.7	18	33.6	572	18.0	918	19.2

[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 2017 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, 2017

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	3586	151.9	2896	119.0	6482	135.2
Cryptosporidiosis	561	23.8	631	25.9	1192	24.9
Gastroenteritis[b]	149	6.3	174	7.2	325	6.8
Giardiasis	847	35.9	801	32.9	1648	34.4
Hepatitis A	29	1.2	29	1.2	58	1.2
Listeriosis[c]	11	0.5	10	0.4	21	0.4
Salmonellosis	597	25.3	521	21.4	1119	23.3
Shigellosis	135	5.7	110	4.5	245	5.1
VTEC/STEC infection	261	11.1	286	11.8	547	11.4
Yersiniosis	468	19.8	450	18.5	918	19.2

[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 four perinatal cases.

Table 74. Number of cases and rates of selected notifiable diseases per 100,000 population by age group, 2017

	<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	146	241.0	633	257.9	320	98.1	243	80.6	380	120.1	979	136.4	682	113.5	672	108.7	856	138.3	772	154.4	796	163.3	6482	135.2
Cryptosporidiosis	20	33.0	319	130.0	149	45.7	70	23.2	71	22.4	215	30.0	146	24.3	84	13.6	58	9.4	39	7.8	21	4.3	1192	24.9
Gastroenteritis	23	38.0	37	15.1	11	3.4	7	2.3	14	4.4	36	5.0	45	7.5	42	6.8	39	6.3	24	4.8	40	8.2	325	6.8
Giardiasis	22	36.3	270	110	104	31.9	47	15.6	44	13.9	209	29.1	371	61.8	204	33.0	175	28.3	145	29.0	57	11.7	1648	34.4
Hepatitis A	0	-	5	2.0	4	-	4	-	10	3.2	13	1.8	11	1.8	5	0.8	1	-	3	-	2	-	58	1.2
Listeriosis	1	-	0	-	0	-	0	-	0	-	0	-	1	-	1	-	3	-	5	1.0	10	2.1	21	0.4
Salmonellosis	69	113.9	161	65.6	53	16.2	42	13.9	54	17.1	165	23.0	119	19.8	106	17.1	156	25.2	115	23.0	79	16.2	1119	23.3
Shigellosis	1	-	28	11.4	13	4.0	4		15	4.7	46	6.4	32	5.3	31	5.0	33	5.3	22	4.4	20	4.1	245	5.1
VTEC/STEC infection	36	59.4	120	48.9	31	9.5	28	9.3	23	7.3	59	8.2	44	7.3	36	5.8	47	7.6	48	9.6	75	15.4	547	11.4
Yersiniosis	62	102.4	141	57.5	33	10.1	38	12.6	32	10.1	118	16.4	103	17.1	96	15.5	111	17.9	102	20.4	82	16.8	918	19.2

[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 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, 2017

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	253	766	532	467	562	158	228	53	226	270	92	270	151	347	79	212	61	864	147	744	6482
Cryptosporidiosis	53	108	85	140	120	20	33	26	25	20	18	59	7	35	20	83	6	150	37	147	1192
Gastroenteritis[a]	17	23	50	20	8	9	10	1	0	2	16	38	21	51	1	1	5	36	2	14	325
Giardiasis	79	176	216	189	168	49	105	38	26	65	20	34	27	112	29	47	5	145	25	93	1648
Hepatitis A	3	7	6	21	7	0	0	0	0	0	0	4	0	3	0	0	0	5	0	2	58
Listeriosis	2	1	3	4	1	0	3	0	0	1	1	1	0	0	0	2	0	1	1	0	21
Salmonellosis	59	107	119	71	105	24	37	22	27	29	11	38	22	78	13	30	5	200	22	100	1119
Shigellosis	8	32	60	58	6	4	4	1	2	11	2	3	3	19	0	1	1	15	0	15	245
VTEC/STEC infection	71	78	39	60	35	12	24	1	12	11	5	5	2	10	1	8	2	24	11	136	547
Yersiniosis	22	116	104	69	59	21	56	10	25	34	10	16	38	84	15	8	3	157	17	54	918

