Ministry for Primary Industries
Manatū Ahu Matua

Foodborne Disease in New Zealand 2016

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Prepared for the Ministry for Primary Industries
By Isabelle Pattis, Liza Lopez, Peter Cressey, Beverley Horn and Rebekah Roos

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Growing and Protecting New Zealand

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Publications Logistics Officer
Ministry for Primary Industries
PO Box 2526
WELLINGTON 6140

Email: brand@mpi.govt.nz
Telephone: 0800 00 83 33
Facsimile: 04-894 0300

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Scientific Interpretative Summary

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

Annual report concerning foodborne disease in New Zealand 2016

ESR Report FW17008

Foodborne illness is important to New Zealand and to MPI as the gatekeeper for New Zealand's food safety system, protecting the health and wellbeing of consumers here and overseas. Human health surveillance and its relationship to foodborne illness determine the strategic direction that MPI takes in relation to focus on food safety and the drive to reduce foodborne illness in the New Zealand population.

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

Campylobacter remains our top priority foodborne pathogen of concern and MPI 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 can be viewed in the section titled **Reporting against Targets** (Table 4 and Figure1).

Other potentially foodborne pathogens such as the shiga-toxigenic *Escherichia coli* (STEC) in relation to raw drinking milk, and *Yersinia* species in relation to fresh produce, continue to be watched closely but often available information shows weak association with food.

It is important to note that there is a gradual and continuing shift towards molecular methodology by laboratories in New Zealand and this will impact on results seen in the foodborne illness statistics, such as for VTEC/STEC. Further follow up with laboratories introducing methodology changes will be needed to determine if and how these changes affect the human case notification rates and trends recorded for specific pathogens.

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2016

Prepared for Ministry for Primary Industries under
Project MRP/16/02 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2016,
as part of an overall contract for scientific services

by

Isabelle Pattis
Liza Lopez
Peter Cressey
Beverley Horn
Rebekah Roos

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Client Report FW17008

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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 2016 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 appendix 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 medical 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:
    - Reported risk factors: for a proportion of the notified cases, supplemental information is obtained by public health units (PHUs) on risk factors. This information should be interpreted with some caution as it is self-reported by cases, no external validation of this information is undertaken, and often the cases will report several potentially important risk factors. The quality of information from notifiable disease surveillance as an indication for foodborne disease transmission has been reviewed in more detail [2].
    - 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 [3], as presented in relevant report sections. These are not fixed values; future changes to the New Zealand food chain may require the values to be amended.

* Note that water is not considered a food.

- 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 [3] and five sets of published country-specific estimates are given in Table 1, for the USA [4], Canada [5], Australia [6, 7], England and Wales [8] and the Netherlands [9]. In addition, a WHO project to estimate the global burden of foodborne diseases derived estimates for 14 international regions [10, 11]. The estimates for New Zealand, Australia, Canada, the Netherlands and the international WHO estimates are based on expert opinion, the estimates for England and Wales are based on outbreak analysis, while the US estimates are based on data from surveillance, risk factor studies and a literature review. 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 2016 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 2016 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 it was considered that a significant proportion would be 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.

Table 2. Potentially foodborne conditions included in the report

Disease	Type	Source(s)	ICD-10 code[a]
Bacillus cereus intoxication	Bacterium	N, O, H	A05.4 Foodborne *Bacillus cereus* intoxication
Campylobacteriosis	Bacterium	N, O, H	A04.5 *Campylobacter* enteritis
Ciguatera fish poisoning	Toxin	N, O, H	T61.0 Toxic effect: Ciguatera fish poisoning
Clostridium perfringens intoxication	Bacterium	N, O, H	A05.2 Foodborne *Clostridium perfringens* [*Clostridium welchii*] intoxication
Cryptosporidiosis	Protozoan	N, O, H	A07.2 Cryptosporidiosis
Giardiasis	Protozoan	N, O, H	A07.1 Giardiasis [lambliasis]
Histamine (scombroid) fish poisoning	Toxin	N, O, H	T61.1 Toxic effect: scombroid fish poisoning
Hepatitis A infection	Virus	N, O, H	B15 Acute hepatitis A
Listeriosis (total and perinatal)	Bacterium	N, O, H, L	A32 Listeriosis
Norovirus infection	Virus	N, O, H, L	A08.1 Acute gastroenteropathy due to Norwalk agent
Salmonellosis	Bacterium	N, O, H, L	A02.0 Salmonella enteritis
Sapovirus infection	Virus	N, O, L	No specific ICD-10 code
Shigellosis	Bacterium	N, O, H, L	A03 Shigellosis
Staphylococcus aureus intoxication	Bacterium	N, O, H	A05.0 Foodborne staphylococcal intoxication
Toxic shellfish poisoning	Toxin	N, O, H	T61.2 Other fish and shellfish poisoning
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].

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 [3]. In the current report these food-attributable proportions have been used to estimate the number of food-associated cases of relevant diseases. The estimated proportion of travel-associated cases from reported risk factors were subtracted from the total cases before application of the food-associated proportion. Travel-associated cases are those where the individual reported being outside New Zealand during the incubation period for the disease.

This report includes both 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

Changes in enteric testing methods and screening criteria have been introduced in some laboratories during 2015. Since 22 June 2015, 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. However, as more laboratories are shifting to molecular methods in 2017 it needs to be determined if and how this affects notification rates and trends. 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 predicted by culture, may be masked by the increased sensitivity of the PCR methodology.

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 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.

For these same DHBs, before June 2015, *Giardia* spp. and *Cryptosporidium* spp. were only screened for in those specimens where parasite screening was requested.

REPORTING

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.

Performance targets

- Campylobacteriosis: 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 2020.

Rationale

The above disease is the most commonly notified, potentially foodborne disease in New Zealand.

Specific targets previously seen for salmonellosis and listeriosis have been removed for 2015 and 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. This has been due to 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 continues to fund active surveillance projects that provide primary information on food attribution such as the advanced attribution study of human C*ampylobacter* 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 [3]. 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.

Campylobacteriosis

Performance target

- Campylobacteriosis: 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 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 2016 is given in Table 4.

Table 4. Estimated proportion and incidence of foodborne campylobacteriosis for 2016

	Cases	Proportion (%)	Rate (per 100,000, mid-year estimated population)
Total notified	7456		158.9
Confirmed very large [a] outbreaks not associated with food	964		
Total corrected for very large outbreaks	6492		138.3
Estimated not related to overseas travel[d]	5875	90.5	125.2
Estimated foodborne transmission	3748	63.8 (44.1-83.2)[b]	80.0 (55.2-104.2)[c]

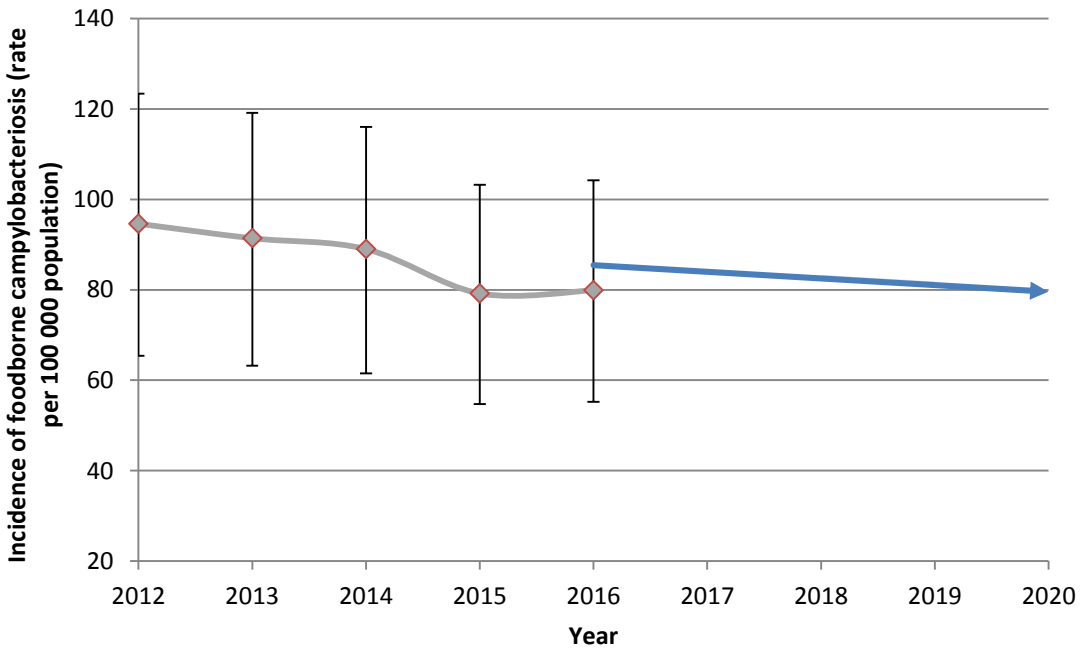
[a] 300 or more cases of campylobacteriosis with a confirmed source that is not categorised as food
[b] Most likely (95th percentile credible interval) estimates of proportion foodborne, from expert consultation
[c] Most likely (95th percentile credible interval) estimates of foodborne rate
[d] Removing very large outbreak data, the estimated percentage of cases relating to overseas travel is 9.5%

Presentation

The trend in relative rates (and ranges) compared with the 2016 to 2020 goal is shown in Figure 1. The estimated foodborne rates for 2012 to 2016 are calculated using the estimates of the proportion foodborne from the expert consultation in 2013.

* 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

Figure 1. Incidence of foodborne campylobacteriosis



The blue arrowed line represents the new target for 2016 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 [3]. Note that these estimates are only available for some of the conditions included in this report;
- statement of estimated foodborne percentage and range for any specific foods provided by the same expert elicitation process;
- information on pathogen typing (principally from data generated by ESR's Enteric Reference Laboratory), 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 2016 by data source

During 2016, one case of *B. cereus* intoxication was reported in EpiSurv. Note that not all cases of *B. cereus* intoxication are necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.4 was used to extract *B. cereus* intoxication hospitalisation data from the Ministry of Health (MoH) National Minimum Dataset (NMDS). Of the two hospital admissions recorded in 2016, one was reported with *B. cereus* intoxication as the primary diagnosis and the other 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 2016, a single outbreak caused by *B. cereus* intoxication was reported in EpiSurv, with seven associated cases (Table 5). This outbreak, involving two groups was associated with a common food service outlet.

Testing by ESR's Public Health Laboratory found *B. cereus* diarrheal toxin in two faecal samples, but no *B. cereus* was detected in the faecal samples. High counts of *C. perfringens* were also found in the faecal samples, but no associated toxin was detected. No food samples were tested.

Table 5. *B. cereus* outbreak reported, 2016

Measure	Foodborne *B. cereus* outbreaks	All *B. cereus* outbreaks
Outbreaks	1	1
Cases	7	7
Hospitalised cases	0	0

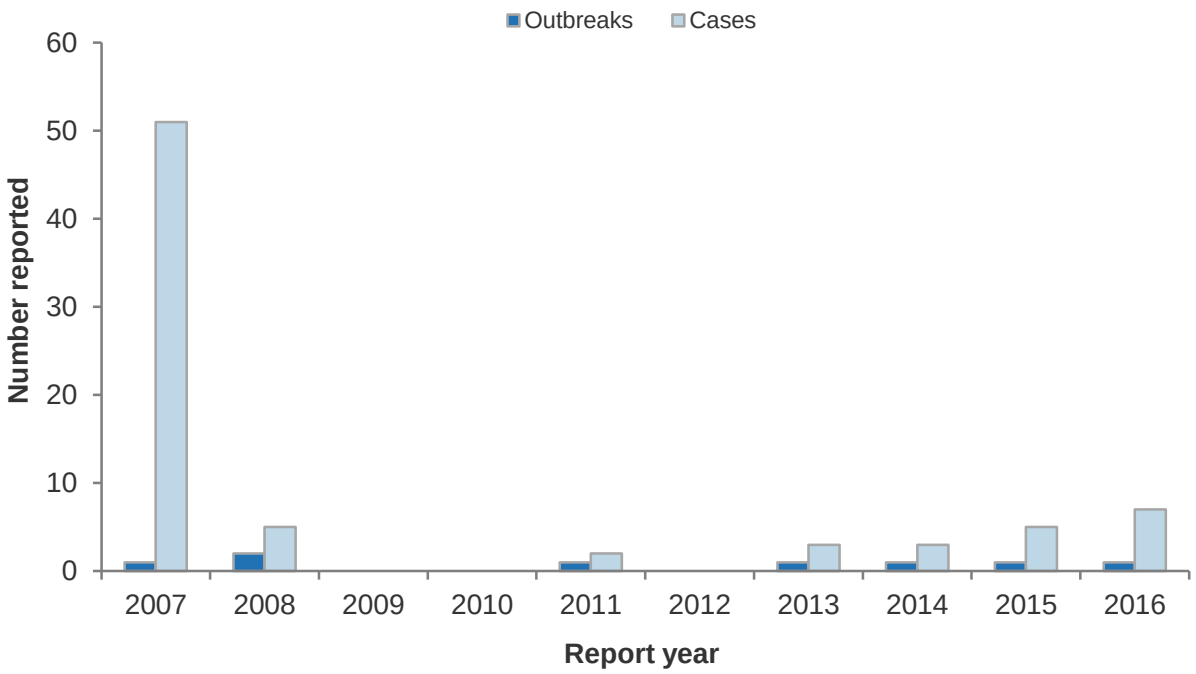
Table 6. Details of foodborne *B. cereus* outbreak, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Regional	Feb	Dosai	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C, 5P

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

Outbreaks of *B. cereus* intoxication are rarely reported, with eight outbreaks reported since 2007 (Figure 2). The largest outbreak, with 51 associated cases, was reported in 2007.

Figure 2. Foodborne *B. cereus* outbreaks and associated cases reported by year, 2007–2016



Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

A Risk Profile was prepared on *B. cereus* in dairy products [15]. The Risk Profile concluded that the most important sources of *B. cereus* in New Zealand dairy products are likely to be soil and faecal contamination of animal teats, and subsequent transfer of bacilli to raw milk during the milking process. Available data indicate that raw milk is the major determinant of the occurrence of *B. cereus* in milk and dairy products, although contribution from biofilms or added ingredients must also be considered. *B. cereus* is most likely to be detected in pasteurised milk but it may be present in most, if not all dairy foods, due to the ability of the organism to form resistant spores.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *B. cereus* and other pathogenic *Bacillus* spp. in ready-to-eat foods [16].

Standard 1.6.1 (Microbiological limits in food) of the Australia New Zealand Food Standards Code was amended in line with Proposal P1039 [17] to remove the limit for *B. cereus* in powdered infant formula products.

An Animal Products Notice: *Raw Milk for Sale to Consumers. Regulated Control Scheme* was published requiring testing for *B. cereus* on request [18].

Campylobacteriosis

NOTE: This section provides data on all notified cases of campylobacteriosis, whatever the cause in 2016, including those associated with the drinking water related outbreak in the Hawke's Bay region (964 cases).

Summary data for campylobacteriosis in 2016 are given in Table 7.

Table 7. Summary of surveillance data for campylobacteriosis, 2016

Parameter	Value in 2016	Source
Number of notified cases	7456	EpiSurv
Notification rate (per 100,000)	158.9	EpiSurv
Hospitalisations (% of notifications)[a]	712 (9.5%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	700 (9.4%)	EpiSurv
Estimated food-related cases (%)[b]	4310 (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 diarrhoea, and often bloody stools.
Laboratory test for diagnosis:	Isolation of *Campylobacter* 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 in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for a range of pathogens, including *Campylobacter*. It is unclear at this stage how laboratory changes have affected the notification rates.

Campylobacteriosis cases reported in 2016 by data source

During 2016, 7456 cases (158.9 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv.

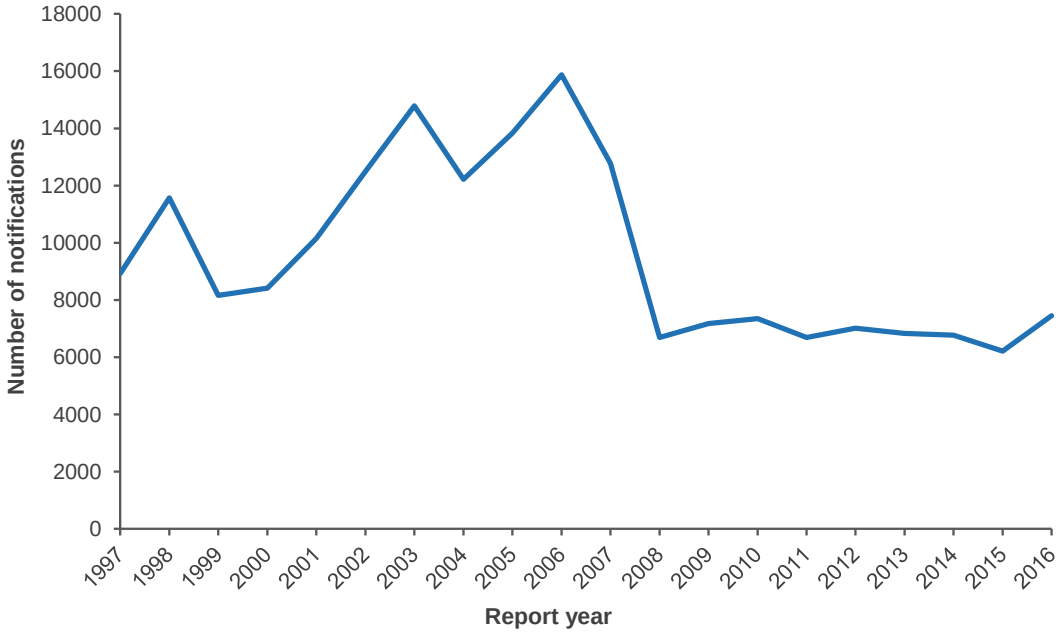
The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the MoH NMDS database. Of the 712 hospital admissions (15.2 admissions per 100,000 population) recorded in 2016, 595 were reported with campylobacteriosis as the principal diagnosis and 117 with campylobacteriosis as another relevant diagnosis.

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

Notifiable disease data

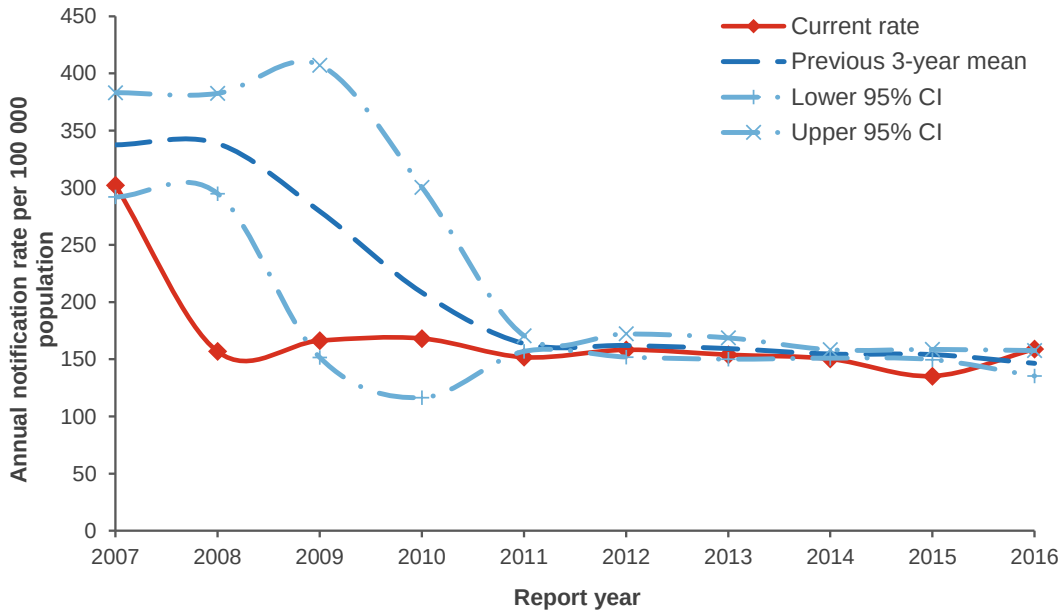
The number of campylobacteriosis notifications reported each year generally increased from 1997, up to the highest number recorded in 2006 (15,873 cases). During 2007 and 2008, there was a significant decrease in the number of cases reported (Figure 3). The number of notifications each year has remained stable from 2008 to 2015 with a statistically significant increase in 2016, due to one outbreak in Hawke's Bay attributed to contaminated drinking water [19].

Figure 3. Campylobacteriosis notifications by year, 1997–2016



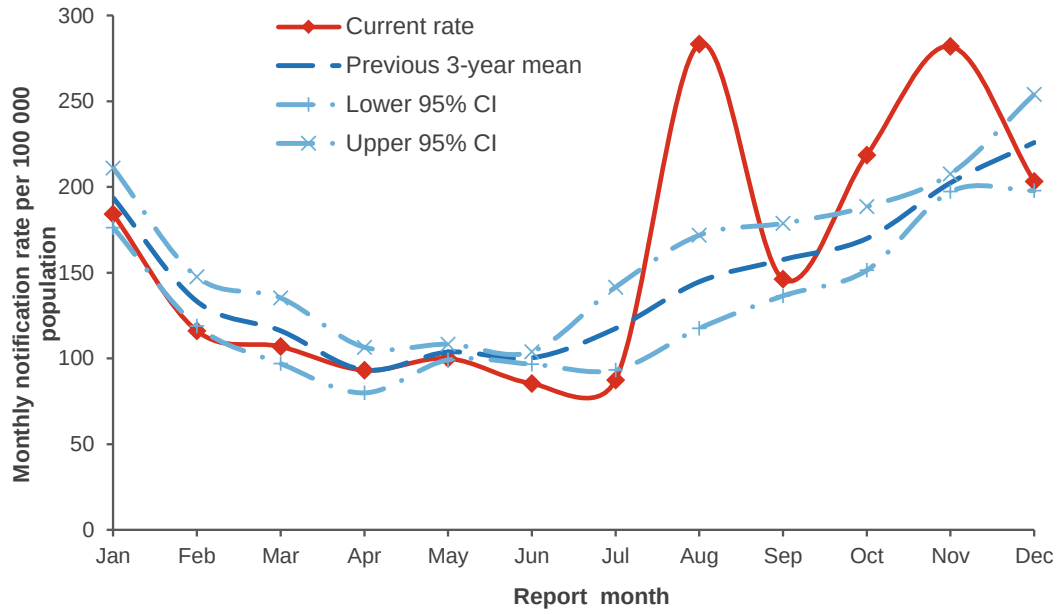
The campylobacteriosis annual rate trend (Figure 4) was very similar to the corresponding annual notification trend; with the notification rate remaining stable between 2008 and 2016. The notification rate was slightly higher in 2016 (158.9 cases per 100,000 population) than the previous three year average (146.5 cases per 100,000), due to one outbreak in Hawke's Bay attributed to contaminated drinking water [19].

Figure 4. Campylobacteriosis notification rate by year, 2007–2016



The number of notified cases of campylobacteriosis per 100,000 population by month for 2016 is shown in Figure 5. The monthly number of notifications in 2016 ranged from 334 notifications (June) to 1108 notifications (August). The lowest notification rates occurred between February and July in 2016. Rates by month in 2016 followed a similar pattern as seen in the previous three years (2013-2015) with the exception of two peaks in August and November caused by an outbreak in Hawke's Bay attributed to contaminated drinking water [19]. 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 5. Campylobacteriosis monthly rate (annualised), 2016



Similar to previous years, the rate of notifications and hospitalisations for campylobacteriosis was higher for males (177.3 notifications and 16.9 admissions per 100,000 population) than for females (141.0 notifications and 13.6 admissions per 100,000 population) in 2016 (Table 8).

Table 8. Campylobacteriosis cases by sex, 2016

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	4093	177.3	389	16.9
Female	3361	141.0	323	13.6
Total[c]	**7456**	**158.9**	**712**	**15.2**

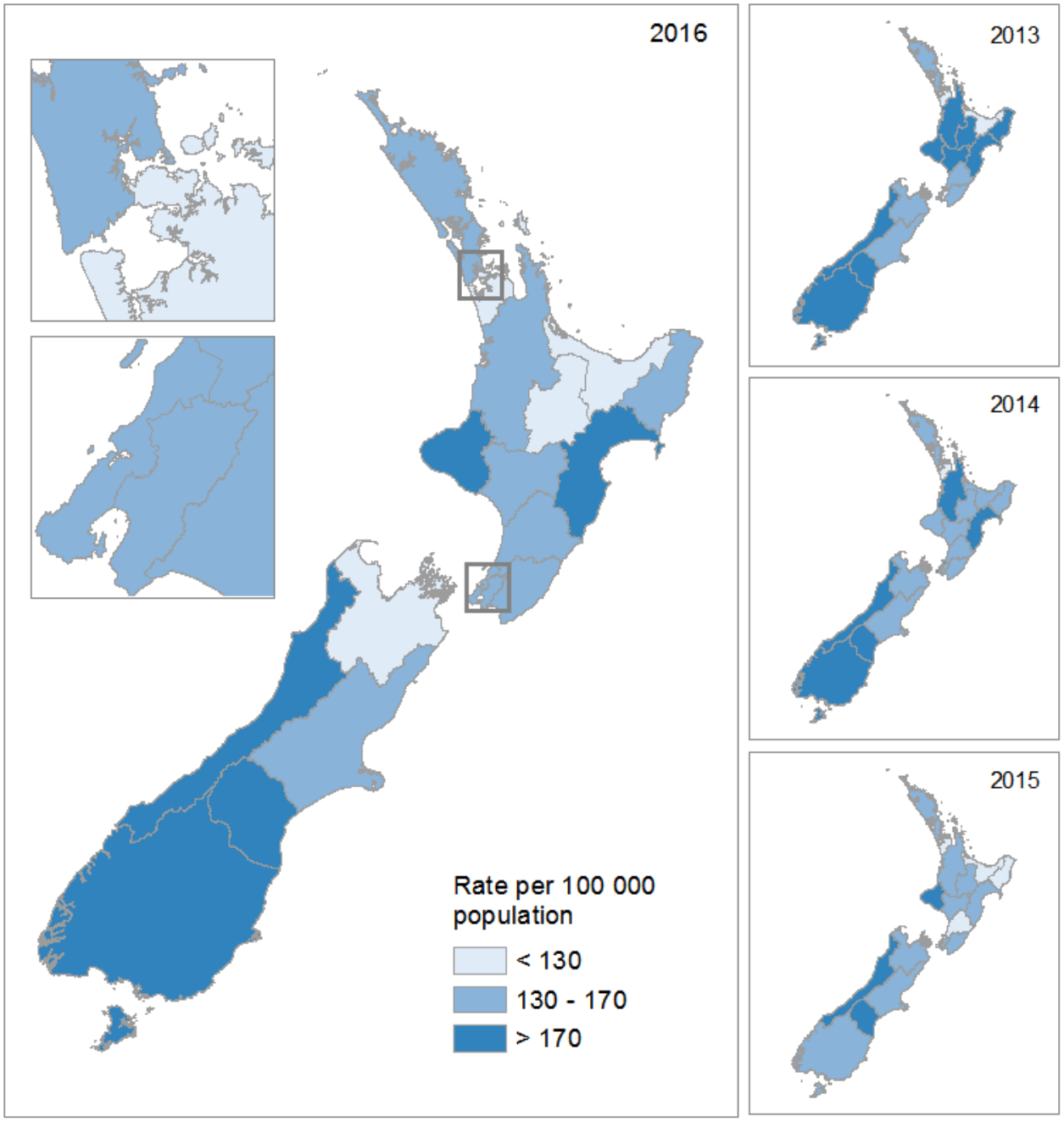
[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

[c] Total includes 2 cases where sex was not reported

Campylobacteriosis rates varied throughout the country in 2016 as shown in Figure 6. The highest DHB rates were in Hawke's Bay (825.9 per 100,000 population, 1333 cases) due to the drinking water related outbreak in August 2016. In the South Island, South Canterbury DHB (253.4 per 100,000 population, 150 cases), the West Coast DHB (178.5 per 100,000 population, 58 cases) and Southern DHB (177.8 per 100,000 population, 567 cases) were higher than other DHBs in the South Island (range 118.2-140.8 per 100,000 population). After Hawke's Bay, Taranaki DHB (202.1 per 100,000, 236 cases) had the highest rate for the North Island. The lowest rate in New Zealand was for Counties-Manukau DHB (94.7 per 100,000, 506 cases).

Figure 6. Geographic distribution of campylobacteriosis notifications, 2013–2016



The highest age-specific notification rates for campylobacteriosis in 2016 were reported for children aged 1 to 4 years (273.6 per 100,000 population, 671 cases) and infants aged less than 1 year (251.5 per 100,000, 149 cases). The highest hospitalisation rate was for the 70 years and over age group (41.9 admissions per 100,000 population), which was noticeably higher than any other age group (Table 9).

Table 9. Campylobacteriosis cases by age group, 2016

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	149	251.5	14	23.6
1 to 4	671	273.6	33	13.5
5 to 9	345	107.1	22	6.8
10 to 14	292	99.2	14	4.8
15 to 19	452	142.0	45	14.1
20 to 29	1083	157.6	96	14.0
30 to 39	766	132.5	60	10.4
40 to 49	795	128.3	74	11.9
50 to 59	964	157.3	72	11.7
60 to 69	876	178.6	87	17.7
70+	1063	228.6	195	41.9
Total	**7456**	**158.9**	**712**	**15.2**

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

[b] per 100,000 of population

The risk factors recorded for campylobacteriosis notifications in 2016 are shown in Table 10. The most common risk factors reported were consumption of untreated water (48.1%), consumption of food from retail premises (46.9%) and contact with farm animals (39.3%).

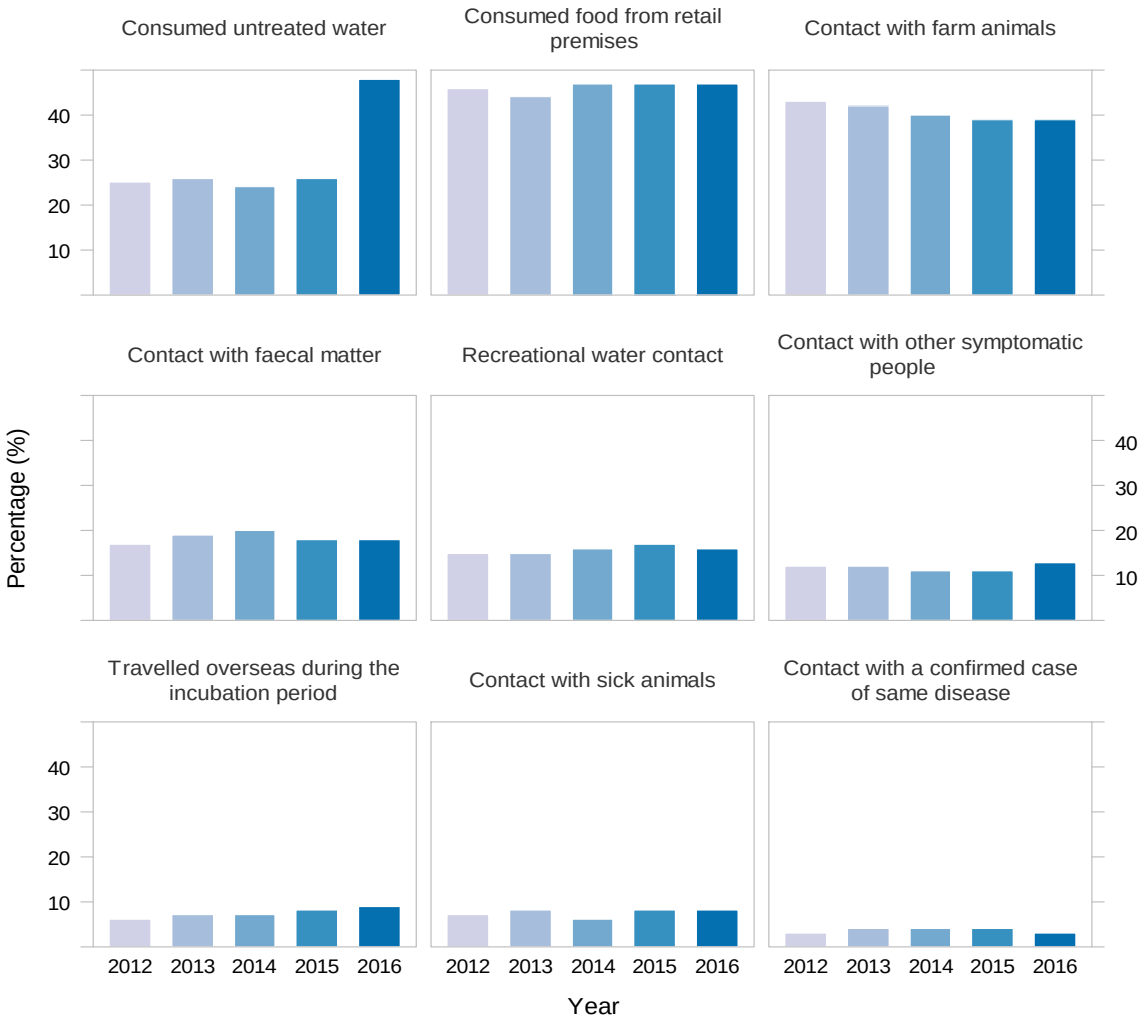
Table 10. Exposure to risk factors reported for campylobacteriosis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Consumed untreated water	1489	1608	4359	48.1
Consumed food from retail premises	1014	1150	5292	46.9
Contact with farm animals	929	1433	5094	39.3
Contact with faecal matter	381	1794	5281	17.5
Recreational water contact	357	1912	5187	15.7
Contact with other symptomatic people	294	1914	5248	13.3
Travelled overseas during the incubation period	282	2728	4446	9.4
Contact with sick animals	155	1906	5395	7.5
Contact with a confirmed case of same disease	49	1609	5798	3.0

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

Between 2012 and 2016, consumption of food from retail premises, contact with farm animals, and consumption of untreated water were consistently the most commonly reported risk factors for campylobacteriosis. The percentages of cases exposed to the reported risk factors were similar in 2016 compared to 2012–2015 with the exception of consumption of untreated water in 2016 (Figure 7). Part of the increase in the percentage of cases reporting consumption of untreated water is due to 898 out of 964 cases of the Hawkes Bay August Outbreak answering yes to this risk factor. Excluding the Hawkes Bay outbreak cases, the percentage of cases answering this risk factor question indicating consumption of untreated water would be 29.1%.

Figure 7. Percentage of cases with exposure to risk factors reported for campylobacteriosis and year, 2012–2016



For cases where information on travel was provided in 2016, 9.4% (95% CI 8.3-10.5%) 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 2016. The resultant distribution has a mean of 698 cases (95% CI 606-797).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 7.9% (95% CI 7.5-8.4%).

Outbreaks reported as caused by *Campylobacter* spp.

In 2016, 8 (53.3%) of the outbreaks caused by *Campylobacter* spp. and 28 (2.8%) of the associated cases were reported as foodborne (Table 11). 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 2.7% (15/561) of all enteric outbreaks and 9.7% (1008/10,378) of all associated cases reported in 2016.

