New Zealand Food Safety
Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2020

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Cover Image: medical illustration of *Staphylococcus aureus*
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Scientific Interpretative Summary

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

Annual report concerning Foodborne Diseases in New Zealand 2020

ESR Report FW21005

Human health surveillance and its relationship to foodborne illness is essential for informing the strategic direction that New Zealand Food Safety (NZFS) takes and regulatory measures it puts in place to minimise foodborne illness in New Zealand and overseas consumers. The annual ESR foodborne disease reports are critical, allowing NZFS to monitor trends in foodborne illness in New Zealand by describing in a consistent manner evidence from notifications, case enquiries, outbreak investigations and other epidemiological studies of human enteric diseases.

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

The COVID-19 pandemic and public health measures had a strong impact on notification rates of all communicable disease including foodborne disease in New Zealand in 2020. To aid understanding of this impact on the reporting numbers a list of public health and social measures that are likely to affect notifications for potentially foodborne diseases is included in the report.

The reduction of human cases of foodborne campylobacteriosis is a top priority for NZFS. In 2015, MPI established a performance target for campylobacteriosis to reduce the number of human cases of domestically acquired foodborne campylobacteriosis by 10% from 88.4 to 79.6 per 100,000 population by the end of 2020. The section entitled Reporting Against Targets identifies that this target was successfully achieved.

As the reporting period for this performance target has expired a new performance target has been established. This is: “The number of human cases of foodborne campylobacteriosis reduced by 20% from 88 to 70 per 100,000 population by the end of 2024”. To reflect the increasing understanding of campylobacteriosis this performance target uses a new attribution factor for foodborne campylobacteriosis. Following recommendations of the 2020 Expert Colloquium[1] on Foodborne Campylobacteriosis, Yersiniosis and STEC Infection NZFS adopted an attribution factor of 75% for foodborne campylobacteriosis. This is an increase from the 64% attribution used during the previous reporting period. NZFS underscores that both total numbers of human campylobacteriosis cases and rates per 100,000 population are consistently, albeit slowly, decreasing.

Since 2015, NZ diagnostic laboratories have started to replace traditional culture-based methods for enteric pathogens by culture-independent diagnostic tests (CIDT) using molecular polymerase chain reaction. In 2019, about 78% of all human faecal samples referred to laboratories nationwide were tested using CIDT only. During 2020, Taranaki DHB moved to PCR-based methods in February, no other laboratory method changes have been recorded. Appendix B of this report presents an analysis of notification trends for bacterial infections in areas using CIDT tests and areas still to change to CIDT. That analysis suggests the change in methodology is having a significant impact on reporting rates for *Escherichia coli* (STEC infections), but not for *Campylobacter spp., Salmonella spp., Shigella spp.* and *Yersinia enterocolitica.*

Observed trends in changes in STEC notification rates between 2015 and 2020 must be considered in the context of changes to testing approaches and beginning of wider

[1] https://www.mpi.govt.nz/dmsdocument/46693-Foodborne-transmission-of-Campylobacteriosis-Yersiniosis-and-STEC-infection-in-New-Zealand

screening. A continuing apparent sharp increase in notification of STEC infections has been recorded, despite the absence of evidence that foodborne sources of the infection are increasing. The report suggests the national increase in STEC notifications observed since 2015 is due to ascertainment, that is **diagnosing** more people with STEC infection from an existing constant burden of disease , rather than an underlying real increase in the rate of incidence of STEC infections in New Zealand, i.e. the number of STEC circulating in the environment and population and available to cause infection, has increased. Similar anomalies resulting from changes in diagnostic methods have been observed internationally. For example, in the United States of America, the incidence of non-0157 STEC infections in 2015 significantly increased in comparison to the average incidence in 2012-2014. This was attributed in full or at least in part to the use of CIDTs more than doubling during the same period (Huang *et al*. 2016[2]).

Determining the impact of ascertainment as a result of the change in methodology is the subject of research projects currently underway. These projects may not be completed for several years however, preliminary observations could prove to be useful and will be factored into further NZFS analysis of this issue.

In contrast to other enteric diseases yersiniosis has a wide range of clinical manifestations and sequelae. Consequently, case notifications often rely on laboratory results only. The wider screening of clinical samples by CIDT now occurring in New Zealand with more samples being screened for *Yersinia* spp. than previously with conventional methods will contribute to the observed trend. The actual impact of the changes in scope of application of testing methodology and its comparative sensitivity compared with conventional diagnostic methods, needs to be established to inform future public health and food safety actions. Notably, yersiniosis is not a nationally notifiable disease in many countries including Australia.

Although all effort was made to investigate risk factors for all potentially foodborne outbreaks, some outbreaks reported as foodborne with an unidentified food source might be attributed to other routes of transmission, such as water, animal contact or person to person. NZFS and ESR alongside the Ministry of Health will continue to further improve the reporting, analysis and presentation of foodborne human illness surveillance and investigation data.

[2] Huang, J.Y., Henao, O.L., Griffin, P.M., Vugia, D.J., Cronquist, A.B., Hurd, S., Tobin-D'Angelo, M., Ryan, P., Smith, K., Lathrop. S., Zansky, S., Cieslak, P.R., Dunn, J., Holt, K.G., Wolpert, B.J., Patrick, M.E. 2016. Infection with Pathogens Transmitted Commonly Through Food and the Effect of Increasing Use of Culture-Independent Diagnostic Tests on Surveillance – Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2012-2015. *Morbidity and Mortality Weekly Report*, 65, 368-371.

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Science for Communities

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2020

Prepared for New Zealand Food Safety under
Project MRP/20/01 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2020,
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Disclaimer

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INTRODUCTION

New Zealand Food Safety, part of the Ministry for Primary Industries (MPI), leads New Zealand's food safety system, protecting the health and wellbeing of consumers here and overseas. This includes reducing food-related risks to human health. Human health surveillance is an essential element of the monitoring and review component of New Zealand Food Safety's risk management framework. In addition, evidence from notifications, case enquiries, outbreak investigations and other epidemiological studies of human enteric diseases are used as sources of data for risk profiles and assessments. There is ongoing interest in foodborne disease statistics within New Zealand Food Safety and its stakeholders.

This report for the calendar year 2020 is part of a series providing a consistent source of data and method of presentation to allow monitoring of foodborne illness in New Zealand.

Human health surveillance data and foodborne disease

The information in this report concerns reported cases of notifiable disease and reported outbreaks collected in the EpiSurv database (for a description of EpiSurv, see the Methods section of this report, page 114). Some notifiable illnesses may be caused by transmission of pathogens through foods*, but it is important to remember that most of the information relates to the illness, not the mode of transmission. The information needs to be considered with two caveats:

1. Notified cases of illness and reported outbreaks represent a subset of all the cases and outbreaks that occur in New Zealand each year. Many sick individuals do not visit a GP or otherwise come to the attention of the health system. By using these data as indicators, we are assuming that they are representative of all the cases and outbreaks that occur [1].
2. 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 some indicators from which we can get information on the proportion of cases caused by foodborne transmission:
    - Outbreak reports: the circumstances of an outbreak (multiple cases from a single event) mean that an investigation is more likely to identify a source of exposure to the pathogen than investigation of sporadic cases.
    - Expert opinion: based on their experience in laboratories and epidemiological investigations, as well as knowledge of factors influencing the risk, experts can provide estimates of the proportion of cases caused by foodborne transmission. Estimates for New Zealand have been developed for some foodborne diseases [2, 3], as presented in relevant report sections. These are not fixed values; future changes to the New Zealand food chain may require the values to be amended.
    - Overseas analyses and estimates: information for countries with food supplies similar to New Zealand can be helpful, especially for illnesses where a foodborne estimate could not be developed from local studies. New Zealand estimates [2, 3] and published country-specific estimates, for the USA [4], Canada [5], Australia [6, 7], England and Wales [8] and the Netherlands [9] are given in Table 1. In addition, a WHO project to estimate the global burden of foodborne diseases derived estimates for 14 international regions [10, 11]. The estimates for New Zealand, Australia, Canada, the Netherlands and the international WHO estimates are based on expert opinion, the estimates for England and Wales are based on outbreak analysis, while the US estimates are based on data from surveillance, risk factor studies and a literature review.

* Note that water is not considered a food.

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

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

Hazard		Percentage foodborne (%)					
	New Zealand (2013, 2021)	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.	75	51–76	80	62	77[c]	80	42
Clostridium perfringens	NE	100	100	93	98[c]	94	91
Shiga toxin-producing *Escherichia coli* (STEC) O157:H7	20	40–60[d]	68	61	56[c,d]	63	40
STEC non-O157	40	40–60[d]	82	60	56[c,d]	63	42
Listeria monocytogenes	88	100	99	77	98[c]	99	69
Salmonella non-typhoidal	62	46–76	94	63	72[c]	92	55
Shigella spp.	NE	7–36	31	26	12[c]	8	NE
Staphylococcus aureus	NE	100	100	78	100	96	87
Yersinia enterocolitica[e]	75	NE	90	83	84	90	NE
Parasites							
Cryptosporidium parvum	NE	8–16	8	11	10	6	12
Giardia lamblia	NE	11–14	7	7	5	10	13
Viruses							
Hepatitis A virus	NE	29–42	7	30	12[c]	11	11
Norovirus	33	12–26	26	18	18[c]	NE	17
Sapovirus	NE	NE	<1	17	NE	0	NE

[a] The WHO study estimated proportions for 14 international regions. Figures presented here are the range of those estimates

[b] The Dutch study also collected opinions on the proportion of disease due to travel. A proportion of this will also be foodborne. Of the other studies, the US study only considered domestically acquired cases, while the other studies did not specifically address whether cases were travel-related or domestically acquired

[c] The 2014 Australian publication did not cover the full range of organisms covered in the 2005 publication. Estimates marked with a superscript are from the 2014 publication

[d] Estimate was derived for total STEC

[e] For England and Wales the estimate refers to *Yersinia* spp., for all other countries the estimate refers to *Yersinia enterocolitica*

NE = not estimated

This report considers information for the 2020 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 2020 becomes available in the future.

Conditions included in this report

The conditions that have been selected for inclusion in the report are those that have:

1. The potential to be caused by foodborne transmission; and,
2. Available historical and current national data sources.

The potentially foodborne conditions included in this report are listed in Table 2. Data have been drawn from a number of sources including disease notification, hospitalisation, outbreak reports and laboratory surveillance databases.

Notifiable conditions were selected for inclusion in the report where a significant proportion is expected to be foodborne or the disease organism has been reported as the cause of foodborne outbreaks. Typhoid and paratyphoid fever are not included as the majority of cases acquire their infection overseas. Case definitions for conditions were obtained from the Communicable Disease Control Manual, published by the Ministry of Health [12].

Table 2. Potentially foodborne conditions included in the report

Disease	Type	Source(s)	ICD-10 code[a]
Bacillus cereus intoxication	Bacterium	N, O, H	A05.4 Foodborne *Bacillus cereus* intoxication
Campylobacteriosis	Bacterium	N, O, H	A04.5 *Campylobacter* enteritis
Ciguatera fish poisoning	Toxin	N, O, H	T61.0 Toxic effect: Ciguatera fish poisoning
Clostridium perfringens intoxication	Bacterium	N, O, H	A05.2 Foodborne *Clostridium perfringens* [*Clostridium welchii*] intoxication
Cryptosporidiosis	Protozoan	N, O, H	A07.2 Cryptosporidiosis
Giardiasis	Protozoan	N, O, H	A07.1 Giardiasis [lambliasis]
Hepatitis A infection	Virus	N, O, H, L	B15 Acute hepatitis A
Histamine (scombroid) fish poisoning	Toxin	N, O, H	T61.1 Toxic effect: scombroid fish poisoning
Listeriosis (total and perinatal)	Bacterium	N, O, H, L	A32 Listeriosis
Norovirus infection	Virus	N, O, H, L	A08.1 Acute gastroenteropathy due to Norwalk agent
Salmonellosis	Bacterium	N, O, H, L	A02.0 *Salmonella* enteritis
Sapovirus infection	Virus	N, O, L	No specific ICD-10 code
Shigellosis	Bacterium	N, O, H, L	A03 Shigellosis
Staphylococcus aureus intoxication	Bacterium	N, O, H	A05.0 Foodborne staphylococcal intoxication
Toxic shellfish poisoning	Toxin	N, O, H	T61.2 Other fish and shellfish poisoning
STEC infection	Bacterium	N, O, H, L	A04.3 Enterohaemorrhagic *Escherichia coli* infection
Vibrio parahaemolyticus infection	Bacterium	N, O, H	A05.3 Foodborne *Vibrio parahaemolyticus* intoxication
Yersiniosis	Bacterium	N, O, H, L	A04.6 Enteritis due to *Yersinia enterocolitica*

Data sources: EpiSurv notifications (N), EpiSurv outbreaks (O), Ministry of Health hospitalisations (H), ESR laboratory data (L)
STEC = Shiga toxin-producing *Escherichia coli*
[a] International statistical classification of diseases and related health problems, 10th revision [13]

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

For the conditions listeriosis and salmonellosis the attribution of disease incidence to foodborne transmission is based on an expert consultation held on 5 June 2013. For campylobacteriosis, shiga toxin-producing *Escherichia coli* (STEC) infection, and yersiniosis the attribution of disease incidence

to foodborne transmission was estimated by a New Zealand Food Safety (NZFS) expert colloquium in November 2020 [2, 3].