[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, 2017

Disease	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	144.2	126.4	101.6	85.4	137.5	145.6	98.3	109.3	191.4	164.7	143.5	152.9	102.1	111.0	177.5	142.5	187.7	156.7	246.6	229.4	135.2
Cryptosporidiosis	30.2	17.8	16.2	25.6	29.4	18.4	14.2	53.6	21.2	12.2	28.1	33.4	4.7	11.2	44.9	55.8	18.5	27.2	62.1	45.3	24.9
Gastroenteritis	9.7	3.8	9.6	3.7	2.0	8.3	4.3	-	-	-	25.0	21.5	14.2	16.3	-	-	15.4	6.5	-	4.3	6.8
Giardiasis	45.0	29.0	41.3	34.6	41.1	45.2	45.3	78.4	22.0	39.7	31.2	19.3	18.3	35.8	65.2	31.6	15.4	26.3	41.9	28.7	34.4
Hepatitis A	-	1.2	1.1	3.8	1.7	-	-	-	-	-	-	-	-	-	-	-	-	0.9	-	-	1.2
Listeriosis	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.4
Salmonellosis	33.6	17.7	22.7	13.0	25.7	22.1	16.0	45.4	22.9	17.7	17.2	21.5	14.9	24.9	29.2	20.2	15.4	36.3	36.9	30.8	23.3
Shigellosis	4.6	5.3	11.5	10.6	1.5	-	-	-	-	6.7	-	-	-	6.1	-	-	-	2.7	-	4.6	5.1
VTEC/STEC infection	40.5	12.9	7.4	11.0	8.6	11.1	10.3	-	10.2	6.7	7.8	2.8	-	3.2	-	5.4	-	4.4	18.5	41.9	11.4
Yersiniosis	12.5	19.1	19.9	12.6	14.4	19.4	24.1	20.6	21.2	20.7	15.6	9.1	25.7	26.9	33.7	5.4	-	28.5	28.5	16.7	19.2

[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
VTEC/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, VTEC/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 VTEC/STEC infection confirmed in New Zealand was reported in October 1993 [43]. Note: cell is blank where data are unavailable.

Table 78. Number of cases of selected notifiable diseases by year, 2003–2017

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

[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 (2017)	Australia[a] (2017)	USA[b] (2017)	Canada[d] (2015)	UK (2016)	EU Total (2016)	Other high
Campylobacteriosis	135.2	110.3	19.1	25.3	90.2[e]	66.3[e]	228.2 (Czech Republic)[e] 140.5 (Slovakia)[e]
Cryptosporidiosis	24.9	19.4	3.7	2.4	9.1[f]	3.1[f]	9.4 (Ireland)[f]
Giardiasis	34.4	NN	6.4[c]	10.4	7.0[f]	5.3[f]	17.3 (Bulgaria)[f] 15.1 (Sweden)[f]
Hepatitis A	1.2	0.9	0.6[c]	0.5	0.5[f]	3.0[f]	33.3 (Romania)[f] 15.7 (Hungary)[f]
Listeriosis	0.4	0.3	0.3	0.40	0.31[e]	0.47[e]	1.22 (Finland)[e] 0.92 (Belgium)[e]
Salmonellosis	23.3	67.9	16.0	21.6	15.1[e]	20.4[e]	110.0 (Czech Republic)[e] 97.7 (Slovakia)[e]
Shigellosis	5.1	7.2	4.3	2.5	3.4[f]	1.7[f]	5.7 (Bulgaria)[f] 3.5 (Slovakia)[f]
VTEC/STEC infection	11.4	2.0	4.2	1.8	2.1[e]	1.8[e]	15.6 (Ireland)[e] 6.5 (Sweden)[e]
Yersiniosis	19.2	NN	1.0	NN	0.1[e]	1.8[e]	7.4 (Finland)[e] 5.8 (Czech Republic)[e]

NN: Not notifiable

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

[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 2016 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 2016 http://onlinelibrary.wiley.com/doi/10.2903/j.efsa.2017.5077/epdf

[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 2015 year. At the time of publication of the current report the 2015 ECDC report on hepatitis A had not been published and figures here relate to the 2014 year).

Table 80. Foodborne outbreaks and associated cases by pathogen/condition, 2017

Pathogen/Condition	Outbreaks (n = 61)[d]		Cases (n = 719)[d]	
	No.	%[a]	No.	%[b]
Norovirus	17	27.4	308	42.4
Salmonella	4	6.5	15	2.1
Campylobacter	4	6.5	19	2.6
Shigella	3	4.8	17	2.3
Ciguatera fish poisoning	2	3.2	31	4.3
Staphylococcus	2	3.2	12	1.7
Hepatitis A	2	3.2	8	1.1
Histamine (scombroid) fish poisoning	2	3.2	7	1.0
VTEC/STEC infection	1	1.6	157	21.6
Vibrio fluvialis	1	1.6	27	3.7
Giardia	1	1.6	3	0.4
Neurotoxin	1	1.6	3	0.4
Pathogen not identified[c]	19	30.6	102	14.0

[a] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (61). 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 (719).