Table 11. *Campylobacter* spp. outbreaks reported, 2016

Measure	Foodborne *Campylobacter* spp. Outbreaks	All *Campylobacter* spp. outbreaks
Outbreaks	8	15
Cases	28	1008
Hospitalised cases	1	41

During 2007 to 2016, excluding 2014, the number of reported foodborne outbreaks of campylobacteriosis has ranged between seven and 16 outbreaks reported each year with between 28 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, 2007–2016

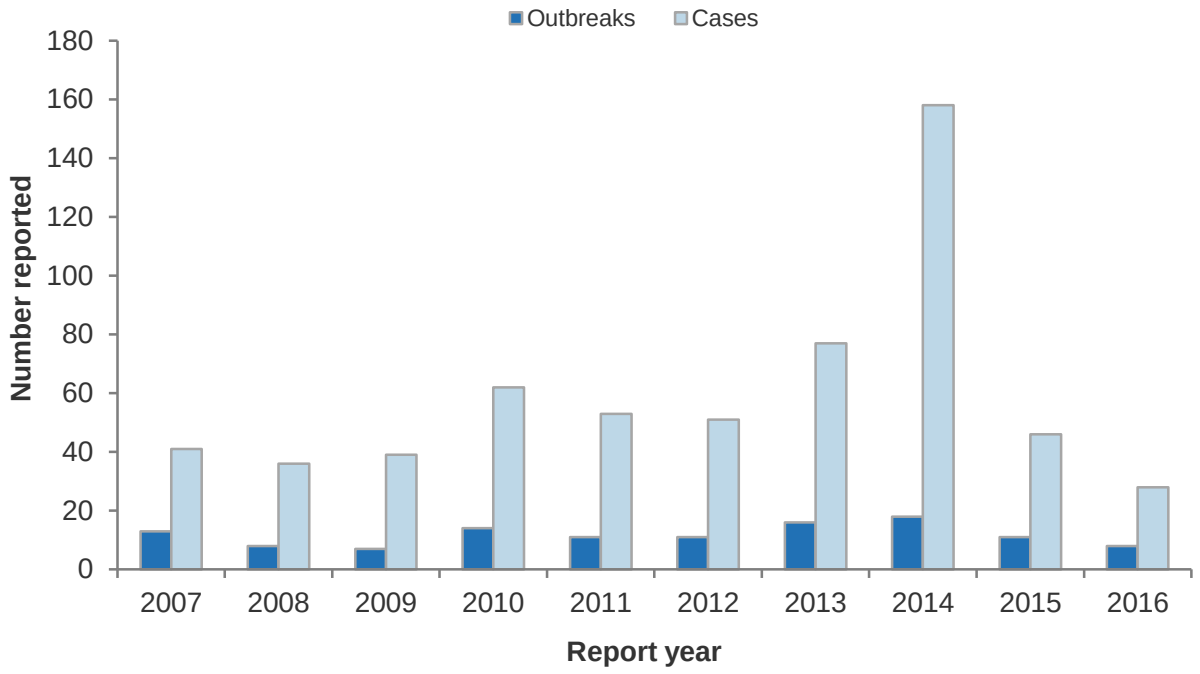


Table 12 contains details of the 8 foodborne outbreaks of campylobacteriosis reported in 2016. In all outbreaks with a suspected food vehicle (Table 12), the evidence for the implicated food was weak.

Table 12. Details of foodborne *Campylobacter* spp. outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Regional	May	Chicken liver pate	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C
MidCentral	May	Raw milk	Other food outlet	Other food outlet	4C
MidCentral	Aug	Raw milk	Other food outlet	Other food outlet	7C
Regional	Sep	Chicken liver pate	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C
PH South	Oct	Raw milk	Farm	Farm	2C
Regional	Dec	Unknown	Long term care facility	Long term care facility	3C
C and PH	Dec	Chicken liver pate	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C
Nelson Marlborough	Dec	Raw milk	Other food outlet	Other food outlet	5C[a]

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

[a] Of the confirmed cases linked to the outbreak, 3 cases had giardiasis and 2 cases campylobacteriosis. Reporting includes total number of cases linked to the outbreak by pathogen.

During the investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory in 2016, culture samples for typing were received from the Regional Public Health December outbreak in Table 12.

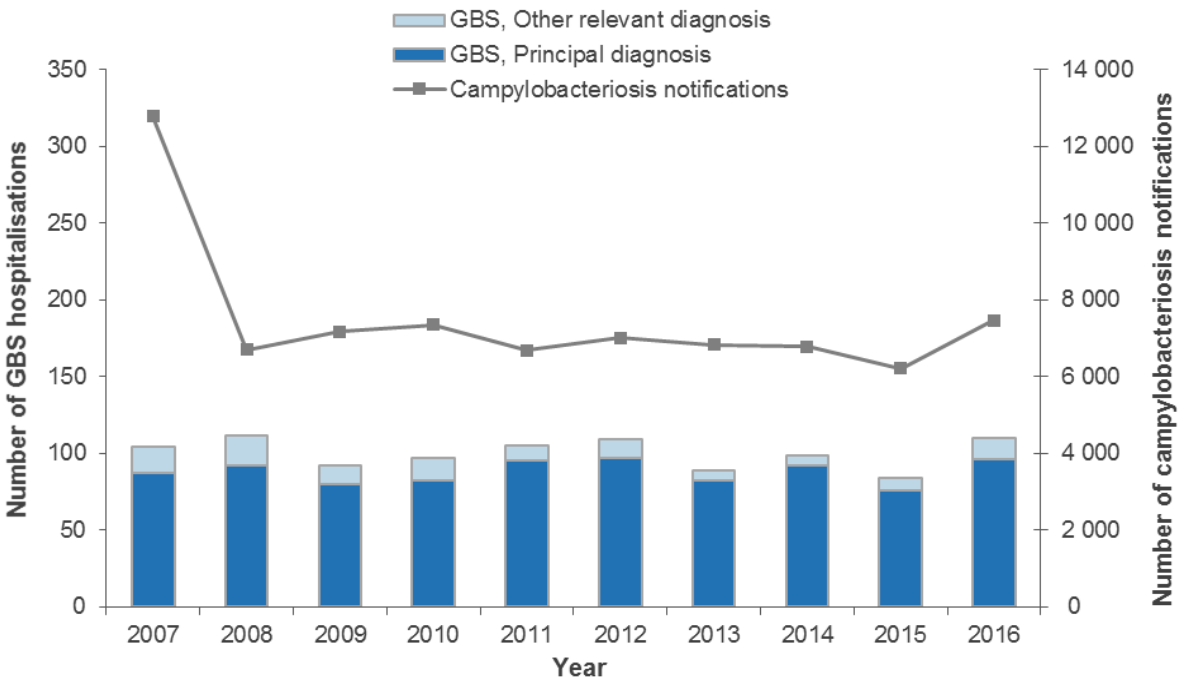
Disease sequelae - Guillain-Barré syndrome

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 2016 were considered, rather than all cases that were hospitalised in 2016. That is, if a GBS cases hospitalised in 2016 had been hospitalised with GBS in a previous year, the 2016 admission was considered to be a readmission, rather than an incident case. There were 110 incident hospitalised cases recorded in 2016 (2.3 admissions per 100,000 population), 96 were reported with GBS as the primary diagnosis and 14 with this condition as another relevant diagnosis.

Between 2007 and 2016, the annual number of incident hospitalised cases (any diagnosis code) for GBS ranged from 84 to 112 (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, 2007–2016



In 2016, the number of incident hospitalised cases due to GBS was similar for males and females (Table 13). There was a marked difference in incident hospitalised GBS case numbers between males and females in 2015 (49 male and 33 female cases), which is consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2016 (Table 8).

Table 13. Guillain-Barré syndrome hospitalised cases by sex, 2016

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	56	2.4
Female	54	2.3
Total	**110**	**2.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2016, the highest rates of incident hospitalisation for GBS were in the 70 years and over age group, followed by the 60 to 69 years age group (Table 14).

Table 14. Guillain-Barré syndrome hospitalised cases by age group, 2016

Age group (years)	Hospitalised cases	
	No.	Rate[b]
<5	3	-
5 to 9	7	2.2
10 to 14	2	-
15 to 19	3	-
20 to 29	11	1.6
30 to 39	10	1.7
40 to 49	11	1.8
50 to 59	14	2.3
60 to 69	25	5.1
70+	24	5.2
Total	**110**	**2.3**

[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

Bayesian Specification and Multiple Imputation methods were compared to predict values for missing data in New Zealand campylobacteriosis notification risk factors [20]. The methods were applied to reporting of notified case travel during the organism incubation period. The estimated proportion of travel-related cases was highest in highly urbanised regions (up to 37% of cases) and lowest in predominantly rural areas (as low as 2% of cases).

A survey of 80 dairy farms, carried out during 2011-2012, detected *C. jejuni* in 0.6% of bulk tank milk samples [21]. Milk quality data such as coliform counts, total bacterial counts, and somatic cell counts were also collected. By treating the total bacterial count as a proxy for faecal contamination of milk and utilising farm and animal level prevalence and shedding rates of *Campylobacter*, a predictive model for the concentration of *Campylobacter* in bulk tank raw milk was developed.

Campylobacter coli isolates from the Manawatu sentinel site were typed by multi-locus sequence typing (MLST) and typing data used to estimate attribution of cases to three main sources (poultry, ruminant, environmental) [22]. Different models gave similar source attribution estimates, with the majority of *C. coli* cases attributed to ruminant (55%) or poultry (38%) sources.

Reports

A further report was published in the ongoing series on source attribution of *C. jejuni* cases in the Manawatu [23]. Reservoir attribution modelling revealed that 45–70% of human cases could be attributed to poultry, with 25–50% attributed to ruminants in calendar year 2015.

EpiSurv data for campylobacteriosis for 2014 were examined to determine if they were suitable for comparison with 2017 data, to decide if there have been any changes in notification or hospitalisation rates for campylobacteriosis following changes to the regulation of raw milk sales [24]. Cases were matched to hospital records and analysis conducted on the association of risk factors (including raw milk) with hospitalisation, length of stay, and death. It was concluded that the 2014 EpiSurv data are not suitable for use as a baseline, primarily due to data quality issues that result in difficulties in classifying cases as exposed to raw milk or not exposed to raw milk, and to missing data resulting in uncertainty and bias. It was also noted that the data did not distinguish between consumption of raw milk purchased from a raw milk supplier and non-commercial consumption of raw milk, such as a dairy farmer drinking from the vat.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *Campylobacter* spp. in ready-to-eat foods and process hygiene criteria for *Campylobacter* spp. in raw chicken meat [16].

Standard 1.6.1 (Microbiological limits in food) of the Australia New Zealand Food Standards Code was amended in line with Proposal P1022 [25], omitting criteria for *Campylobacter* spp. in butter made from unpasteurised milk and/or unpasteurised milk products and raw milk unripened cheeses.

An Animal Products Notice: *Raw Milk for Sale to Consumers. Regulated Control Scheme* was published requiring testing for *Campylobacter* spp. at a standard frequency of once every 10 days, or a reduced frequency of once per calendar month if certain performance criteria are met [18].

A further Animal Products Notice: *Specifications for National Microbiological Database Programme* set specifications relating to the National Microbiological Database (NMD), including for *Campylobacter* spp. in poultry [26].

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 2016 by data source

During 2016, five cases (0.1 per 100,000 population) of ciguatera fish poisoning were reported in EpiSurv. Note that not all cases of ciguatera fish poisoning are necessarily notifiable, only those where there is a suspected common source.

The ICD-10 code T61.0 was used to extract ciguatera fish poisoning hospitalisation data from the MoH NMDS database. Of the eight hospital admissions (0.2 admissions per 100,000 population) recorded in 2016, six were reported with ciguatera fish poisoning as the primary diagnosis and two were reported as another relevant diagnosis. It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified.

Outbreaks reported as caused by ciguatera fish poisoning

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.

During 2016, a single outbreak of ciguatera fish poisoning was reported in EpiSurv, with four associated cases (Table 15). In EpiSurv, this outbreak was weakly linked to consumption of imported eel. No samples were submitted to ESR's Public Health Laboratory. It should be noted that, while the EpiSurv record of this outbreak reported that none of the cases were hospitalised, the outbreak was also reported in a journal paper, which stated that all four cases were hospitalised [27].

Table 15. Ciguatera fish poisoning outbreaks reported, 2016

Measure	Foodborne ciguatera fish poisoning outbreaks
Outbreaks	1
Cases	4
Hospitalised cases[a]	0

[a] Source: EpiSurv

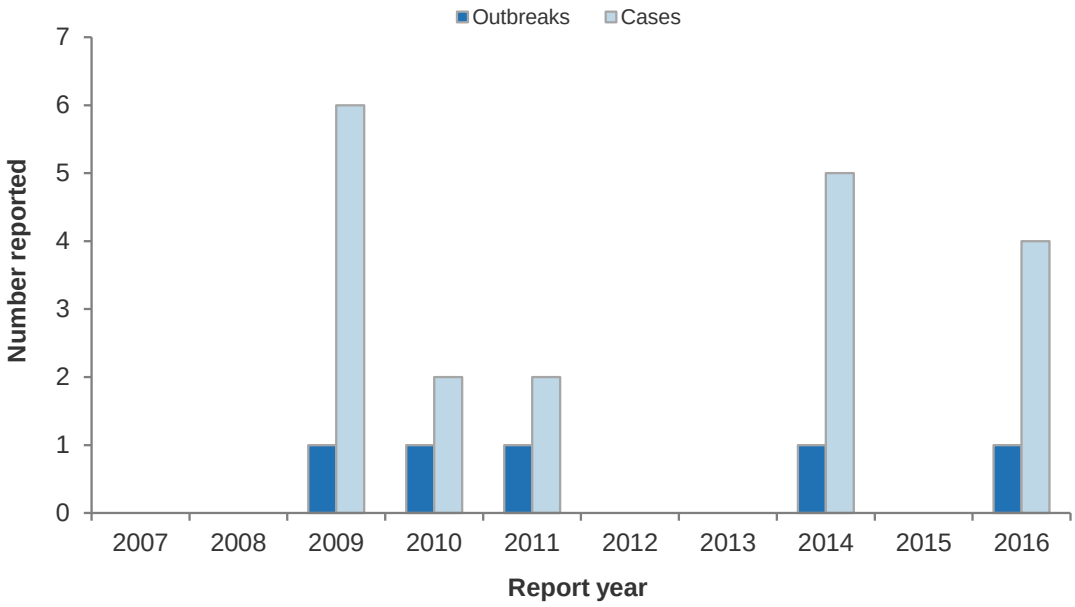
Table 16. Details of ciguatera fish poisoning outbreak, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Regional	Jan	Imported Eel (Samoa)	Home	Home	4C, 0P

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

Over the 10-year period from 2007 to 2016, five outbreaks of ciguatera fish poisoning were reported, with no more than one outbreak of ciguatera fish poisoning reported in any year (Figure 10).

Figure 10. Ciguatera fish poisoning outbreaks and associated cases reported by year, 2007–2016



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Details of four cases of ciguatera fish poisoning, presenting at Wellington Hospital, were reviewed [27]. All four cases had shared a meal including eel. The eel was brought from Samoa by one of the cases and tested positive for ciguatoxin-1B. Three cases presented with cardio toxicity, while the fourth had severe gastrointestinal symptoms. An analysis of notified and hospitalised cases for the period 2006-2014 was also presented, suggesting that ciguatera fish poisoning is heavily under-reported.

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 2016 by data source

During 2016, four cases (0.09 per 100,000 population) of *C. perfringens* intoxication and one death was 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 2016 with *C. perfringens* intoxication as a diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

There was only one outbreak of *C. perfringens* intoxication with 2 associated cases reported in 2016. The source of the outbreak is unknown (Table 17). 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 17. *C. perfringens* outbreaks reported, 2016

Measure	Foodborne *C. perfringens* outbreaks	All *C. perfringens* outbreaks
Outbreaks	1	1
Cases	2	2
Hospitalised cases	0	0

Between 2007 and 2015, the number of foodborne outbreaks associated with *C. perfringens* ranged from three (in 2009 and 2014) to 13 outbreaks (in 2006) (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 2016 the lowest number of outbreaks (1) and cases (2) was recorded since 2006.

Figure 11. Foodborne *C. perfringens* outbreaks and associated cases reported by year, 2007–2016

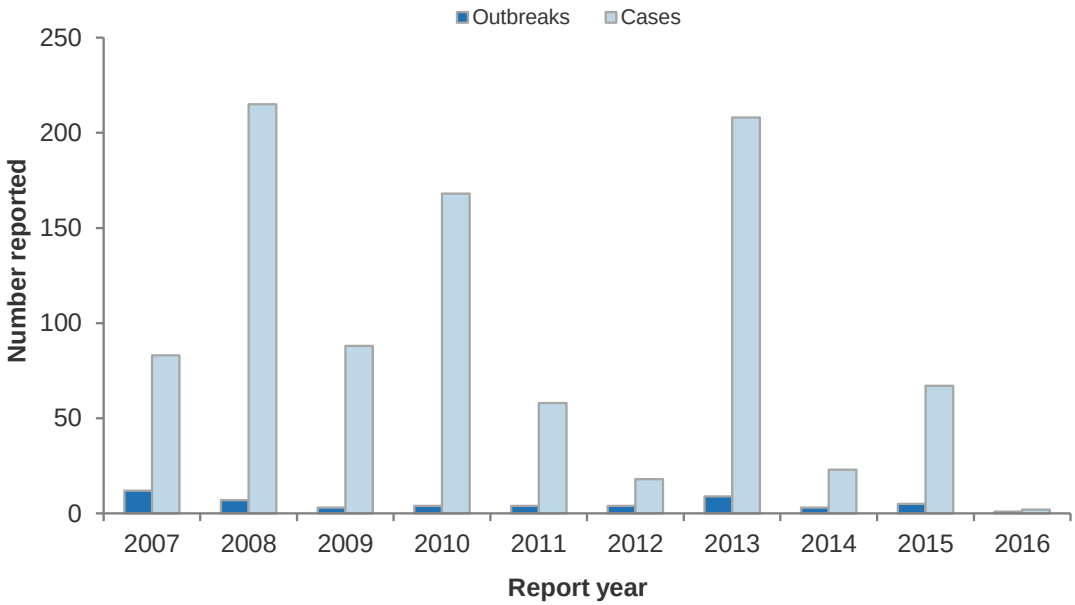


Table 18 contains details of the foodborne outbreak of *C. perfringens* intoxication reported in 2016. For this outbreak (Table 18) weak evidence was provided to implicate a suspected food vehicle.

Table 18. Details of foodborne *C. perfringens* outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
MidCentral	Jan	Unknown	Home	Supermarket/delicatessen	1C, 1P

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

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory in 2016, faecal and food samples were received from the outbreak detailed in Table 18. *C. perfringens* and *C. perfringens* spores were detected in faecal samples from one case.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *C. perfringens* in ready-to-eat foods [16].

Cryptosporidiosis

Summary data for cryptosporidiosis in 2016 are given in Table 19.

Table 19. Summary of surveillance data for cryptosporidiosis, 2016

Parameter	Value in 2016	Source
Number of notified cases	1062	EpiSurv
Notification rate (per 100,000)	22.6	EpiSurv
Hospitalisations (% of notifications)[a]	50 (4.7%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	117 (11.1%)	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 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 in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for a range of pathogens, including *Cryptosporidium*. Before June 2015, *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.

Cryptosporidiosis cases reported in 2016 by data source

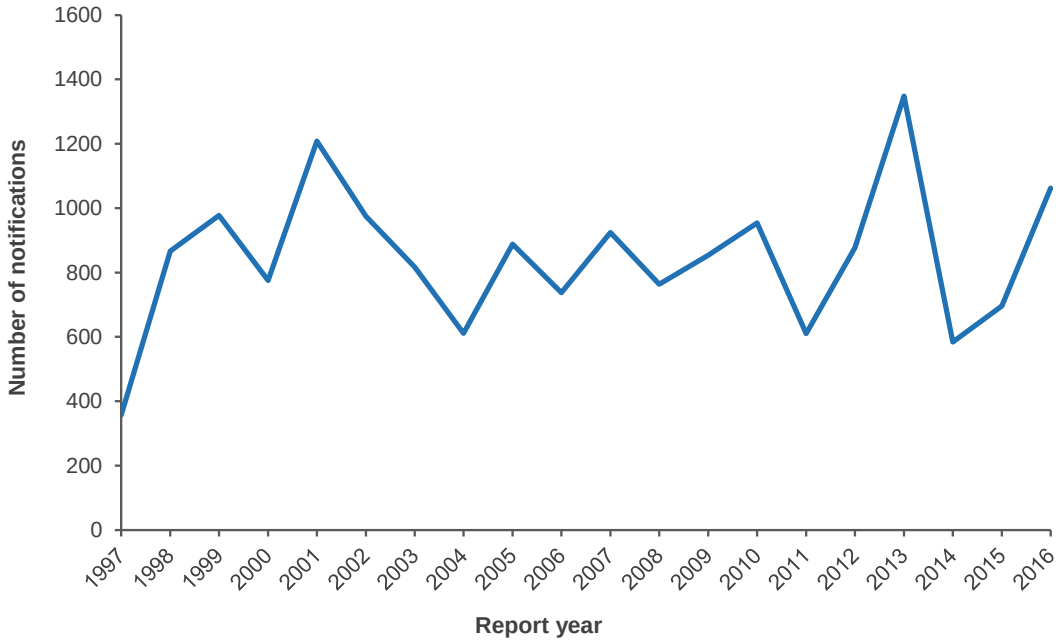
During 2016, 1062 cases (22.6 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 50 hospital admissions (1.1 admissions per 100,000 population) recorded in 2016, 39 were reported with cryptosporidiosis as the principal diagnosis and 11 with cryptosporidiosis as another relevant diagnosis.

Notifiable disease data

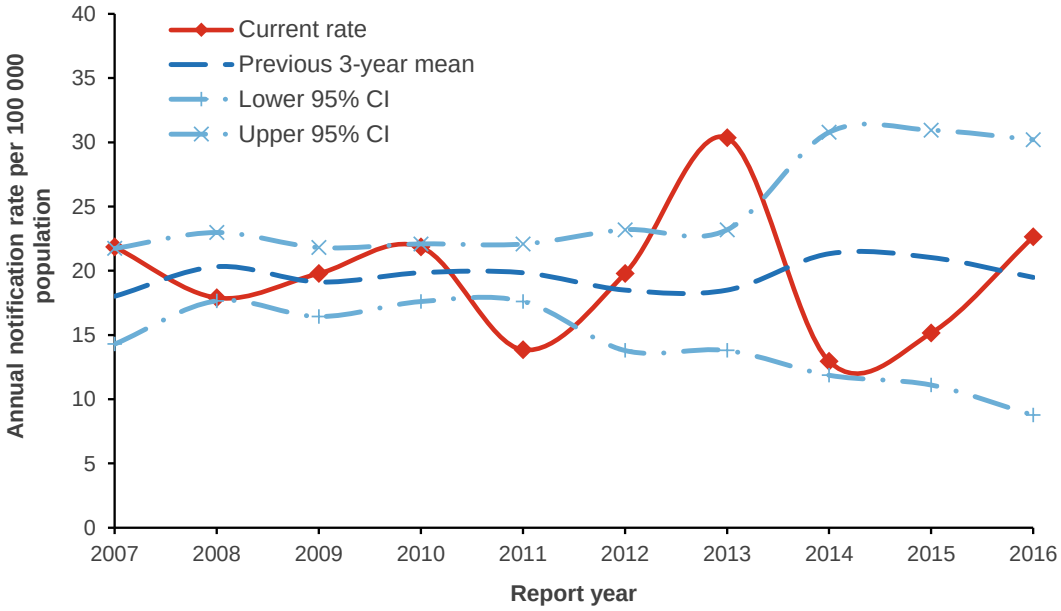
The highest recorded number of cryptosporidiosis notifications since cryptosporidiosis became a notifiable disease in 1996 was 1384 notifications in 2013 followed by 1208 notifications in 2001 and 1062 notifications in 2016. There are no clear trends regarding the number of cryptosporidiosis notifications over the 20 year time period (Figure 12).

Figure 12. Cryptosporidiosis notifications by year, 1997–2016



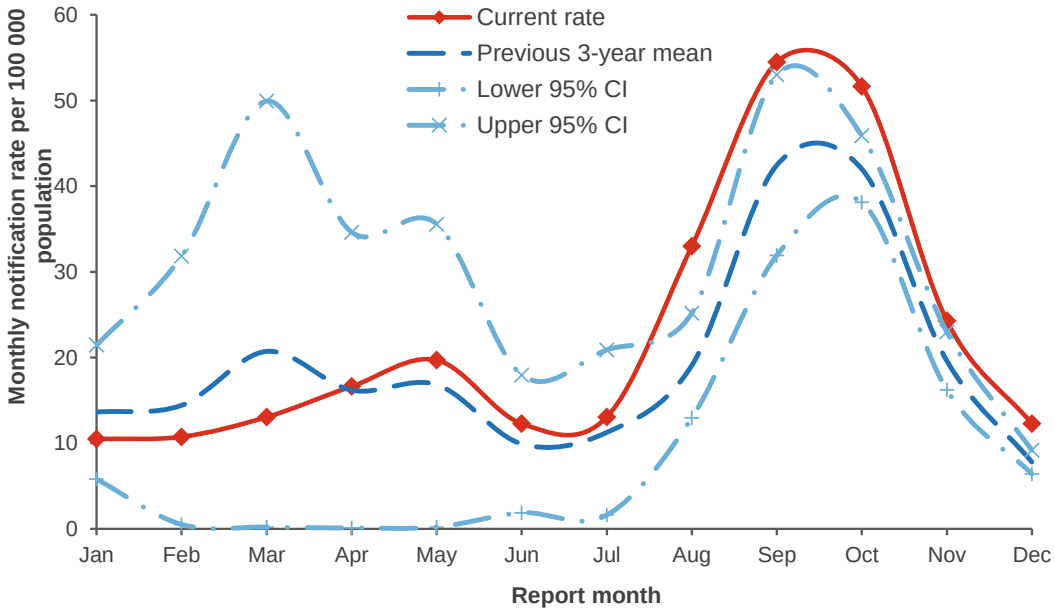
The notification rate was slightly higher in 2016 (22.6 cases per 100,000 population) than the previous three year average (19.5 cases per 100,000) (Figure 13).

Figure 13. Cryptosporidiosis notification rate by year, 2007–2016



The number of notified cases of cryptosporidiosis reported per 100,000 population by month for 2016 was different compared to the previous three years (2013-2015). The spring peak in September/October was consistent with previous years, but with slightly higher notification rates. The notification rate in the first half of the year in 2014 to 2016 did not show the strong March to May peak seen in 2013 (Figure 14).

Figure 14. Cryptosporidiosis monthly rate (annualised), 2016



In 2016, the rate of notifications for cryptosporidiosis was higher for females (24.0 per 100,000 population) compared with males (21.3 per 100,000 population), however similar numbers of females and males were admitted to hospital (1.0 and 1.1 per 100,000 population for males and females, respectively) (Table 20).

Table 20. Cryptosporidiosis cases by sex, 2016

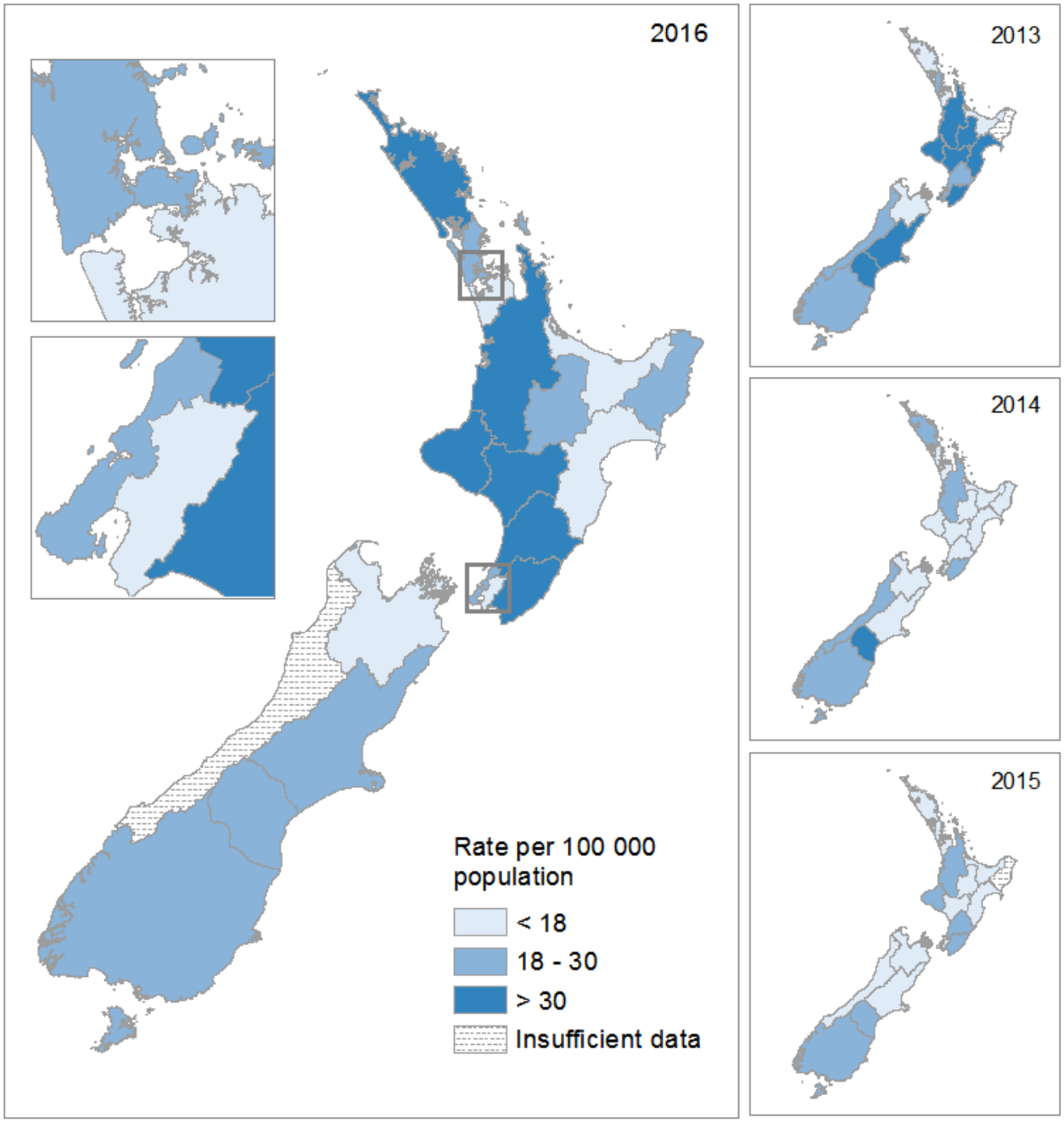
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	491	21.3	26	1.1
Female	571	24.0	24	1.0
Total	**1062**	**22.6**	**50**	**1.0**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

In 2016, the highest rates of cryptosporidiosis were for Northland (61.8 per 100,000, 106 cases), Wairarapa (45.9 per 100,000, 20 cases), Taranaki (37.7 per 100,000, 44 cases), Whanganui (31.7 per 100,000, 20 cases), and Mid Central (31.6 per 100,000, 55 cases). South Canterbury DHB (27.0 per 100,000 population, 16 cases) had the highest rate in the South Island. Overall, the notification rates have increased in a number of DHBs since 2015, most notably in Northland (2015: 16.0 per 100,000, 27 cases) and Wairarapa (2015: 25.5 per 100,000, 11 cases) DHBs (Figure 15).

Figure 15. Geographic distribution of cryptosporidiosis notifications, 2013–2016



During 2016, the highest cryptosporidiosis age-specific notification rates were for the 1 to 4 years age group (124.3 per 100,000 population, 305 cases), followed by 5 to 9 (41.6 per 100,000, 134 cases) and the less than 1 year (30.4 per 100,000, 18 cases) age groups (Table 21). The hospitalisation rate was also highest in the 1 to 4 years age group.

Table 21. Cryptosporidiosis cases by age group, 2016

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	18	30.4	0	-
1 to 4	305	124.3	17	6.9
5 to 9	134	41.6	10	3.1
10 to 14	61	20.7	2	-
15 to 19	57	17.9	2	-
20 to 29	161	23.4	3	-
30 to 39	148	25.6	5	0.9
40 to 49	74	11.9	3	-
50 to 59	52	8.5	3	-
60 to 69	32	6.5	4	-
70+	20	4.3	1	-
Total	**1062**	**22.6**	**50**	**1.1**

[a] MoH NMDS data for hospital admissions

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

During 2016, the most commonly reported risk factors for cryptosporidiosis were contact with farm animals (49.1%), consumption of untreated water (36.3%) and consumed food from retail premises (30.5%) (Table 22).

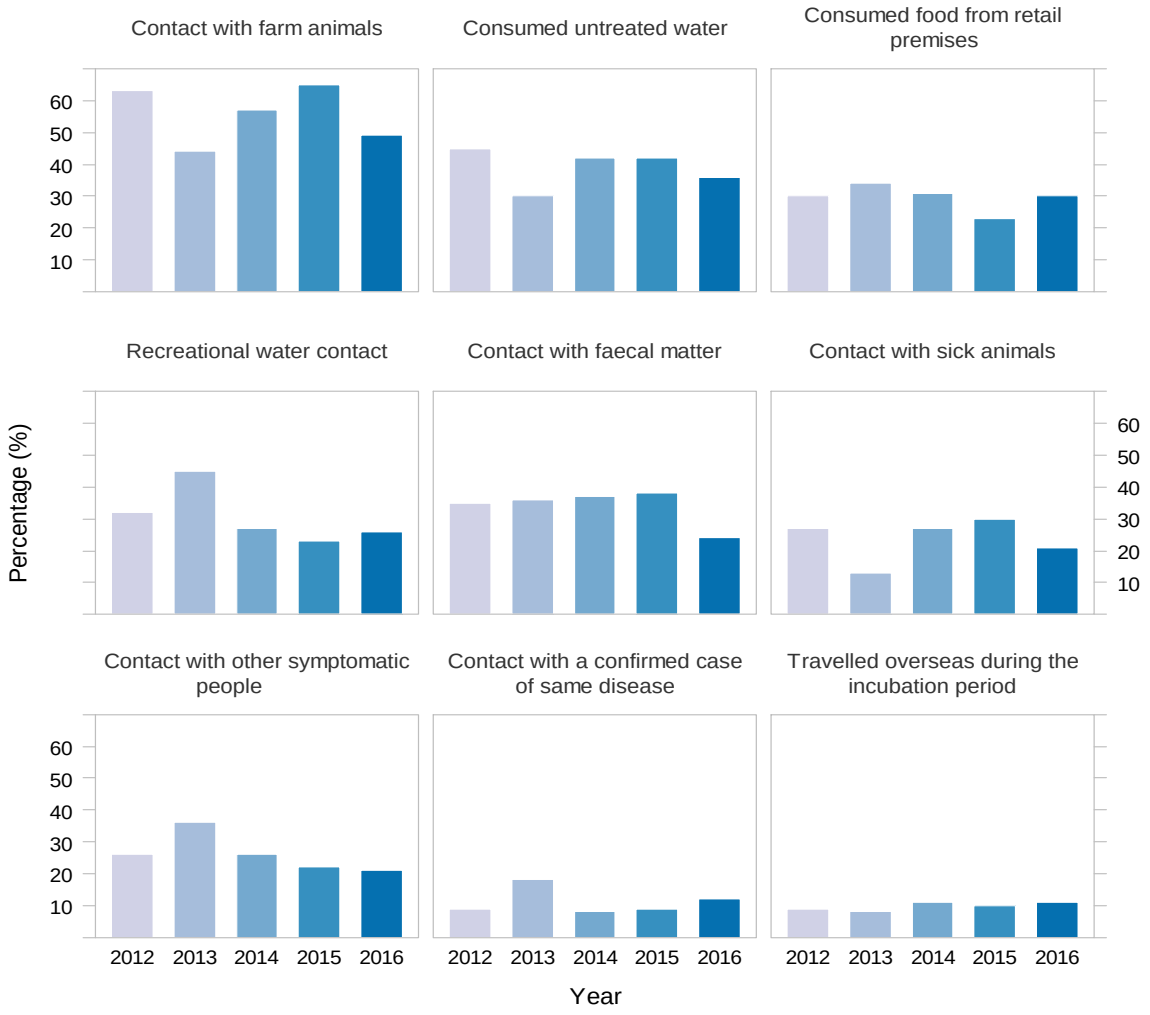
Table 22. Exposure to risk factors reported for cryptosporidiosis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Contact with farm animals	377	391	294	49.1
Consumed untreated water	251	441	370	36.3
Consumed food from retail premises	163	372	527	30.5
Recreational water contact	187	530	345	26.1
Contact with faecal matter	153	482	427	24.1
Contact with other symptomatic people	158	583	321	21.3
Contact with sick animals	140	532	390	20.8
Contact with a confirmed case of same disease	75	550	437	12.0
Travelled overseas during the incubation period	100	805	157	11.1

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

Between 2012 and 2016, the most commonly reported risk factor for cryptosporidiosis was contact with farm animals followed by consumption of untreated water and contact with faecal matter (Figure 16). The percentage of cases reporting recreational water contact peaked in 2013 after increasing from 2011, but has reduced as a risk factor since 2014 back to the 2011 value (23%). A similar trend is shown for contact with other symptomatic people (2011 value was 21%).