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

This report includes both potentially foodborne notifiable diseases and two sequelae which are considered to result from preceding infections (Table 3). The two sequelae included in the report, haemolytic uraemic syndrome (HUS) and Guillain-Barré syndrome (GBS), are severe illnesses and occasionally life threatening.

Table 3. Sequelae to potentially foodborne conditions included in the report

Disease	Source(s)	Comment
Guillain-Barré syndrome (GBS)	H (G61.0 Guillain-Barré syndrome)	Sequela to infection with *Campylobacter* [a]
Haemolytic uraemic syndrome (HUS)	H (D59.3 Haemolytic-uraemic syndrome)	Sequela to infection with STEC

Data Sources: Ministry of Health hospitalisations (H)

[a] While there is evidence that GBS can be triggered by other microbial infections (e.g. cytomegalovirus, Epstein-Barr virus, *Mycoplasma pneumonia*), *Campylobacter* infection is the only recognised triggering organism that is potentially foodborne

Changes in laboratory testing methodology

Since 2015, NZ diagnostic laboratories gradually introduced changes in enteric testing methods and screening criteria. Traditional culture-based methods for enteric bacteria and microscopy for parasites are gradually being replaced by molecular techniques such as multiplex Polymerase Chain Reaction (PCR). All faecal specimens in the affected DHBs are screened by multiplex PCR for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.*, STEC, and *Yersinia enterocolitica*. In some of the affected DHBs all faecal specimens are also routinely screened for *Giardia* spp., *Cryptosporidium spp.*, *Yersinia pseudotuberculosis* and *Vibrio parahaemolyticus.* An overview when laboratories servicing different DHBs moved to PCR detection methods and which pathogens are included in the respective PCR panels[*] is provided in Table 77 in Appendix B.

For the 2020 reporting year, nationally reported notification rates are a mixture of notifications based on PCR and non-PCR approaches. During 2020, Taranaki DHB moved to PCR-based methods in February, no other laboratory method changes have been recorded.

Multiple different testing related factors (e.g., change in sensitivity of methods, proportion of faecal specimens being tested) affect the notification rates on top of any underlying changes to disease incidence happening in New Zealand. The impact of the move to using PCR methods on notification rates of individual diseases is disease specific and is therefore discussed in more detail in the respective sections of this report.

Initial analyses comparing notification trends for bacterial infections in areas using community PCR-based culture independent diagnostic tests (CIDT) and areas still to change to CIDT (see Appendix B) suggest the change in methodology is having a significant impact on reporting rates for STEC infections, but not for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.* and *Yersinia enterocolitica*. Any observed trends in changes in STEC notification rates between 2015 and 2020 must be considered in the context of changes to testing approaches.

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

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

The global pandemic of Coronavirus disease 19 (COVID-19), caused by SARS-CoV-2, started to unfold in early 2020 with the first confirmed case reported in New Zealand on 26 February 2020. To prevent the spread of COVID-19 New Zealand introduced rapid public health measures, including border restrictions, followed by border closure to all but New Zealand citizens and residents on 20 March 2020. From 24 March 2020 until 14 May 2020 firm restrictions, including a complete lockdown were applied to all of New Zealand. Due to a localised outbreak in Auckland in August 2020, Level 3 restrictions were introduced to Auckland from 12 August to 31 August 2020. A gradual easing of alert levels occurred after the August outbreak (Table 4).

Table 4. New Zealand public health measures in response to the COVID-19 pandemic

Dates	Public Health Measures
16 Mar 2020	Border restrictions, compulsory self-isolation, cruise ships prohibited
20 Mar 2020	Border closed to all but New Zealand citizens and residents
22 Mar 2020	Alert Level 2 - Reduce
24 Mar 2020	Alert Level 3 - Restrict
26 Mar 2020	Alert Level 4 - Lockdown
28 Apr 2020	Alert Level 3 - Restrict
14 May 2020	Alert Level 2 - Reduce
9 Jun 2020	Alert Level 1 - Prepare
12 Aug 2020 (L2, AKL L3)	Auckland Alert Level 3 - Restrict, rest of New Zealand Alert Level 2 - Reduce
31 Aug 2020 (L2)	Alert Level 2 - Reduce
22 Sep 2020 (L1, AKL L2)	Auckland Alert Level 2 - Reduce (24 Sep), rest of New Zealand Alert Level 1 - Prepare (22 Sep)
8 Oct 2020 (L1)	Alert Level 1 - Prepare

Source: New Zealand COVID-19 Surveillance Dashboard (esr.cri.nz)

The impact of public health and social measures on notifications for potentially foodborne diseases is complex. While some diseases did show a significant reduction in notifications in comparison to the previous year others were little affected.

Changes in notification rates during 2020 may be attributed to several contributing factors, including:

- changes in testing priorities of laboratories, resources had to be diverted to the COVID-19 response
- more emphasis on hygiene
- travel restrictions
- physical distancing leading to no socialising, no private functions, no BBQs
- only supermarkets were open during lockdown, restaurants, cafes were closed, more home cooking
- behavioural changes such as fewer visits to healthcare providers (e.g., due to anxiety related to COVID-19, financial insecurity, active encouragement to replace GP visits by phone consultations)
- some of the behavioural changes may have continued onwards even after lockdown restrictions were lifted, their impacts, if any, have not been determined.

The contribution of all the above-mentioned factors makes it difficult to quantify the impact of individual factors. The monthly disease rate graphs for individual diseases will show the 2020 notification rates compared to the notification rates from 2017–2019. This will provide an indication of the possible impact on the 2020 notification rates due to COVID-19.

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2020 in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2020

	Total notified		Estimated foodborne transmission[a]		
	Cases	Rate[b]	Cases	Proportion (%)	Rate
Campylobacteriosis	5289	104.0	3917	75	77
Cryptosporidiosis	735	14.5	NE	-	-
Giardiasis	1141	22.4	NE	-	-
Hepatitis A	22	0.4	NE	-	-
Listeriosis	34	0.7	30	88 [c]	0.6 [d]
Salmonellosis	708	13.9	409	62 [c]	8.0 [d]
Shigellosis	76	1.5	NE	-	
STEC infection	844	16.6	330	40 [e]	6.5
Yersiniosis	1261	24.8	937	75	18

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

[a] For estimation of food-related cases the proportions derived from expert consultation [2, 3] exclude travel-related cases. Estimated foodborne transmission proportions were derived from two expert consultations in 2013 and 2020, respectively [2, 3]

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

[c] Most likely (95th percentile credible interval) estimates of proportion foodborne, from expert consultation[2]

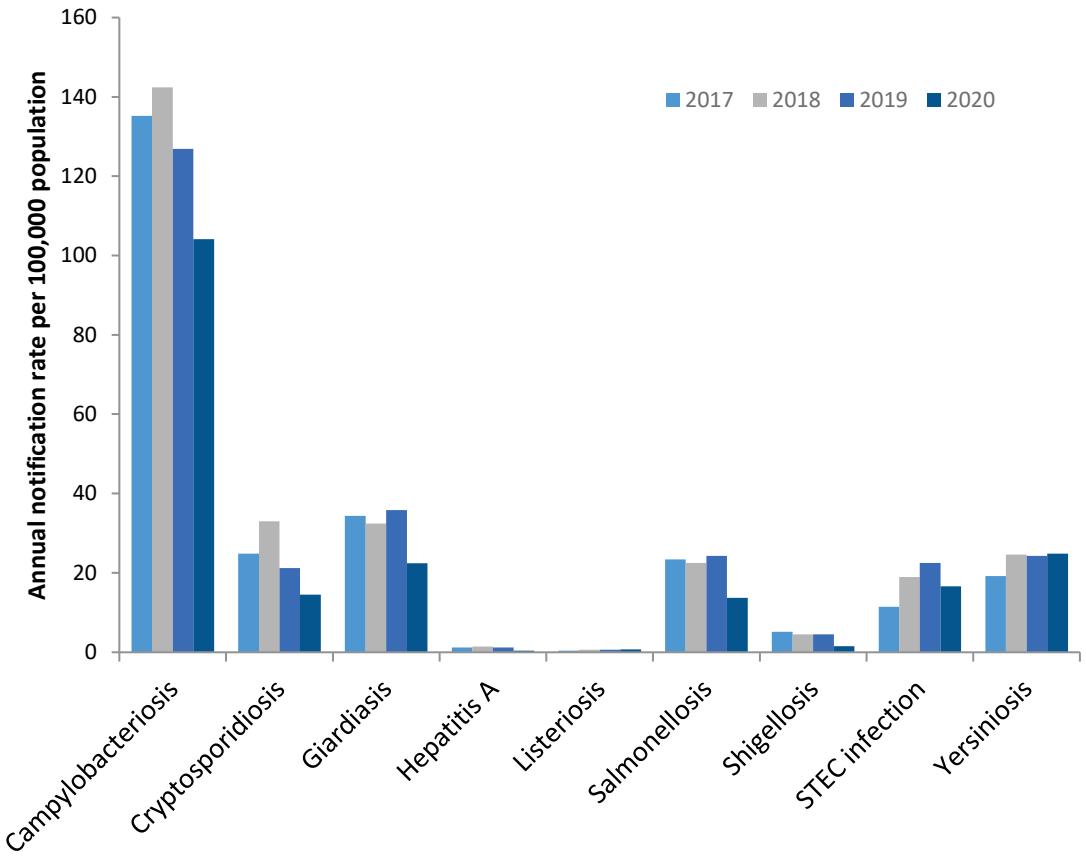
[d] Most likely (95th percentile credible interval) estimates of foodborne rate [2]

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

In 2020, notification rates for all main foodborne diseases with the exception of listeriosis and yersiniosis were lower compared to the previous three years; yersiniosis and listeriosis notification rates were similar to the previous year (Figure 1).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9) and the individual sections of this report.

Figure 1. Notification rates of the main foodborne diseases, 2017–2020



Reporting against targets

The performance targets for potentially foodborne diseases are reviewed by New Zealand Food Safety on an annual basis. In 2015, MPI established a performance target for campylobacteriosis to reduce the number of human cases of domestically acquired foodborne campylobacteriosis by 10% from 88.4 to 79.6 per 100,000 population by the end of 2020. In 2020, New Zealand Food Safety (MPI) introduced a further goal of reducing the number of domestically acquired human cases of foodborne campylobacteriosis by 20% from the mean rate for the years 2017-2019 (87.7) to 70.2 cases per 100,000 population by the end of 2024*. The new target uses the new proportion estimate of foodborne campylobacteriosis (75%) based on the latest expert elicitation process in 2020 [3].

Rationale

Campylobacteriosis is the most commonly notified potentially foodborne disease in New Zealand. A study commissioned by New Zealand Food Safety and conducted in 2018-2019 [14], provided updated information on how New Zealanders become infected with the *Campylobacter* bacterium†. The study identified that food remained the dominant pathway for exposure and infection in New Zealand, with poultry meat still being the main source of *Campylobacter*, especially for the urban population.

* https://www.mpi.govt.nz/dmsdocument/42766-Campylobacter-Action-Plan-2020-21 https://www.mpi.govt.nz/science/food-safety-and-suitability-research/managing-the-risk-of-campylobacter/ (Accessed 30 April 2021)
† http://www.sacnz.org.nz

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

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

Methodology, tools and reporting

Historical baseline data on the number of reported cases of the targeted potentially foodborne diseases are available from the *Notifiable Diseases in New Zealand Annual Report,* produced by ESR for the Ministry of Health (MoH) [15].

The annual number of notified cases is adjusted for the proportion of cases reported as having travelled overseas during the likely incubation period. The number of notified cases is also adjusted for the proportion of disease estimated to be due to foodborne transmission. In the event of very large outbreaks of campylobacteriosis (>300 notified cases) with a confirmed non-food cause, these cases are subtracted from the total number of cases before calculation of the target metric. Estimates for the proportion of campylobacteriosis due to foodborne transmission were revised in 2020 to 75% of cases through an expert elicitation process taking new studies and increased knowledge into account [3]. Prior to 2020, the estimate of the proportion of campylobacteriosis cases assigned to foodborne transmission was 64% (credible interval 44-83), based on an expert elicitation in 2013 [2].

The annual incidence of campylobacteriosis is reported in terms of calendar year cases per 100,000 population (*Notifiable Diseases in New Zealand Annual Report,* ESR) [15]. This allows for demographic changes within the New Zealand population to be appropriately captured. The proportion of infections acquired overseas is estimated through data from the EpiSurv programme administered by ESR and MoH.