[c] All enteric outbreaks with no pathogen identified in 2017 were recorded as gastroenteritis.

[d] Two agents were reported in one foodborne outbreaks with 27 associated cases, therefore percentage totals add to more than 100%.

Table 81. Foodborne outbreaks and associated cases by exposure setting, 2017

Exposure setting	Outbreaks (n = 61)[c]		Cases (n = 719)[c]	
	No.	%[a]	No.	%[b]
Commercial food operators	**32**	**52.5**	**238**	**33.1**
Restaurant/café/bakery	19	31.1	150	20.9
Fast food outlet	4	6.6	12	1.7
Takeaway	3	4.9	6	0.8
Other food outlet	3	4.9	14	1.9
Supermarket/delicatessen	3	4.9	15	2.1
Caterers	2	3.3	52	7.2
Institutions	**14**	**23.0**	**310**	**43.1**
Hotel/motel	3	4.9	56	7.8
Long-term care facility	2	3.3	77	10.7
School	2	3.3	123	17.1
Marae	2	3.3	16	2.2
Childcare centre	1	1.6	7	1.0
Camp	1	1.6	7	1.0
Hospital (acute care)	1	1.6	5	0.7
Hostel/boarding house	1	1.6	5	0.7
Other institution	1	1.6	14	1.9
Other	**16**	**26.2**	**248**	**34.5**
Private home	7	11.5	32	4.5
Community gathering	2	3.3	30	4.2
Cruiseship	1	1.6	157	21.8
Workplace	1	1.6	8	1.1
Other setting[d]	5	8.2	21	2.9
Unknown exposure setting	**2**	**3.3**	**10**	**1.4**

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (61). 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 (719).

[c] Five outbreaks had two or more exposure settings (98 cases).

[d] Three outbreaks with other setting had an overseas exposure setting.

Table 82. Foodborne outbreaks and associated cases by preparation setting, 2017

Preparation setting	Outbreaks (n = 61)[c]		Cases (n = 719)	
	No.	%[a]	No.	%[b]
Commercial food operators	**31**	**50.8**	**241**	**33.5**
Restaurant/café/bakery	19	31.1	150	20.9
Other food outlet	3	4.9	34	4.7
Takeaway	3	4.9	8	1.1
Caterers	2	3.3	35	4.9
Fast food outlet	2	3.3	5	0.7
Supermarket/delicatessen	2	3.3	9	1.3
Institutions	**10**	**16.4**	**246**	**34.2**
Long term care facility	2	3.3	77	10.7
Marae	2	3.3	16	2.2
School	2	3.3	104	14.5
Hotel/motel	1	1.6	23	3.2
Hospital (acute care)	1	1.6	5	0.7
Childcare centre	1	1.6	7	1.0
Other institution	1	1.6	14	1.9
Other	**13**	**21.3**	**249**	**34.6**
Home	8	13.1	55	7.6
Cruise ship	1	1.6	157	21.8
Community, church, sports gathering	1	1.6	5	0.7
Other setting	1	1.6	1	0.1
Overseas manufacturer	2	3.3	31	4.3
Unknown exposure setting	**9**	**14.8**	**41**	**5.7**

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (61). 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 (719).

[C] Two outbreaks had two or more preparation settings (58 cases).

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INSTITUTE OF ENVIRONMENTAL
SCIENCE AND RESEARCH LIMITED

Kenepuru Science Centre
34 Kenepuru Drive, Kenepuru, Porirua 5022
PO Box 50348, Porirua 5240
New Zealand
T: +64 4 914 0700 **F:** +64 4 914 0770

Mt Albert Science Centre
120 Mt Albert Road, Sandringham, Auckland 1025
Private Bag 92021, Auckland 1142
New Zealand
T: +64 9 815 3670 **F:** +64 9 849 6046

NCBID – Wallaceville
66 Ward Street, Wallaceville, Upper Hutt 5018
PO Box 40158, Upper Hutt 5140
New Zealand
T: +64 4 529 0600 **F:** +64 4 529 0601

Christchurch Science Centre
27 Creyke Road, Ilam, Christchurch 8041
PO Box 29181, Christchurch 8540
New Zealand
T: +64 3 351 6019 **F:** +64 3 351 0010

www.esr.cri.nz