Figure 16. Percentage of cases with exposure to risk factors reported for cryptosporidiosis and year, 2012–2016



For 2016 cases, where information on travel was provided, 11.1% (95% CI 9.1-13.3%) 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 2016. The resultant distribution has a mean of 117 cases (95% CI 88-150).

If data from the last four years are considered, the estimated proportion of cases travelling overseas within the incubation period of the organism was 9.9% (95% CI 8.9-11.1%).

Outbreaks reported as caused by *Cryptosporidium* spp.

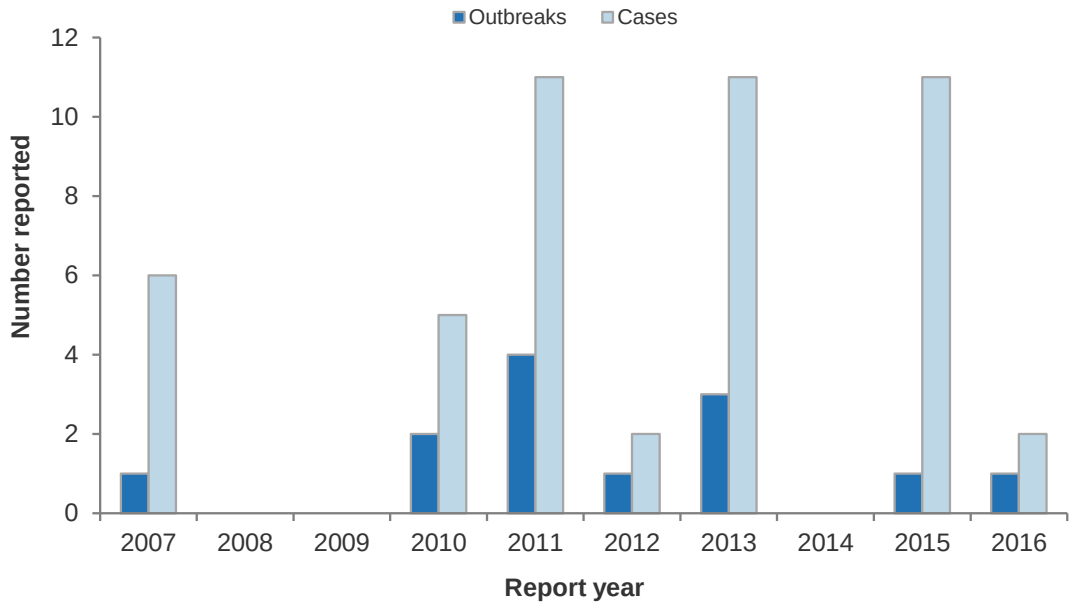
In 2016, one (3.0%) of the *Cryptosporidium* spp. outbreaks with 2 (1.1%) associated cases was reported as potentially foodborne (Table 23). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks of cryptosporidiosis accounted for 5.9% (33/561) of all enteric outbreaks and 1.8% (188/10,378) of all associated cases.

Table 23. *Cryptosporidium* spp. outbreaks reported, 2016

Measure	Foodborne *Cryptosporidium* spp. outbreaks	All *Cryptosporidium* spp. outbreaks
Outbreaks	1	33
Cases	2	188
Hospitalised cases	0	1

Foodborne transmission was rarely reported for *Cryptosporidium* spp. outbreaks, with not more than four outbreaks reported each year in the ten year period, 2007−2016. The outbreak in 2015 had the largest number of cases (11) associated with a single outbreak (Figure 17).

Figure 17. Foodborne *Cryptosporidium* spp. outbreaks and associated cases reported by year, 2007–2016



In the *Cryptosporidium* spp. outbreak with a suspected food vehicle (Table 24), weak evidence was found to implicate food. The cases all had overseas travel recorded as a risk factor and developed symptoms after returning to New Zealand.

Table 24. Details of the foodborne *Cryptosporidium* spp. outbreak, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Jul	Unknown	Other setting	Other setting	2C, 2P

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

In 2016, no food or clinical samples were submitted to ESR's Public Health Laboratory relating to the food-associated *Cryptosporidium* spp. outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Cryptosporidiosis cases in New Zealand children less than five years of age, notified during the period 1997-2008, were examined in relation to dairy cattle densities [28]. The risk of cryptosporidiosis was found to be significantly positively associated with medium or high dairy cattle densities, compared to areas with no dairy cattle.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2016 are given in Table 25.

Table 25. Summary of surveillance data for giardiasis, 2016

Parameter	Value in 2016	Source
Number of notified cases	1617	EpiSurv
Notification rate (per 100,000)	34.5	EpiSurv
Hospitalisations (% of notifications)[a]	47 (2.6%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	403 (24.9%)	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 or malabsorption. The infection may be asymptomatic.
Laboratory test for diagnosis:	Detection of *Giardia* cysts or trophozoites in a specimen from the human intestinal tract OR detection of *Giardia* antigen in faeces.
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 in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for a range of pathogens, including *Giardia*. Before June 2015, *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.

Giardiasis cases reported in 2016 by data source

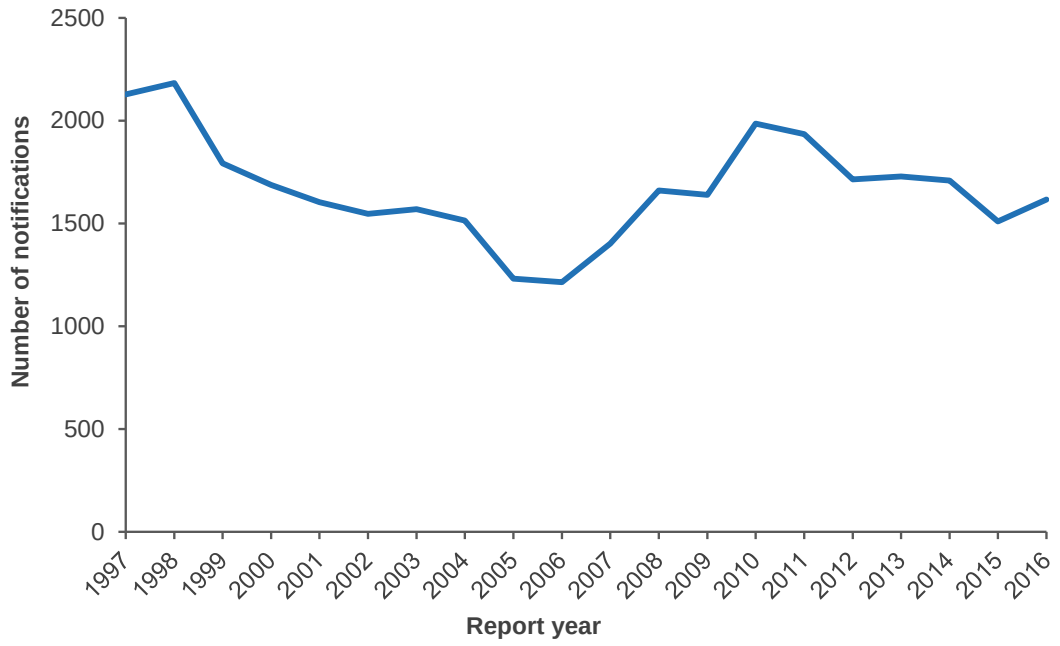
During 2016, 1617 cases (34.5 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 47 hospital admissions (1.0 admissions per 100,000 population) recorded in 2016, 27 were reported with giardiasis as the principal diagnosis and 20 with giardiasis as another relevant diagnosis.

Notifiable disease data

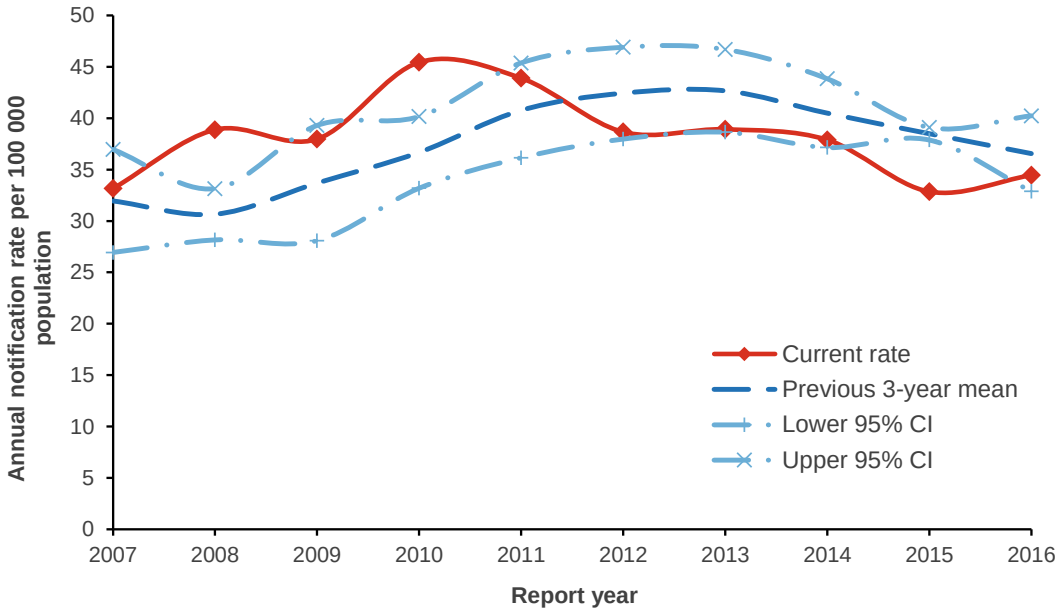
There was a steady decrease in the number of giardiasis cases reported each year from 1998 to 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 followed by decreases in the number of notifications. The highest number of notifications since 1999 was reported in 2010 (1985 cases), followed by 2011 (1934 cases) (Figure 18).

Figure 18. Giardiasis notifications by year, 1997–2016



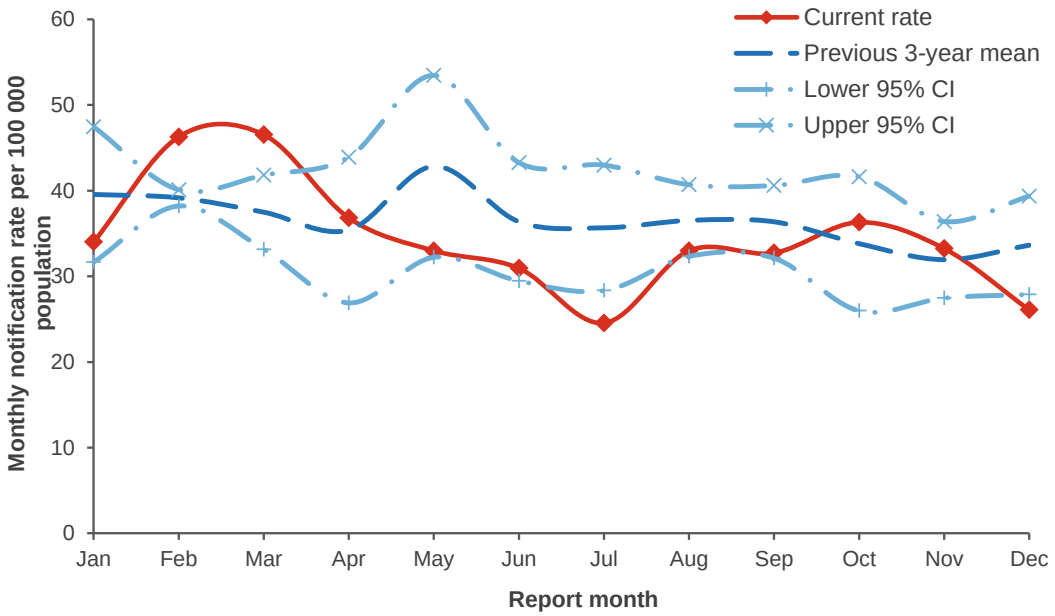
The 2016 notification rate was lower than 2012 to 2014 and similar to 2015, maintaining the downward trend since 2010. Between 2007 and 2010 there had been a generally increasing trend (Figure 19).

Figure 19. Giardiasis notification rate by year, 2007–2016



There was no strong seasonal pattern in the population rate of giardiasis notifications reported by month either historically in the previous three years (2013-2015) or in 2016 (Figure 20). The lowest number of notifications was reported in July and December.

Figure 20. Giardiasis monthly rate (annualised), 2016



In 2016 the number and rate for notifications were slightly higher for males than females, however hospital admission rates per 100,000 population were similar for females and males (Table 26).

Table 26. Giardiasis cases by sex, 2016

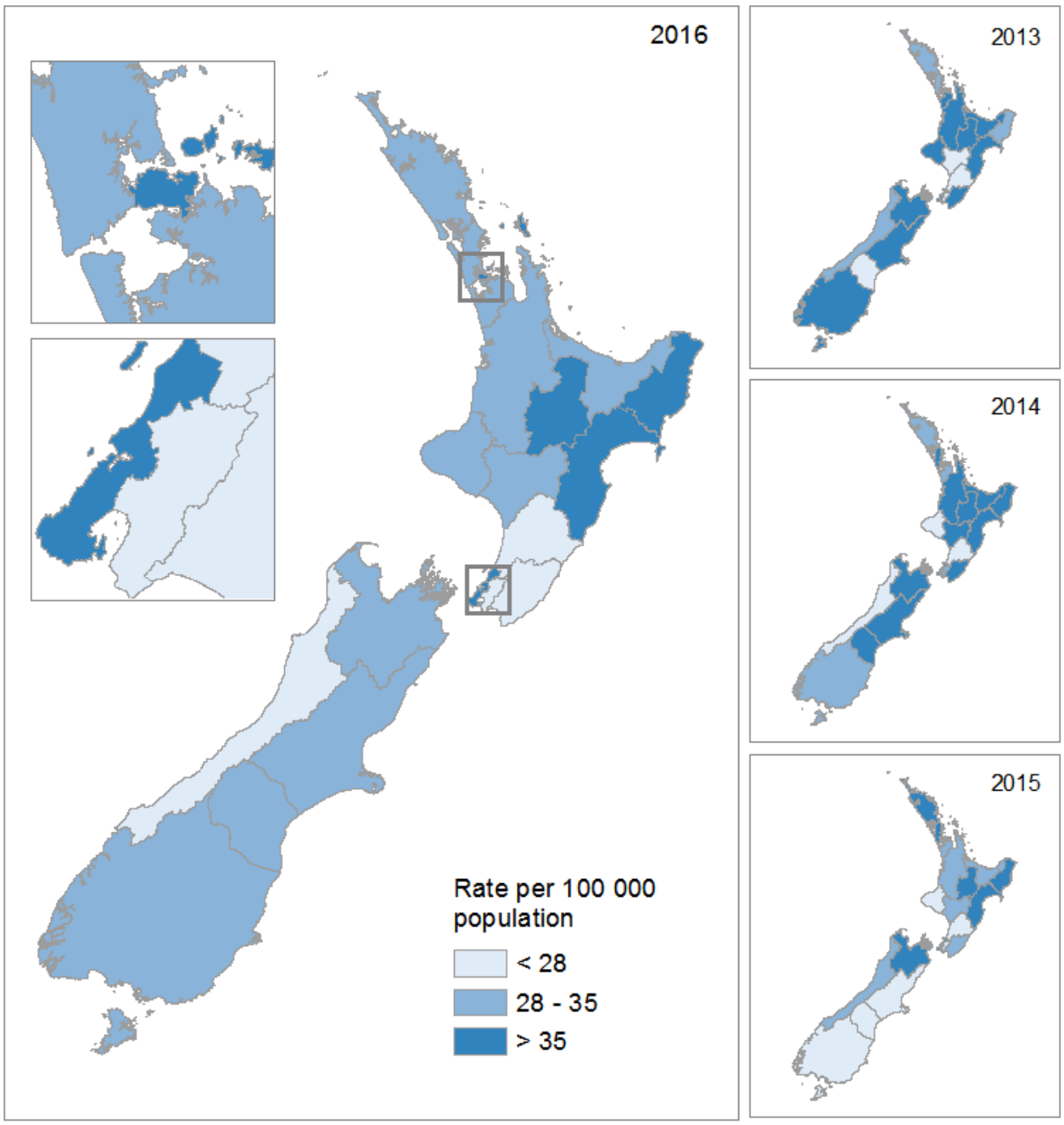
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	828	35.9	21	0.9
Female	789	33.1	26	1.0
Total	**1617**	**34.5**	**47**	1.0

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

Giardiasis rates varied throughout the country during 2016 (Figure 21). The highest rate was for Tairawhiti (156.9 per 100,000 population, 75 cases), followed by Hawke's Bay (47.7 per 100,000, 77 cases) and Lakes DHB (45.0 per 100,000, 48 cases). The lowest rates were reported for West Coast (21.5 per 100,000, 7 cases), Hutt Valley (22.6 per 100,000, 33 cases) and MidCentral (22.4 per 100,000 population, 39 cases) DHBs. Lakes and Hawke's Bay DHBs have consistently been in the highest quantile in the last four years.

Figure 21. Geographic distribution of giardiasis notifications, 2013–2016



In 2016, the highest notification rate was for the 1 to 4 years age group (110.9 per 100,000 population, 272 cases), followed by the 30 to 39 years age group (55.4 per 100,000, 320 cases) and the under 1 age group (43.9 per 100,000, 26 cases) (Table 27). The highest hospitalisation rate was also for the 1 to 4 years age group.

Table 27. Giardiasis cases by age group, 2016

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	26	43.9	0	-
1 to 4	272	110.9	11	4.5
5 to 9	125	38.8	1	-
10 to 14	42	14.3	3	-
15 to 19	46	14.4	0	-
20 to 29	197	28.7	5	0.7
30 to 39	320	55.4	8	1.4
40 to 49	201	32.4	5	0.8
50 to 59	183	29.9	6	1.0
60 to 69	154	31.4	2	-
70+	51	11.0	6	1.3
Total	**1617**	**34.5**	**47**	**1.0**

[a] MoH NMDS data for hospital admissions

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

In 2016, the most commonly reported risk factor for notified giardiasis cases was contact with faecal matter (40.5%). Between 33.4% and 35.7% of cases reported the risk factors of consuming untreated water, consuming food from retail premises, contact with other symptomatic people, and contact with recreational water (Table 28).

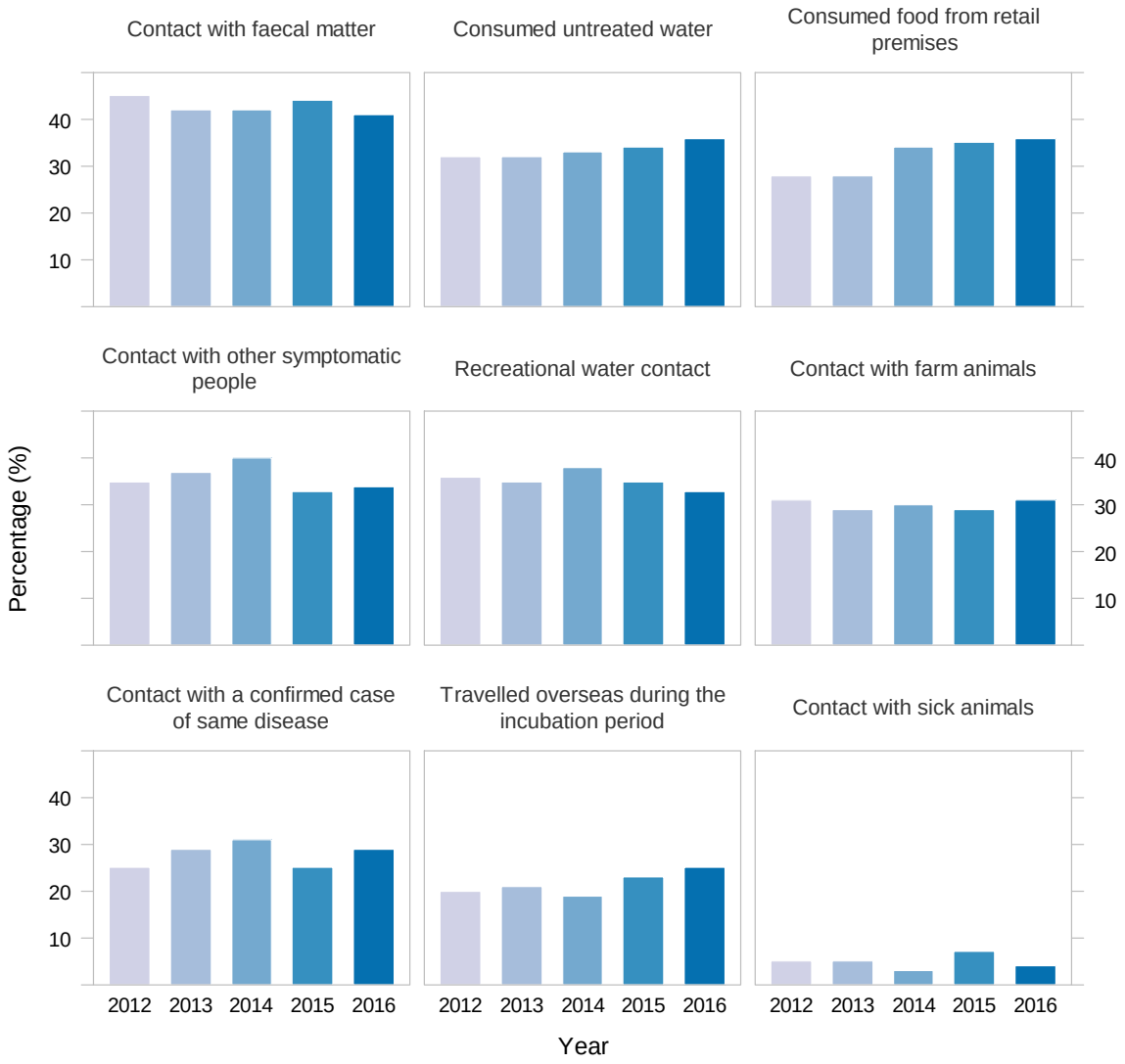
Table 28. Exposure to risk factors reported for giardiasis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Contact with faecal matter	306	449	862	40.5
Consumed untreated water	261	471	885	35.7
Consumed food from retail premises	237	431	949	35.5
Contact with other symptomatic people	268	513	836	34.3
Recreational water contact	264	528	825	33.3
Contact with farm animals	252	559	806	31.1
Contact with a confirmed case of same disease	175	433	1009	28.8
Travelled overseas during the incubation period	236	713	668	24.9
Contact with sick animals	33	708	876	4.5

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

The risk factors for giardiasis between 2012 and 2016 are presented in Figure 22.

Figure 22. Percentage of cases with exposure to risk factors reported for giardiasis and year, 2012–2016



For cases where information on travel was provided in 2016, 24.9% (95% CI 22.1-27.8%) 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 2016. The resultant distribution has a mean of 402 cases (95% CI 339-468).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 22.1% (95% CI 20.7%-23.5%).

Outbreaks reported as caused by *Giardia* spp.

In 2016, there were 45 *Giardia* spp. outbreaks reported, four of these were associated with a suspected or known foodborne source (Table 29). 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 8.0% (45/561) of all enteric outbreaks and 2.3% (238/10,378) of all associated cases.

Table 29. Giardia spp. outbreaks reported, 2016

Measure	Foodborne *Giardia* spp. outbreaks	All *Giardia* spp. outbreaks
Outbreaks	4	45
Cases	18	238
Hospitalised cases	1	2

The highest number of foodborne *Giardia* spp. outbreaks and associated cases reported in the period from 2007 to 2016 was in 2013 (10 outbreaks and 36 associated cases). Between 2007 and 2016, two to six foodborne *Giardia* spp. outbreaks were reported each year, with the exception of 2009 when no outbreaks were reported and 2013 (Figure 23). For the last six years the annual number of cases has been in the range 17 to 36 cases, which was higher than in the preceding seven years.

Figure 23. Foodborne *Giardia* spp. outbreaks and associated cases reported by year, 2007–2016

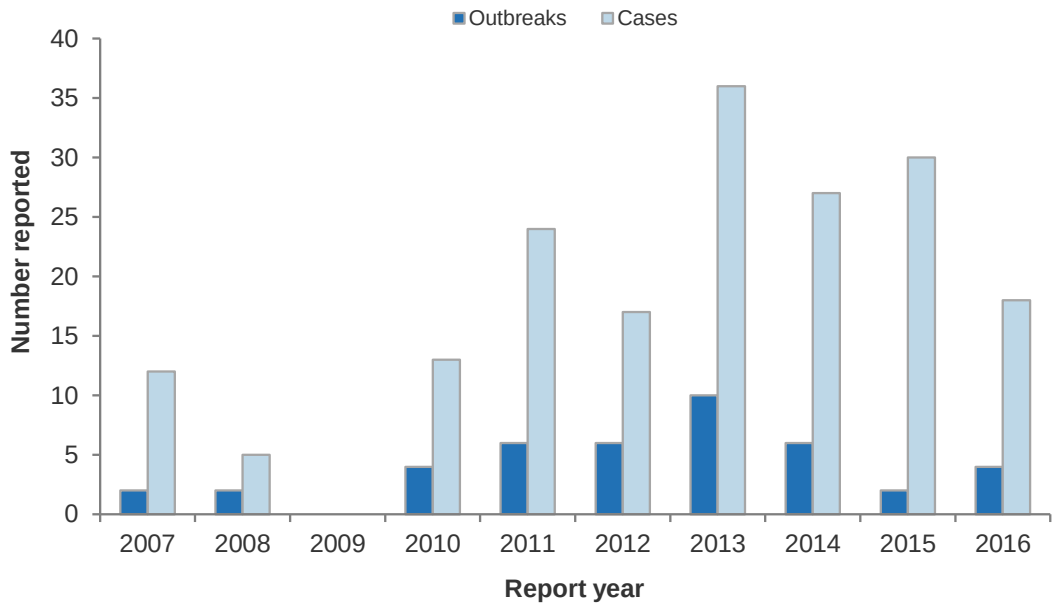


Table 30 contains details of the four foodborne *Giardia* spp. outbreaks reported in 2016. For both outbreaks that reported raw milk as the suspected vehicle of infection, the evidence for foodborne transmission was weak.

Table 30. Details of foodborne *Giardia* spp. outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
MidCentral	Aug	Raw milk	Other food outlet	Other food outlet	7C, 0P[a]
Auckland	Dec	Unknown	Home	Home	4C, 0P
Nelson Marlborough	Dec	Raw milk	Other food outlet	Other food outlet	5C, 0P[b]
PH South	Dec	Unknown	Unknown	Unknown	2C, 0P

PHU: Public Health Unit, Auckland: Auckland Regional Public Health Service, MidCentral: MidCentral Public Health Service, PH South: Public Health South, Nelson Marlborough: Nelson Marlborough Public Health Service, C: confirmed, P: probable.

[a] Of the confirmed cases linked to the outbreak, 1 case had giardiasis and 6 cases campylobacteriosis. Reporting includes total number of cases linked to the outbreak by pathogen.

[b] Of the confirmed cases linked to the outbreak, 3 cases had giardiasis and 2 cases campylobacteriosis. Reporting includes total number of cases linked to the outbreak by pathogen.

In 2016, no food or clinical samples were submitted to ESR's Public Health Laboratory relating to the food-associated *Giardia* spp. outbreaks.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2016 are given in Table 31.

Table 31. Summary of surveillance data for hepatitis A, 2016

Parameter	Value in 2016	Source
Number of notified cases	35	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalisations[b]	19	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Travel-related cases (%)[a]	20 (57.1%)	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).
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 2016 by data source

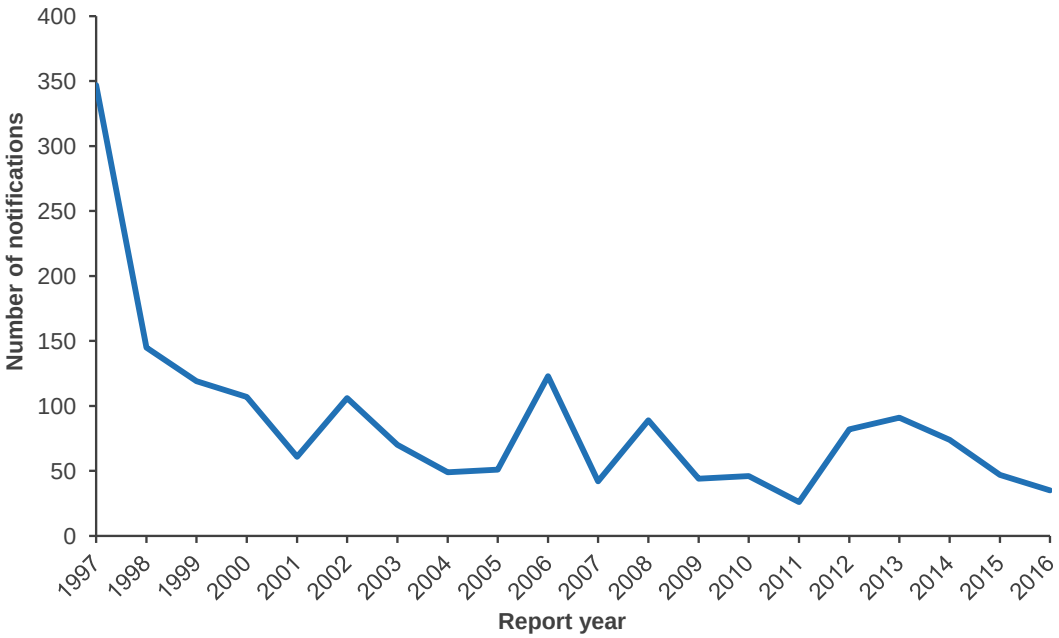
During 2016, 35 cases (0.7 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv.

The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the MoH NMDS database. Of the 84 hospital admissions (1.4 admissions per 100,000 population) recorded in 2016, 19 were reported with acute hepatitis A as the principal diagnosis and 65 with acute hepatitis A as another relevant diagnosis.

Notifiable disease data

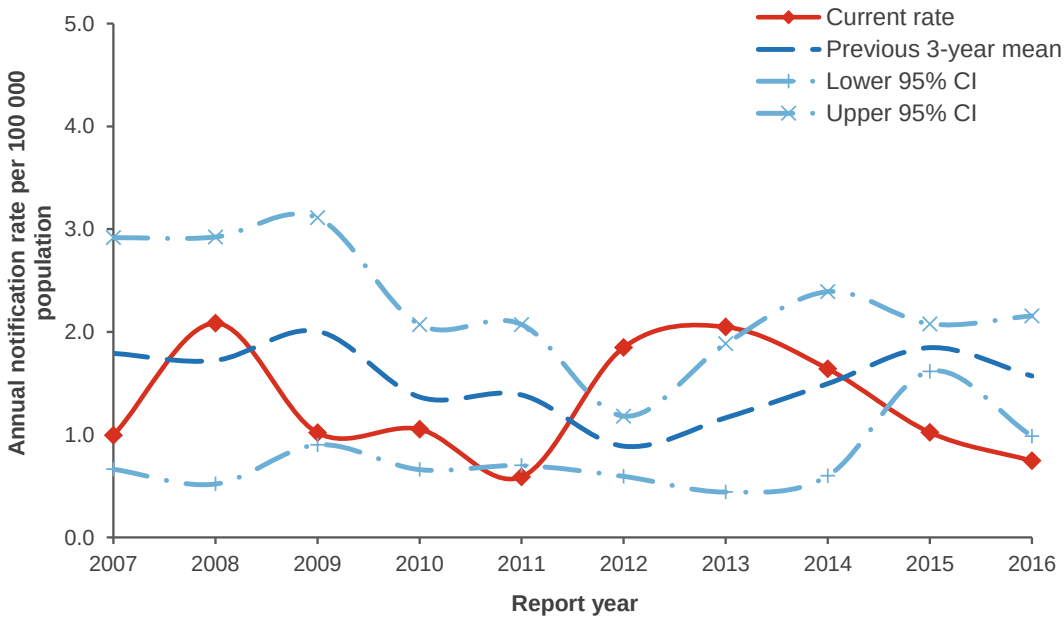
Between 2001 and 2016, the annual number of notifications has remained in the range of 26 (2011) to 123 (2006), having decreased from 347 in 1997 (Figure 24).

Figure 24. Hepatitis A notifications by year, 1997–2016



Hepatitis A notification rates have varied throughout the 10-year period 2007–2016 in the range of 0.6 to 2.1 per 100,000 population (Figure 25). The lowest notification rate for the ten year period was in 2011, after which the rate showed an increasing trend in 2012 and 2013, followed by a decrease.

Figure 25. Hepatitis A notification rate by year, 2007–2016



In 2016, hepatitis A notifications and hospital admissions were higher for males than for females (Table 32). Over previous years there has not been one sex with consistently higher notifications than the other.

Table 32. Hepatitis A cases by sex, 2016

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	22	1.0	13	0.6
Female	13	0.5	6	0.2
Total	**35**	**0.7**	**19**	**0.4**

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

[b] per 100,000 of population

In 2016, the highest notification rate was reported for the 20 to 39 years age group (1.2 per 100,000, 15 cases) with lower rates for the less than 20 and 40 to 59 age group (0.6 and 0.7 per 100,000, respectively). Hospitalisation rates were similar for the less than 20, 20 to 39 and 40 to 59 age groups (Table 33). No rates were calculated for the 60+ age group as fewer than five cases were reported.

Table 33. Hepatitis A cases by age group, 2016

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<20	7	0.6	5	0.4
20 to 39	15	1.2	7	0.6
40 to 59	9	0.7	5	0.4
60+	4	-	2	-
Total	**35**	**0.7**	**19**	**0.4**

[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)

The most commonly reported risk factor for hepatitis A in 2016 was travelling overseas during the incubation period (57.1%), followed by contact with contaminated food or drink (41.7%) (Table 34).