Campylobacteriosis 2015 to 2020 Performance Target

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

Measurement

The measurement used is the annual (calendar year) rate (per 100,000 mid-year population estimate) of notified cases of human domestically-acquired foodborne campylobacteriosis, with the baseline being the average foodborne rate for 2012 to 2014 (88.4 cases per 100,000 mid-year population). The estimated incidence of domestically-acquired foodborne campylobacteriosis in 2020 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2020

	Cases	Proportion (%)	Rate (per 100,000, mid-year estimated population)
Total notified	5289	-	104.0
Estimated not related to overseas travel[a]	5223	98.8	102.8
Estimated foodborne transmission	3917	64 (44-83)	66 (45-86)

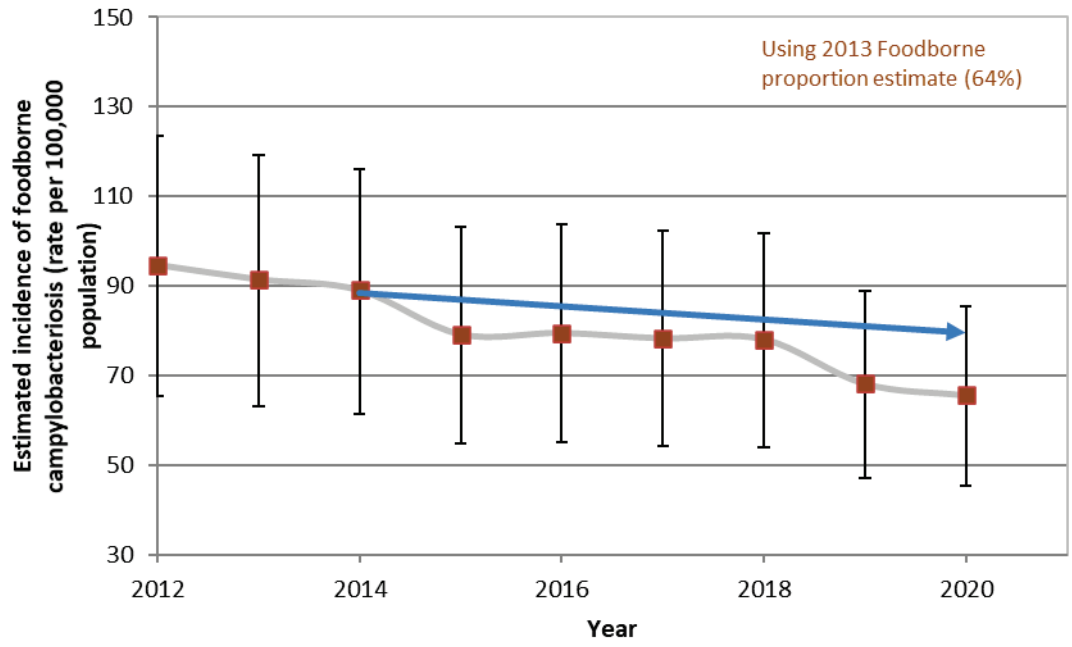
[a] The estimated percentage of cases relating to overseas travel in 2020 is 1.2%
[b] From expert consultation in 2013 [2]].

Presentation

The trend in the domestically-acquired foodborne campylobacteriosis rate (the measurement, most likely estimates) compared with the 2014 to 2020 goal (blue arrow) is shown in Figure 2. The measurements for 2012 to 2019 are calculated using the estimates of the proportion foodborne from

the expert consultation in 2013 (squares). The goal for a reduction in the measurement ending in 2020 has been achieved.

Figure 2. Estimated incidence of domestically acquired foodborne campylobacteriosis compared to 2015 to 2020 performance target



(Arrow indicates performance target)

Campylobacteriosis 2020 to 2024 performance target

Performance target: The number of human cases of foodborne campylobacteriosis reduced by 20% from 87.7 to 70.2 per 100,000 population by the end of 2024.

Measurement

The measurement that will be used is the annual (calendar year) rate (per 100,000 mid-year population estimate) of notified cases of human domestically-acquired foodborne campylobacteriosis, with the baseline being the average foodborne rate for 2017 to 2019 (88 cases per 100,000 mid-year population). The 2020 data have been excluded for setting the baseline, due to COVID-19 related changes in notification rates (see page 9).

Based on the campylobacteriosis data for 2020 in Table 6 and assuming 75% of domestic cases are due to foodborne transmission, the estimated rate for notified cases of human domestically-acquired foodborne campylobacteriosis is 77 per 100,000 population.

Reporting of incidence and severity of selected foodborne conditions

This report 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. The individual sections include the following information, where available:

- statement of estimated foodborne percentage and range provided by expert elicitation processes conducted in 2013 [2] and 2020 [3]. Note that these estimates are only available for some of the conditions included in this report.
- statement of estimated foodborne percentage and range for any specific foods provided by the same expert elicitation process.
- information on pathogen typing (principally from data generated by ESR's Enteric Reference Laboratory), where it is available and informative about foodborne disease.
- comments on specific food related incidents or outbreaks of the disease that were reported to the notification system during the calendar year.
- studies 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 from surveys conducted during the calendar year.
- regulatory or other risk management actions in New Zealand that might be expected to affect the foodborne disease data.

Interpreting data

Data in this report may differ from those published in other reports depending on:

- the date of extraction of data.
- the date used to aggregate data (e.g. date reported or date of onset of illness).
- filters used to extract the data, such as exclusion of records classified as 'not a case'.

The information in this report shows disease trends by age group, sex, and district health board (DHB) of the place of residence.

Due to low numbers of cases for some foodborne illnesses such as listeriosis the rates calculated in this report may be highly variable from year to year and it is necessary to interpret trends with caution.

Bacillus cereus intoxication

Case definition

Clinical description:	Gastroenteritis where either vomiting or profuse watery diarrhoea dominate.
Laboratory test for diagnosis:	Isolation of ≥10^3/g *Bacillus cereus* from a clinical specimen or ≥10^4 *B. cereus* from leftover food or detection of diarrhoeal toxin in a faecal sample.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Bacillus cereus intoxication cases reported in 2020 by data source

During 2020, one individual case of *B. cereus* intoxication was reported in EpiSurv in October. Testing by ESR of the remains of curry with rice eaten by the case detected *B. cereus.*

Note that not every case of *B. cereus* intoxication is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.4 was used to extract foodborne *B. cereus* intoxication hospitalisation data from the MoH National Minimum Dataset (NMDS). There were three hospital admissions (0.06 admissions per 100,000 population) recorded in 2020 two of which had *B. cereus* intoxication as the primary diagnosis and one with *B. cereus* intoxication as another relevant diagnosis.

Foodborne Estimate

Expert consultation estimated that 97% (minimum = 90%, maximum = 100%) of *B. cereus* intoxication will be due to foodborne transmission [16]. 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 2020 there was one *B. cereus* intoxication outbreak reported in EpiSurv with two associated cases.

Table 7. *B. cereus* intoxication outbreaks reported, 2020

	***B. cereus* intoxication outbreaks**	
	Possible foodborne transmission with a suspected or confirmed source	**All [a]**
Outbreaks	1	1
Outbreak-associated cases	2	2
Hospitalised Cases	0	0

[a] All *Bacillus cereus* outbreaks, including non-foodborne outbreaks

Table 8 contains details of the foodborne *B. cereus* intoxication outbreak reported in 2020. The suspected vehicle of this outbreak was a rice meal. The level of evidence for the outbreak being foodborne was weak.

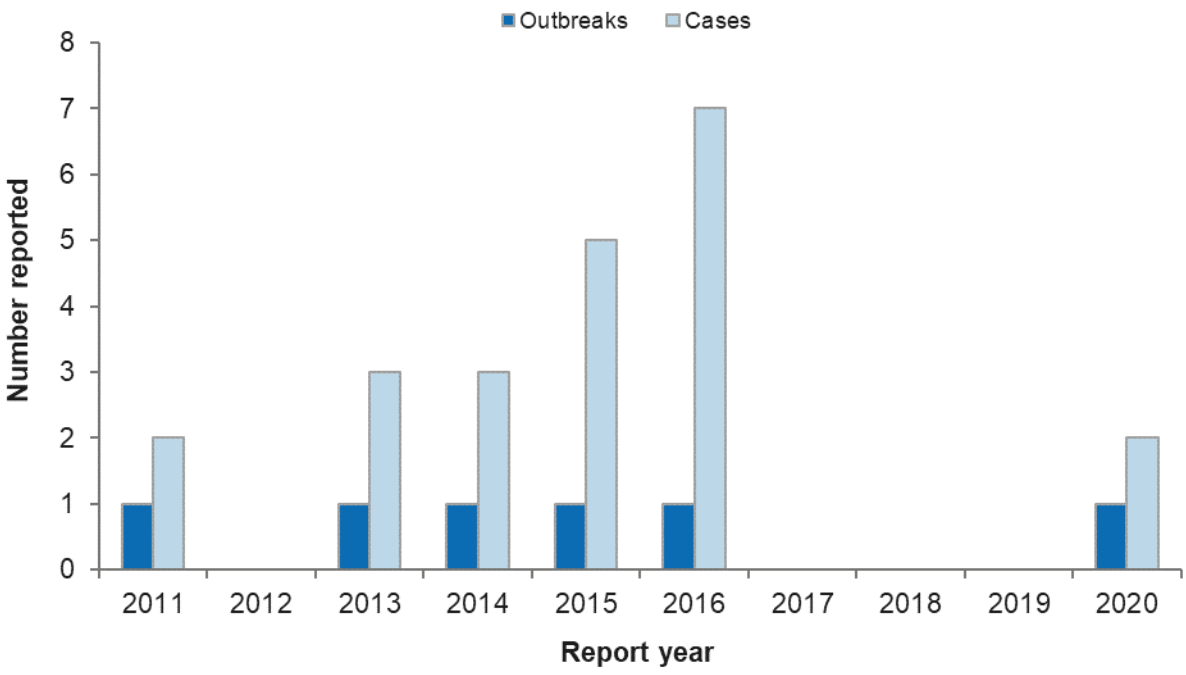
Table 8. Details of *B. cereus* intoxication outbreaks with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. ill
C and PH	July	Rice	Symptoms attributable to specific organism. Consumption from a common source	Takeaway	2P

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

Outbreaks of *B. cereus* intoxication are rare, with only six outbreaks reported since 2011. The number of cases associated with the outbreaks ranged between two and seven cases (Figure 3).

Figure 3. *B. cereus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2020 are given in Table 9.

Table 9. Summary of surveillance data for campylobacteriosis, 2020

Parameter	Value in 2020	Source
Number of notified cases	5289	EpiSurv
Notification rate (per 100,000)	104.0	EpiSurv
Hospitalisations[a]	718	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	66 (1.2%)	EpiSurv
Estimated food-related cases (%)[d]	3917 (75%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020.
[d] For estimation of food-related cases, the proportions derived from expert consultation [3] exclude travel-related cases. It has been estimated that 75.4% of foodborne transmission would be due to transmission via poultry [2].

Case definition

Clinical description:	An illness of variable severity with symptoms of abdominal pain, fever and watery diarrhoea, and often bloody stools. Less frequently, *Campylobacter* can present as an invasive disease.
Laboratory test for diagnosis:	Isolation of *Campylobacter* from a clinical specimen OR detection of *Campylobacter* nucleic acid OR detection of antigen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source - that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, community faecal specimens in all DHBs except for Canterbury, MidCentral, South Canterbury, Tairawhiti, West Coast and Whanganui, were screened by PCR methods for *Campylobacter* spp.

There is no evidence that campylobacteriosis notification rates have been affected by the introduction of PCR methods by diagnostic laboratories (refer to Appendix B) [3].

Effect of COVID-19 on campylobacteriosis notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, there was a reduction in campylobacteriosis notifications compared to the same period in the previous three years. During April and May 2020, there were 267 notified cases compared to 642 cases in 2019. From June to November 2020, notifications were slightly lower compared to the previous three years, with notifications in December being within the range of the previous three years (Figure 6).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes

to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9).

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

Campylobacteriosis cases reported in 2020 by data source

During 2020, 5289 individual cases (104.0 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv. Of the 5289 cases, the symptoms of 4776 cases (90%) were reported as fitting the clinical description for campylobacteriosis, the symptoms were unknown for 517 cases, and for 6 cases the symptoms are listed as not fitting the clinical description.

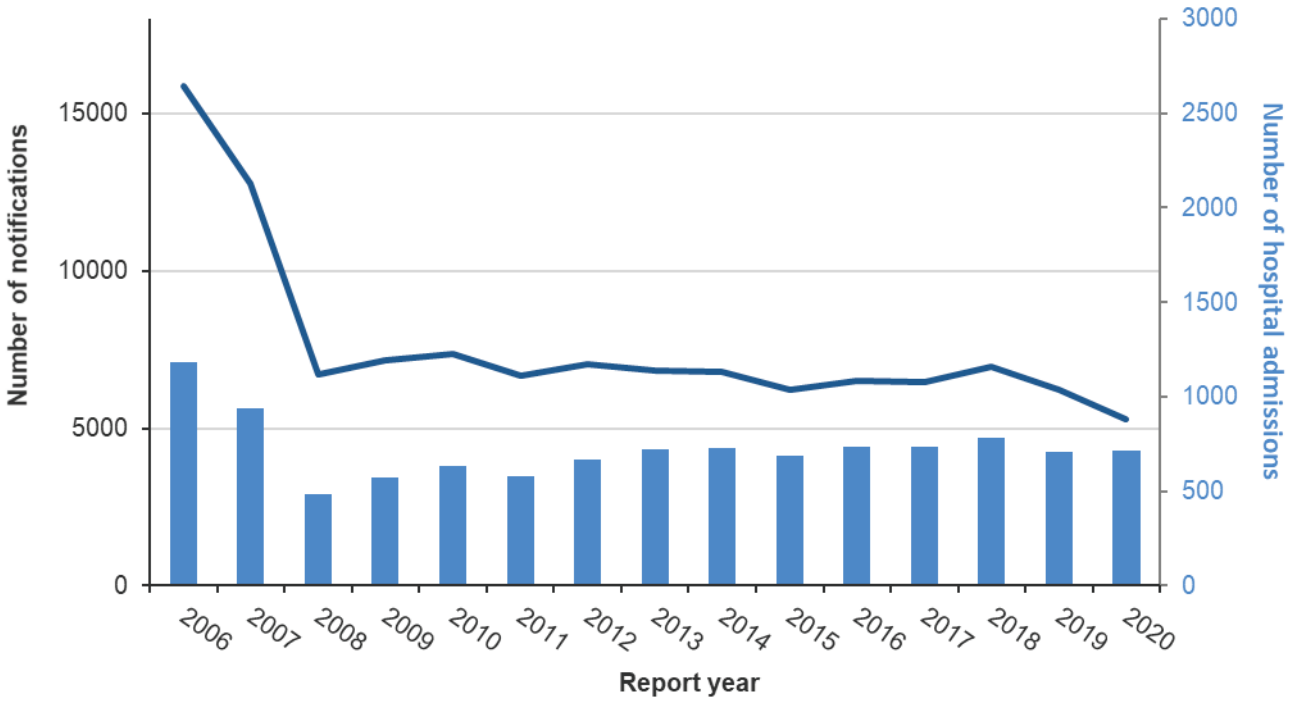
The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the NMDS database. Of the 718 hospital admissions (14.1 admissions per 100,000 population) recorded in 2020, 609 cases were reported with campylobacteriosis as the primary diagnosis and 109 were reported with campylobacteriosis as another relevant diagnosis.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

The number of campylobacteriosis notifications reported each year generally increased up to the highest number recorded in 2006 (15,873 cases). Due to the measures taken by New Zealand Food Safety and the poultry industry, there was a significant decrease from 2006 to 2008 in the number of reported cases (Figure 4). The number and rate of notifications each year has remained relatively stable from 2008 to 2018, with a decrease in 2019 and a further drop in notifications in 2020 (Figure 4 and Figure 5). The number of hospital admissions with campylobacteriosis as a primary or secondary diagnosis varied slightly year by year and has ranged between 485 (2008) and 780 (2018) hospitalisations since 2008.