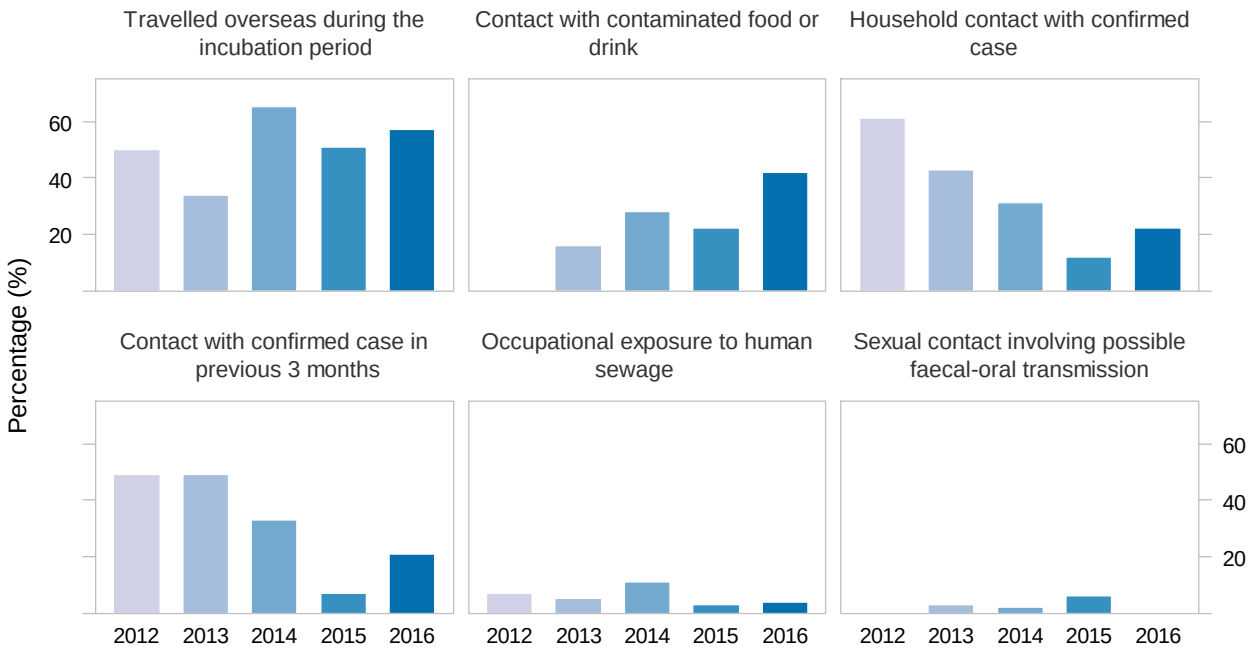
Table 34. Exposure to risk factors reported for hepatitis A notifications, 2016

Risk Factor	Notifications			
	Yes	No	Unknown	%[a]
Travelled overseas during the incubation period	20	15	0	57.1
Contact with contaminated food or drink	5	7	23	41.7
Household contact with confirmed case	7	25	3	21.9
Contact with confirmed case in previous 3 months	6	23	6	20.7
Occupational exposure to human sewage	1	26	8	3.7
Sexual contact involving possible faecal-oral transmission	0	24	11	0.0

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

The percentage of cases reporting overseas travel during the incubation period has been variable over the period 2012 to 2016 (Figure 26). The percentage of cases reporting household contact with a confirmed case and contact with a confirmed case in the previous three months has decreased since 2012 and 2013 respectively, but increased slightly in 2016.

Figure 26. Hepatitis A risk factors by percentage of cases and year, 2012–2016

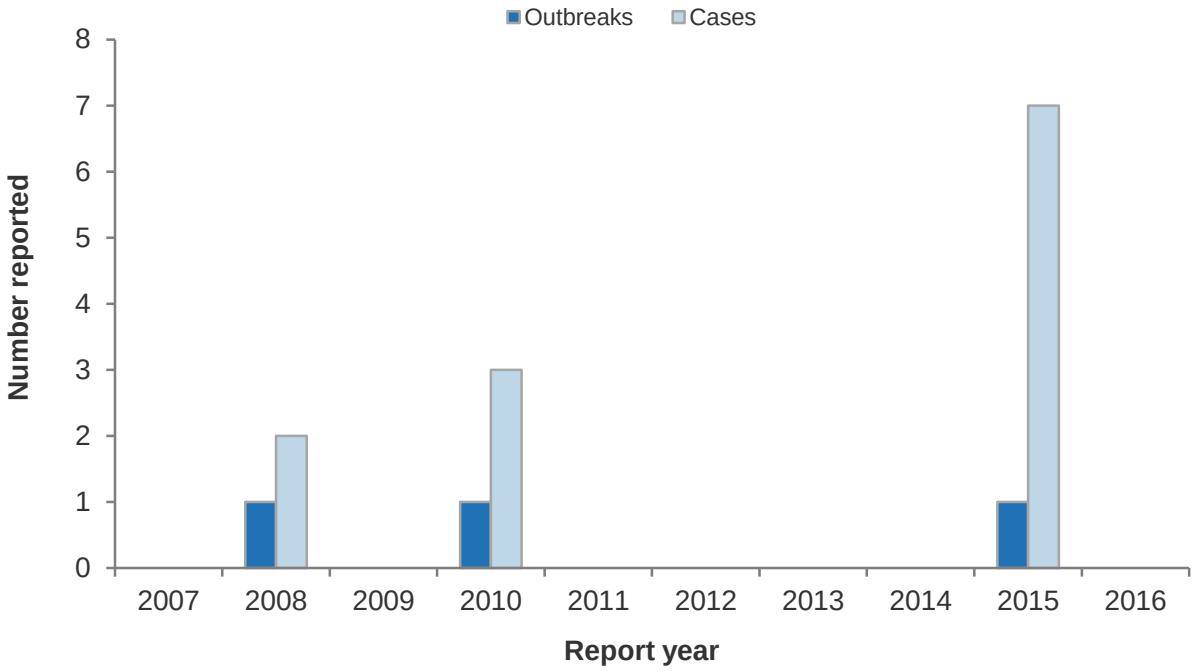


In 2016, all 35 hepatitis A cases provided information on overseas travel, and 57.1% (95% CI 39.5-73.2%) had travelled overseas during the incubation period. If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 49.6% (95% CI 43.2-56.0%).

Outbreaks reported as caused by hepatitis A virus

There were no outbreaks caused by hepatitis A virus reported in 2016. Foodborne hepatitis A outbreaks are rare with only three outbreaks reported in the period 2007 to 2016 (Figure 27). Although occurring infrequently, foodborne outbreaks of hepatitis A virus infection can be associated with many cases (34 cases for an outbreak reported in 2006). However, the food-associated outbreaks in 2008, 2010 and 2015 involved only 2, 3 and 7 cases, respectively.

Figure 27. Foodborne hepatitis A virus outbreaks and associated cases reported by year, 2007–2016



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 2016 by data source

Two cases of histamine (scombroid) fish poisoning were reported in EpiSurv during 2016 (0.04 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 seven hospital admissions (0.15 admissions per 100,000 population) recorded in 2016, all were reported with scombroid fish poisoning as the principal diagnosis.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

Two histamine (scombroid) fish poisoning outbreaks were reported in 2016 involving five associated cases, none of whom were reported as hospitalised (Table 35). 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 35. Histamine (scombroid) fish poisoning outbreaks reported, 2016

Measure	Foodborne histamine fish poisoning outbreaks	All histamine fish poisoning outbreaks
Outbreaks	2	2
Cases	5	5
Hospitalised cases	0	0

Between 2007 and 2016 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 28). 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 (21 cases).

Figure 28. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2007–2016

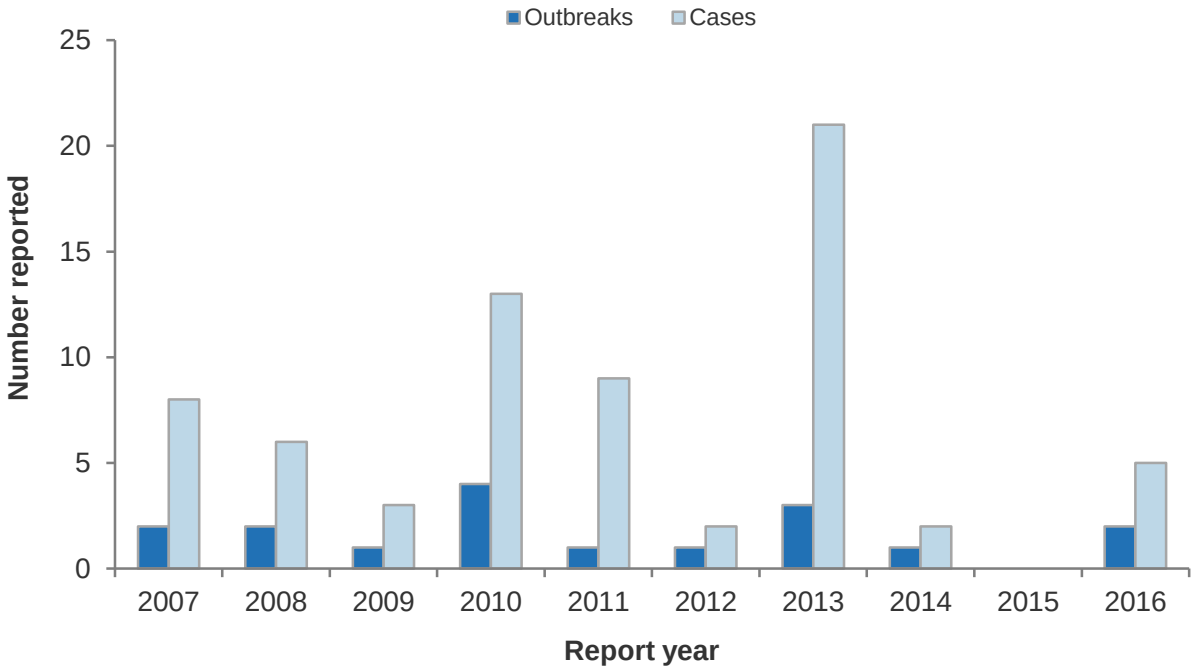


Table 36 contains details of the two foodborne histamine fish poisoning outbreaks reported in 2016. For the outbreak reporting fish as a suspected vehicle of infection the evidence for foodborne transmission was listed as weak in EpiSurv.

Table 36. Details of foodborne histamine fish poisoning outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Regional	Jun	fish bought from store	Other food outlet	Home	0C, 3P
Auckland	Nov	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C, 0P

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

In 2016, smoked fish samples were submitted to ESR's Public Health Laboratory relating to a Regional Public Health histamine fish poisoning outbreak (3 cases). The fish had high levels of histamine present. Prawns and chicken samples relating to the Auckland outbreak were tested and had low levels of histamine present. As these foods are not associated with histamine fish poisoning, cross contamination at the food premise was suspected.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2016 are given in Table 37.

Table 37. Summary of surveillance data for listeriosis, 2016

Parameter	Value in 2016	Source
Number of notified cases[a]	37	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalisations	41	MoH NMDS
Deaths (%)[b]	2 (5.4%)	EpiSurv
Travel-related cases (%)[b]	3 (7.7%)	EpiSurv
Estimated food-related cases (%)[c]	30 (87.8%)	Expert consultation

[a] Includes non-perinatal (33) and perinatal cases (4).

[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* 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 7 days before birth until 7 days after birth.

Listeriosis cases reported in 2016 by data source

During 2016, 37 cases (0.8 per 100,000 population) of listeriosis were reported in EpiSurv, of which 4 were perinatal.

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 41 hospital admissions (0.8 admissions per 100,000 population) recorded in 2016, 21 were reported with listeriosis as the principal diagnosis and 20 with listeriosis as another relevant diagnosis.

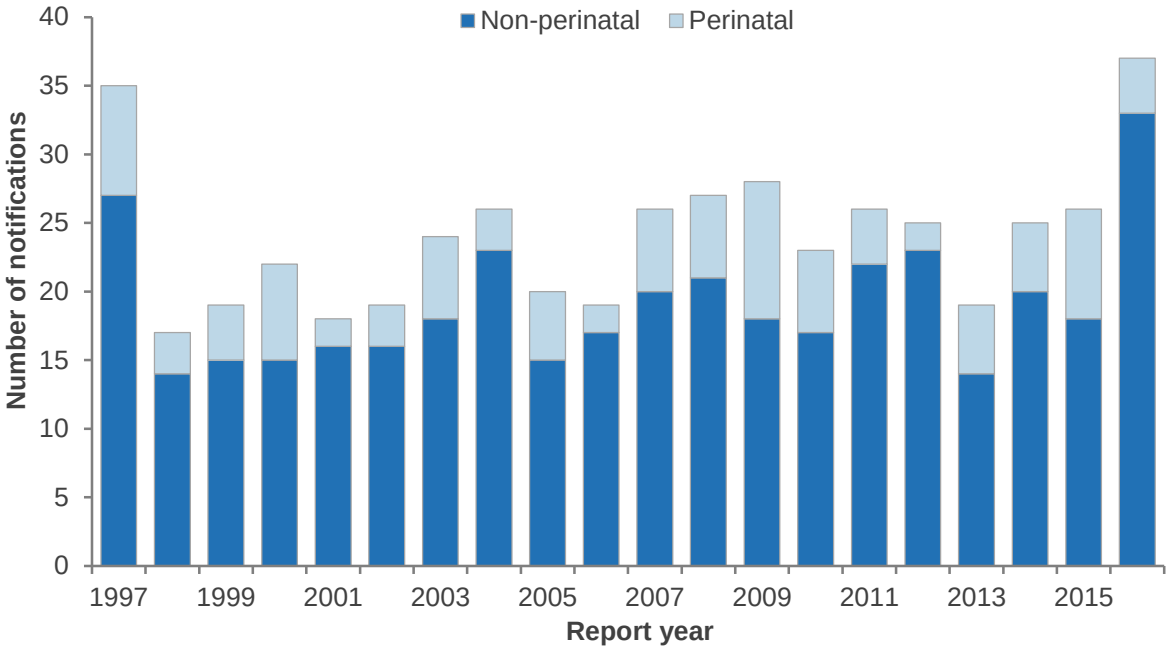
Two deaths were recorded in EpiSurv in 2016, both perinatal.

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 2015, the annual number of listeriosis notifications has fluctuated between 17 (1998) and 28 (2009) (Figure 29). In 2016, the total number of notifications (37) was higher than in previous 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.

Figure 29. Listeriosis non-perinatal and perinatal notifications by year, 1997–2016



In 2016, the rate of notifications for listeriosis was slightly higher for females (0.8 per 100,000 population, 22 cases) than males (0.6 per 100,000, 15 cases). The number and rate of hospitalisations were also higher for females than males (Table 38). 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 38. Listeriosis cases by sex, 2016

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	15	0.6	16	0.6
Female	22	0.8	25	0.9
Total	**37**	**0.7**	**41**	**0.8**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

In 2016, rates for listeriosis were highest in the 60 years and over age group for both the notifications (2.5 per 100,000 population, 24 cases) and hospitalisations (2.6 per 100,000, 25 admissions) (Table 39).

Table 39. Listeriosis cases by age group, 2016

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<20	2	-	5	0.4
20 to 39	6	0.5	5	0.4
40 to 59	5	0.4	6	0.5
60+	24	2.5	25	2.6
Total	**37**	**0.7**	**41**	**0.8**

[a] MoH NMDS data for hospital admissions (ICD-10 code A32)

[b] For perinatal cases the age reported is the mother's age

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

During 2016, the most common risk factors reported for non-perinatal listeriosis cases were having an underlying illness (86.7%), receiving immunosuppressive drugs (60.0%), and admission to hospital for another illness (39.3%) (Table 40).

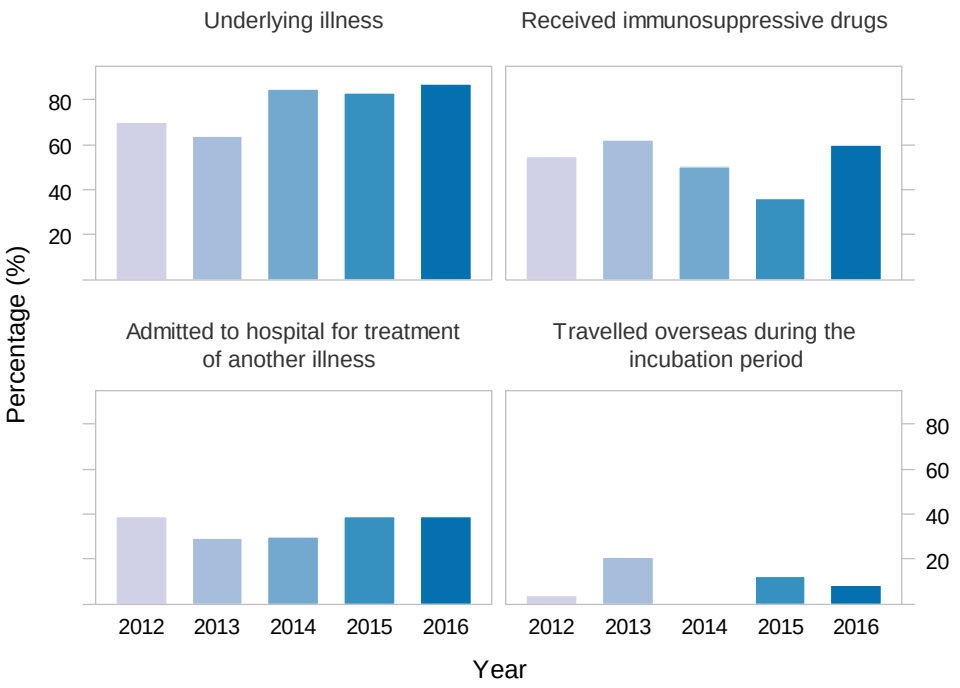
Table 40. Exposure to risk factors reported for listeriosis (non-perinatal) notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Underlying illness	26	4	3	86.7
Received immunosuppressive drugs	15	10	8	60.0
Admitted to hospital for treatment of another illness	11	17	5	39.3
Travelled overseas during the incubation period	2	24	7	7.7

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

Having an underlying illness was the risk factor most commonly associated with listeriosis cases each year between 2012 and 2016 (Figure 30).

Figure 30. Percentage of cases with exposure to risk factors reported for listeriosis (non-perinatal) and year, 2012–2016



Outbreaks reported as caused by *Listeria* spp.

There were no *Listeria* spp. outbreaks reported in 2016. 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 37 isolates of *L. monocytogenes* during 2016.

Table 41 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2012 and 2016. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of 11 to 20 isolates over the period 2012 to 2016, with the exception of only 7 O4 isolates in 2013.

Table 41. *L. monocytogenes* serotypes identified by the Special Bacteriology Laboratory, 2012–2016

Serotype	2012		2013		2014		2015		2016	
	No.	%	No.	%	No.	%	No.	%	No.	%
O4	12	48.0	7	36.8	16	57.1	11	42.3	20	54.1
O1/2	13	52.0	12	63.2	12	42.9	15	57.7	17	45.9
Total	**25**		**19**		**28**		**26**		**37**	

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A survey of 80 dairy farms, carried out during 2011-2012 detected *L. monocytogenes* in 4.0% of bulk tank milk samples [21]. Milk quality data such as coliform counts, total bacterial counts, and somatic cell counts were also collected. By treating the total bacterial count as a proxy for faecal contamination of milk and utilising farm and animal level prevalence and shedding rates of *L. monocytogenes*, a predictive model for the level of *L. monocytogenes* in bulk tank raw milk was developed.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *L. monocytogenes* in ready-to-eat foods [16]. Separate guidelines are specified for ready-to-eat foods in which growth of *L. monocytogenes* can occur and ready-to-eat foods in which growth of *L. monocytogenes* will not occur.

Standard 1.6.1 (Microbiological limits in food) of the Australia New Zealand Food Standards Code was similarly amended during 2016, in line with Proposal P1017 [29].

During 2016, MPI published the first five of a planned seven fact sheets to support control of *L. monocytogenes* in the food industry. The fact sheets published in 2016 were:

- *L. monocytogenes* and ready-to-eat foods [30]
- *Listeria* control measures [31]
- Cleaning and sanitising [32]
- Environmental testing for *Listeria* [33]
- Product testing for *L. monocytogenes* [34].

MPI also published an Animal Products Notice, *Specifications for Products Intended for Human Consumption*, which includes a section entitled "*Listeria* requirements for processors of certain ready-to-eat animal products" [35] .

A training video on swabbing for *Listeria* was released by MPI through YouTube [36].

An Animal Products Notice: *Raw Milk for Sale to Consumers. Regulated Control Scheme* was published requiring testing for *L. monocytogenes* at a standard frequency of once every 10 days, or a reduced frequency of once per calendar month if certain performance criteria are met [18].

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 2016 by data source

During 2016, 155 cases (3.3 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 2016 there were 5548 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 444 hospital admissions (9.5 admissions per 100,000 population) recorded in 2016, 219 were reported with norovirus infection as the principal diagnosis and 225 with norovirus infection as another relevant diagnosis. Of the 444 hospital admissions, 208 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 2016, 18 (9.7%) of the 185 norovirus outbreaks and 542 (9.8%) of the 5548 outbreak-associated cases were reported as foodborne (Table 42). 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 33.0% (185/561) of all enteric outbreaks and 53.5% (5548/10,378) of all outbreak-associated cases reported in 2016.

Table 42. Norovirus outbreaks reported, 2016

Measure	Foodborne norovirus infection outbreaks	All norovirus infection outbreaks
Outbreaks	18	185
Cases	542	5548
Hospitalised cases	0	29

Between 2007 and 2016 the annual number of foodborne norovirus outbreaks reported each year ranged from 10 (2007) to 30 (2009) (Figure 31).The total number of cases associated with these outbreaks each year ranged from 177 (2013) to 618 cases (2008).

Figure 31. Foodborne norovirus outbreaks and associated cases reported by year, 2007–2016

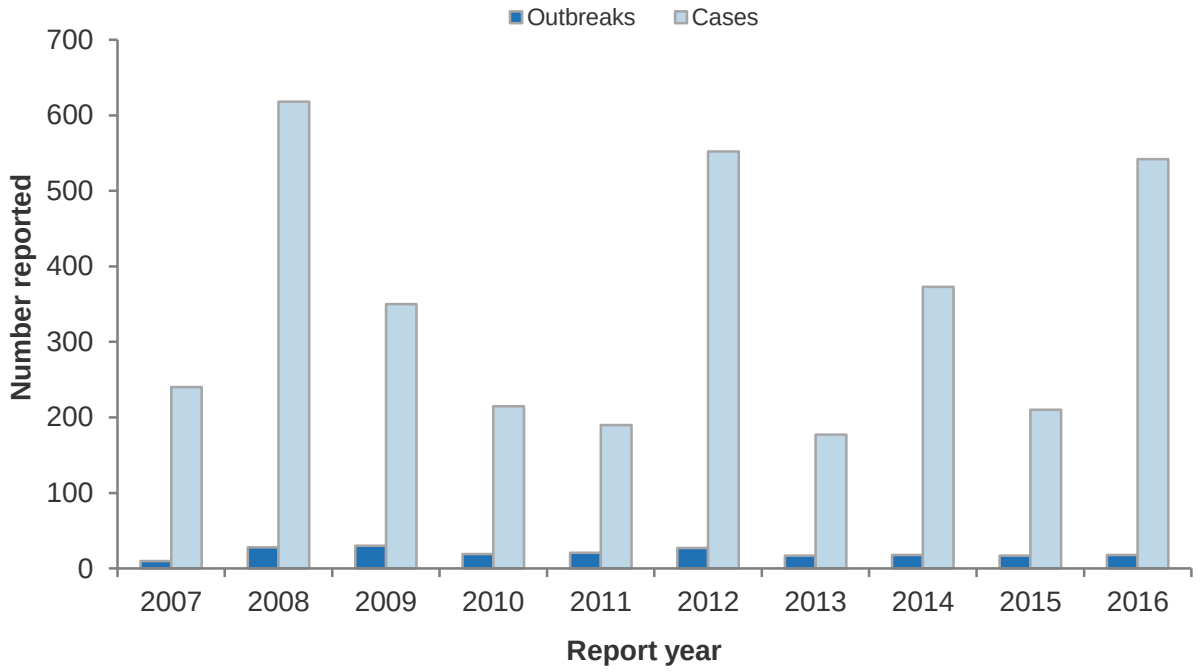


Table 43 contains details of the 18 foodborne norovirus outbreaks reported in 2016. A suspected food vehicle was not identified in any of these outbreaks. Four outbreaks (Auckland in March and July, Hawke's Bay in October and November) were strongly associated with preparation of food by a norovirus infected food handler.

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric Virus/Norovirus Reference Laboratory in 2016, faecal samples were received relating to 17 of the 18 foodborne outbreaks (Table 43). Norovirus was detected in faecal samples from these 17 foodborne outbreaks.

Table 43. Details of foodborne norovirus outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Taranaki	Mar	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 11P
Auckland	Mar	unknown [a]	Restaurant/cafe/bakery	Restaurant/cafe/bakery	4C, 18P
Regional	May	unknown	Community, church, sports gathering	Community, church, sports gathering	3C, 25P
Regional	Jun	unknown	School	School	5C, 63P
Auckland	Jul	unknown [a]	Restaurant/cafe/bakery	Restaurant/cafe/bakery	3C, 6P
Auckland	Aug	unknown	Childcare centre	unknown	2C, 31P
Auckland	Aug	unknown	unknown	unknown	5C, 125P
Northland	Sep	unknown	Workplace	Workplace	1C, 4P
Regional	Oct	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 5P
Hawke's Bay	Oct	unknown [a]	Restaurant/cafe/bakery	Restaurant/cafe/bakery	31C
Regional	Nov	unknown	Restaurant/cafe/bakery	unknown	4C, 41P
Toi Te Ora	Nov	unknown	Camp	Camp	24C
Regional	Nov	unknown	Other setting	Other setting	4C, 92P
Hawke's Bay	Nov	unknown [a]	Restaurant/cafe/bakery	Restaurant/cafe/bakery	7C
Toi Te Ora	Nov	unknown	Fast food restaurant	Fast food restaurant	1C, 6P
C and PH	Dec	unknown	School	unknown	2C, 8P
Regional	Dec	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C, 2P
Regional	Dec	unknown	Restaurant/cafe/bakery / Other food outlet	Restaurant/cafe/bakery	3C

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

[a] Outbreaks with a food handler tested positive for norovirus

Table 44 shows the number of hospitalised cases and total cases by genotype for the 18 foodborne norovirus outbreaks reported during 2016. 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 two outbreaks due to GII.4 (105 cases) and one outbreak due to GI.3 (130 cases).

Table 44. Norovirus genotypes reported in foodborne outbreaks, 2016

Norovirus	Outbreaks	Total cases	Hospitalised cases
GII.P16/GII.2	5	45	0
GII.17	3	64	0
GII.4	2	105	0
GI.Pb/GI.6	2	55	0
GI.1	2	35	0
GI.3	1	130	0
GII.7	1	68	0
GII.P12/GII.3	1	7	0
Genotype unknown	1	33	0

During 2016 it was possible to test for norovirus in the following foods; bivalve molluscan shellfish, soft berry fruit and leafy salads.

Norovirus types commonly reported

Norovirus genotyping data from ESR's Norovirus Reference Laboratory are shown in Table 45. The data relates to outbreaks not individual cases and includes all outbreaks, including those which are not associated with foodborne transmission.

In 2016, norovirus genogroup II (GII) was identified in 159/188 (84.6%) outbreaks. In the previous four years GII was identified in between 70.1% (2013) and 94.1% (2012) of outbreaks. In 2016, genogroup I (GI) was identified in 29/188 (15.4%) outbreaks. The norovirus genotype was determined for 98.9% (182/184) of ESR laboratory-confirmed norovirus outbreaks. As in previous years, GII.4 was the predominant norovirus genotype identified (84/186, 45.2% of outbreaks).

Table 45. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2012–2016

Norovirus genotypes	2012	2013	2014	2015	2016
Genogroup I	**9**	**45**	**51**	**13**	**29**
GI untyped	1	-	1	-	1
GI.1	-	1	-	-	2
GI.2	5	1	12	7	3
GI.3	-	12	17	2	15
GI.4	1	23	-	-	-
GI.5	-	1	1	2	-
GI.6	2	4	10	2	6
GI.7	-	1	1	-	-
GI.9	-	2	9	-	2
Genogroup II	**208**	**110**	**253**	**167**	**159**
GII untyped	2	-	4	5	1
GII.1	1	-	-	-	-
GII.2	1	13	2	14	1
GII.3	-	-	1	2	-
GII.4	160	55	203	90	84
GII.5	-	1	-	-	-
GII.6	30	4	22	19	2
GII.7	1	18	6	2	6
GII.8	-	-	1	1	-
GII.17	-	-	2	6	-
GII.20	-	-	1	-	-
GII.Pb/GII.3	2	-	-	-	-
GII.P12/GII.3	3	2	-	18	19
GII.P16/GII.2	5	-	-	-	27
GII.P16/GII.13	-	9	2	-	-
Other GII recombinants	3	8	9	10	19
Mixed GI and GII	**4**	**2**	**8**	**4**	**-**
Total outbreaks	**221**	**157**	**312**	**184**	**188**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

The emergence of a novel GII.17 norovirus was first detected in New Zealand in 2014 (3 outbreaks; April, July and November) but not identified again until September 2015. Between November 2015 and March 2016, GII.P17-GII.17 was identified in another 14 outbreaks, eight of which (298 cases) occurred in long-term care facilities. Viruses belonging to the GII.P17-GII.17 genotype have quickly replaced the GII.4 Sydney_2012 variant as the predominant norovirus circulating in Asia. GII.4 Sydney_2012 variant is still the predominant strain in New Zealand and it is yet unclear if GII.P17-GII.17 will become the

predominant circulating virus globally or in New Zealand, or lead to an increase in reported norovirus outbreaks [37].

A multi-site study of norovirus molecular epidemiology in Australia and New Zealand revealed that following its emergence in 2012, GII.4 Sydney 2012 variant continued to be the predominant cause of norovirus-associated acute gastroenteritis in Australia and New Zealand between 2013 and 2014 [38].

Relevant regulatory developments

Nil.

Salmonellosis

Summary data for salmonellosis in 2016 are given in Table 46.

Table 46. Summary of surveillance data for salmonellosis, 2016

Parameter	Value in 2016	Source
Number of notified cases	1091	EpiSurv
Notification rate (per 100,000)	23.2	EpiSurv
Hospitalisations (% of notifications)[a]	207 (19.0%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	338 (31%)	EpiSurv
Estimated food-related cases (%)[b]	468 (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 from any 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 in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for a range of pathogens, including *Salmonella* spp.. It is unclear at this stage how laboratory changes have affected the notification rates.

Salmonellosis cases reported in 2016 by data source

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

During 2016, 1091 cases (23.2 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 1071 cases infected with non-typhoidal *Salmonella* spp. (22.8 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 207 hospital admissions (4.4 admissions per 100,000 population) recorded in 2016, 154 were reported with salmonellosis as the principal diagnosis and 53 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 (954 cases) (Figure 32, Figure 33).

Figure 32. Salmonellosis notifications and laboratory-reported cases by year, 1997–2016

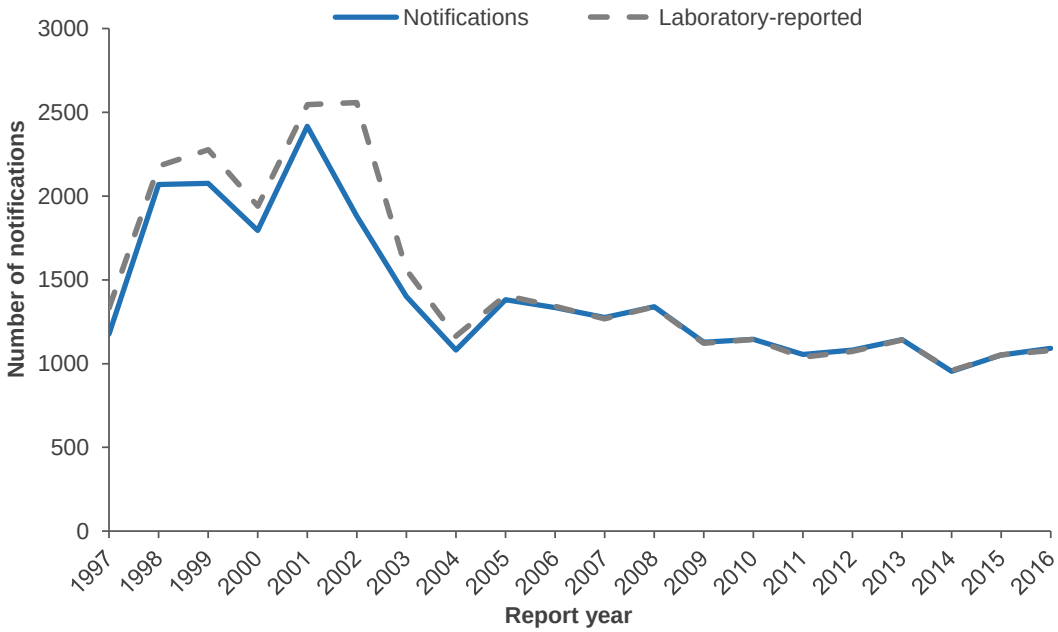
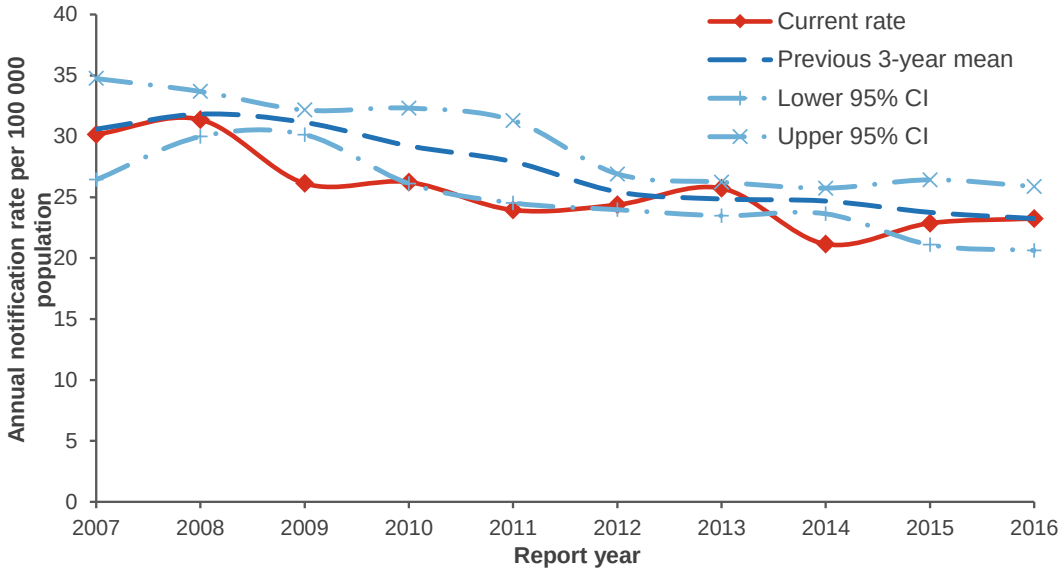
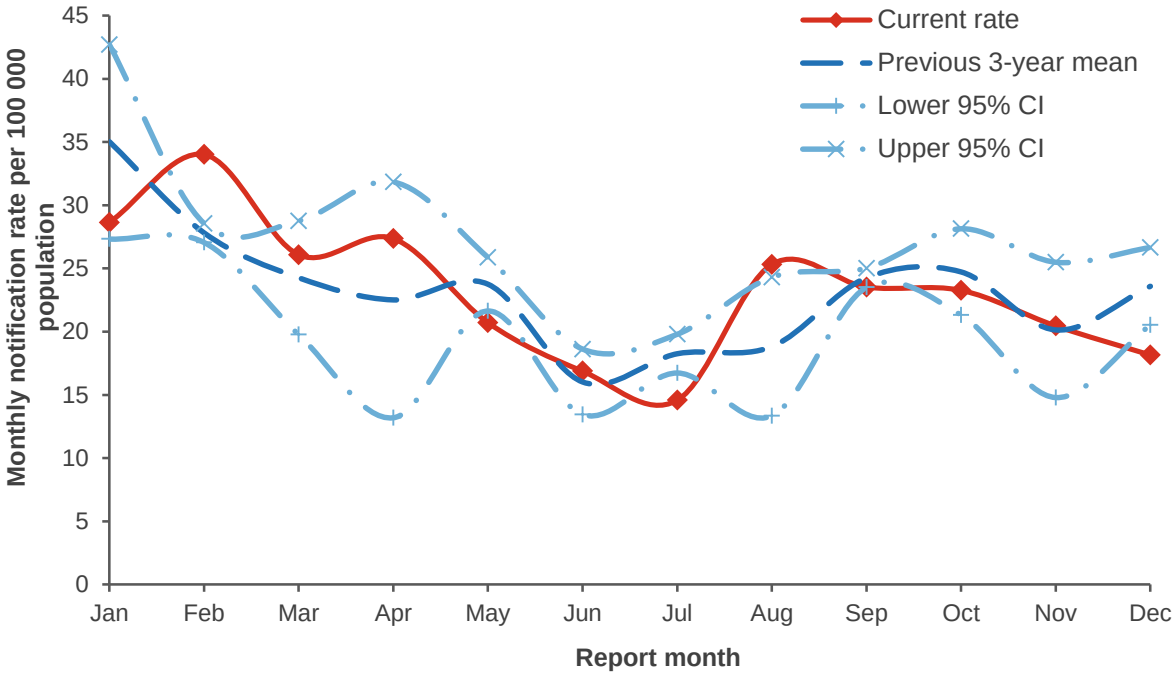


Figure 33. Salmonellosis notification rate by year, 2007–2016



The number of notified cases of salmonellosis per 100,000 population by month for 2016 is shown in Figure 34. The overall pattern for 2016 was similar to the previous three year mean with the highest rate during summer months (January and February) and lowest rates during the winter months (June and July). However, unlike the previous three years (2013-2015), where the highest peak was observed in January, in 2016 the highest number of notified cases was recorded in February (34.0 per 100,000 population).

Figure 34. Salmonellosis monthly rate (annualised), 2016



In 2016, the number and rate of notifications were similar for males and females, however hospitalisation rates were higher for males (Table 47). In 2015 notification rates and hospitalisation rates were similar for males and females.

Table 47. Salmonellosis cases by sex, 2016

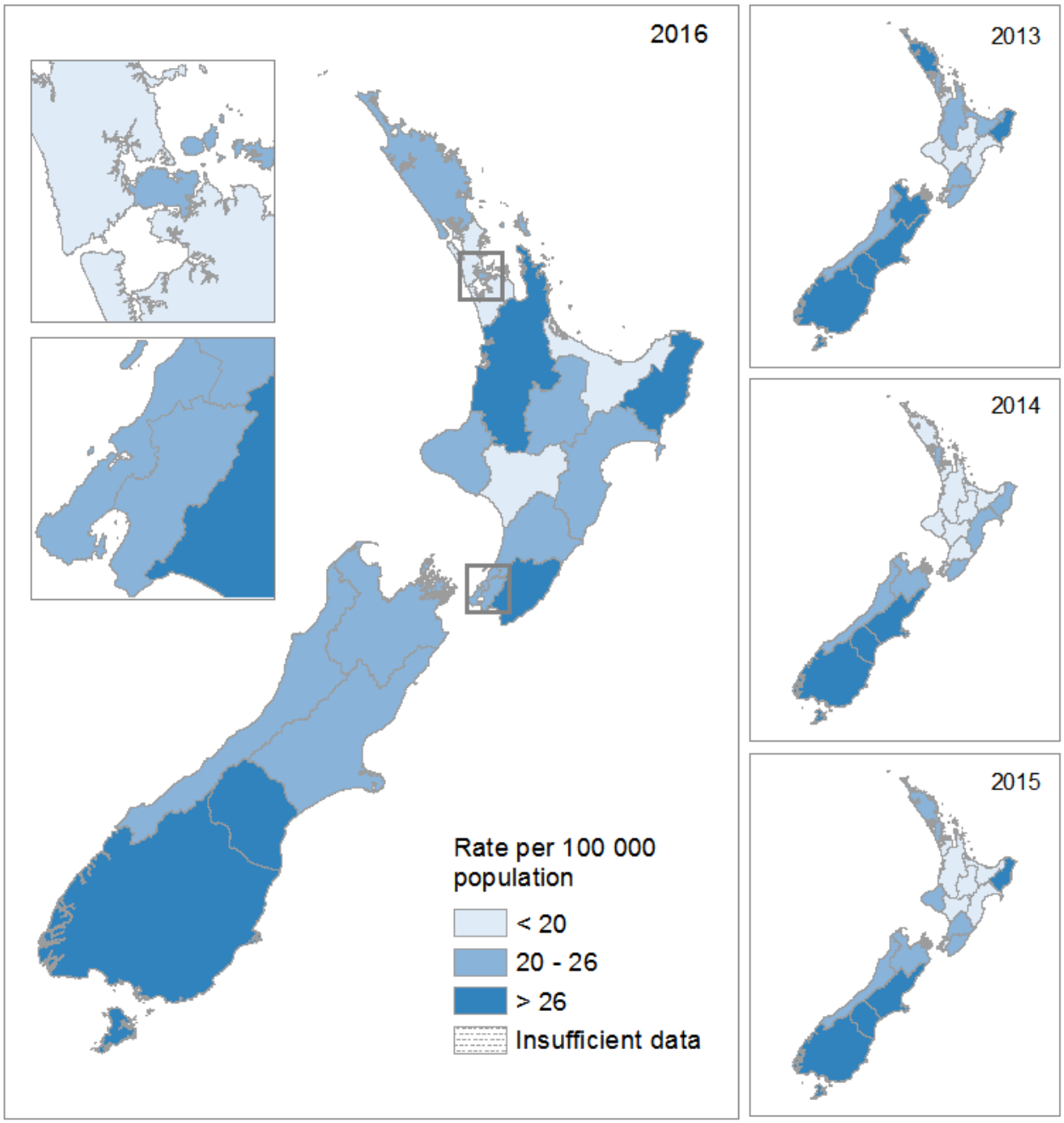
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	549	23.8	108	4.7
Female	542	22.7	99	4.1
Total	**1091**	**23.2**	**207**	**4.4**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

Rates of salmonellosis varied throughout the country as illustrated in Figure 35. The highest salmonellosis notification rate in 2016 was for Tairawhiti DHB (108.8 per 100,000, 52 cases), followed by South Canterbury DHB (37.2 per 100,000 population, 22 cases), Southern DHB (33.9 per 100,000, 108 cases), Waikato DHB (28.5 per 100,000, 114 cases) and Wairarapa DHB (27.5 per 100,000, 12 cases). South Canterbury and Southern DHBs had consistently high salmonellosis notification rates between 2013 and 2016 compared to the rest of the country.

Figure 35. Geographic distribution of salmonellosis notifications, 2013–2016



In 2016, notification rates and hospitalisation rates of salmonellosis were highest for infants aged less than 1 year (114.8 cases and 23.6 admissions per 100,000 population) and children aged 1 to 4 years (66.9 cases and 11.4 admissions per 100,000 population) when compared to other age groups (Table 48).

Table 48. Salmonellosis cases by age group, 2016

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	68	114.8	14	23.6
1 to 4	164	66.9	28	11.4
5 to 9	64	19.9	4	-
10 to 14	32	10.9	3	-
15 to 19	50	15.7	3	-
20 to 29	155	22.6	32	4.7
30 to 39	114	19.7	17	2.9
40 to 49	143	23.1	19	3.1
50 to 59	134	21.9	27	4.4
60 to 69	89	18.1	18	3.7
70+	78	16.8	42	9.0
Total	**1091**	**23.2**	**207**	**4.4**

[a] MoH NMDS data for hospital admissions

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

The most commonly reported risk factors for notified salmonellosis cases during 2016 were consumption of food from retail premises (45.8%), travelling overseas during the incubation period of the organism (31.0%) and contact with farm animals (24.6%) (Table 49).

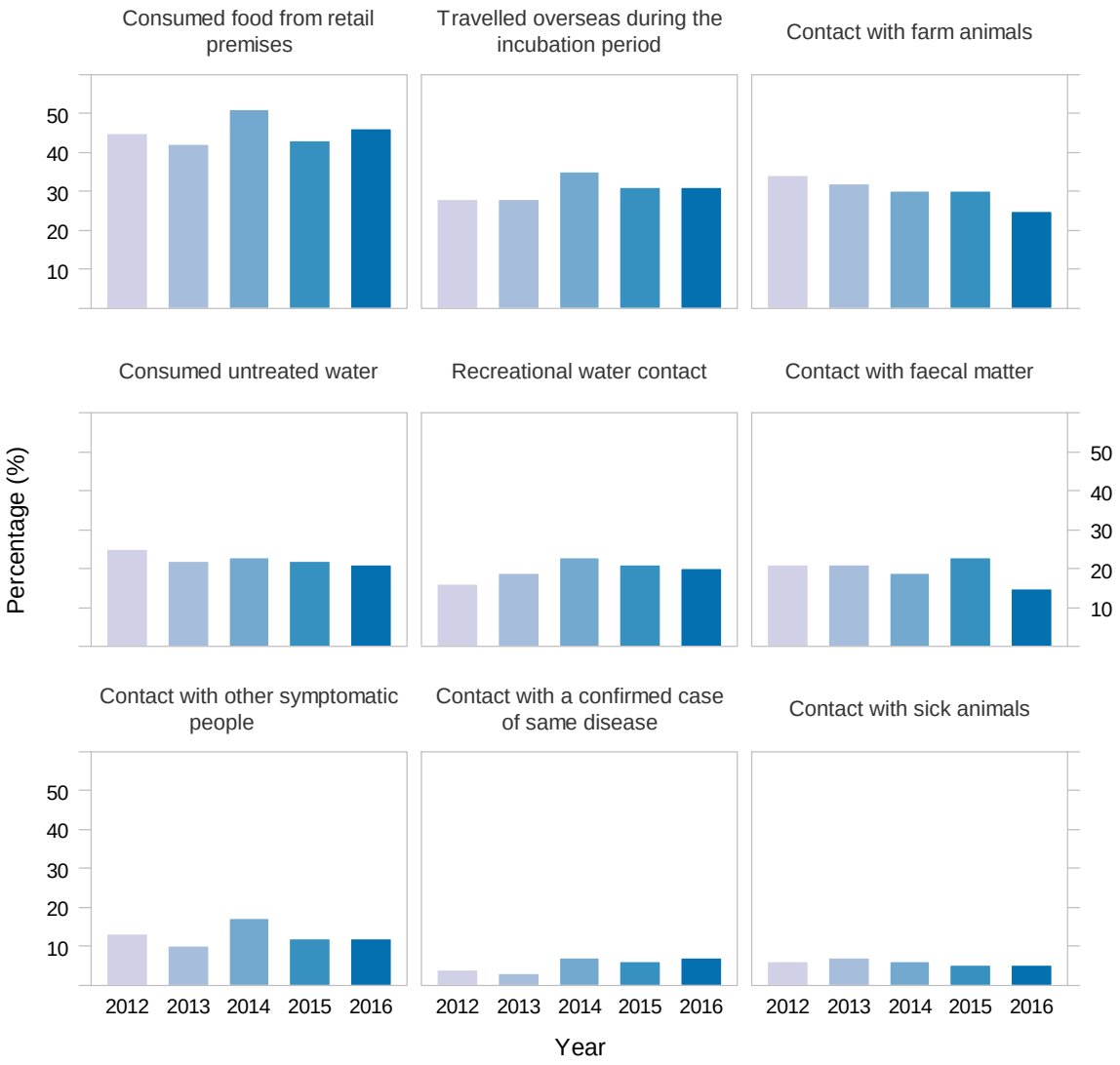
Table 49. Exposure to risk factors reported for salmonellosis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Consumed food from retail premises	275	325	491	45.8
Travelled overseas during the incubation period	288	640	163	31.0
Contact with farm animals	173	530	388	24.6
Consumed untreated water	130	503	458	20.5
Recreational water contact	135	534	422	20.2
Contact with faecal matter	97	537	457	15.3
Contact with other symptomatic people	89	647	355	12.1
Contact with a confirmed case of same disease	42	546	503	7.1
Contact with sick animals	30	623	438	4.6

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

The most commonly reported risk factor for salmonellosis cases between 2012 and 2016 was consumption of food from retail premises (Figure 36).

Figure 36. Percentage of cases with exposure to risk factors reported for salmonellosis and year, 2012–2016



For cases where information on travel was provided in 2016, 31.0% (95% CI 28.1-34.1%) 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 2016. The resultant distribution has a mean of 339 cases (95% CI 288-394).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 30.9% (95% CI 29.2-32.6%).

Outbreaks reported as caused by *Salmonella*

In the following sections the term *Salmonella* refers to serotypes of *Salmonella enterica* subspecies *enterica*, excluding *S.* Typhi and *S.* Paratyphi.

In 2016, there were 24 *Salmonella* outbreaks reported, of which 12 (50%) were reported as foodborne (Table 50). 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. Fourteen of the 15 hospitalisations due to *Salmonella* infection were associated with foodborne outbreaks.

Table 50. *Salmonella* outbreaks reported, 2016

Measure	Foodborne *Salmonella* spp. outbreaks	All *Salmonella* spp. outbreaks
Outbreaks	12	24
Cases	78	130
Hospitalised cases	14	15

The number of foodborne *Salmonella* outbreaks reported between 2007 and 2016 ranged from three (2015) to 12 (2016), (Figure 37). 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 37. Foodborne *Salmonella* outbreaks and associated cases reported by year, 2007–2016

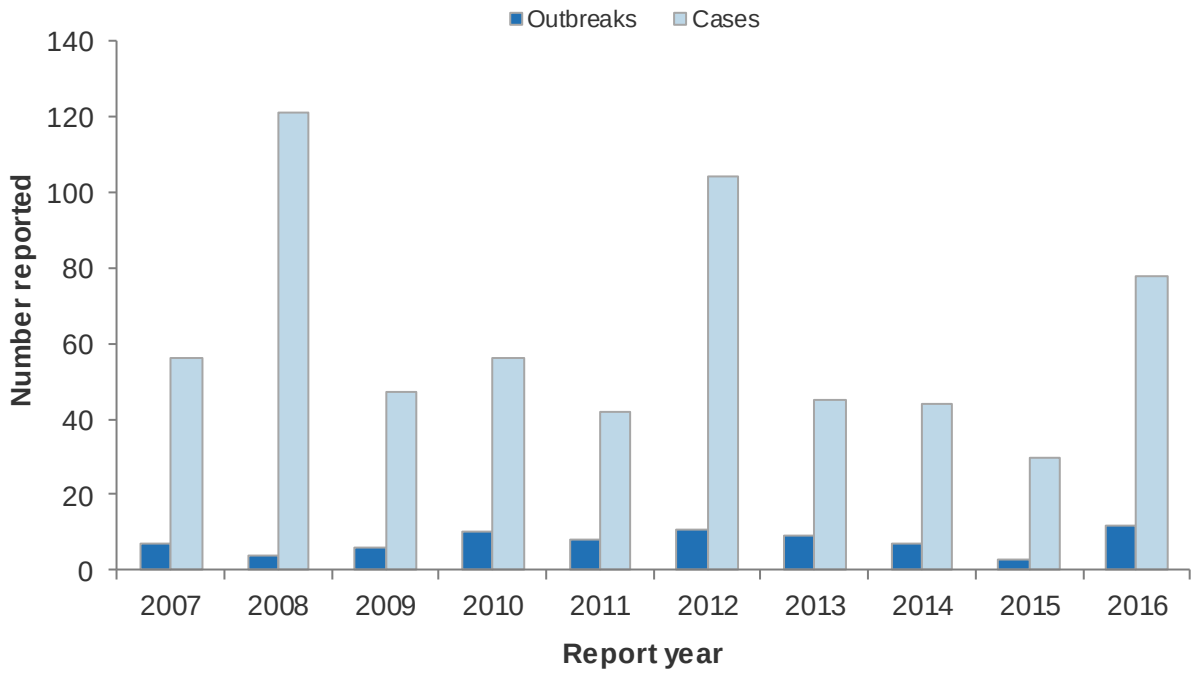


Table 51 contains details of the twelve foodborne *Salmonella* outbreaks reported in 2016. For one foodborne *Salmonella* outbreak (Regional Public Health in January) the evidence linking the outbreak to a suspected food vehicle was strong. Biscuit and biscuit dough samples relating to the outbreak were submitted to ESR's Public Health Laboratory. *S.* Typhimurium 60 was isolated from the food.

For the other outbreaks weak evidence linking the outbreak to food was recorded in EpiSurv. No other outbreak samples were submitted to ESR's Public Health Laboratory. One outbreak (Tairawhiti in March) was associated with preparation of food by a *Salmonella* infected food handler.

Table 51. Details of foodborne *Salmonella* outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Jan	spit roast (under cooked)	Home	Home	2C, 9P
Regional	Jan	Christmas cookies	Other setting	Home	3C, 5P
Auckland	Jan	tuna sushi	Restaurant/cafe/bakery	Restaurant/cafe/bakery	2C, 2P
Auckland	Feb	eggs, raw peppers, soft brie cheese	Supermarket/delicatessen	Supermarket/delicatessen	3C, 0P
Tairawhiti	Mar	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	27C, 0P
Toi Te Ora	Apr	unknown	Hotel/motel	Hotel/motel	2C, 0P
Waikato	Jul	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 2P
Auckland	Aug	unknown	Unknown	unknown	2C, 0P
MidCentral	Sep	unknown	Other institution / Other setting	unknown	11C, 0P
Auckland	Sep	unknown	Other setting	unknown	2C, 1P
Auckland	Nov	unknown	Home	unknown	1C, 1P
South	Dec	unknown	Unknown	unknown	1C, 1P

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

Salmonella types commonly reported

1. Human isolates

Isolates from 1071 cases infected with non-typhoidal *Salmonella* were typed by the ESR Enteric Reference Laboratory during 2016. Of these cases, 391 (36.5%) were *Salmonella* serotype Typhimurium.

Table 52 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 2016, of which *S.* Typhimurium phage type 56 variant (prior to 2012 known as RDNC-May 06 (65 cases)) and *S.* Typhimurium phage type 101 (47 cases) were most commonly detected. The most common of the other serotypes were *S.* Brandenburg (67 cases) and *S.* Stanley (60 cases).

Salmonella serotypes showing an increase in 2016 compared with 2015 included: *S.* Bovismorbificans, *S.* Brandenburg, and *S.* Stanley.

Table 52. *Salmonella* case serotypes and subtypes identified by the Enteric Reference Laboratory, 2012–2016

Serotype[a]	2012	2013	2014	2015	2016
***S.* Typhimurium**	**459**	**481**	**392**	**447**	**389**
1	35	30	22	38	34
9	11	13	17	27	42
12a	26	15	20	18	6
56 variant[b]	73	122	72	96	64
101	26	26	41	56	47
135	44	48	35	64	30
156	21	17	9	27	12
160	58	69	27	9	6
Other or unknown	157	134	166	112	148
***S.* Enteritidis**	**125**	**137**	**116**	**110**	**114**
1b	9	14	5	4	8
11[c]	52	27	39	45	46
Other or unknown	58	77	58	44	60
Other serotypes	**460**	**523**	**450**	**496**	**570**
S. Agona	11	11	15	12	18
S. Bovismorbificans	8	8	4	23	39
S. Brandenburg	34	52	35	52	67
S. Infantis	52	70	56	52	14
S. Mississippi	12	20	21	16	21
S. Montevideo	26	11	7	3	2
S. Saintpaul	27	43	26	37	35
S. Stanley	22	31	34	25	60
S. Thompson	2	16	5	32	13
S. Virchow	17	15	5	16	10
S. Weltevreden	24	28	31	18	18
S. enterica (I) ser. 4,[5],12 : i : -	38	27	27	22	23
Other or unknown	187	191	184	188	250
Total	**1044**	**1141**	**958**	**1053**	**1073**

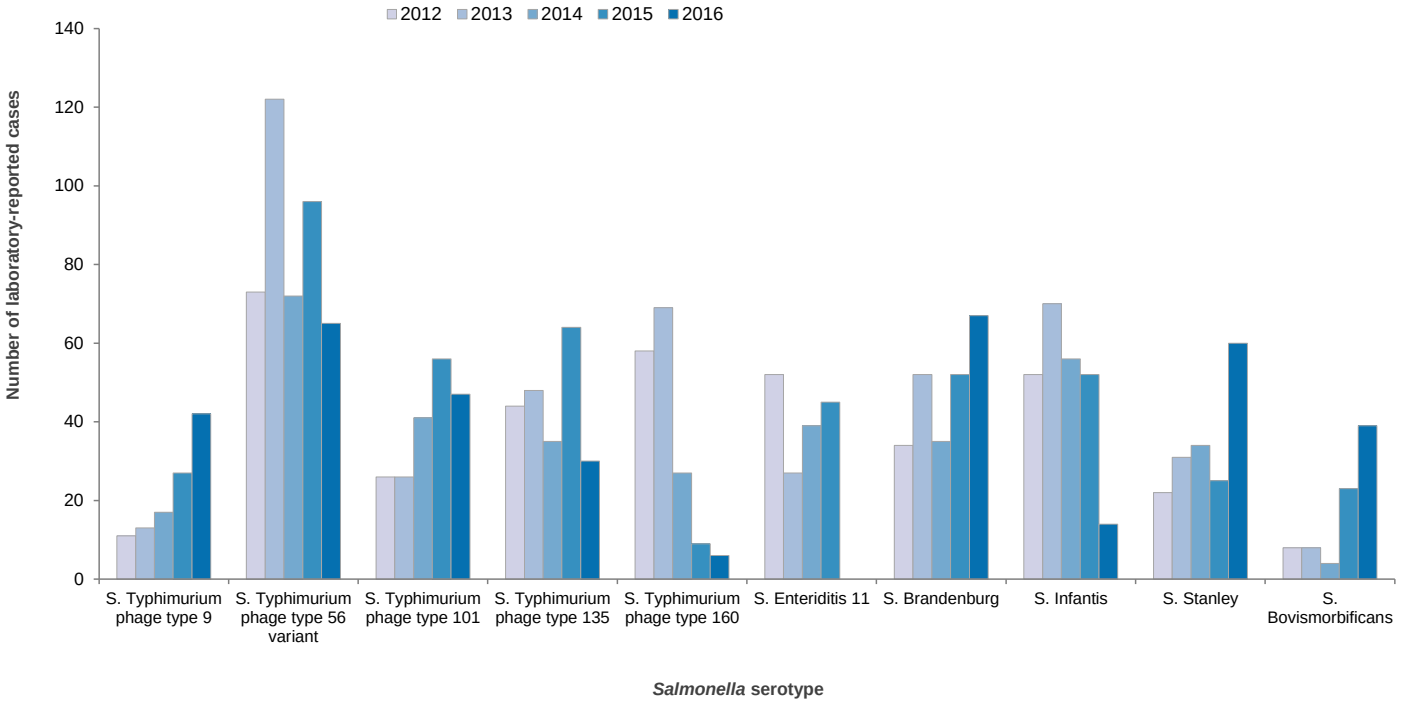
[a] Excludes *S.* Paratyphi and *S.* Typhi.

[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 38 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 2012 and 2016, with numbers remaining high relative to the other serotypes shown. *S.* Typhimurium phage type 160 has continued with a decreasing trend with only 6 cases of that serotype in 2016. An increased number of cases were serotyped as *S.* Typhimurium phage type 9, *S.* Stanley and *S*. Bovismorbificans in 2016 compared to the previous four years.

Figure 38. Number of laboratory-reported cases for selected *Salmonella* serotypes by year, 2012–2016



2. Non-human isolates

A total of 684 non-human *Salmonella* isolates were typed by the Enteric Reference Laboratory during 2016. *S.* Typhimurium and *S.* Enteritidis were the most commonly isolated serotypes in non-human samples in 2016, of which *S.* Typhimurium phage type 56 variant (prior to 2012 known as RDNC-May 06 (43 cases)) and *S.* Typhimurium phage type 101 (45 cases) were most commonly detected. The most common of the other serotypes were *S*. Bovismorbificans and *S.* Brandenburg with 135 and 127 cases, respectively (Table 53). 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 53. *Salmonella* serotypes and subtypes from non-human sources identified by the Enteric Reference Laboratory, 2012–2016

Serotype	2012	2013	2014	2015	2016	Major sources, 2016
S. Typhimurium	**421**	**358**	**220**	**258**	**249**	
1	57	26	13	16	14	Bovine (10)
9	9	39	9	9	12	Bovine (7), ovine (4)
12a	50	12	12	19	1	Bovine (1)
56 variant[a]	33	79	38	56	43	Bovine (10), feline (5), avian(9), environmental poultry(4), equine(8)
101	53	57	48	32	45	Bovine (34), avian(6)
135	12	15	12	18	10	Bovine (10)
RDNC	33	32	16	41	31	Bovine (20)
Unknown or other	174	98	72	67	93	
Other serotypes	**600**	**609**	**509**	**379**	**435**	
S. Agona	26	42	17	22	10	Bovine (3), meat/bone meal (3)
S. Anatum	10	28	23	6	9	Meat/bone meal (7)
S. Bovismorbificans	3	14	13	71	135	Bovine (122)
S. Brandenburg	113	197	129	102	127	Bovine (58), ovine (30), meat/bone meal (27)
S. Hindmarsh	77	56	77	49	48	Ovine (30), bovine (16),
S. Infantis	78	67	27	14	20	Meat/bone meal (9), environmental (7)
S. Mbandaka	35	26	20	10	6	Environmental (5)
S. Saintpaul	13	22	22	12	9	Reptile (3), canine (3)
S. Senftenberg	8	12	19	15	4	No major source
Other or unknown serotypes	237	145	162	78	67	
Total	**1021**	**967**	**729**	**637**	**684**	

[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.

3. Outbreak types

Table 54 shows the number of hospitalised cases and total cases by subtype for the 12 foodborne *Salmonella* outbreaks reported during 2016. A *Salmonella* subtype was determined for six of the 12 foodborne *Salmonella* outbreaks in 2016. No serotype was identified for three outbreaks. All 11 cases associated with a *S.* Enteritidis phage type 7 outbreak were hospitalised.

Table 54. *Salmonella* subtypes reported in foodborne outbreaks, 2016

Pathogen and subtype	Outbreaks	Total cases	Hospitalised cases
S. Brandenburg	1	11	0
S. Typhimurium phage type 60	1	8	0
S. Typhimurium phage type 9	1	3	0
S. Stanley	1	27	0
S. Javiana	1	2	0
S. Typhimurium phage type 1	1	3	0
S. Enteritidis phage type RDNC-Aug16	1	2	2
S. Enteritidis phage type 7	1	11	11
S. Enteritidis phage type 1b	1	2	0
Serotype unknown	3	9	1
Total	**12**	**78**	**14**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A survey of 80 dairy farms, carried out during 2011-2012 did not detect *Salmonella* in any bulk tank milk samples [21]. Milk quality data such as coliform counts, total bacterial counts, and somatic cell counts were also collected. By treating the total bacterial count as a proxy for faecal contamination of milk and utilising farm and animal level prevalence and shedding rates of *Salmonella*, a predictive model for the level of *Salmonella* in bulk tank raw milk was developed.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *Salmonella* spp. in ready-to-eat foods [16].

Standard 1.6.1 (Microbiological limits in food) of the Australia New Zealand Food Standards Code was amended in line with Proposal P1039 [17] to change the requirements for *Salmonella* in powdered infant formula products from not detected in 10 x 25 g samples to not detected in 60 x 25 g samples for powdered infant formula products and powdered follow-on formula.

Further amendments in line with Proposal P1022 [25] were made to criteria for raw/unpasteurised milk products, with criteria for butter made from unpasteurised milk and/or unpasteurised milk products, all raw milk cheese and raw milk unripened cheese being omitted and criteria for raw milk cheese being substituted. The actual criterion (not detected in 5 x 25 g samples) remained unchanged.

An Animal Products Notice: *Raw Milk for Sale to Consumers. Regulated Control Scheme* was published requiring testing for *Salmonella* spp. at a standard frequency of once every 10 days, or a reduced frequency of once per calendar month if certain performance criteria are met [18].

A further Animal Products Notice: *Specifications for National Microbiological Database Programme* set specifications relating to the National Microbiological Database (NMD), including for *Salmonella* spp. in red meat and poultry [26].

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 2016 by data source

In 2016, four individual cases of sapovirus infection were reported in EpiSurv. 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 2016, 24 sapovirus outbreaks were reported in EpiSurv with 268 associated cases and no deaths. One of the outbreaks was reported to be foodborne (Table 55) with 65 associated cases. 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.

The number of outbreaks in 2016 (24 outbreaks) was higher than the number of sapovirus outbreaks reported in previous years: 9 outbreaks in 2015, 16 outbreaks in 2014 and 8 outbreaks in 2013.

Table 55. Sapovirus outbreaks reported, 2016

Measure	Foodborne sapovirus outbreaks	All sapovirus outbreaks
Outbreaks	1	24
Cases	65	268
Hospitalised cases	0	22

One of the outbreaks with 65 associated cases was listed as potentially foodborne. In the last five years there has been 0 and 2 foodborne outbreaks notified each year.

Table 56 contains details of the foodborne sapovirus outbreak reported in 2016, the evidence linking the outbreak to the suspected foods was recorded as strong in EpiSurv.

Table 56. Details of foodborne Sapovirus outbreak, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Waikato	Mar	Mixed leaf salad, fruit salad	Hotel/motel	Hotel/motel	63C, 2P

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

In 2016, no food or clinical samples relating to the food-associated sapovirus outbreak were submitted to ESR's Public Health Laboratory.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2016 are given in Table 57.

Table 57. Summary of surveillance data for shigellosis, 2016

Parameter	Value in 2016	Source
Number of notified cases	174	EpiSurv
Notification rate (per 100,000)	3.7	EpiSurv
Hospitalisations (% of notifications)[a]	30 (17.2%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	105 (60.8%)	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: Isolation of any *Shigella* spp. from a stool sample or rectal swab and confirmation of genus.

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 in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs are screened by multiplex PCR for a range of pathogens, including *Shigella* spp.. It is unclear at this stage how laboratory changes have affected the notification rates.

Shigellosis cases reported in 2016 by data source

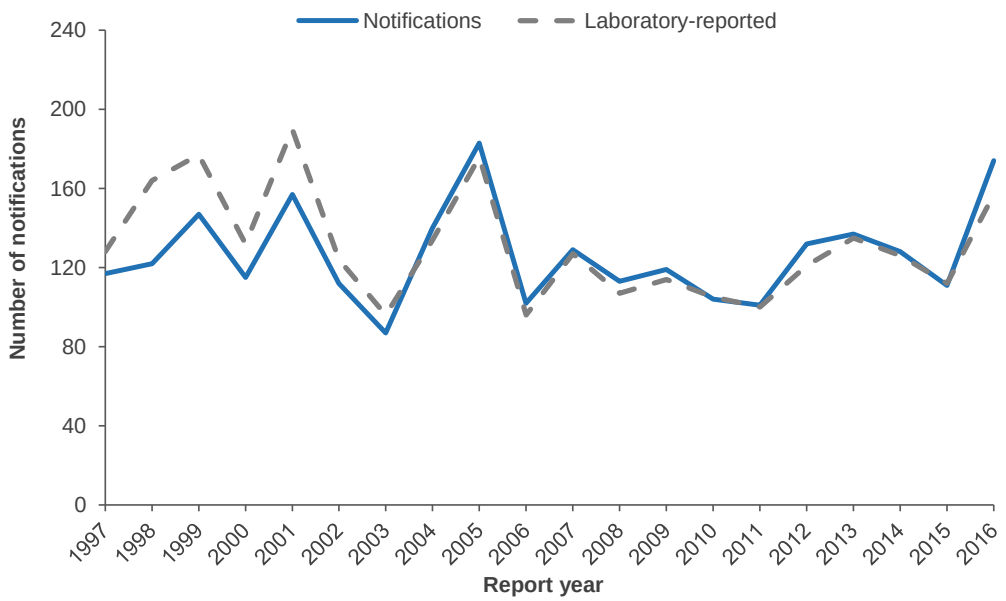
During 2016, 174 cases (3.7 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 157 cases (3.3 per 100,000 population) infected with *Shigella* in 2016.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 30 hospital admissions (0.6 admissions per 100,000 population) recorded in 2016, 20 were reported with shigellosis as the principal diagnosis and 10 with shigellosis as another relevant diagnosis.

Notifiable disease data

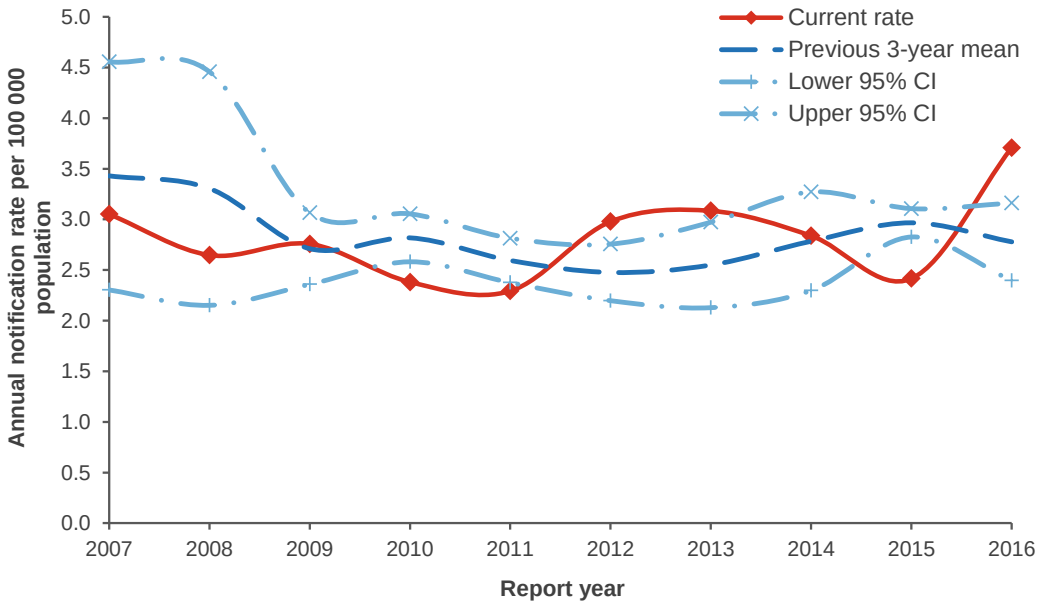
The number of notifications and laboratory reported cases of shigellosis was variable from year to year with the highest peak in notifications in 2005 (183 cases) followed by the second highest number of notifications in 2016 (174). Between 2006 and 2015 the number of notifications has been in the range of 101 to 137 cases (Figure 39).