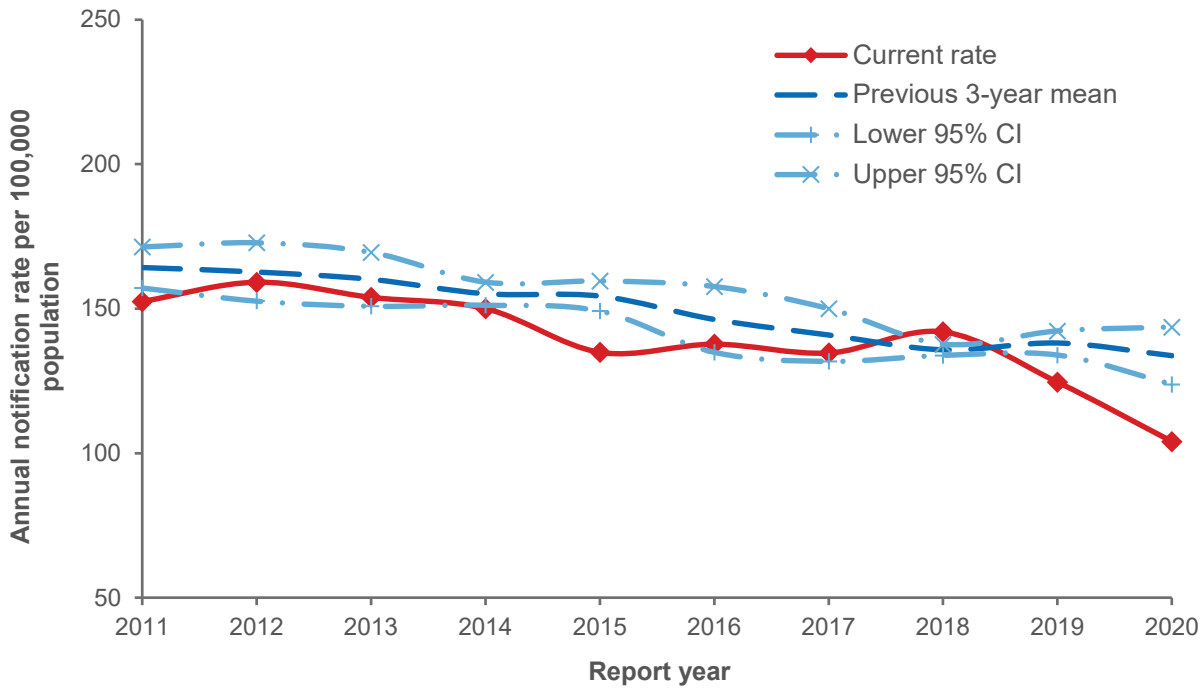
Figure 4. Campylobacteriosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



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

Between 2011 and 2019, the notification rate of campylobacteriosis was in the range of 124.6 to 158.2 notifications per 100,000 population (Figure 5). The trend for the calculated previous three-year mean is generally downward over that period. In 2020, the campylobacteriosis notification rate (104.0 cases per 100,000 population) was much lower compared to 2019 (124.6 cases per 100,000 population), due to the impact of COVID-19.

Figure 5. Campylobacteriosis notification rate by year, 2011–2020

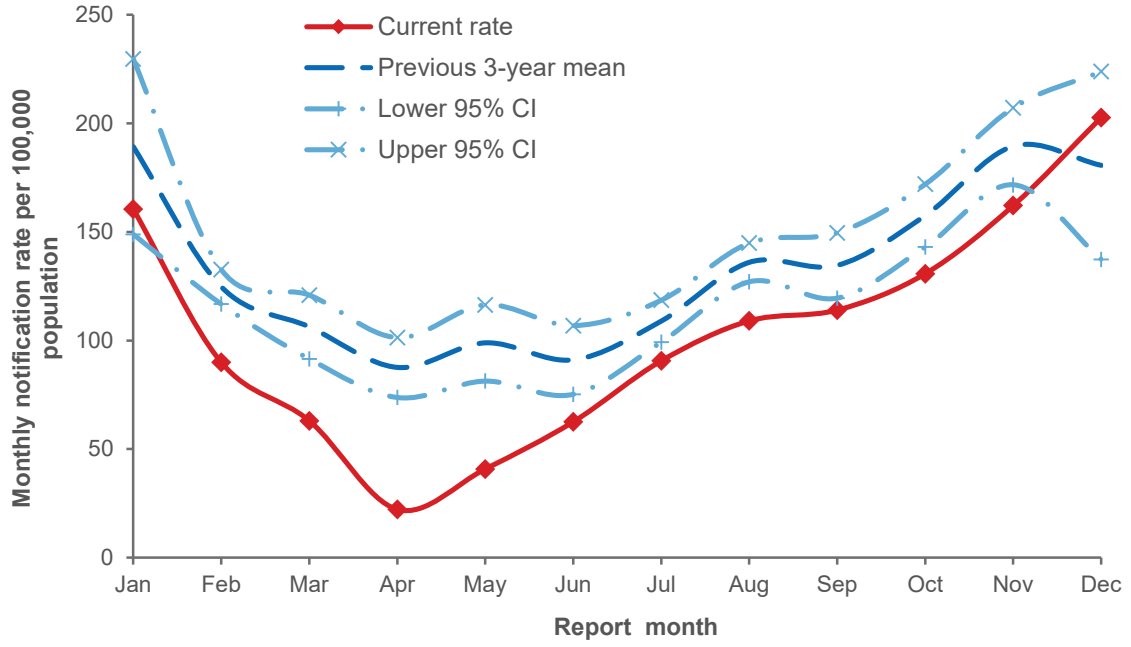


Note: 2016 campylobacteriosis notifications have been adjusted to exclude 964 cases associated with the Hawke's Bay drinking water-related campylobacteriosis outbreak

Seasonal data

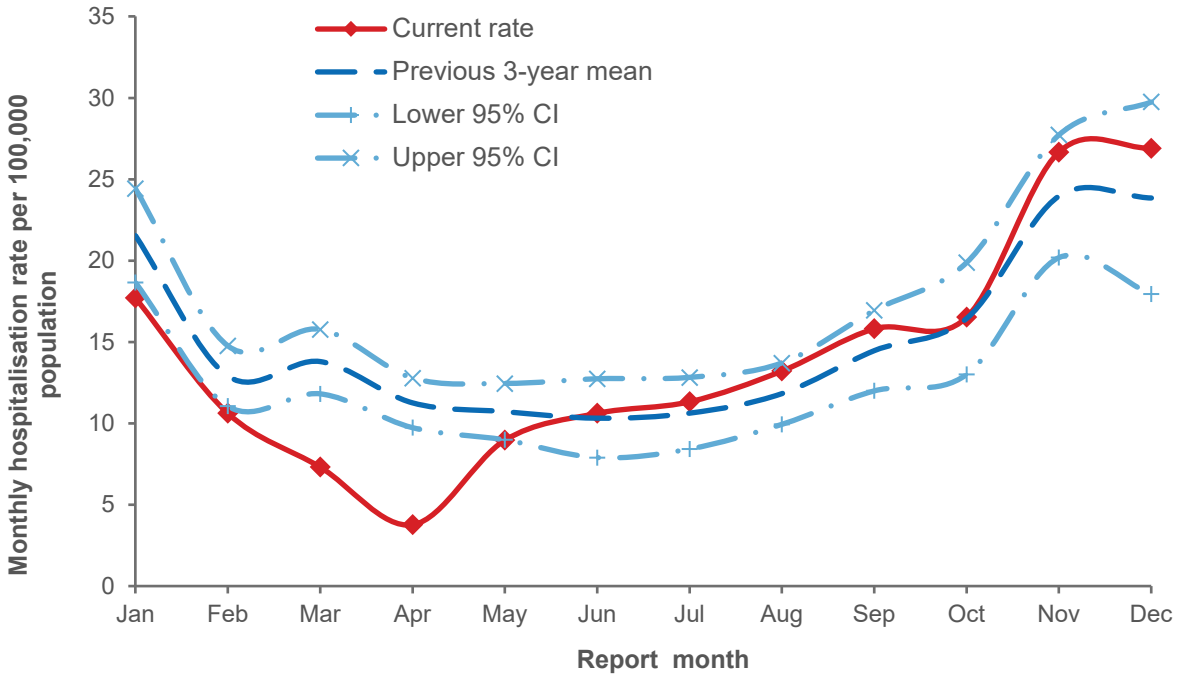
The number of notified cases of campylobacteriosis per 100,000 population by month for 2020 is shown in Figure 6. The monthly number of notifications in 2020 ranged from 94 notifications (April) to 859 notifications (December). In 2020, notification rates followed the same trend but were generally lower than the previous three-year mean. The monthly notification rates in 2020 showed a pronounced drop in April and May, related to the impact of the COVID-19 Level 4 public health response.

Figure 6. Campylobacteriosis monthly rate (annualised), 2020



In 2020, the monthly hospitalisation rates were mostly very similar compared to the previous three-year average with the exception of the months March and April, where the monthly hospitalisation rate was much lower than the previous three-year average (Figure 7).

Figure 7. Campylobacteriosis monthly hospitalisation rate (annualised), 2020



Demographics

In 2020, the rate of notifications and hospitalisations for campylobacteriosis was higher for males (118.0 and 15.5 per 100,000 population) compared with females (90.1 and 12.7 per 100,000 population) (Table 10).

Table 10. Campylobacteriosis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	2980	118.0	392	15.5
Female	2305	90.1	326	12.7
Total[c]	**5289**	**104.0**	**718**	**14.1**

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

The highest age-specific notification rates for campylobacteriosis in 2020 were reported for children aged 0 to 4 years (220.1 per 100,000 population, 672 cases). The highest hospitalisation rates were for the 70 years and over age group (39 admissions per 100,000 population) (Table 11).

Table 11. Campylobacteriosis cases by age group, 2020

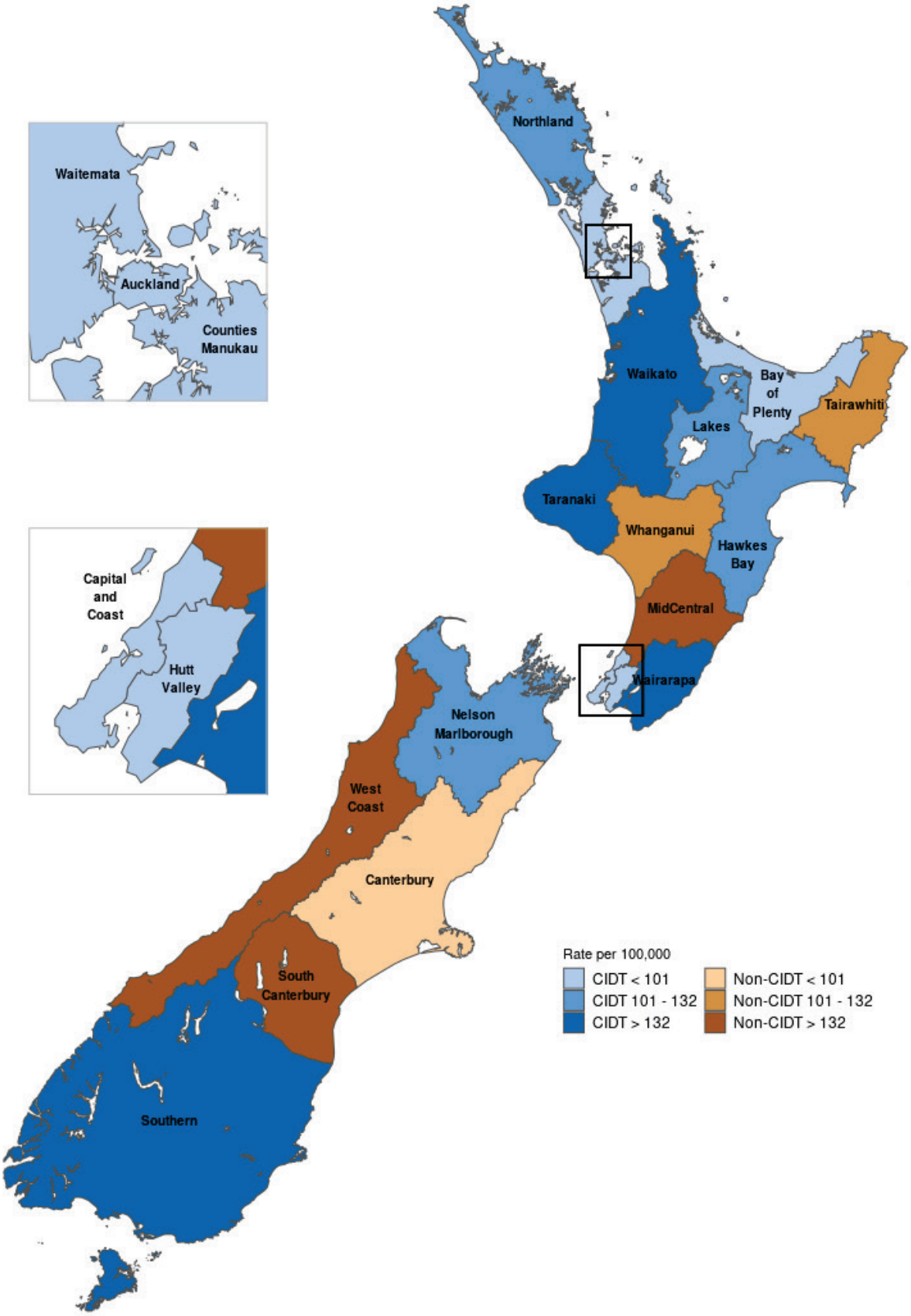
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	672	220.1	54	17.7
5 to 9	225	68.4	18	5.5
10 to 14	179	53.9	22	6.6
15 to 19	285	89.7	42	13.2
20 to 29	790	109.9	96	13.4
30 to 39	568	80.2	46	6.5
40 to 49	526	82.1	48	7.5
50 to 59	660	101.3	78	12.0
60 to 69	656	122.7	102	19.0
70+	722	132.8	212	39.0
Total[c]	**5289**	**104.0**	**718**	**14.1**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported)
[c] total includes notifications where age is unknown