Figure 39. Shigellosis notifications and laboratory-reported cases by year, 1997–2016



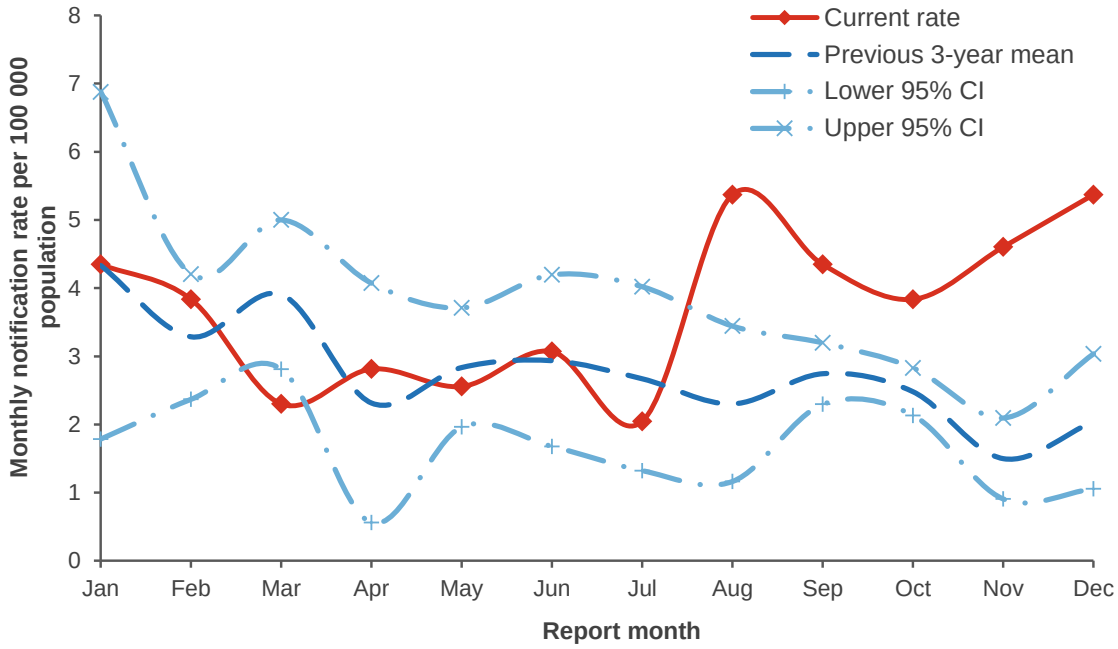
Between 2007 and 2015, the shigellosis notification rate has consistently been in the range of 2.3 to 3.1 notifications per 100,000 population (Figure 40), with an increase noted in 2016 (3.7 per 100,000 population).

Figure 40. Shigellosis notification rate by year, 2007–2016



The number of notified cases of shigellosis per 100,000 population by month for 2016 is shown in Figure 41. In 2015, the shigellosis notification rate was lower in March than the previous three year mean for the month, but higher in August to December. The number of notifications per month was small, ranging from 8 in July to 21 in August and December.

Figure 41. Shigellosis monthly rate (annualised), 2016



In 2016, the rates of notification for shigellosis were slightly higher for males compared to females, with hospitalisation rates similar for males and females (Table 58). This is similar to the pattern seen in 2015.

Table 58. Shigellosis cases by sex, 2016

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	95	4.1	15	0.6
Female	79	3.3	15	0.6
Total	**174**	**3.7**	**30**	**0.6**

[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 age group (7.3 per 100,000 population, 18 cases). The number of hospitalisation was low in all age groups, ranging from 0 to 6 hospitalisations across all age groups (Table 59).

Table 59. Shigellosis cases by age group, 2016

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	3	-	0	-
1 to 4	18	7.3	5	2.0
5 to 9	14	4.3	6	1.9
10 to 14	4	-	2	-
15 to 19	5	1.6	0	-
20 to 29	26	3.8	2	-
30 to 39	25	4.3	5	0.9
40 to 49	25	4.0	2	-
50 to 59	19	3.1	0	-
60 to 69	23	4.7	3	-
70+	12	2.6	5	1.1
Total	**174**	**3.7**	**30**	**0.6**

[a] MoH NMDS data for hospital admissions

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

The most commonly reported risk factor for shigellosis cases in 2016 was overseas travel during the incubation period (60.8%), followed by consuming food from retail premises (45.0%) (Table 60).

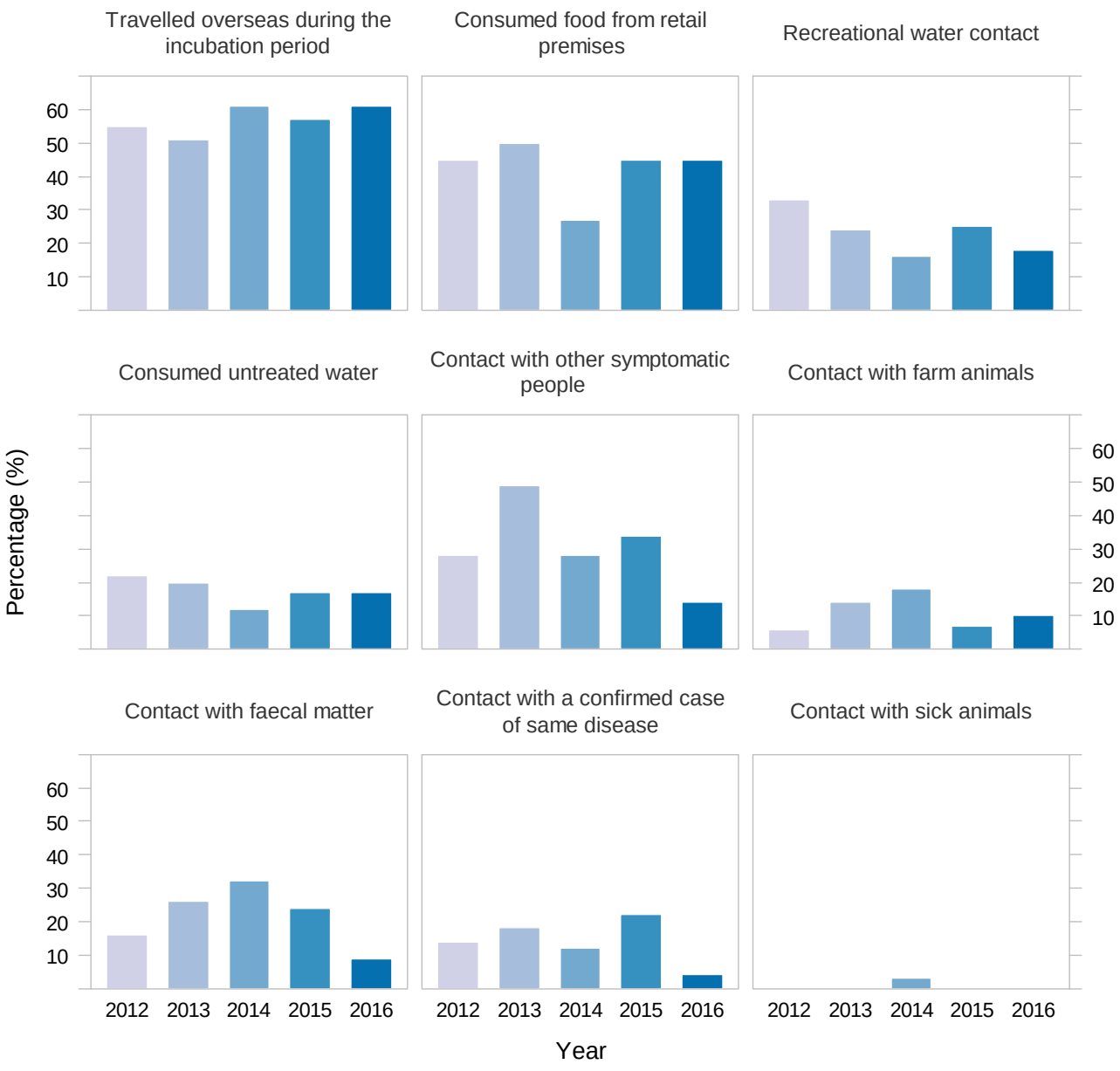
Table 60. Exposure to risk factors reported for shigellosis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Travelled overseas during the incubation period	101	64	9	61.2
Consumed food from retail premises	27	33	114	45.0
Recreational water contact	13	58	103	18.3
Consumed untreated water	11	54	109	16.9
Contact with other symptomatic people	16	101	57	13.7
Contact with farm animals	8	72	94	10.0
Contact with faecal matter	6	62	106	8.8
Contact with a confirmed case of same disease	4	95	75	4.0
Contact with sick animals	0	72	102	0.0

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

During the period 2012–2016, overseas travel during the incubation period has been the leading reported risk factor for shigellosis, followed by consuming food from retail premises (Figure 42).

Figure 42. Percentage of cases by exposure to risk factors associated with shigellosis and year, 2012-2016



For cases where information on travel was provided in 2016, 61.2% (95% CI 53.3-68.6%) 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 2016. The resultant distribution has a mean of 107 cases (95% CI 79-137).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 57.6% (95% CI 53.3-61.9%).

Outbreaks reported as caused by *Shigella* spp.

In 2016, there were two *Shigella* spp. outbreaks reported and one of these was reported to be foodborne (Table 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. There were no hospitalisations due a *Shigella* spp. associated outbreak.

Table 61. *Shigella* spp. outbreaks reported, 2016

Measure	Foodborne *Shigella* spp. outbreaks	All *Shigella* spp. outbreaks
Outbreaks	1	2
Cases	8	13
Hospitalised cases	0	0

The number of foodborne shigellosis outbreaks was steady over the five year period 2011–2015, with four or five foodborne outbreaks being reported each year. The highest number of cases associated with outbreaks in a year was 39 cases in 2015. From 2007 to 2010 and in 2016 there were no more than two outbreaks reported each year (Figure 43).

Figure 43. Foodborne *Shigella* spp. outbreaks and associated cases reported by year, 2007–2016

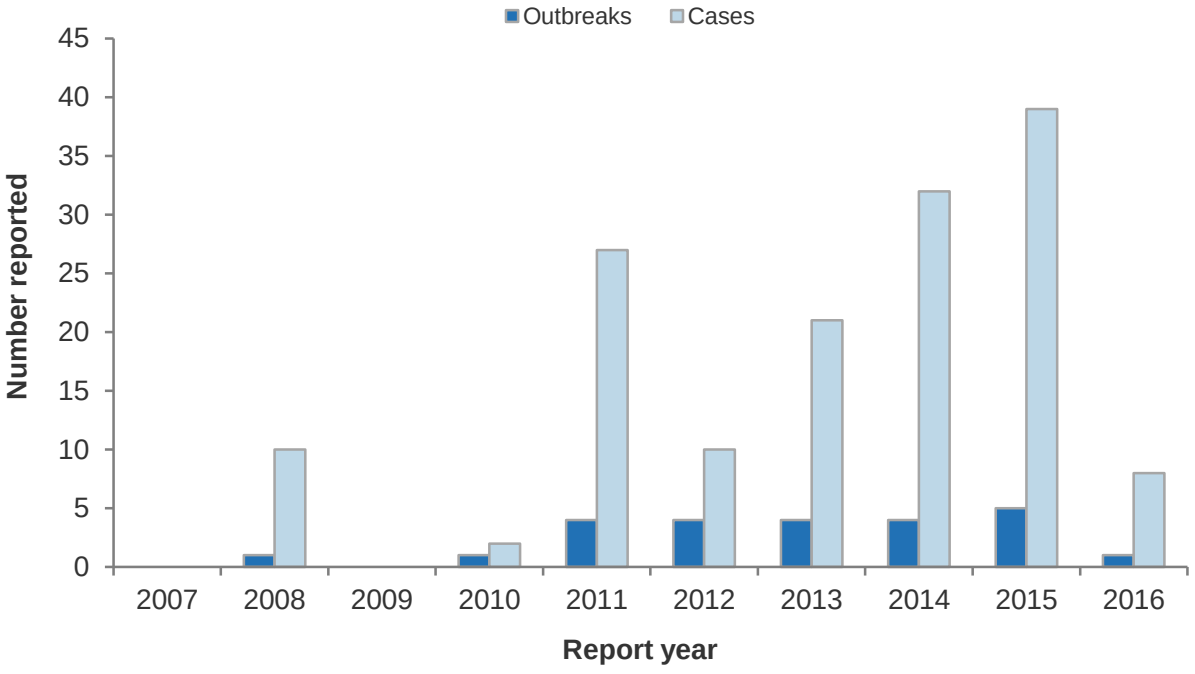


Table 62 contains details of the foodborne *Shigella* spp. outbreak reported in 2016. The evidence linking this outbreak to specific foods or food in general was weak.

Table 62. Details of foodborne *Shigella* spp. outbreaks, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Toi Te Ora	Aug	Unknown	Hotel/motel	unknown	1C, 7P

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

No clinical or food samples relating to the August *Shigella* spp. outbreak listed in Table 62 were submitted to ESR's Public Health Laboratory.

Shigella types commonly reported

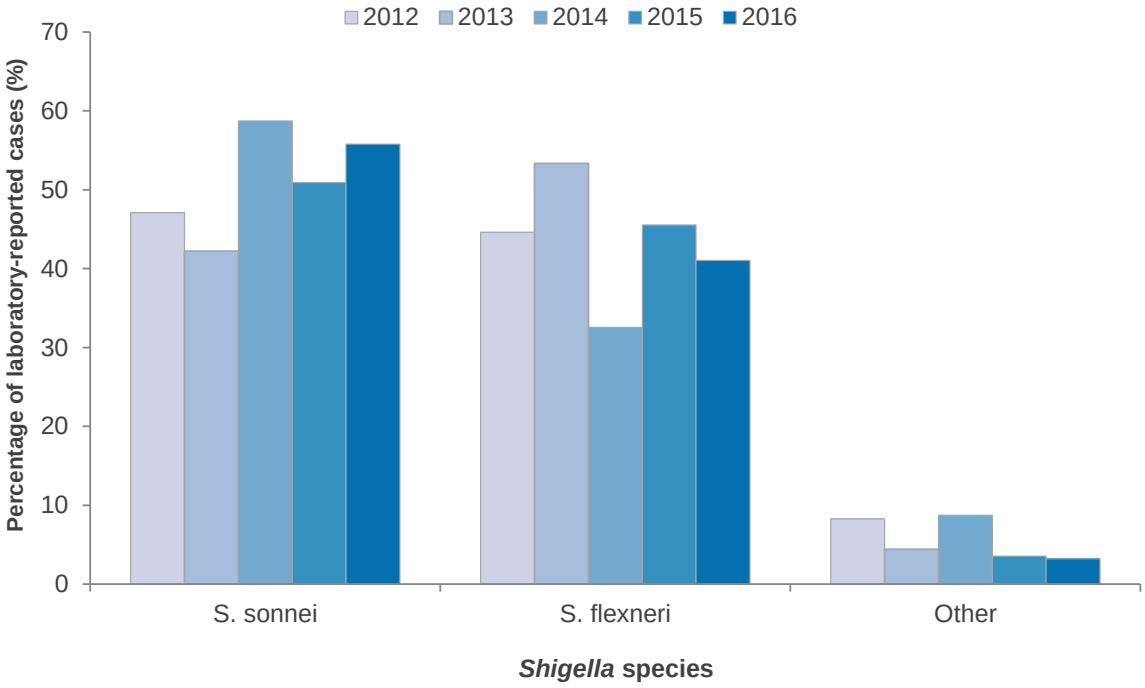
In 2016, the Enteric Reference Laboratory at ESR reported 157 cases infected with *Shigella* spp. *S. sonnei* and *S. flexneri* were the species most often identified. Of these, *S. sonnei* biotype g was most common in 2016 (Table 63).

Table 63. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2012–2016

Species	2012	2013	2014	2015	2016
S. sonnei	**57**	**57**	**74**	**57**	**87**
biotype a	27	35	32	20	31
biotype f	3	1	6	0	1
biotype g	27	21	36	37	55
S. flexneri	**54**	**72**	**41**	**51**	**64**
1	1	6	7	8	1
2a	10	12	11	14	16
2b	3	2	6	6	4
3a	3	10	4	7	18
Other	37	42	13	16	4
Other	**10**	**6**	**11**	**4**	1
S. boydii	7	5	9	4	20
S. dysenteriae	3	1	1	0	**6**
Shigella species not identified	0	0	1	0	3
Total	**121**	**135**	**126**	**112**	**157**

The percentage of shigellosis cases infected with *S. sonnei* in 2016 (55%) was within the range of values observed between 2012 and 2015 (between 42% and 59%). The percentage of shigellosis cases with *S. flexneri* in 2016 (41%) was also within the range of values observed between 2012 and 2015 (between 33% and 53%) (Figure 44).

Figure 44. Percentage of laboratory-reported cases by *Shigella* species and year, 2012–2016



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 2016 by data source

During 2016, there was one notification of *S. aureus* intoxication and no resulting deaths 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 was one hospital admission recorded in 2016 with *S. aureus* intoxication recorded as the principal diagnosis.

Outbreaks reported as caused by *Staphylococcus aureus*

In 2016, one foodborne *S. aureus* outbreak was reported with 14 associated cases (Table 64). 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 64. *S. aureus* outbreaks reported, 2016

Measure	Foodborne *S. aureus* outbreaks	All *S. aureus* outbreaks
Outbreaks	1	1
Cases	14	14
Hospitalised cases	0	0

The number of foodborne outbreaks associated with *S. aureus* reported each year between 2007 and 2016 ranged from zero to two (Figure 45). No *S. aureus* outbreaks were reported in EpiSurv in three of the last ten years.

Figure 45. Foodborne *S. aureus* outbreaks and associated cases reported by year, 2007–2016

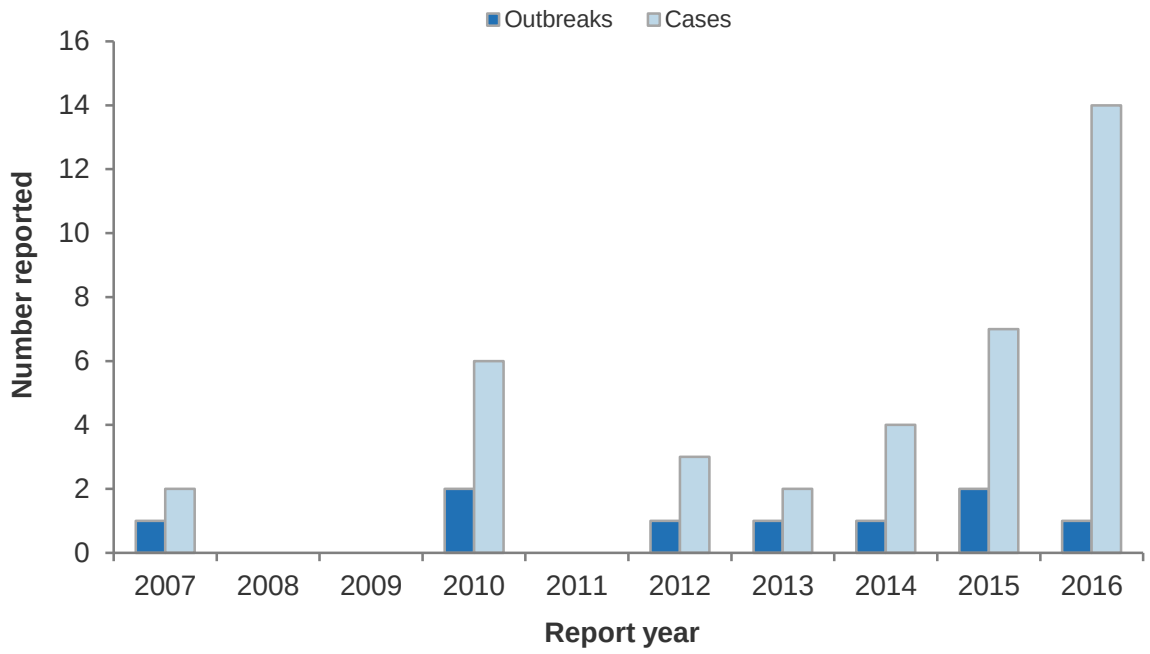


Table 65 contains details of the foodborne *S. aureus* outbreak reported in 2016. The level of evidence for suspected foods was weak.

Table 65. Details of foodborne *S. aureus* outbreak, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
South	Apr	unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 13P

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

In 2016, a faecal specimen was submitted to ESR's Public Health Laboratory relating to the outbreak listed in Table 65. Staphylococcal enterotoxin was detected in the faecal sample.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for *S. aureus* in ready-to-eat foods [16].

Standard 1.6.1 (Microbiological limits in food) of the Australia New Zealand Food Standards Code was amended in line with Proposal P1039 [17] to remove the limit for Coagulase-positive staphylococci in powdered infant formula products.

An Animal Products Notice: *Raw Milk for Sale to Consumers. Regulated Control Scheme* was published requiring testing for Coagulase-positive staphylococci at a standard frequency of once every 10 days, or a reduced frequency of once per calendar month if certain performance criteria are met [18].

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
NSP: 20 MU/100 g shellfish
DSP: 20 g/100 g or 5 MU/100 g shellfish
PSP: 80 g/100 g shellfish
(MU = mouse units)

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 2016

During 2015, three cases (0.06 per 100,000 population) of toxic shellfish poisoning and no resulting deaths were reported in EpiSurv.

The ICD-10 code T61.2 was used to extract hospitalisation data for 'other fish and shellfish poisoning' from the MoH NMDS database. Of the 14 hospital admissions (0.3 admissions per 100,000 population) reported in 2016, 11 were reported with 'other fish and shellfish poisoning' as the primary diagnosis and three were reported as another relevant diagnosis. Note that this ICD-10 code includes shellfish and other fish. It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified.

Outbreaks reported as caused by toxic shellfish poisoning

In 2016, 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 2 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

Nil.

VTEC/STEC infection

Summary data for VTEC/STEC infection in 2016 are given in Table 66.

Table 66. Summary of surveillance data for VTEC/STEC infection, 2016

Parameter	Value in 2016	Source
Number of notified cases	418	EpiSurv
Notification rate (per 100,000)	8.9	EpiSurv
Hospitalisations (% of notifications)[a]	15 (3.6%)	MoH NMDS, EpiSurv
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	39 (9.3%)	EpiSurv
Estimated food-related cases (%)[b]	113 (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.*

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” [39].

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*" [40]. At this stage, the current report will maintain terminology that aligns with the New Zealand schedule.

Changes to laboratory methods in 2015

In June 2015 some Auckland laboratories changed the methodology for testing faecal specimens. These changes include using polymerase chain reaction (PCR) for molecular detection of VTEC/STEC and all faecal samples being tested for VTEC/STEC instead of only faecal samples with blood, or those from under 5 year olds. These changes have resulted in an increased notification rate for VTEC/STEC for the Auckland and Northland areas.

VTEC/STEC infection cases reported in 2016 by data source

During 2016, 418 cases (8.9 per 100,000 population) of VTEC/STEC infection and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 491 cases (10.5 cases per 100,000) infected with VTEC/STEC in 2016.

The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E. coli* infection hospitalisation data from the MoH NMDS database. Of the 15 hospital admissions (0.3 admissions per 100,000 population) recorded in 2016, nine were reported with enterohaemorrhagic *E. coli* infection as the principal diagnosis and six 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 (Figure 46 and Figure 47).

Figure 46. VTEC/STEC infection notifications by year, 1997–2016

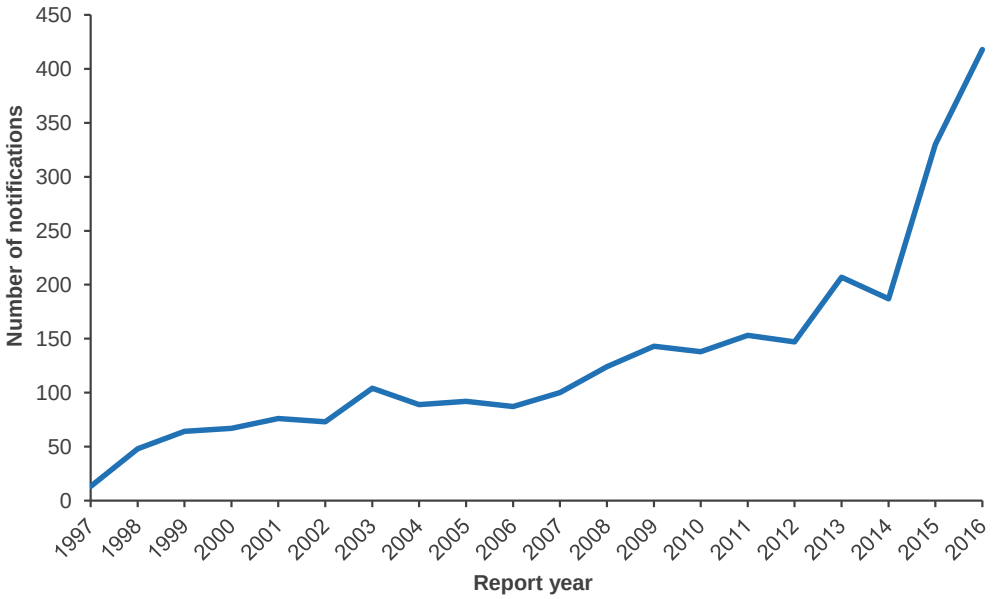
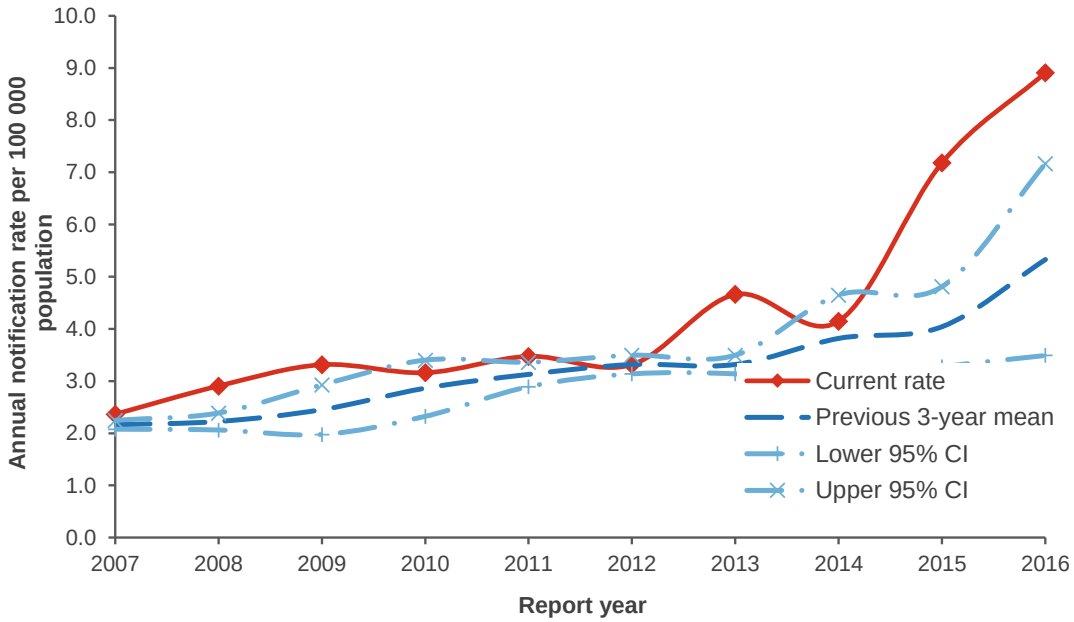
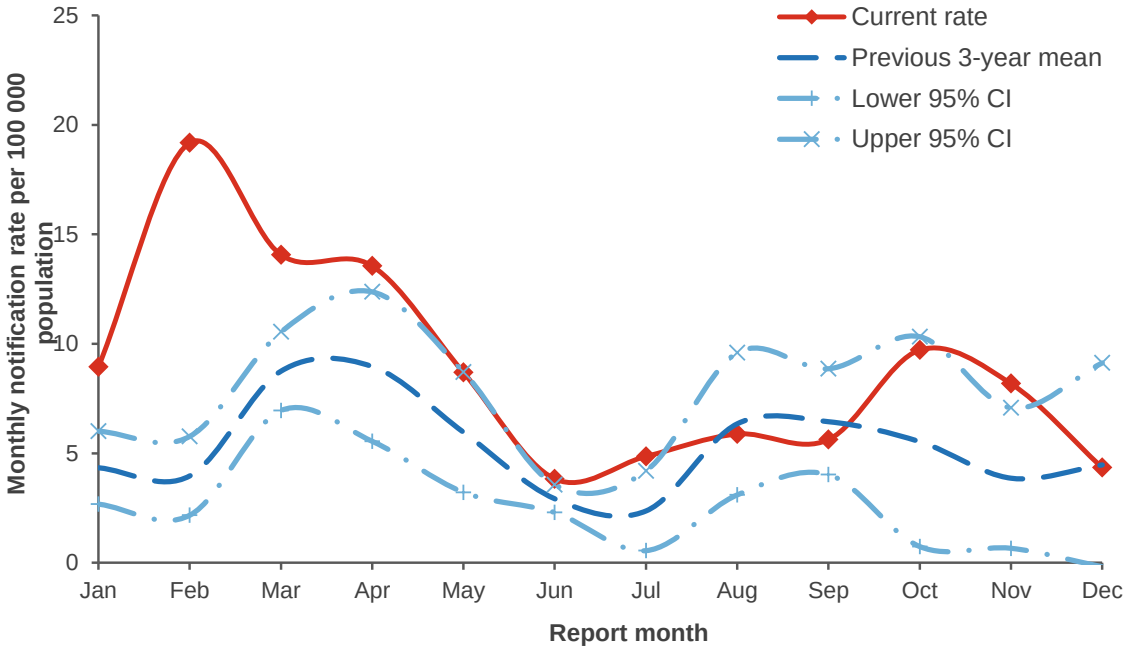


Figure 47. VTEC/STEC infection notification rate by year, 2007–2016



The number of notified cases of VTEC/STEC infection per 100,000 population by month for 2016 are shown in Figure 48. The 2016 monthly notification rate trend was generally similar to the trend in recent years (2013-2015) with slight peaks in autumn and spring, with the exception of a higher peak in February.

Figure 48. VTEC/STEC infection monthly rate (annualised), 2016



In 2016 notification rates were higher for females compared to males, however, hospitalisation rates were similar for females and males (Table 67).

Table 67. VTEC/STEC infection cases by sex, 2016

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	175	7.6	7	0.3
Female	243	10.2	8	0.3
Total	**418**	**8.9**	**15**	**0.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

In 2016, the VTEC/STEC infection notification rate was highest for the 1 to 4 years age group (44.4 per 100,000 population, 109 cases) and the less than 1 year age group (43.9 per 100,000, 26 cases). The number of hospitalisations ranged between zero and five for each of the age groups (Table 68).

Table 68. VTEC/STEC infection cases by age group, 2016

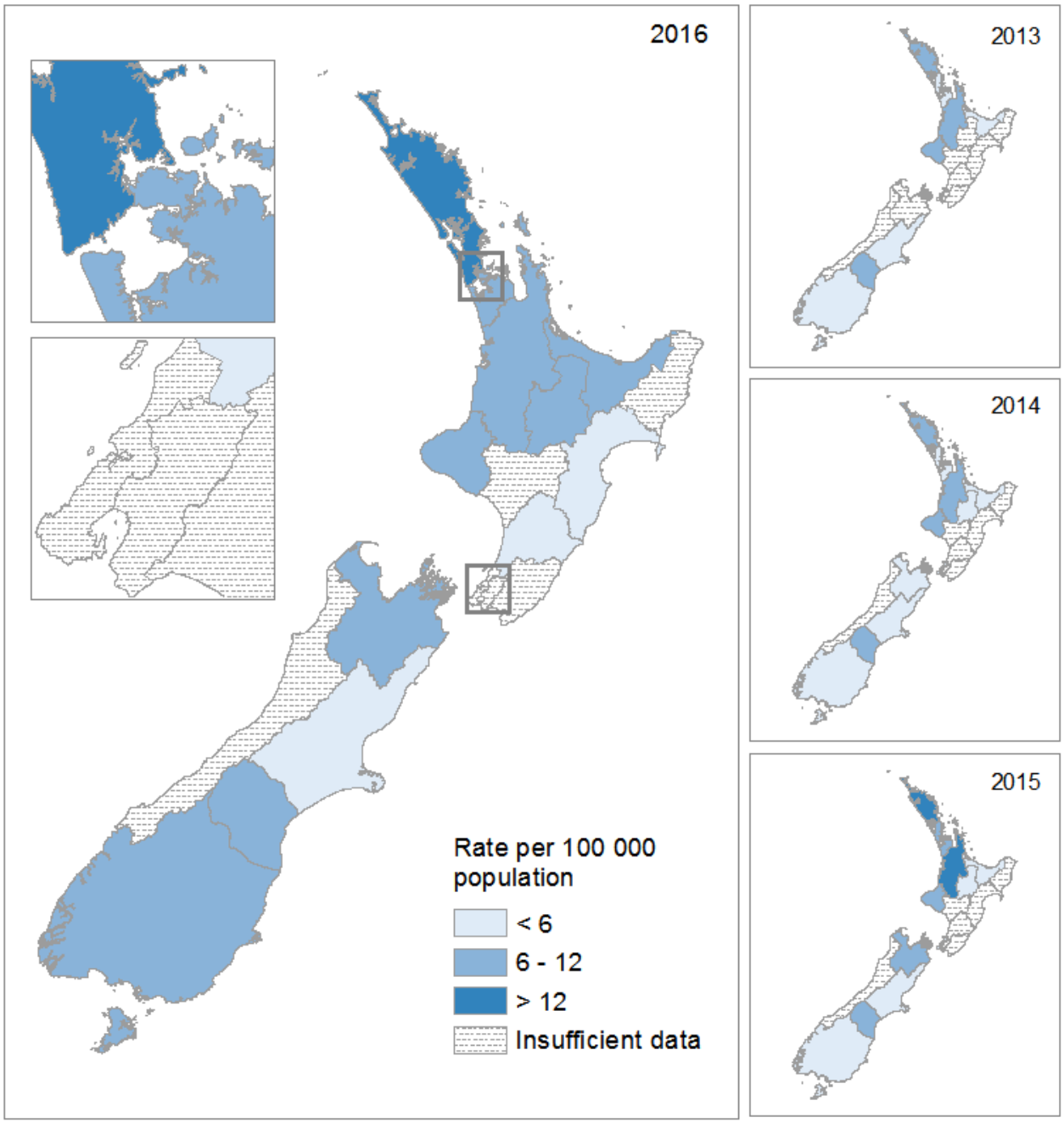
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	26	43.9	0	-
1 to 4	109	44.4	5	2.0
5 to 9	27	8.4	0	-
10 to 14	18	6.1	1	-
15 to 19	21	6.6	0	-
20 to 29	49	7.1	1	-
30 to 39	27	4.7	1	-
40 to 49	32	5.2	2	-
50 to 59	27	4.4	1	-
60 to 69	41	8.4	3	-
70+	41	8.8	1	-
Total	**418**	**8.9**	**15**	**0.3**

[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 49. In 2016, the highest rates of VTEC/STEC infection were reported for Northland (27.4 per 100,000, 47 cases), Waitemata (14.9 per 100,000, 88 cases), Counties Manukau (12.0 per 100,000, 64 cases), and Taranaki (12.0 per 100,000, 14 cases) DHBs. South Canterbury DHB (11.8 per 100,000, 7 cases) had the highest rate in the South Island. Note that rates were not calculated for 6 DHBs where there were insufficient (less than 5) cases notified in 2016.

Figure 49. Geographic distribution of VTEC/STEC infection notifications, 2013–2016



It should be noted that VTEC/STEC infection cases are reported using a different report form to other enteric diseases, resulting in an expanded range of investigated risk factors. In 2016, the most commonly reported risk factors for VTEC/STEC infection cases were contact with household pets (90.8%), consumption of raw fruit or vegetables (83.5%), and consumption of dairy products (77.7%) (Table 69).

Table 69. Exposure to risk factors reported for notifications of VTEC/STEC infection, 2016

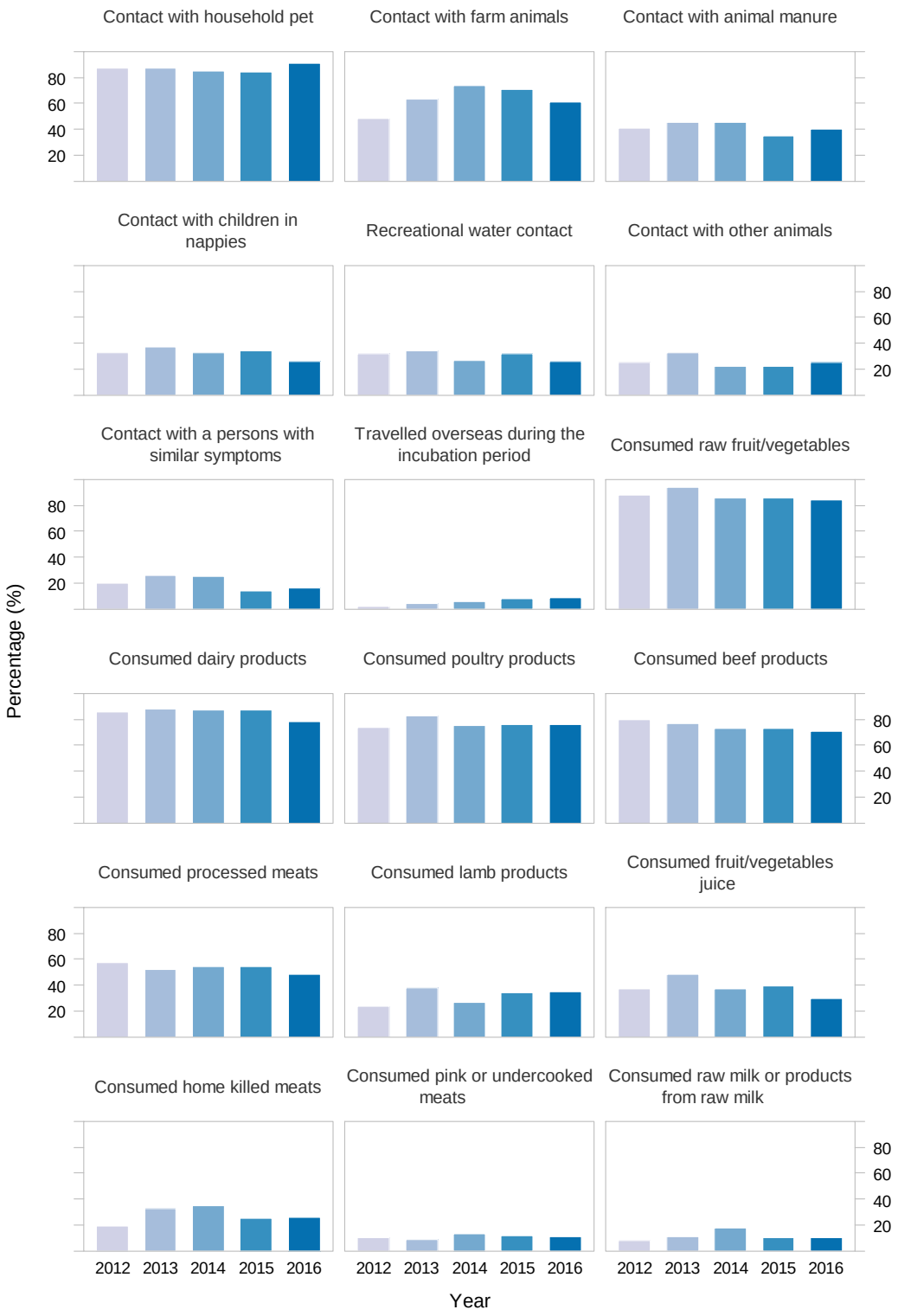
Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Contact with household pets	158	16	244	90.8
Consumed raw fruit/vegetables	167	33	218	83.5
Consumed dairy products	157	45	216	77.7
Consumed poultry products	145	45	228	76.3
Consumed beef products	137	55	226	71.4
Contact with farm animals	89	58	271	60.5
Consumed processed meats	91	97	230	48.4
Contact with animal manure	41	61	316	40.2
Consumed lamb, hogget or mutton products	63	119	236	34.6
Consumed fruit/vegetables juice	54	126	238	30.0
Contact with recreational water	72	204	142	26.1
Consumed home killed meats	49	141	228	25.8
Contact with children in nappies	59	171	188	25.7
Contact with other animals	29	85	304	25.4
Contact with persons with similar symptoms	62	315	41	16.5
Consumed pink or undercooked meats	19	149	250	11.3
Consumed raw milk or products from raw milk	21	187	210	10.1
Travelled overseas during the incubation period	37	360	21	9.3

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied.

Cases may have more than one risk factor recorded.

Between 2012 and 2016, the risk factors reported by VTEC/STEC infection cases generally occurred in the same order of importance and to a similar magnitude (Figure 50). The most commonly reported risk factors (excluding consumption of various commonly-consumed foods) were contact with household pets and contact with farm animals. The foods with the highest reporting frequency by cases were raw fruit and vegetables, and dairy products, followed closely by beef and poultry products, and processed meats.

Figure 50. Percentage of cases with exposure to risk factors reported for VTEC/STEC infection and year, 2012–2016



For cases where information on travel was provided in 2016, 9.3% (95% CI 6.7-12.7%) 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 2016. The resultant distribution has a mean of 39 cases (95% CI 23-58).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 7.6% (95% CI 6.0-9.5%).

Outbreaks reported as caused by VTEC/STEC

Of the 16 outbreaks (52 cases) of VTEC/STEC infection during 2016, one outbreak was classed as foodborne (Table 70). 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 70. VTEC/STEC outbreaks reported, 2016

Measure	Foodborne VTEC/STEC outbreaks	All VTEC/STEC outbreaks
Outbreaks	1	16
Cases	11	52
Hospitalised cases	0	6

The number of foodborne VTEC/STEC outbreaks reported between 2007 and 2016 ranged from one to four (2014), with no outbreaks reported for four of the ten years (Figure 51). 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).

Figure 51. Foodborne VTEC/STEC outbreaks and associated cases reported by year, 2007–2016

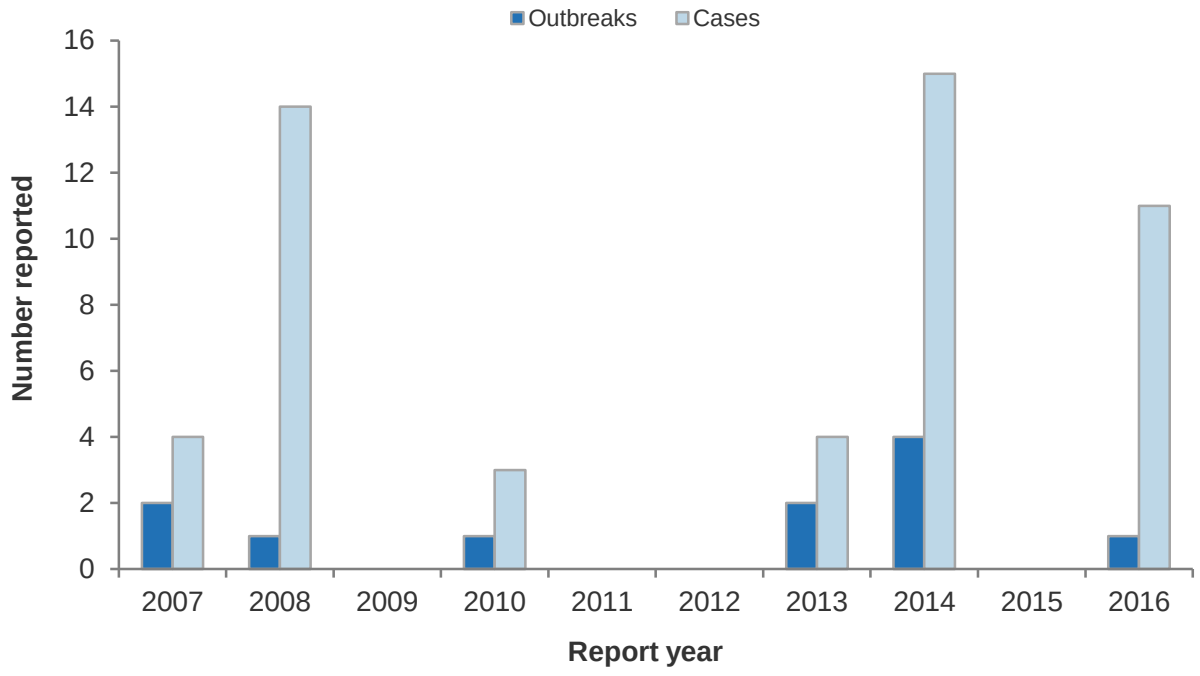


Table 71 contains details of the foodborne VTEC/STEC outbreak reported in 2016. The evidence linking the outbreak to consumption of raw milk was strong. The serotype was identified as *E. coli* O157:H7.

Table 71. Details of foodborne VTEC/STEC outbreaks reported, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Feb	Raw milk	Other food outlet	Other food outlet	11C, 0P

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

In 2016, raw milk samples were submitted to ESR's Public Health Laboratory relating to the food-associated VTEC/STEC outbreak listed in Table 71 (Auckland). *E.coli* O157:H7 was isolated from the associated raw milk samples.

VTEC/STEC types commonly reported

A total of 491 cases infected with VTEC/STEC were reported by the ESR Enteric Reference Laboratory in 2016. Of these, 205 (41.8%) isolates were identified as *E. coli* O157:H7, 181 (36.9%) as non-O157 and for 105 (21.4%) isolates the serotype was not identified.

Of the 181 non-O157 isolates, 46 were typed as O26:H11, 25 as O128:H2 and 10 as O38:H26 (Table 72). The percentage of non-O157 VTEC/STEC cases in 2015 was higher than 2013 and 2014 due to the changes in laboratory methods and the screening of all faecal samples submitted to an Auckland laboratory (Figure 52). The further increase in the percentage of non-O157 case isolates in 2016 may be due to a full year of applying the new approach in Auckland compared to half a year in 2015.

Figure 52. Percentage of *E. coli* O157 and non-O157 laboratory-reported cases by year, 2012–2016

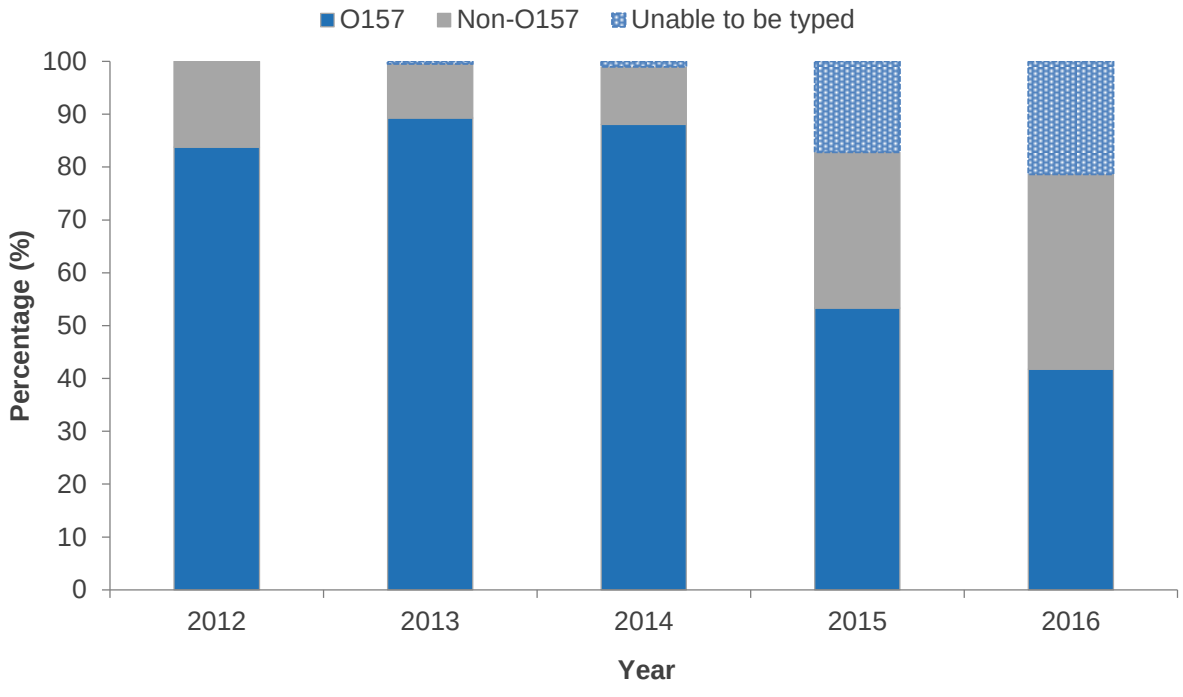


Table 72. VTEC/STEC subtypes identified by the Enteric Reference Laboratory, 2012–2016

Serotype	2012	2013	2014	2015	2016
O157	**119**	**192**	**170**	**183**	**205**
O157:H7	119	192	170	183	205
Non-O157	**23**	**22**	**21**	**101**	**181**
O26:H11	1	1	1	14	46
O26:HNM					5
O176:HNM	1	-	3	10	2
ONT:HNM	9	1	2	10	6
ONT:H2	-	1	1	9	3
O38:H26	1	1	2	5	10
O5:HNM					4
O64:H20					3
O91:HNM	-	-	-	5	2
O128:H2	-	1	-	4	25
O128:HNM					5
O153:H2	-	-	-	4	2
ORough:HNM	-	1	-	3	2
ORough:H2					6
O103:H2	-	-	-	2	2
O145:H2					3
O146:H21	1	-	1	2	4
O183:H18					3
ONT:H2					3
ONT:H7					3
ONT:HNM					3
Other types[a]	8	14	11	25	39
Unable to be typed		**1**	**2**	**59**	**105**
Total	**142**	**215**	**193**	**343**	**491**

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

2012: O26:H7, O68:HNM, O84:HNM, O128:HNM, O146:HRough, O176:HRough, O180:HNM, ONT:H7

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:HNM, ONT:H10, ONT:H13, ONT:H14, ONT:H21, ONT:H28, ONT:H5, ONT:HNT (two cases), ORough:H21, ORough:H7

Most human isolates of O157:H7 are further genotyped by pulsed-field gel electrophoresis (PFGE). Table 73 summarises PFGE typing of human O157:H7 isolates each year from 2012 to 2016.

Table 73. PFGE genotypes of human *E. coli* O157:H7 isolates, 2012–2016

Genotype	Number of isolates				
	2012	2013	2014	2015	2016
Xb0079	24	29	12	20	45
Xb0097	12	30	22	21	28
Xb0168	14	7	13	11	15
Xb0049	4	8	7	1	10
Xb0048	2	-	-	2	5
Xb0263	-	1	3	-	5
Xb0370	8	2	4	3	4
Xb0014	5	2	4	1	4
Xb0332	1	11	1	2	4
Xb0092	5	1	-	3	3
Xb0019	-	4	2	1	3
Xb0379	2	1	2	3	3
Xb0206	-	-	-	-	3
Xb0547	-	-	-	-	3
Xb0233	1	10	4	9	1
Xb0352	-	-	3	9	-
Xb0207	1	1	-	4	1
Xb0483	-	-	-	4	1
Xb0536	-	-	-	4	-
Xb0110	2	5	4	3	1
Xb0117	2	12	4	3	-
Other types	35	65	87	79	66
Total	**118**	**189**	**172**	**183**	**205**

PFGE pattern designations are sequential numbers given to each different PFGE patterns, with pattern numbers assigned in the order the patterns are identified. During 2014, the PFGE pattern database was reviewed, and some pattern designations changed. Isolates reported previously may now have a different PFGE pattern designation from that previously reported

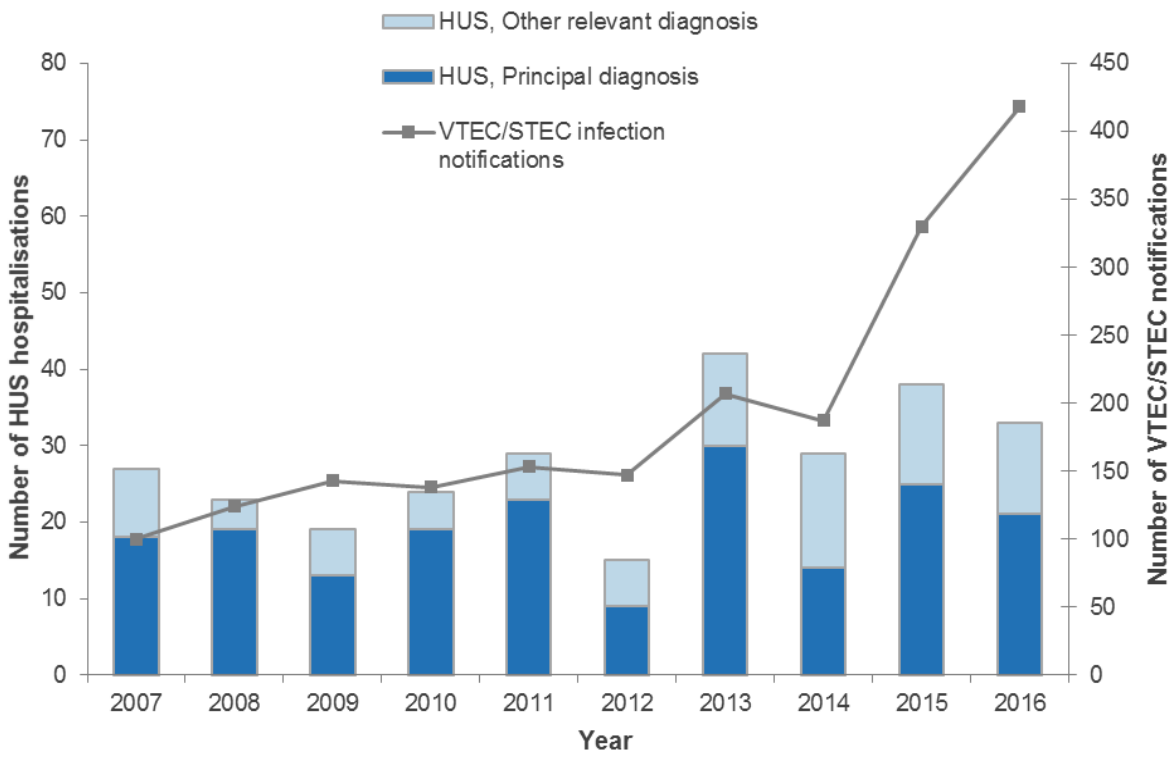
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from a VTEC/STEC infection. HUS is usually preceded by a VTEC/STEC infection [41]. While most HUS cases are associated with *E. coli* O157 infections, non-O157 genotypes differ markedly in their virulence with respect to HUS causation [42].

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 2016 year were considered, rather than all cases that were hospitalised in that year. That is, if a HUS cases hospitalised in 2016 had been hospitalised with HUS in a previous year, the 2016 admission was considered to be a readmission, rather than an incident case. Of the 33 incident hospital admissions recorded in 2016 (0.7 per 100,000 population), 21 were reported with HUS as the primary diagnosis and 12 with HUS as another relevant diagnosis.

Between 2007 and 2016, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 42 (Figure 53). In 2016, the number of incident hospitalised cases decreased to 33 from 38 in 2015. This decrease corresponded with an increase in the number of VTEC/STEC notifications (Figure 46).

Figure 53. Haemolytic-uraemic syndrome (HUS) hospitalised cases, 2007–2016



In 2016, the number of female incident hospitalised cases due to HUS was greater than the number of male cases (Table 74). The relative proportion of female and male cases was similar between 2015 and 2016.

Table 74. Haemolytic uraemic syndrome hospitalised cases by sex, 2016

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	14	0.6
Female	19	0.8
Total	**33**	**0.7**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 of population

In 2016, the highest age-specific rates of incident hospitalised cases due to HUS were in the less than 5 years age group (Table 75). The age distribution of incident hospitalised HUS cases in 2016 was notable for the small number of cases in the older age categories, compared to 2015 when 10 of 38 incident cases were 60 years or older.

Table 75. Haemolytic uraemic syndrome hospitalised cases by age group, 2016

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
<5	19	6.2
5 to 9	7	2.2
10 to 14	1	-
15 to 19	0	-
20 to 29	2	-
30 to 39	0	-
40 to 49	1	-
50 to 59	0	-
60 to 69	2	-
70+	1	-
Total	**33**	**0.7**

[a] MoH NMDS data for hospital admissions

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

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

During 2016, 14 cases of HUS were reported to the NZPSU, of which 11 had a diarrhoeal prodrome. The median age at presentation of diarrhoeal cases was 2.4 years (range 1.7 to 4.4 years). Eight of 11 cases had *E. coli* O157:H7 isolated from their stools. All the *E. coli* O157 positive cases were in the North Island except one case from Dunedin.

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

PFGE analysis of meat isolates of E. coli O157:H7 in New Zealand (2015)

This report describes the results of PFGE analysis of 57 *E. coli* O157:H7 isolates from meat enrichment samples received by ESR during the period 1 January 2015 to 31 December 2015 [43]. All of the isolates have been analysed by PFGE using both *Xba*I and *Bln*I enzymes. When the two PFGE types were combined 44 *Xba*I:*Bln*I types were observed

Relevant New Zealand studies and publications

Journal papers

The prevalence and risk factors for faecal carriage of *E. coli* O157 and O26 was examined in 695 young calves and 895 adult cattle, sampled at slaughter [44]. Prevalence of the two genotypes combined was higher in young calves (42/695; 6.9%) than in adult cattle (16/895; 1.8%). *E. coli* O26 was more frequently detected than O157 in young calves, while O157 was more frequently detected in adult cattle. Presence of the other genotype was a risk factor for faecal carriage of either genotype.

A survey of 80 dairy farms, carried out during 2011-2012 detected *E. coli* O157 in 0.6% of bulk tank milk samples [21]. Milk quality data such as coliform counts, total bacterial counts, and somatic cell counts were also collected. By treating the total bacterial count as a proxy for faecal contamination of milk and utilising farm and animal level prevalence and shedding rates of *E. coli* O157, a predictive model for the level of *E. coli* O157 in bulk tank raw milk was developed.

Reports

EpiSurv data for VTEC infections for 2014 were examined to determine if they were suitable for comparison with 2017 data [24]. Cases were matched to hospital records and analysis conducted on the association of risk factors (including raw milk) with hospitalisation, length of stay, and death. It was concluded that the 2014 EpiSurv data are not suitable for use as a baseline, primarily due to data quality issues that result in difficulties in classifying cases as exposed to raw milk or not exposed to raw milk, and to missing data resulting in uncertainty and bias. It was also noted that the data did not distinguish between consumption of raw milk purchased from a raw milk supplier and non-commercial consumption of raw milk, such as a dairy farmer drinking from the vat.

Relevant regulatory developments

Food Standards Australia New Zealand (FSANZ) published a *Compendium of Microbiological Criteria for Food*, including guideline levels for VTEC/STEC in ready-to-eat foods [16].

Yersiniosis

Summary data for yersiniosis in 2016 are given in Table 76.

Table 76. Summary of surveillance data for yersiniosis, 2016

Parameter	Value in 2016	Source
Number of notified cases	857	EpiSurv
Notification rate (per 100,000)	18.3	EpiSurv
Hospitalisations (% of notifications)[a]	65 (7.6%)	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	69 (8.1%)	EpiSurv
Estimated food-related cases (%)[b]	498 (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 5 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 circulating antigen by ELISA or agglutination test.

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 2016 by data source

During 2016, 857 cases (18.3 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv.

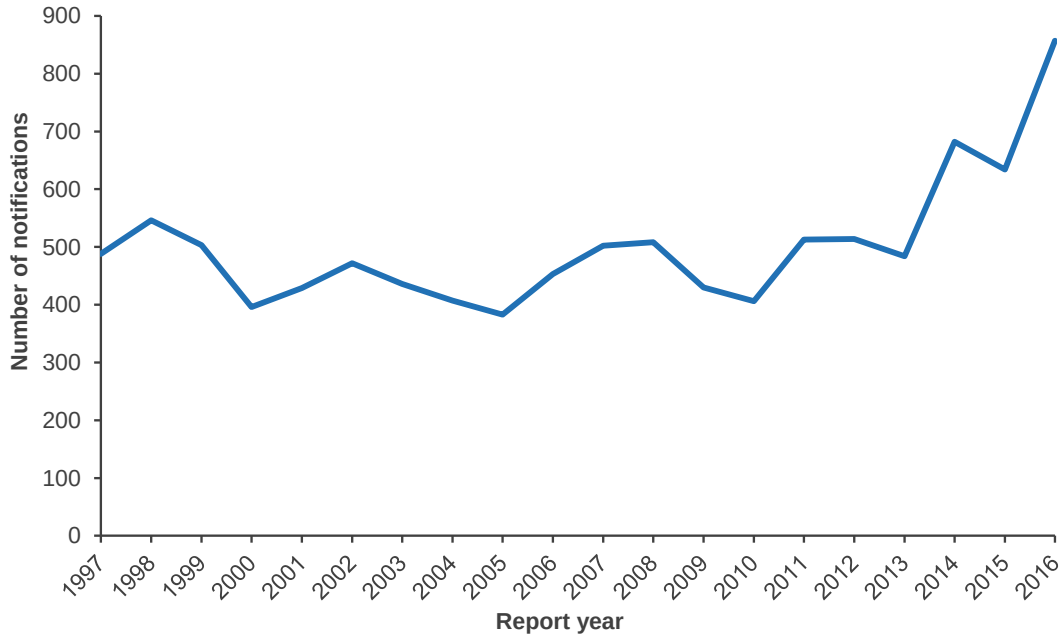
The ICD-10 code A04.6 was used to extract yersiniosis (*Y. enterocolitica)* hospitalisation data from the MoH NMDS database. Of the 65 hospital admissions (1.4 admissions per 100,000 population) recorded in 2016, 41 were reported with yersiniosis as the principal diagnosis and 24 with yersiniosis as another relevant diagnosis.

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

Notifiable disease data

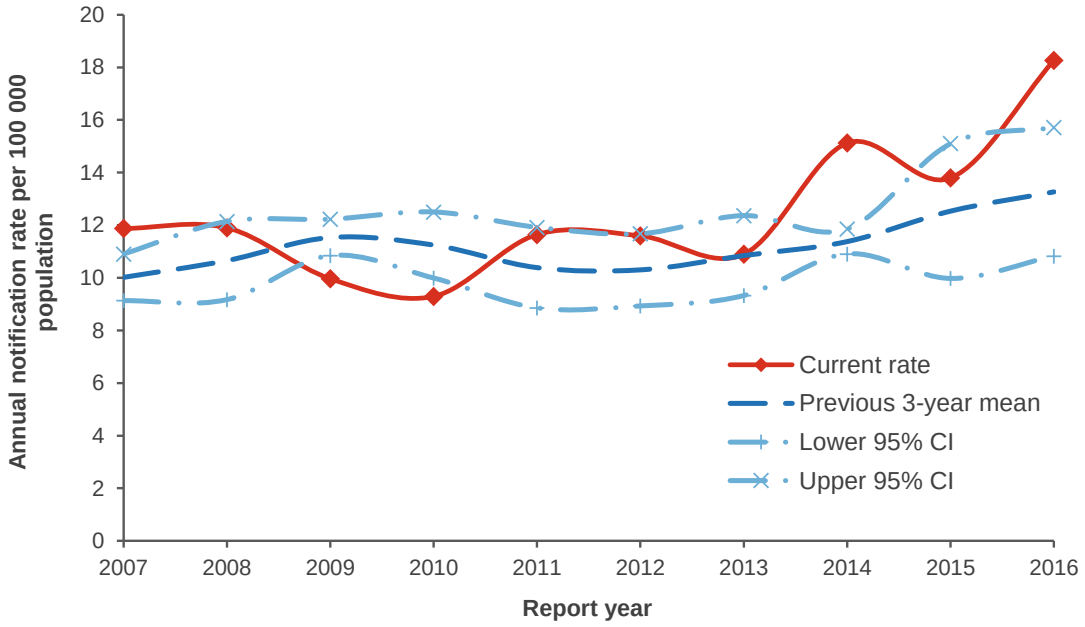
Yersiniosis became notifiable in 1996. Between 1998 and 2013 the annual number of notifications reported ranged between 383 and 546. Since 2013, higher number of notifications have been recorded, with the highest number of notifications reported in 2016 (857) (Figure 54).

Figure 54. Yersiniosis notifications by year, 1997–2016



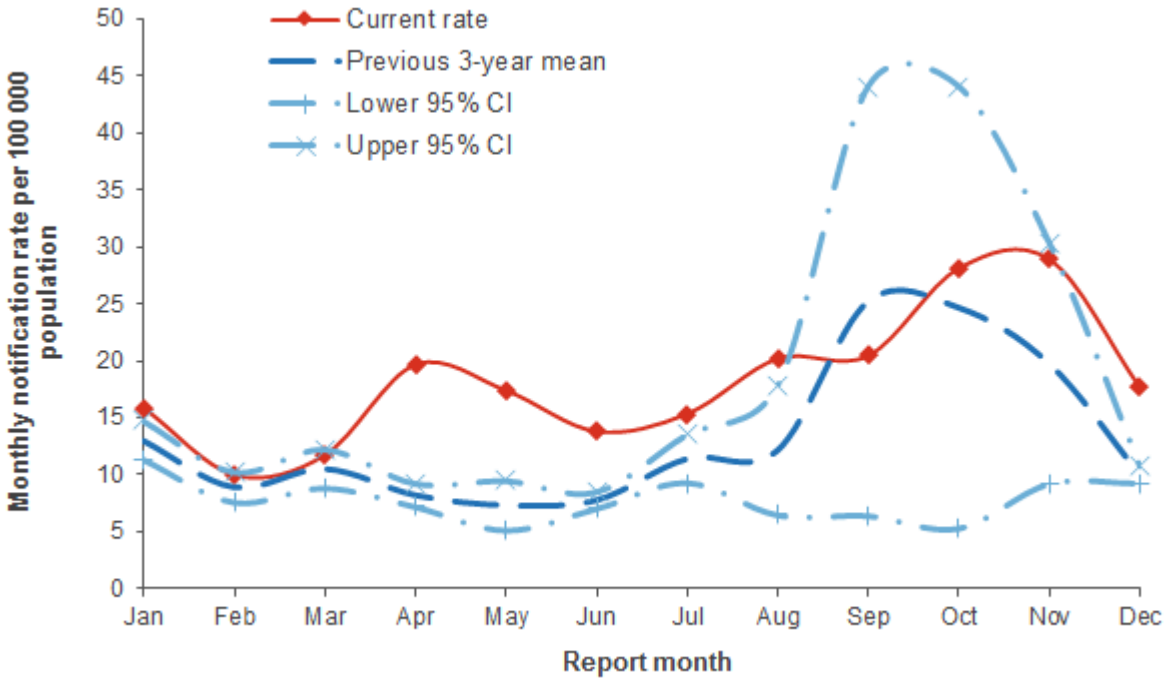
The yersiniosis annual notification rate has remained stable between 2007 and 2013 (ranging from 9.3 to 11.9 per 100,000) (Figure 55). In 2016, the rate has increased to 18.3 per 100,000 population.

Figure 55. Yersiniosis notification rate by year, 2007–2016



The number of notified cases of yersiniosis per 100,000 population by month for 2016 is shown in Figure 56. The 2016 monthly notification rate trend was similar to the mean monthly rate in previous years (2013-2015) for July to December, with a small peak in April and a peak in cases observed in October and November. In 2014 there was a large peak in notifications during September and October, associated with a single large outbreak (220 cases).

Figure 56. Yersiniosis monthly rate (annualised), 2016



In 2016 the yersiniosis notification rates were slightly higher for females than for males, however hospitalisation rates were similar (Table 77). In 2015 the notification and hospitalisation rates were slightly higher for females than for males.