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 8. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

Figure 8. Geographic distribution of campylobacteriosis notifications, 2020



In 2020, the highest notification rates of campylobacteriosis were reported in South Canterbury DHB (208.1 per 100,000, 129 cases), Wairarapa DHB (173.8 per 100,000, 85 cases), West Coast DHB (166.7 per 100,000, 54 cases), Taranaki DHB (155.6 per 100,000, 194 cases) and Southern DHB (148.4 per 100,000, 519 cases). The DHBs South Canterbury and West Coast are using non-CIDT community testing, while the other three DHBs are using CIDT methods.

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

Outbreaks reported as caused by *Campylobacter* spp.

In 2020, there were 20 campylobacteriosis outbreak notifications in EpiSurv, six (30%) of which recorded food as a possible mode of transmission (Table 12). It is important to note that a single outbreak may have multiple pathogens, settings and possible modes of transmission.

Table 12. Campylobacteriosis outbreaks reported, 2020

	Campylobacteriosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	4	2	20
Outbreak-associated cases	22	8	157
Hospitalised Cases	0	0	2

[a] All campylobacteriosis outbreaks, including non-foodborne outbreaks

Table 13 contains details of the six campylobacteriosis outbreaks reported in 2020 with food as a possible mode of transmission.

Table 13. Details of campylobacteriosis outbreaks with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. ill
South	Feb	Raw Milk	Household Cluster Roof water also suspected exposure route	Home	3C
C and PH	July	Unknown	Common meal	Long term care facility	4C
Hawke's Bay[a]	Aug	Raw Milk	Common source	Home	6C 2P
Auckland	Sept	Unknown	Increase in disease incidence	Long term care facility	4C
Northland	Oct	Unknown / food handler	None	Homes with inter-household contact	1C 5P
C and PH	Nov	Takeaway Meal	Common meal	Fast food restaurant, other food outlet	4C 1P

[a] Part of the information concerning the August Hawke's Bay has been derived from New Zealand Food Safety outbreak investigations.

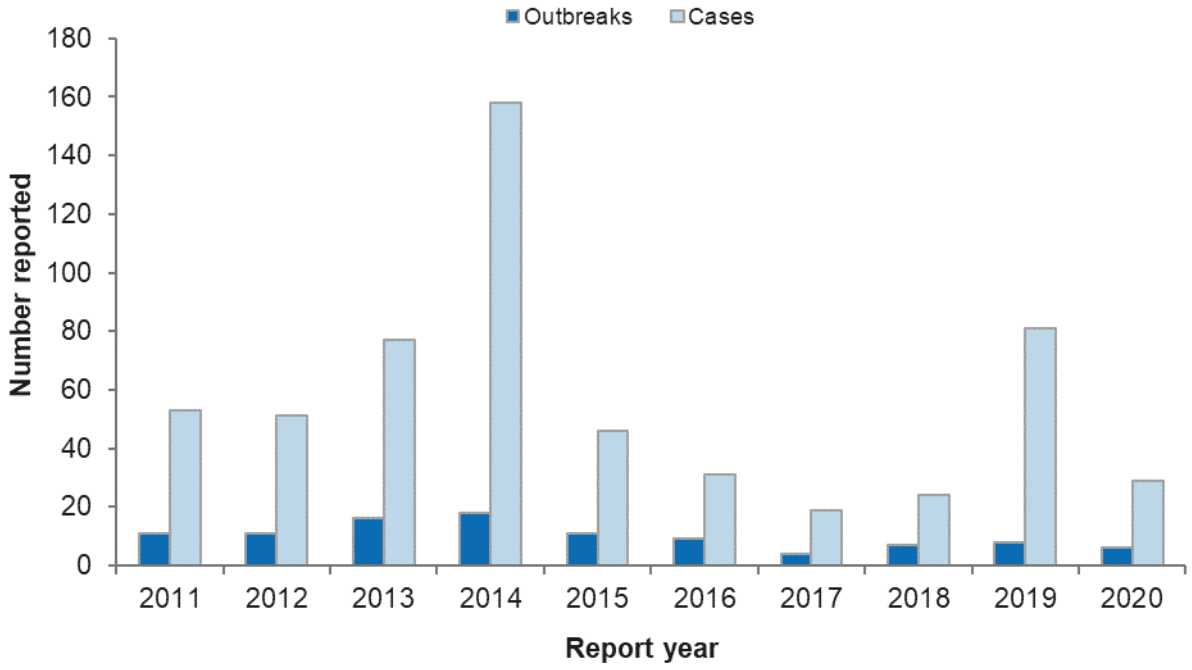
PHU: Public Health Units, South: Public Health South, C and PH: Community and Public Health, Hawke's Bay: Hawke's Bay District Health Board, Auckland: Auckland Regional Public Health Service, Northland: Ngā Tai Ora – Public Health Northland

Number ill: C: confirmed, P: probable

Of the six outbreaks and 30 associated cases where food was identified as a possible mode of transmission (Table 13), no cases were hospitalised. For the Hawke's Bay outbreak in August STEC (one case) and *Yersinia* spp. (one case) were implicated as additional pathogens. For the Auckland outbreak in September STEC was implicated as an additional pathogen.

Over the 10-year period 2011 to 2020, excluding 2014, the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission has ranged between four and 16 outbreaks reported each year with between 19 and 81 annual outbreak-associated cases (Figure 9). The greater number of outbreak-associated cases in 2014 was due to three outbreaks with high numbers of cases (51, 32 and 17).

Figure 9. Campylobacteriosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



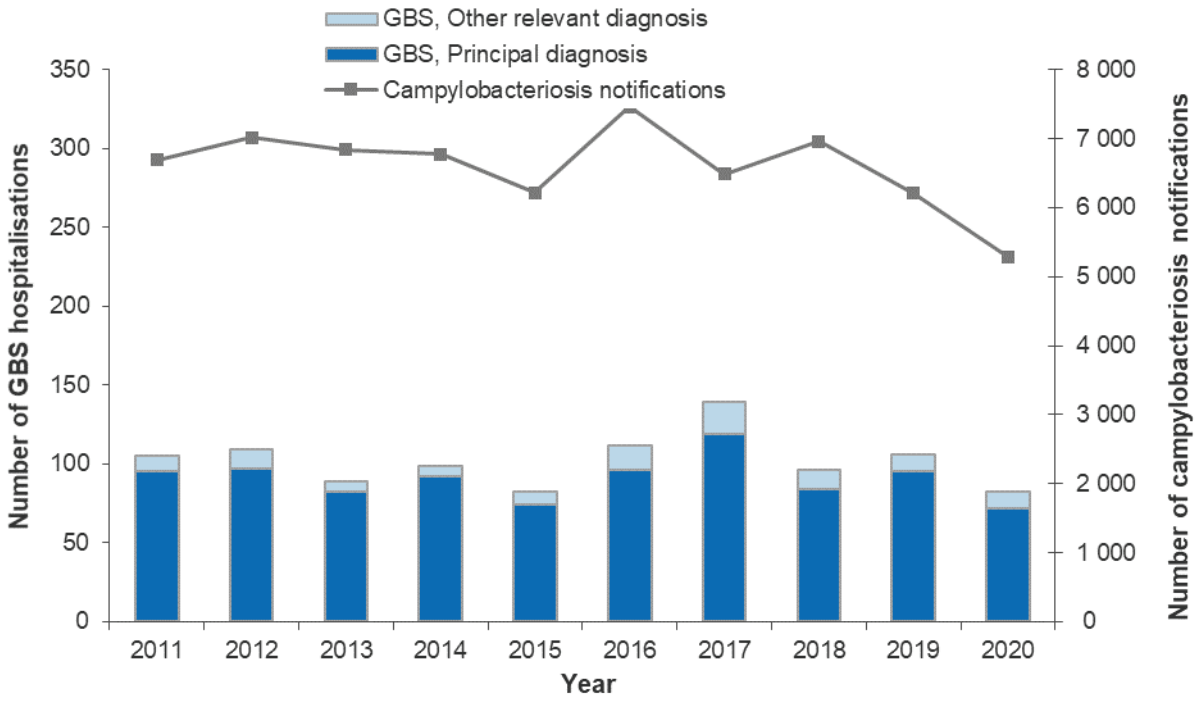
Disease sequelae - Guillain-Barré syndrome

Guillain-Barré syndrome (GBS) is a post-infectious disorder, which may be preceded by a range of respiratory or intestinal infections but is predominantly associated with *Campylobacter jejuni* infections.

The ICD-10 code G61.0 was used to extract GBS hospitalisation data from the MoH NMDS database. Only GBS cases that were incident in 2020 were considered, rather than all cases that were hospitalised in 2020. That is, if a GBS case hospitalised in 2020 had been hospitalised with GBS in a previous year, the 2020 admission was considered to be a readmission, rather than an incident case. There were 82 incident hospitalised cases recorded in 2020 (1.6 admissions per 100,000 population), 72 were reported with GBS as the primary diagnosis and 10 with GBS as another relevant diagnosis.

Between 2011 and 2020, the annual number of incident hospitalised cases (any diagnosis code) for GBS ranged from 82 to 139 (Figure 10). The numbers of campylobacteriosis notifications during the same period are also included in Figure 10 for comparison.

Figure 10. Guillain-Barré syndrome hospitalised cases, 2011–2020



In 2020, the number of incident hospitalised cases due to GBS was slightly higher for males than for females (Table 14). This is consistent with the pattern seen for GBS in most previous years, except 2016 when case numbers for males and females were almost identical. It is also consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2020 (Table 10).

Table 14. Guillain-Barré syndrome hospitalised cases by sex, 2020

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	45	1.8
Female	37	1.4
Total	**82**	**1.6**

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

In 2020, the highest rates of incident hospitalisation for GBS were in the 70+ years age group, followed by the 15-19 years age group (Table 15).

Table 15. Guillain-Barré syndrome hospitalised cases by age group, 2020

Age group (years)	Hospitalised cases	
	No.	Rate[b]
0 to 4	1	-
5 to 9	5	1.5
10 to 14	6	1.8
15 to 19	8	2.5
20 to 29	12	1.7
30 to 39	5	0.7
40 to 49	4	-
50 to 59	9	1.4
60 to 69	12	2.2
70+	20	3.7
Total	**82**	**1.6**

[a] MoH NMDS data for hospital admissions

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

Source assigned campylobacteriosis in New Zealand study (SACNZS)(*Lake et al. 2020*).

To better inform a comprehensive food-borne campylobacteriosis risk management strategy, New Zealand Food Safety commissioned a year-long source-assigned case-control study of notified human cases of campylobacteriosis [14]. The methodology incorporated a case control study and a nested source attribution study to estimate the relative contributions of different reservoirs and exposure pathways to the burden of human illness.

The number of case interviews completed were 598 in Auckland and 258 in Manawatū- Whanganui, giving a total of 856 interviewed cases. A total of 1080 clinical isolates were obtained from cases, including those who were not interviewed. The number of cases who were interviewed, and for which a clinical isolate was obtained, was 666 (Auckland 445, Manawatū-Whanganui 221).

As targeted, 600 controls were recruited and interviewed, with an age distribution that matched the age distribution of cases.

Source isolates recovered across the study were poultry (209), sheep (194) and cattle (172).

The source assignment models provided estimates of the number of study cases that could be assigned to a source:

- Poultry 553/656 (84%)
- Sheep 0 (0%)
- Cattle 93/656 (14%)
- Unassigned 10 (2%)

The pattern of source assignments for urban and rural cases are quite different, with about 90% of urban campylobacteriosis cases assigned to poultry sources, while less than 75% of rural cases were assigned to this source. The proportion of poultry source-assigned cases increases as the location of the cases becomes more urban.

Poultry is the most commonly consumed meat type in New Zealand and greater than 80% of people involved in the current study as cases or controls had consumed poultry within the previous 7 days. Under these study circumstances, differentiation of poultry consumption between cases and controls as a statistically significant overall risk factor would be less likely to be detected. On the other hand, more specific risk factors associated with consumption of poultry did result in statistically significantly elevated odds ratios e.g. consumption of undercooked chicken, consumption of chicken outside the home. Thus, the overall findings examining the source attribution and specific risk factors indicate that poultry meat remains the dominant pathway for exposure and infection.

Direct exposures to poultry birds with significantly elevated odds ratios include; contact with domestic poultry (reported by 6% of cases), contact with chickens (12% of cases) at home (9% of cases) or outside the home (3% of cases). This indicates that while direct contact with poultry presents a significantly elevated risk, it affects only a small proportion of the poultry attributed cases.

While raw milk consumption was a significant risk factor in the univariate analysis, it was reported in only a small proportion (4.1%) of cases.

The following is a summary of the risk factor calculation results (e.g. odds ratio estimates) for human campylobacteriosis.

- Living and/or working on a farm, and direct animal contact are significant exposure pathways, particularly for cattle-associated cases. This includes exposure to chickens.
- Raw milk consumption is a significant risk factor for urban cattle associated cases.
- Eating chicken outside the home is a significant risk factor for illness. There are many possible reasons for this, and the result is consistent with the previous case-control study.
- Although chicken consumption is not significant, there is elevated risk from a number of risk factors associated with poultry handling and preparation in the home.
- Eating a vegetarian meal is a significant risk factor, possibly because it contains uncooked foods.
- Rainwater/roof tank as a water source, either in the home or elsewhere, is a risk factor for campylobacteriosis.
- The use of proton pump inhibitors as a medication is a significant risk factor for infection.
- Contact with another person with gastrointestinal symptoms, particularly close contact, is a risk factor.
- Exposure to compost was a risk for infection in the initial univariate analysis, but after selection of actual compost exposures, this was no longer significant.

Journal papers

Persistent contamination of Salmonella Campylobacter, Escherichia coli, and Staphylococcus aureus at a broiler farm in New Zealand – Castaneda-Gulla et al. 2020

In a study conducted in 2016, broiler shed surfaces (annex, crevices, drinkers, fans, feed loaders, feeders and vents) were swabbed and tested for *Campylobacter* spp. before cleaning and after disinfection across three 6-week growth cycles [17]. While the prevalence of positive swabs decreased following cleaning and disinfection, *Campylobacter* contamination persisted. Microbial counts were enumerated using a correlation between quantitative polymerase chain reaction (qPCR) cycle threshold (C_t) values and conventional plate counts. *Campylobacter* concentrations decreased on most surface types by about 1 $\log_{10}$ CFU/mL or less across the cleaning/disinfection cycles. This study demonstrates the ability of *Campylobacter* to persist in broiler sheds. It should be noted that isolates were not typed and it was not confirmed that the same strains were present in broiler sheds across multiple growth cycles.

Campylobacteriosis associated with the consumption of unpasteurised milk: findings from a sentinel surveillance site – Davys et al. 2020

Recent increases in demand for untreated or 'raw' milk have raised concerns that this exposure may become a more important source of campylobacteriosis in the future [18]. This study described the cases of notified campylobacteriosis from a sentinel surveillance site. Previously collected data from notified cases of raw milk-associated campylobacteriosis were examined and compared with campylobacteriosis cases who did not report raw milk consumption. Raw milk campylobacteriosis cases differed from non-raw milk cases on comparison of age and occupation demographics, with raw milk cases more likely to be younger (median 26 years compared to 39 years for non-raw milk cases) and categorised as children or students for occupation. Raw milk cases were more likely to be associated with outbreaks than non-raw milk cases. However, raw milk cases were not significantly more likely to live in a rural location than an urban location.

Shifts in molecular Campylobacter jejuni infections in a sentinel region of New Zealand following implementation of food safety interventions by the poultry industry – Nohra et al. 2020.

A study was carried out to examine the impact of targeted food safety interventions implemented by the New Zealand poultry industry on the source attribution of *Campylobacter jejuni* infections in a sentinel region [19]. *Campylobacter jejuni* isolates collected from the Manawatu region of New Zealand between 2005 and 2007 ("before intervention") and 2008 and 2015 ("after intervention") from human clinical cases, chicken meat, ruminant faeces, environmental water, and wild bird sources were subtyped by Multi Locus Sequence typing. Viable counts of *Campylobacter* spp. from carcasses were analysed using a zero-inflated Poisson regression model. In the period before intervention, sequence type 474 (ST-474) was the most common sequence type (ST) recovered from human cases, accounting for 28.2% of the isolates. After intervention, the proportion of human cases positive for ST-474 reduced to 9.3%. Modelling indicated that chicken meat, primarily from one supplier, was the main source of *C. jejuni* infection in the Manawatu region before intervention. However, after intervention poultry collectively had a similar attribution to ruminants, but more human cases were attributed to ruminants than any single chicken supplier. Viable counts on carcasses were lower in all poultry suppliers after intervention. This study provides evidence of changes in the source attribution of campylobacteriosis following targeted food safety interventions in one sector of the food supply chain.

Importance of the farm environment and wildlife for transmission of Campylobacter jejuni in a pasture-based dairy herd – Rapp et al. 2020

A 6-month study was conducted to evaluate sources and pathways governing long-term presence of *Campylobacter jejuni* in a pasture-based dairy herd [20]. *C. jejuni* was detected in all sample types (soil, pasture, stock drinking-water, bird, rodent and cow faeces). *C. jejuni* was persistently detected from cow (54%; 49/90 samples) and bird (36%; 77/211 samples) faeces. Genetic comparison of 252 *C. jejuni* isolates identified 30 Multi-Locus Sequence Types (ST). ST-61 and ST-42 were persistent in the herd and accounted for 43% of the cow isolates. They were also detected on pasture collected from fields both recently and not recently grazed, indicating that grazed pasture is an important pathway and reservoir for horizontal transmission among cows. ST-61 accounted for 9% of the bird isolates and was detected at four of the six sampling events, suggesting that bird populations might contribute to the cycling of ruminant-adapted genotypes on-farm. Overall, the results indicated that management of grazed pasture and supplementary feed contaminated by bird droppings could be targeted to effectively reduce transmission of *C. jejuni* to dairy herds, the farm environment and ultimately to humans.

A meta-analysis of case-control studies examining sporadic campylobacteriosis in Australia and New Zealand from 1996 to 2016 – Varrone et al. 2020

A meta-analysis of campylobacteriosis case-control studies conducted in Australia and New Zealand was carried out to identify locally relevant risk factors for sporadic campylobacteriosis [21]. In total, 325 relevant articles were identified, from which 10 were included that described case-control studies. Four risk factors were statistically significant in the meta-analysis: eating undercooked poultry (OR=4.28, 95%CI 3.09-5.93); eating poultry cooked outside the home (OR=2.13, 95%CI 1.66-2.72);

having pet chickens (OR=3.29, 95%CI 2.12-5.10); and overseas travel (OR=5.55, 95%CI 3.20-9.63). Among children, having pet dogs showed elevated but not significant risk (OR=1.57, 95%CI 0.99-2.49). It should be noted that this meta-analysis did not include data from the recently completed SACNZ source-assigned case-control study.

Relevant regulatory developments

New Zealand Food Safety published a *Campylobacter* action plan [22]. The Action Plan includes:

- prioritisation of selected actions for immediate evaluation/implementation;
- identification of a further list of potential control measures on the basis of current knowledge, and establishing a framework for their systematic evaluation, prioritisation and implementation;
- setting of a public health improvement goal for the reduction of foodborne campylobacteriosis; and
- a lead into medium-term control measures that will likely be implemented in years 2022 – 2023.

Ciguatera poisoning

Case definition

Clinical description:	Gastroenteritis, possibly followed by neurologic symptoms.
Laboratory test for diagnosis:	Demonstration of ciguatoxin in implicated fish.
Case classification:	Not applicable.

Terminology

A FAO/WHO expert meeting, carried out in 2018 and reported in 2020 [23], concluded that there was sufficiently good evidence for cases of ciguatoxicity from consumption of non-finfish marine species. The meeting proposed that the condition should be known as ciguatera poisoning, rather than ciguatera fish poisoning. Ciguatera poisoning is now the preferred term and will be used throughout this document.

Ciguatera poisoning cases reported in 2020 by data source

During 2020, no individual cases of ciguatera poisoning were reported in EpiSurv. Note that not every case of ciguatera poisoning is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code T61.0 was used to extract foodborne ciguatera poisoning hospitalisation data from the NMDS database. Of the two hospital admissions (0.3 admissions per 100,000 population) recorded in 2020, both cases were reported with ciguatera poisoning as the primary diagnosis. No cases were reported with ciguatera poisoning as another relevant diagnosis.

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

Outbreaks reported as caused by ciguatera poisoning

During 2020, one outbreak of possible ciguatera poisoning was reported in EpiSurv, with one associated probable case and three confirmed cases in a food premises exposure setting. Consumption of imported fish was the suspected cause of the outbreak. It should be noted that all cases of ciguatera poisoning will be categorised as foodborne as consumption of contaminated fish is the only recognised transmission route for this disease.

Over the 10-year period 2010 to 2020, seven outbreaks of ciguatera poisoning were reported, with no more than two outbreaks reported in a single year (Figure 11). In 2017, the number of cases associated with one outbreak was unusually high (27 cases). The preparation setting for this 2017 outbreak was reported as an overseas manufacturer.

Table 16. Ciguatera poisoning outbreaks reported, 2020

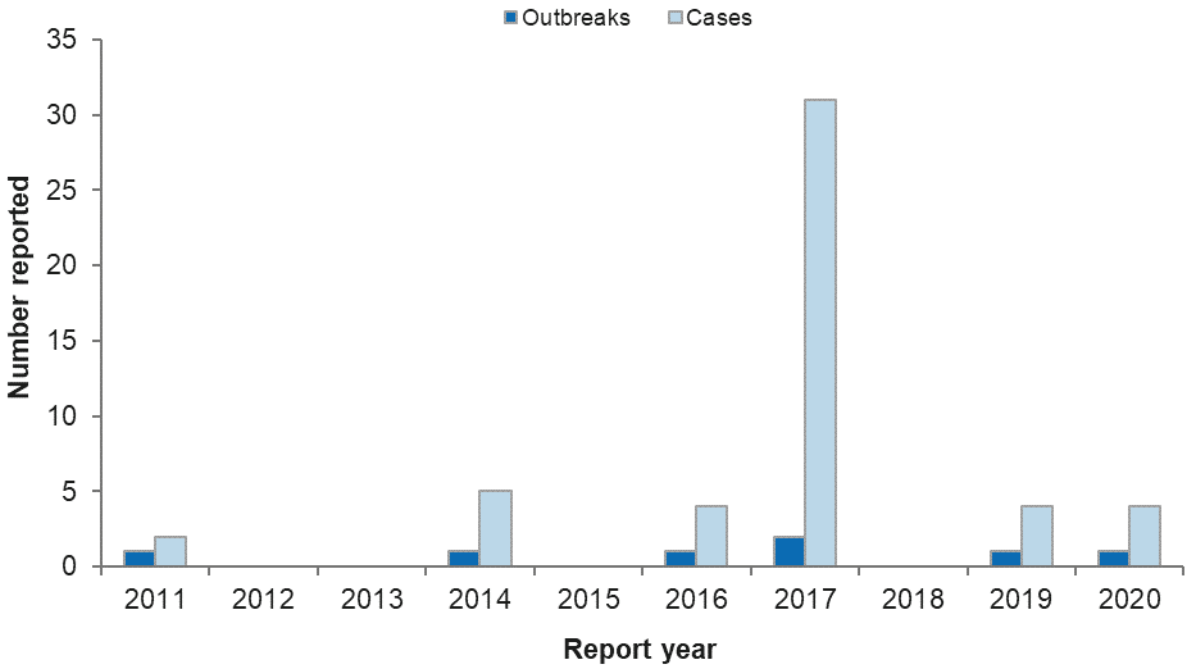
	Ciguatera poisoning outbreaks	
	Possible foodborne transmission with a suspected or confirmed source	All
Outbreaks	1	1
Outbreak-associated cases	4	4
Hospitalised Cases	1	1

Table 17. Details of ciguatera poisoning outbreaks, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. ill
C and PH	May	Preserved Kawa kawa fish from Fiji	Consumption of a common retail food source	Other food outlet, home	3C 1P

PHU: Public Health Units, C and PH: Community and Public Health
Number ill: C: confirmed, P: probable

Figure 11. Ciguatera poisoning outbreaks and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Ciguatera fish poisoning: the risk from an Aotearoa/New Zealand perspective – Rhodes et al. 2020

A review of the risk of ciguatera poisoning impacting on New Zealand was conducted [24]. *Gambierdiscus* and *Fukuyoa* species of dinoflagellates have been identified in Aotearoa/New Zealand's coastal waters and *G. polynesiensis*, a known producer of ciguatoxins, has been isolated from Rangitāhua/Kermadec Islands (a New Zealand territory). The warming of the Tasman Sea and the waters around New Zealand's northern subtropical coastline heighten the risk of *Gambierdiscus* proliferating in New Zealand. If this occurs, the risk of ciguatera poisoning due to consumption of locally caught fish will increase.