Table 77. Yersiniosis cases by sex, 2016

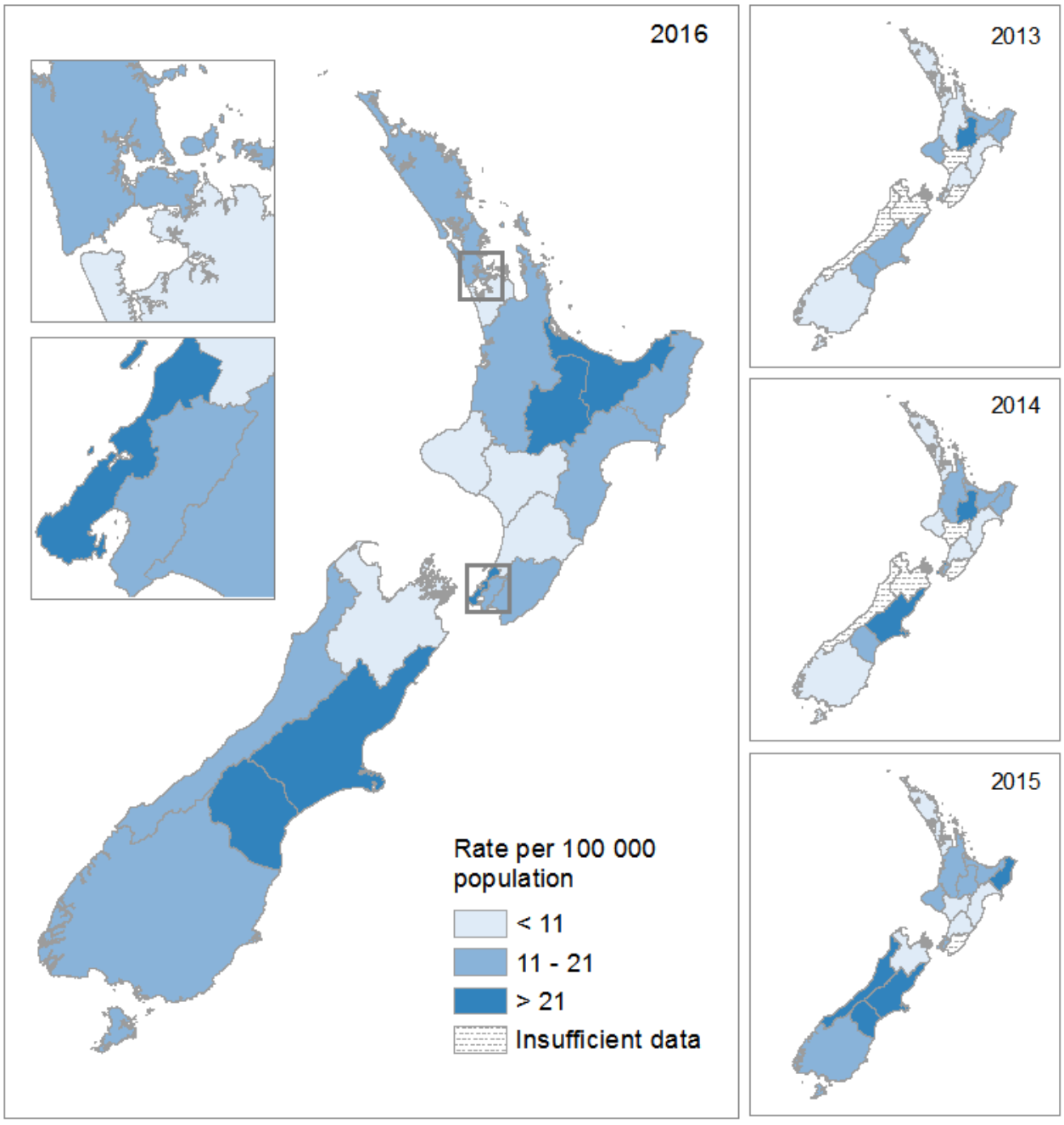
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	395	17.1	34	1.5
Female	462	19.4	31	1.3
Total	**857**	**18.3**	**65**	**1.4**

[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 57. In 2016, the highest rates in the South Island were reported for the Canterbury (34.5 per 100,000 population, 186 cases) and South Canterbury (25.3 per 100,000, 15 cases) DHBs. In the North Island Capital and Coast (28.7 per 100,000 population, 88 cases), Lakes (23.5 per 100,000 population, 25 cases), and Bay of Plenty (22.1 per 100,000 population, 50 cases) DHBs presented with the highest yersiniosis notification rates.

Figure 57. Geographic distribution of yersiniosis notifications, 2013–2016



In 2016, the highest yersiniosis notification rates were for the less than 1 year (77.7 per 100,000 population, 46 cases) and 1 to 4 years (57.9 per 100,000, 142 cases) age groups. Both age groups presented with higher rates compared to 2015. Notification rates for the under five year olds were more than twice the rates for any other age group (Table 78). The highest hospitalisation rate was reported for the 1 to 4 year age group.

Table 78. Yersiniosis cases by age group, 2016

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	46	77.7	4	-
1 to 4	142	57.9	7	2.9
5 to 9	24	7.4	3	-
10 to 14	33	11.2	2	-
15 to 19	36	11.3	3	-
20 to 29	115	16.7	5	0.7
30 to 39	126	21.8	8	1.4
40 to 49	84	13.6	3	-
50 to 59	102	16.6	5	0.8
60 to 69	78	15.9	8	1.6
70+	71	15.3	17	3.7
Total	**857**	**18.3**	**65**	**1.4**

[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)

In 2016, the most commonly reported risk factors for yersiniosis notifications were consumption of food from retail premises (51%), followed by contact with farm animals (21.6%), contact with faecal matter (19.1%), recreational water contact (19.0%) and consuming untreated water (17.9%) (Table 79).

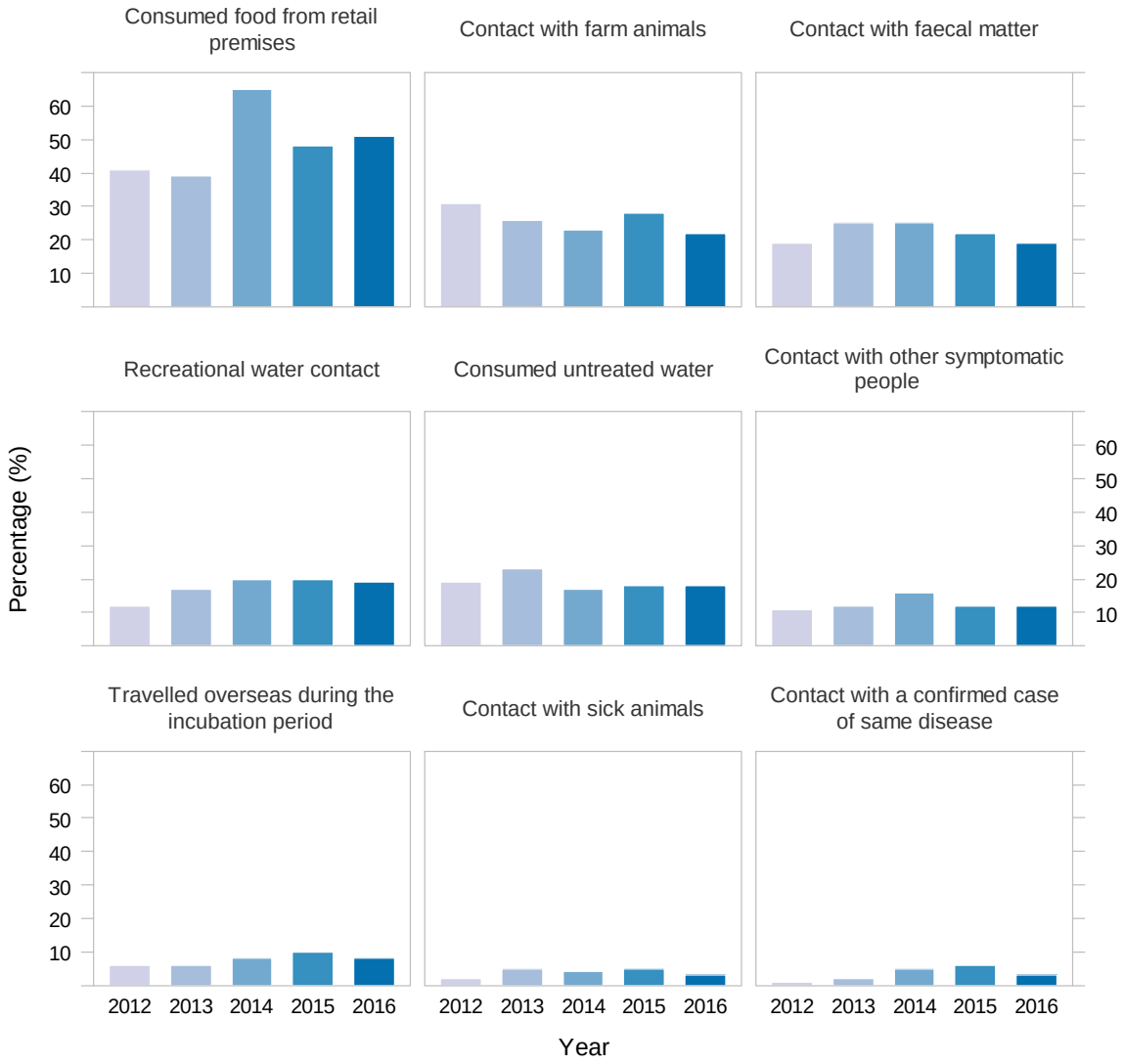
Table 79. Exposure to risk factors reported for yersiniosis notifications, 2016

Risk factor	Notifications			
	Yes	No	Unknown	%[a]
Consumed food from retail premises	215	207	436	50.9
Contact with farm animals	107	388	363	21.6
Contact with faecal matter	85	360	413	19.1
Recreational water contact	89	379	390	19.0
Consumed untreated water	83	381	394	17.9
Contact with other symptomatic people	53	406	399	11.5
Travelled overseas during the incubation period	45	510	303	8.1
Contact with a confirmed case of same disease	9	305	544	2.9
Contact with sick animals	12	440	406	2.7

[a] Percentage refers to the cases that answered "yes" out of the total number of cases for which this information was supplied. Cases may have more than one risk factor recorded.

Between 2012 and 2016, the most commonly reported risk factor for yersiniosis cases was consumption of food from retail premises (Figure 58). Between 2012 and 2016, the risk factors reported by yersiniosis cases generally occurred in the same order of importance and to a similar magnitude.

Figure 58. Percentage of cases with exposure to risk factors reported for yersiniosis and year, 2012–2016



For cases where information on travel was provided in 2016, 8.1% (95% CI 6.0-10.8%) 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 2016. The resultant distribution has a mean of 69 cases (95% CI 46-97).

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 7.1-10.0%).

Outbreaks reported as caused by *Yersinia* spp.

During 2016, there were three *Yersinia* spp. outbreaks, with a total of 88 cases, reported in EpiSurv. Two *Yersinia* spp. outbreaks (75 cases) were associated with a suspected foodborne source. (Table 80). One hospitalisation was associated with the outbreaks. 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 80. *Yersinia* spp. outbreaks reported, 2016

Measure	Foodborne *Yersinia* spp. outbreaks	All *Yersinia* spp. outbreaks
Outbreaks	2	3
Cases	75	88
Hospitalised cases	1	1

Between 2007 and 2016 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 and 2016 was not unusual (two each), but the number of cases involved (232 and 75, respectively) is higher than has been previously seen in New Zealand (Figure 59).

Figure 59. Foodborne *Yersinia* spp. outbreaks and associated cases reported by year, 2007–2016

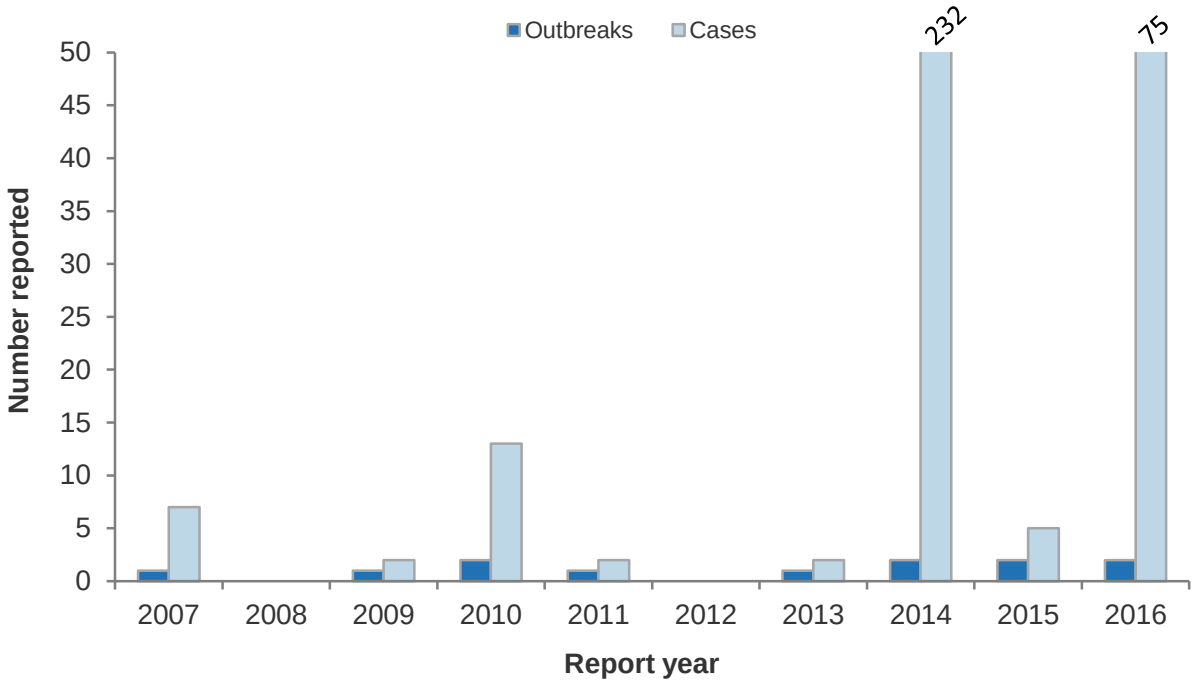


Table 81 contains details of the foodborne *Yersinia* spp. outbreaks reported in 2016. There was strong evidence linking the Auckland outbreak to consumption of bean sprouts. The evidence linking the Toi Te Ora outbreak to the suspected food vehicle was recorded as weak in EpiSurv.

Table 81. Details of foodborne *Yersinia* spp. outbreaks reported, 2016

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	May	Bean sprouts	Other food outlet	unknown	51C
Toi Te Ora	Nov	Sushi	Takeaway	Takeaway	21C, 3P

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

In 2016 no clinical or food samples were submitted to ESR's Public Health Laboratory relating to the *Yersinia* spp. outbreaks.

Yersinia types commonly reported

In 2016, clinical laboratories submitted 880 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 89% of these isolates. The remaining 100 isolates were for either; duplicate samples from the same case, isolates not confirmed as *Yersinia* species or *Yersinia* serotypes 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 notification.

The number of notifiable *Yersinia* spp. cases identified by the Enteric Reference Laboratory at ESR each year is shown in Table 82. Between 2012 and 2016, 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 and a decrease in the percentage of reported cases with *Y. enterocolitica* biotype 4 was observed in the years 2012 to 2016 (Figure 60).

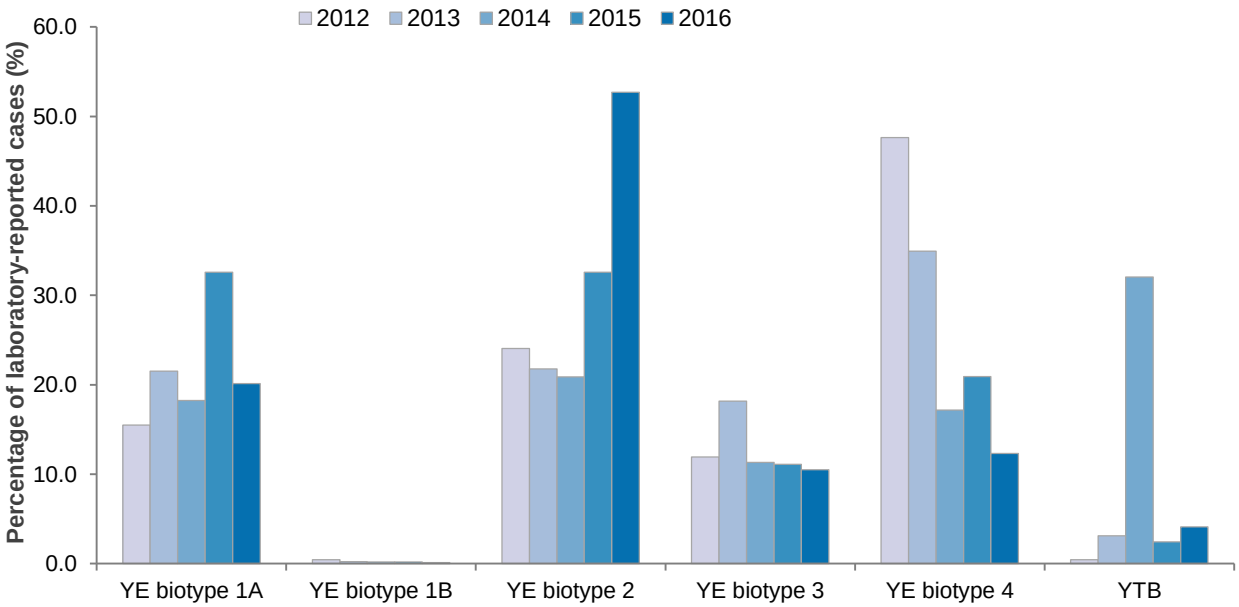
These numbers need to be interpreted with some caution as

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 82. Notifiable *Yersinia* spp. identified by the Enteric Reference Laboratory, 2012–2016

Species	2012	2013	2014	2015	2016
Yersinia enterocolitica	**443**	**405**	**384**	**521**	**748**
biotype 1A	69	90	103	173	157
biotype 1B	2	1	1	1	1
biotype 2	107	91	118	173	411
biotype 3	53	76	64	59	82
biotype 4	212	146	97	111	96
biotype not identified	-	1	1	4	1
Yersinia pseudotuberculosis	**2**	**13**	**181**	**13**	**32**
Total	**445**	**418**	**565**	**534**	**780**

Figure 60. Percentage of laboratory-reported cases of notifiable *Yersinia* spp. by species and year, 2012–2016



YE: *Yersinia enterocolitica*
YTB: *Yersinia pseudotuberculosis*

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Analysis of genomic data from a large potentially food transmitted 2014 outbreak of *Y. pseudotuberculosis* was reported [45]. Multivariate analysis incorporating genomic and clinical epidemiological data strongly suggested a single point-source contamination of the food chain, with subsequent nationwide distribution of contaminated produce.

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 2016, 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.

Further information about notifiable diseases can be found in the *Notifiable Diseases in New Zealand: Annual Report 2016* [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).

Prior to the introduction of processes for matching notifications and laboratory records, the number of laboratory-reported salmonellosis cases had always exceeded the number of notifications. The implementation of data integration processes in 2004 for notifications and laboratory results at ESR has addressed this problem.

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 2016 [46].

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, guideline 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 [3]. 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 16 February 2017. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 7 April 2017. 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 2016 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2016, the New Zealand population was estimated to be 4,692,720. The mid-year population estimate for 2013 used in the analysis of trends was updated in 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 are 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 5 cases).

Risk factors and source of infection

For many diseases an analysis of risk factors for the cases is reported. These risk factors are those included in the current EpiSurv case report forms. Often more than one risk factor is reported for each case. For some diseases the number of cases for which risk factors are unknown can be high.

The reporting of exposure to a risk factor does not imply that this was the source of the infection.

Statistical tests

Confidence intervals have been calculated for the disease rates and displayed on the graphs. The historical mean is calculated from the previous three years data (2013−2015).

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SUMMARY TABLES

SUMMARY TABLES

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

Table 83. Number of cases and rate per 100,000 population of selected notifiable diseases in New Zealand, 2015–2016

Disease	2015		2016		Change [b,c]
	Cases	Rates	Cases	Rates	
Campylobacteriosis	6218	135.3	7456	158.9	➔
Cryptosporidiosis	696	15.1	1062	22.6	➔
Gastroenteritis[a]	503	11.0	510	10.9	→
Giardiasis	1510	32.9	1617	34.5	→
Hepatitis A	47	1.0	35	0.7	←
Listeriosis	26	0.6	37	0.8	→
Salmonellosis	1051	22.9	1091	23.2	→
Shigellosis	111	2.4	174	3.7	➔
VTEC/STEC infection	330	7.2	418	8.9	➔
Yersiniosis	634	13.8	857	18.3	➔

[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 84. Deaths due to selected notifiable diseases recorded in EpiSurv, 1997–2016

Disease	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
Campylobacteriosis	2	2	1	3	1	1	0	0	1	1	1	0	0	0	0	0	1	0	0	0
Gastroenteritis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1
Giardiasis	1	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
Listeriosis - perinatal	6	0	2	4	1	3	2	2	4	1	2	2	2	4	0	2	4	2	3	2
Salmonellosis	2	2	1	7	2	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0
Shigellosis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	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
Yersiniosis	0	2	0	0	0	0	0	1	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 85. MoH mortality data for selected notifiable diseases, 2012–2014

Disease	ICD 10 Codes	2012		2013[a]		2014	
		Und[b]	Cont[c]	Und[b]	Cont[c]	Und[b]	Cont[c]
Campylobacteriosis	A04.5	0	0	2	0	3	1
Hepatitis A	B15	0	0	0	0	0	1
Listeriosis	A32	4	1	1	1	0	0
Salmonellosis	A02	1	0	0	1	1	1
Shigellosis	A03	0	0	1	0	1	0
Yersiniosis	A04.6	2	0	0	0	0	0

[a] Latest year that data are available.

[b] Underlying – main cause of death.

[c] Contributory – selected contributory cause of death (not main cause of death).

Table 86. MoH Hospitalisations data for selected notifiable diseases, 2014–2016

Disease	ICD 10 Codes	2013		2014		2015	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	612	117	574	117	595	117
Cryptosporidiosis	A07.2	22	4	22	9	39	11
Giardiasis	A07.1	43	25	34	21	27	20
Hepatitis A	B15	33	16	27	39	19	65
Listeriosis	A32	15	13	19	14	21	20
Salmonellosis	A02	110	40	148	33	154	53
Shigellosis	A03	12	6	10	10	20	10
VTEC/STEC infection	A04.3	7	5	14	6	9	6
Yersiniosis	A04.6	26	25	38	24	41	24

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 87. Number of cases and rate per 100,000 population of selected notifiable diseases by ethnic group, 2016

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	666	95.5	159	55.1	406	75.4	52	99.5	5798	186.0	7456	158.9
Cryptosporidiosis	121	17.4	17	5.9	48	8.9	9	17.2	831	26.7	1062	22.6
Gastroenteritis[c]	52	7.6	28	9.7	53	9.8	7	13.4	324	10.5	510	10.9
Giardiasis	107	15.4	17	5.9	94	17.5	41	78.4	1290	41.4	1617	34.5
Hepatitis A	2	-	6	2.1	9	1.7	2	-	16	0.5	35	0.7
Listeriosis	6	0.9	4	-	6	1.1	-	-	21	0.7	37	0.8
Salmonellosis	128	18.4	63	21.8	76	14.1	10	19.1	780	25.0	1091	23.3
Shigellosis	12	1.7	47	16.3	13	2.4	-	-	94	3.0	174	3.7
VTEC/STEC infection	48	6.9	16	5.5	40	7.4	7	13.4	297	9.5	418	8.9
Yersiniosis	81	11.6	22	7.6	181	33.6	8	15.3	527	16.9	857	18.3

[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 2016 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 88. Number of cases and rates of selected notifiable diseases per 100,000 population by sex, 2016

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	4093	177.3	3361	141.0	7456	158.9
Cryptosporidiosis	491	21.3	571	24.0	1062	22.6
Gastroenteritis[b]	239	10.4	271	11.4	510	10.9
Giardiasis	828	35.9	789	33.1	1617	34.5
Hepatitis A	22	1.0	13	0.5	35	0.7
Listeriosis[c]	15	0.6	22	0.8	37	0.7
Salmonellosis	549	23.8	542	22.7	1091	23.2
Shigellosis	95	4.1	79	3.3	174	3.7
VTEC/STEC infection	175	7.6	243	10.2	418	8.9
Yersiniosis	395	17.1	462	19.4	857	18.3

[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 89. Number of cases and rates of selected notifiable diseases per 100,000 population by age group, 2016

	<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	149	251.5	671	273.6	345	107.1	292	99.2	452	142.0	1083	157.6	766	132.5	795	128.3	964	157.3	876	178.6	1063	228.6	7456	158.9
Cryptosporidiosis	18	30.4	305	124.3	134	41.6	61	20.7	57	17.9	161	23.4	148	25.6	74	11.9	52	8.5	32	6.5	20	4.3	1062	22.6
Gastroenteritis	51	86.1	92	37.5	24	7.4	14	4.8	19	6.0	52	7.6	59	10.2	46	7.4	53	8.6	47	9.5	48	10.3	510	10.9
Giardiasis	26	43.9	272	110.9	125	38.8	42	14.3	46	14.4	197	28.7	320	55.4	201	32.4	183	29.9	154	31.4	51	11.0	1617	34.5
Hepatitis A			3		3				1		13	1.9	2		6	1.0	3		2		2		35	0.7
Listeriosis	1								1		2		4				5	0.8	7	1.4	17	3.7	37	0.7
Salmonellosis	68	114.8	164	66.9	64	19.9	32	10.9	50	15.7	155	22.6	114	19.7	143	23.1	134	21.9	89	18.1	78	16.8	1091	23.2
Shigellosis	3		18	7.3	14	4.3	4		5	1.6	26	3.8	25	4.3	25	4.0	19	3.1	23	4.7	12	2.6	174	3.7
VTEC/STEC infection	26	43.9	109		27	8.4	18	6.1	21	6.6	49	7.1	27	4.7	32	5.2	27	4.4	41	8.4	41	8.8	418	8.9
Yersiniosis	46	77.7	142	57.9	24	7.4	33	11.2	36	11.3	115	16.7	126	21.8	84	13.6	102	16.6	78	15.9	71	15.3	857	18.3

[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 and the cell has been left blank.

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
- Second (middle) band
- Third (highest) band

Table 90. Number of cases of selected notifiable diseases by District Health Board, 2016

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	289	773	520	506	564	130	246	74	236	1333	102	294	195	413	73	173	58	760	150	567	7456
Cryptosporidiosis	106	145	101	94	122	22	16	12	44	24	20	55	13	62	20	23	2	106	16	59	1062
Gastroenteritis[a]	14	56	101	44	8	12	28	1	8	3	14	43	29	74	10	3	8	40		14	510
Giardiasis	57	195	180	185	132	48	72	75	40	77	18	39	33	125	11	49	7	167	17	90	1617
Hepatitis A	2	7	6	4					1				1	5		4	1	1		3	35
Listeriosis		4	5	4	3		4	1		2			4	2		3		3		2	37
Salmonellosis	38	113	103	75	114	22	41	52	26	38	11	45	32	68	12	30	7	134	22	108	1091
Shigellosis	4	42	31	34	16		8	4		3	1		4	8		2		10		7	174
VTEC/STEC infection	47	88	45	64	43	7	21		14	9	4	5	4	2	1	9	1	16	7	31	418
Yersiniosis	27	105	97	55	52	25	50	6	7	19	6	14	30	88	5	9	6	186	15	55	857

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

Table 91. Rate per 100,000 population of selected notifiable diseases by District Health Board, 2016

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	168.6	130.9	102.5	94.7	141.2	122.0	108.5	154.8	202.1	825.9	161.9	168.8	133.7	134.7	167.4	118.2	178.5	140.8	253.4	177.8	158.9
Cryptosporidiosis	61.8	24.5	19.9	17.6	30.5	20.6	7.1	25.1	37.7	14.9	31.7	31.6	8.9	20.2	45.9	15.7		19.6	27.0	18.5	22.6
Gastroenteritis	8.2	9.5	19.9	8.3	2.0	7.5	12.4		4.3		22.2	24.7	19.9	24.1	22.9		15.4	7.4		3.8	6.3
Giardiasis	33.3	33.0	35.5	34.6	33.0	45.0	31.8	156.9	34.2	47.7	28.6	22.4	22.6	40.8	25.2	33.5	21.5	30.9	28.7	28.2	34.5
Hepatitis A		1.2	1.2											1.6							0.7
Listeriosis			1																		0.7
Salmonellosis	22.2	19.1	20.3	14.0	28.5	20.6	18.1	108.8	22.3	23.5	17.5	25.8	21.9	22.2	27.5	20.5	21.5	24.8	37.2	33.9	23.2
Shigellosis		7.1	6.1	6.4	4.0		3.5							2.6				1.9		2.2	3.7
VTEC/STEC infection	27.4	14.9	8.9	12.0	10.8	6.6	9.3		12.0	5.6		2.9				6.1		3.0	11.8	9.7	8.9
Yersiniosis	15.8	17.8	19.1	10.3	13.0	23.5	22.1	12.6	6.0	11.8	9.5	8.0	20.6	28.7	11.5	6.1	18.5	34.5	25.3	17.2	18.3

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

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 92. 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	10 145	12 493
Cryptosporidiosis[a]									119	357	866	977	775	1208	975
Gastroenteritis[a b]									555	310	492	601	727	942	1088
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 [47]. Note: cell is blank where data are unavailable.

Table 93. Number of cases of selected notifiable diseases by year, 2003–2016

Disease	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
Campylobacteriosis	14 788	12 215	13 836	15 873	12 778	6694	7177	7346	6686	7016	6837	6776	6218	7456
Cryptosporidiosis	817	611	888	737	924	764	854	954	610	877	1348	584	696	1062
Gastroenteritis[a]	1030	1363	560	938	625	687	713	493	570	765	559	756	500	510
Giardiasis	1570	1514	1231	1214	1402	1660	1639	1985	1934	1714	1729	1709	1510	1617
Hepatitis A	70	49	51	123	42	89	44	46	26	82	91	74	47	35
Listeriosis	24	26	20	19	26	27	28	23	26	25	19	25	26	37
Salmonellosis	1401	1081	1382	1335	1275	1339	1128	1146	1055	1081	1143	954	1051	1091
Shigellosis	87	140	183	102	129	113	119	104	101	132	137	128	111	174
VTEC/STEC infection	104	89	92	87	100	124	143	138	153	147	205	187	330	418
Yersiniosis	436	407	383	453	502	508	430	406	513	514	484	682	634	857

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

Table 94. 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 (2016)	Australia[a] (2016)	USA[b] (2016)	Canada[d] (2014)	UK (2015)	EU Total (2015)	Other high	
Campylobacteriosis	158.9	102.0	11.8	28.4	92.2[e]	65.5[e]	198.9 (Czech Republic)[e]	128.2 (Luxembourg)[e]
Cryptosporidiosis	22.6	22.8	3.7	2.5	6.4[f]	2.4[f]	8.4 (Ireland)[f]	
Giardiasis	34.5	NN	5.8[c]	10.3	5.6[f]	5.4[f]	23.9 (Bulgaria)[f]	16.8 (Estonia)[f]
Hepatitis A	0.6	0.6	0.4[c]	0.6	0.5[f]	3.0[f]	33.3 (Romania)[f]	15.7 (Hungary)[f]
Listeriosis	0.7	0.4	0.26	0.41	0.29[e]	0.46[e]	0.99 (Spain)[e]	0.93 (Malta)[e]
Salmonellosis	23.2	76.5	15.4	21.5	14.6[e]	21.2[e]	117.7 (Czech Republic)[e]	89.3 (Slovakia)[e]
Shigellosis	3.7	5.9	4.6	2.2	2.8[f]	1.4[f]	7.1 (Bulgaria)[f]	4.1 (Slovakia)[f]
VTEC/STEC infection	8.9	1.4	2.8	1.8	2.1[e]	1.3[e]	12.9 (Ireland)[e]	5.7 (Sweden)[e]
Yersiniosis	18.3	NN	0.4	1.0	0.1[e]	2.2[e]	10.6 (Finland)[e]	9.5 (Denmark)[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 2016, FoodNet report rates as 'Confirmed' and 'Confirmed or culture-independent diagnostic test positive'. The figure given here are those for 'Confirmed'.

[c] Centers for Disease Control and Prevention. Summary of notifiable disease http://www.cdc.gov/mmwr/mmwr_nd/index.html (CDC data presented here relate to the 2014 year).

[d] Canadian Notifiable Disease Surveillance System (CNDSS) http://dsol-smed.phac-aspc.gc.ca/dsol-smed/ndis/index-eng.php. Yersiniosis is not notifiable in Canada, but information on isolate submission is collected through the National Enteric Surveillance Program (NESP) http://www.publications.gc.ca/site/eng/9.507317/publication.html. Yersiniosis rates calculated in this way are expected to underestimate the rate.

[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 2015 http://www.efsa.europa.eu/en/efsajournal/doc/3547.pdf

[f] European Centre for Disease Prevention and Control (ECDC). Annual epidemiological report on communicable diseases in Europe http://ecdc.europa.eu/en/publications/surveillance_reports/annual_epidemiological_report/Pages/epi_index.aspx (ECDC data presented here relate to the 2014 year).

Table 95. Foodborne outbreaks and associated cases by pathogen/condition, 2016

Pathogen/Condition	Outbreaks (n = 95)[d]		Cases (n = 1139)[d]	
	No.	%[a]	No.	%[b]
Norovirus	18	18.9	542	47.6
Salmonella spp.	12	12.6	78	6.8
Campylobacter spp.	8	8.4	28	2.5
Giardia spp.	4	4.2	18	1.6
Histamine (scombroid) fish poisoning	2	2.1	5	0.4
Yersinia spp.	2	2.1	75	6.6
Bacillus cereus	1	1.1	7	0.6
Ciguatera fish poisoning	1	1.1	4	0.4
Clostridium perfringens	1	1.1	2	0.2
Cryptosporidium spp.	1	1.1	2	0.2
Sapovirus	1	1.1	65	5.7
Shigella spp.	1	1.1	8	0.7
Staphylococcus aureus	1	1.1	14	1.2
VTEC	1	1.1	11	1.0
Pathogen not identified[c]	43	45.3	292	25.6

[a] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (95). 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 (1139).

[c] All enteric outbreaks with no pathogen identified in 2016 were recorded as gastroenteritis.

[d] Two agents were reported in 2 foodborne outbreaks with 12 associated cases, therefore percentage totals add to more than 100%.

Table 96. Foodborne outbreaks and associated cases by exposure setting, 2016

Exposure setting	Outbreaks (n = 95)[c]		Cases (n = 1139)[c]	
	No.	%[a]	No.	%[b]
Commercial food operators	**58**	**61.1**	**422**	**37.1**
Restaurant/café/bakery	36	37.9	277	24.3
Takeaway	11	11.6	48	4.2
Other food outlet	8	8.4	85	7.5
Supermarket/delicatessen	2	2.1	5	0.4
Fast food outlet	1	1.1	7	0.6
Institutions	**14**	**14.7**	**355**	**31.2**
Hotel/motel	3	3.2	75	6.6
Long-term care facility	3	3.2	58	5.1
School	3	3.2	91	8.0
Childcare centre	2	2.1	87	7.6
Camp	1	1.1	24	2.1
Hostel/boarding house	1	1.1	9	0.8
Other institution	1	1.1	11	1.0
Other	**19**	**20.0**	**235**	**20.6**
Private home	9	9.5	42	3.7
Community/church gathering	2	2.1	62	5.4
Farm	1	1.1	2	0.2
Workplace	1	1.1	5	0.4
Other setting[d]	6	6.3	124	10.9
Unknown exposure setting	**5**	**5.3**	**138**	**12.1**

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (95). 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 (1139).

[c] Three outbreaks had two or more exposure settings (16 cases).

[d] Three outbreaks with other setting had an overseas exposure setting (one was in a car, one at a milk station and one at a beach).

Table 97. Foodborne outbreaks and associated cases by preparation setting, 2016

Preparation setting	Outbreaks (n = 95)[c]		Cases (n = 1139)	
	No.	%[a]	No.	%[b]
Commercial food operators	**57**	**60.0**	**329**	**64.6**
Restaurant/café/bakery	35	36.8	232	20.4
Takeaway	12	12.6	52	4.6
Other food outlet	7	7.4	34	3.0
Supermarket/delicatessen	3	3.2	7	0.6
Fast food outlet	1	1.1	7	0.6
Institutions	**8**	**8.4**	**260**	**22.8**
Hotel/motel	2	2.1	67	5.9
Long term care facility	2	2.1	38	3.3
Camp	1	1.1	24	2.1
Childcare centre	1	1.1	54	4.7
Hostel/boarding house	1	1.1	9	0.8
School	1	1.1	68	6.0
Other	**16**	**16.8**	**214**	**18.8**
Private home	9	9.5	45	4.0
Community/church/sports gathering	2	2.1	62	5.4
Other setting	2	2.1	98	8.6
Farm	1	1.1	2	0.2
Overseas manufacturer	1	1.1	2	0.2
Workplace	1	1.1	2	0.2
Unknown exposure setting	**16**	**16.8**	**340**	**29.9**

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (95). 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 (1139).

[C] One outbreaks had 2 or more preparation settings (2 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