Relevant regulatory developments

Nil.

Clostridium perfringens intoxication

Case definition

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

Clostridium perfringens intoxication cases reported in 2020 by data source

During 2020, one individual case of confirmed *C. perfringens* intoxication was reported in EpiSurv. Note that not every case of *C. perfringens* intoxication is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.2 was used to extract foodborne *C. perfringens* intoxication hospitalisation data from the MoH NMDS database. There was one hospital admission recorded in 2020 with *C. perfringens* intoxication as the primary diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

In 2020, there was one *C. perfringens* intoxication outbreak (14 cases) reported in EpiSurv with food as a possible mode of transmission (Table 18). Table 19 contains details of the outbreak with no suspected source of infection recorded.

Table 18. *C. perfringens* intoxication outbreaks reported, 2020

	C. perfringens intoxication outbreaks	
	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	1	1
Outbreak-associated cases	14	14
Hospitalised Cases	0	0

[a] All *C. perfringens* intoxication outbreaks, including non-foodborne outbreaks

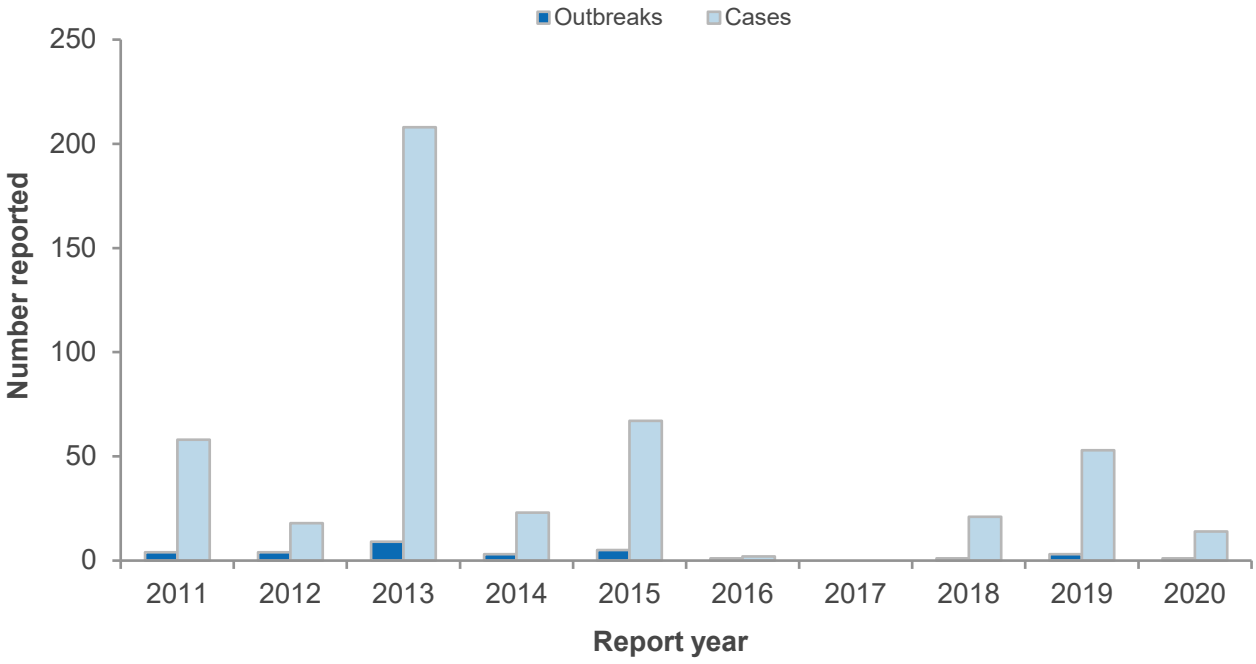
Table 19. Details of *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission, 2020

PHU	Month	Suspected source	Evidence	Setting	No. ill
Auckland	Dec	Unknown	Common event	Community/sports gathering	1C 13P

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

Over the 10-year period 2011-2020, the number of outbreaks of *C. perfringens* intoxication with food reported as a possible mode of transmission ranged from zero (2017 and 2020) to nine outbreaks (in 2013) (Figure 12). The number of cases associated with outbreaks of *C. perfringens* intoxication has also varied markedly over time. The highest number of cases associated with an outbreak of *C. perfringens* intoxication with possible transmission by food occurred in 2013 (208 cases).

Figure 12. *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2020 are given in Table 20.

Table 20. Summary of surveillance data for cryptosporidiosis, 2020

Parameter	Value in 2020	Source
Number of notified cases	735	EpiSurv
Notification rate (per 100,000)	14.5	EpiSurv
Hospitalisations[a]	64	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	7 (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] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020.

Case definition

Clinical description:	An acute illness that includes symptoms of diarrhoea (may be profuse and watery) and abdominal pain. The infection may be asymptomatic.
Laboratory test for diagnosis:	Detection of *Cryptosporidium parvum* oocysts OR *Cryptosporidium* antigen OR *Cryptosporidium* nucleic acid in a faecal specimen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease, or has had contact with the same common source, i.e., is part of an identified common source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, all community faecal specimens in Auckland, Capital & Coast, Counties Manukau, Hawke's Bay, Hutt Valley, Nelson Marlborough, Northland, Southern, Taranaki, Wairarapa, Waitemata DHBs were screened using PCR methods for a range of pathogens, including *Cryptosporidium*. All community faecal specimens in these DHBs are now screened for *Cryptosporidium* spp. when previously only those specimens where parasite screening was requested were tested. The remainder of the DHBs (around 35% of the NZ population) are still serviced by laboratories using microscopic methods or enzyme immunoassay tests (EIA) when parasite screening is specifically requested.

It is unclear at this stage how laboratory changes have affected the notification rates for cryptosporidiosis. The increased number of samples screened for *Cryptosporidium* spp. may impact on the numbers of positive results and subsequently increased notification rates. There does not seem to be a large difference in sensitivity between EIA tests (used by most laboratories prior to enteric PCR introduction) and PCR for the detection of *Cryptosporidium* spp.

Effect of COVID-19 on cryptosporidiosis notification rates

For 2020, the cryptosporidiosis notification rate was below the range based on the previous three years (Figure 14). The monthly rate in April (during the lockdown period) was below the April monthly

rate for the previous three years (Figure 15). However, all monthly rates for 2020 were at the lower end, or below, the monthly rates for the previous three years.

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9).

The frequency of overseas travel has changed due to border restrictions from March 2020. This has had an effect on annual notifications; in 2020, there were 7 cryptosporidiosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 50 in 2019.

Cryptosporidiosis cases reported in 2020 by data source

During 2020, 735 individual cases (14.5 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Of the 735 cases, the symptoms of 679 cases (92%) were reported as fitting the clinical description for cryptosporidiosis and the symptoms were unknown for 56 cases.

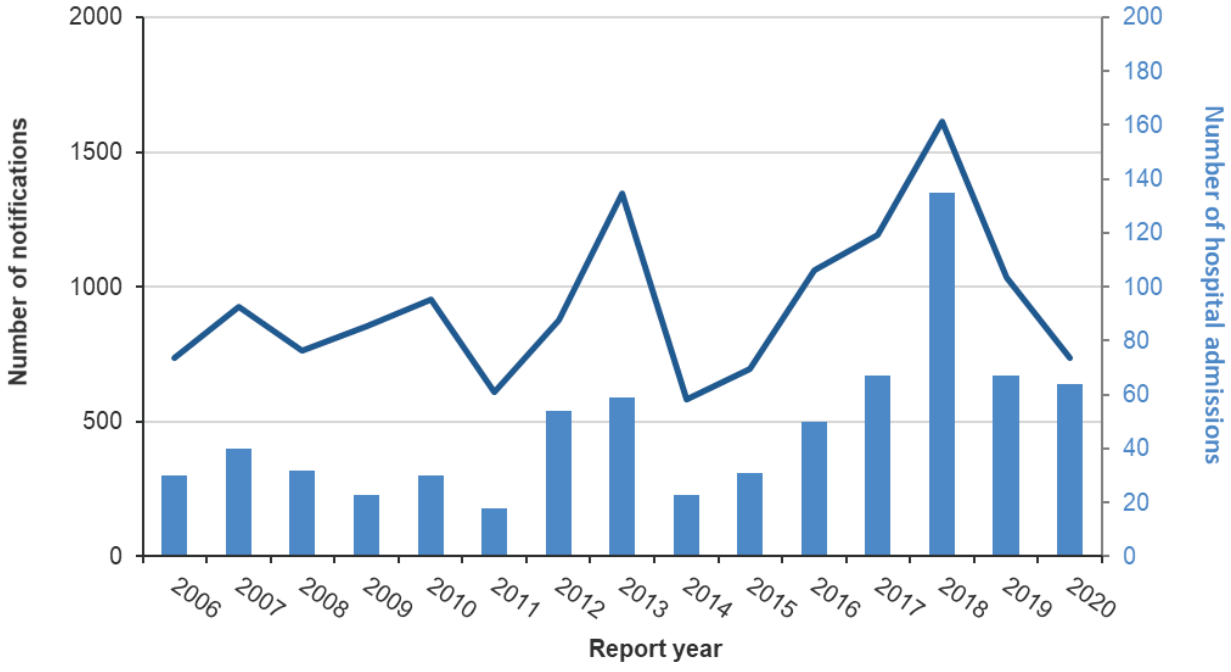
The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 64 hospital admissions (1.3 admissions per 100,000 population) recorded in 2020, 49 cases were reported with cryptosporidiosis as the primary diagnosis and 15 were reported with cryptosporidiosis as another relevant diagnosis.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

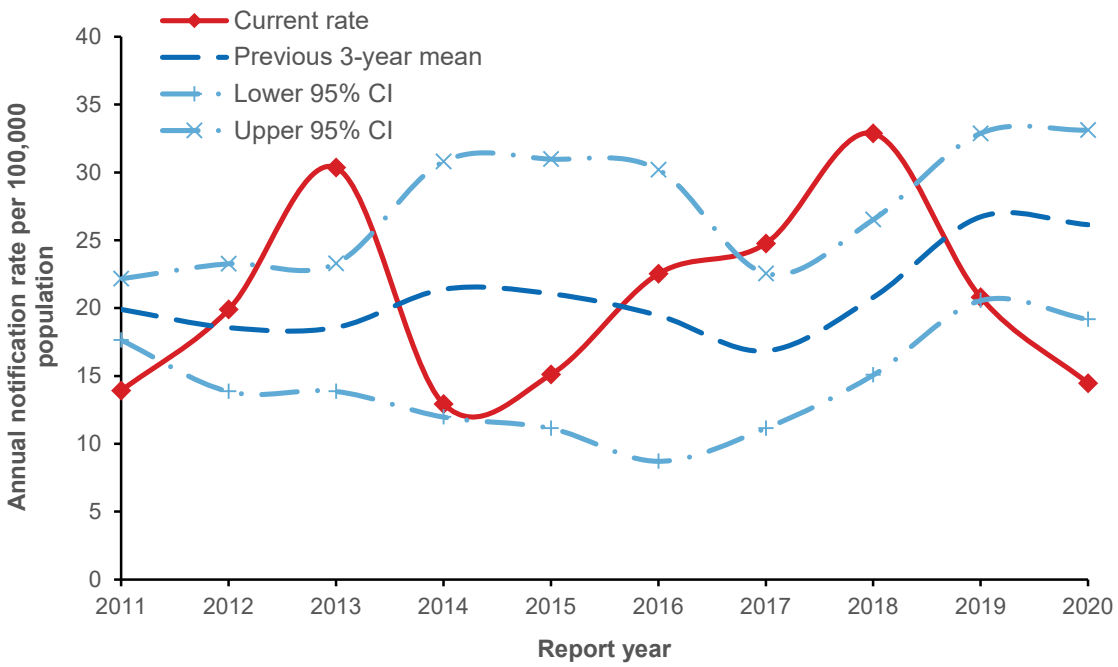
In 2018, the highest number of cryptosporidiosis notifications (1611 notifications) was recorded since cryptosporidiosis became a notifiable disease in 1996. Over the last 20-year time period there were no clear trends regarding the number of cryptosporidiosis notifications (Figure 13). After the peak in 2018, the number of notifications in 2020 (735 cases) has returned to within the range seen in the previous 20 years. The number of hospital admissions with cryptosporidiosis as a primary or secondary diagnosis varied year by year and has ranged between 18 (2011) and 135 (2018).

Figure 13. Cryptosporidiosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



Due to the peak in 2018, the cryptosporidiosis notification rate in 2020 (14.5 cases per 100,000 population) was lower than the previous three-year average (26.1 cases per 100,000 population) (Figure 14).

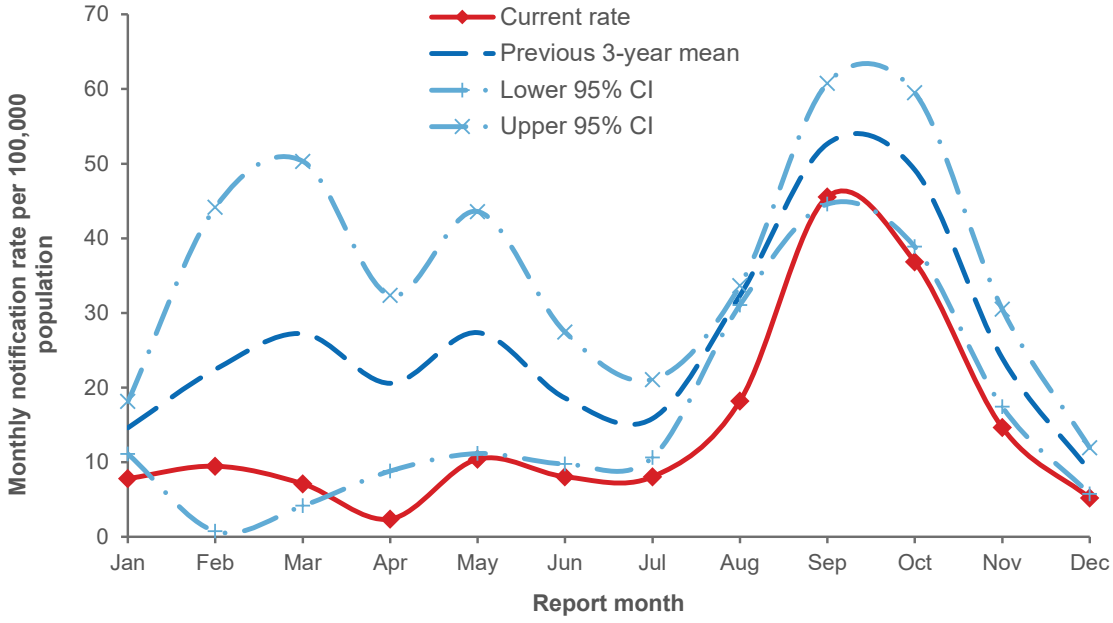
Figure 14. Cryptosporidiosis notification rate by year, 2011–2020



Seasonal data

The number of notified cases of cryptosporidiosis reported per 100,000 population by month for 2020 is shown in Figure 15. The monthly number of notifications in 2020 ranged from 10 notifications (April) to 193 notifications (September). In 2020, monthly notification rates followed the same trend but were generally lower than the previous three-year mean, likely related to the impact of the COVID-19 public health response.

Figure 15. Cryptosporidiosis monthly rate (annualised), 2020



Demographics

In 2020, the rate of notifications for cryptosporidiosis was higher for females (16.1 per 100,000 population) compared with males (12.8 per 100,000 population) whereas the rate of hospitalisations was similar (Table 21).

Table 21. Cryptosporidiosis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	323	12.8	31	1.2
Female	412	16.1	33	1.3
Total	**735**	**14.5**	**64**	**1.3**

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

In 2020, the highest cryptosporidiosis age-specific notification rate was reported for the 0 to 4 years age group (60.6 per 100,000 population, 185 cases) (Table 22). The hospitalisation rate was also highest in this age group (4.3 admissions per 100,000 population, 13 cases).

Table 22. Cryptosporidiosis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	185	60.6	13	4.3
5 to 9	71	21.6	6	1.8
10 to 14	41	12.3	6	1.8
15 to 19	59	18.6	3	-
20 to 29	153	21.3	11	1.5
30 to 39	97	13.7	9	1.3
40 to 49	56	8.7	5	0.8
50 to 59	32	4.9	7	1.1
60 to 69	24	4.5	1	-
70+	17	3.1	3	-
Total	**735**	**14.5**	**64**	**1.3**

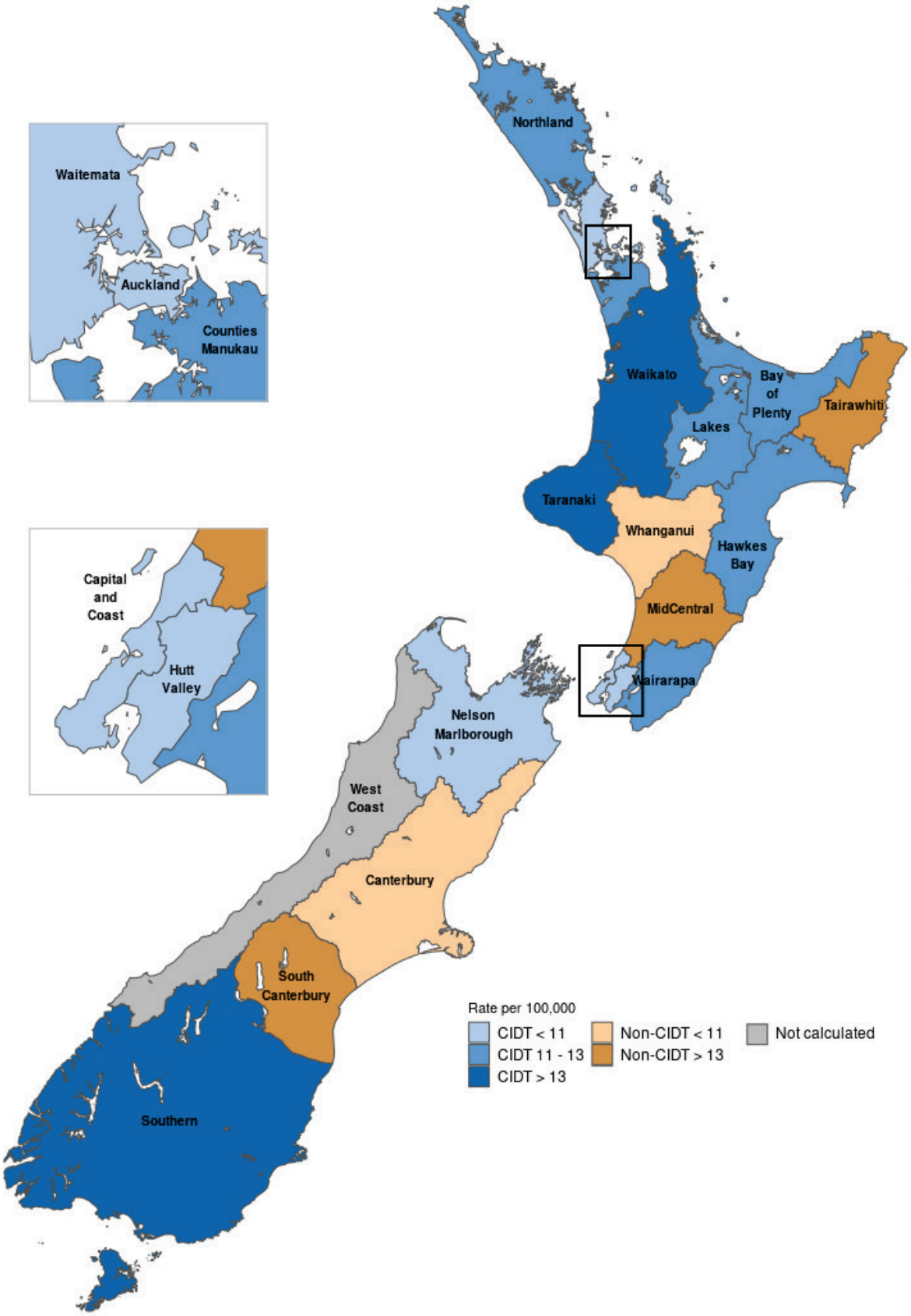
[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported)

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 16. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for West Coast DHB (4 cases) with fewer than 5 cases (grey shading): West Coast DHB is serviced by laboratories using non-CIDT methods.

Notification rates for cryptosporidiosis have been highly variable across New Zealand since 2016.

Figure 16. Geographic distribution of cryptosporidiosis notifications, 2020



In 2020, the highest notification rates of cryptosporidiosis were reported for South Canterbury DHB (48.4 per 100,000, 30 cases), Southern DHB (33.2 per 100,000, 116 cases), Taranaki DHB (28.9 per 100,000, 36 cases), Waikato DHB (25.1 per 100,000, 110 cases), and MidCentral DHB (19.8 per 100,000, 37 cases). The DHBs South Canterbury and MidCentral were serviced by laboratories using

non-CIDT community testing, while the other two DHBs were using CIDT methods for community testing.

Outbreaks reported as caused by *Cryptosporidium* spp.

In 2020 there were four cryptosporidiosis outbreak notifications reported in EpiSurv none of which recorded food as a possible mode of transmission (Table 23). It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

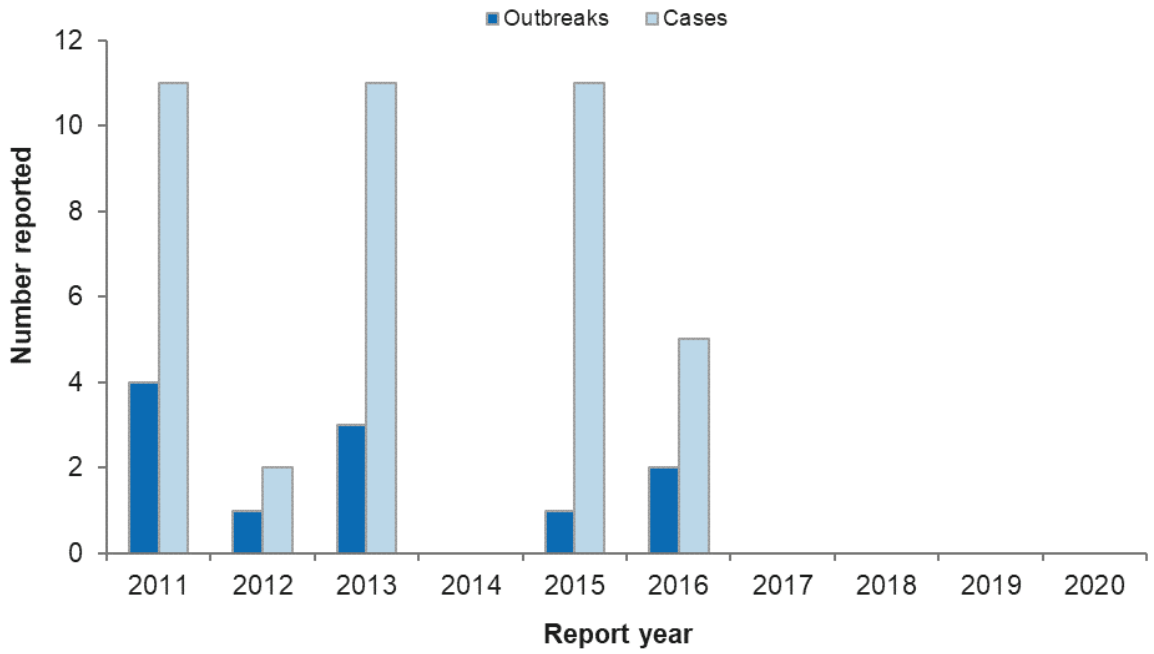
Table 23. Cryptosporidiosis outbreaks reported, 2020

	Cryptosporidiosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	0	0	4
Outbreak-associated cases	0	0	29
Hospitalised Cases	0	0	0

[a] All cryptosporidiosis outbreaks, including non-foodborne outbreaks

Between 2011 and 2016 there have been 11 outbreaks of potentially foodborne cryptosporidiosis (Figure 17). The number of cases associated with these outbreaks ranged between two and eleven. There have been no cryptosporidiosis outbreaks with food reported as a possible mode of transmission in the last four years. The last outbreaks were in 2016 (two outbreaks, five cases) and 2015 (one outbreak, 11 cases).

Figure 17. Cryptosporidiosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2020 are given in Table 24.

Table 24. Summary of surveillance data for giardiasis, 2020

Parameter	Value in 2020	Source
Number of notified cases	1141	EpiSurv
Notification rate (per 100,000)	22.4	EpiSurv
Hospitalisations[a]	66	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	59 (5%)	EpiSurv
Estimated food-related cases	NE	-

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

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

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

Case definition

Clinical description:	An illness characterised by diarrhoea, abdominal cramps, bloating, flatulence, nausea, weight loss and malabsorption. The infection may be asymptomatic.
Laboratory test for diagnosis:	Detection of *Giardia* cysts or trophozoites OR *Giardia* antigen OR *Giardia* nucleic acid in a specimen from the human gastrointestinal tract.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, all community faecal specimens in Auckland, Capital & Coast, Counties Manukau, Hawke's Bay, Hutt Valley, Nelson Marlborough, Northland, Southern, Taranaki, Wairarapa, Waitemata DHBs were screened by PCR methods for a range of pathogens, including *Giardia*. All community faecal specimens in these DHBs are now screened for *Giardia* spp. when previously only those specimens where parasite screening was requested were tested. The remainder of the DHBs (35% of the New Zealand population) are still serviced by community laboratories using microscopic methods or enzyme immunoassay tests (EIA) when parasite screening is specifically requested.

Notification rates for giardiasis have not changed significantly since the introduction of PCR-based methods that enabled the testing of increased numbers of samples. This suggests that symptoms of gardiasis were generally well recognised.

Effect of COVID-19 on giardiasis notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, there was a reduction in giardiasis notifications compared to the previous three years. During April and May 2020, there were 135 notified cases compared to 317 cases in 2019. From April to November 2020, notifications were consistently slightly lower compared to the previous years (Figure 20).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9).

The frequency of overseas travel has changed due to border restrictions from March 2020. This is reflected in the notifications; in 2020, there were 59 giardiasis notifications in EpiSurv listing overseas travel as a risk factor, compared to 179 in 2019. In the months affected by border restrictions (April to December 2020) there were 14 giardiasis notifications in EpiSurv listing overseas travel as a risk factor, compared to 136 for the same time period in 2019. The reduction in overseas travel explains a proportion of the consistent reduction in notifications April to November 2020.

Giardiasis cases reported in 2020 by data source

During 2020, 1141 individual cases (22.4 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv. Of the 1141 cases, the symptoms of 1020 cases (89%) were reported as fitting the clinical description for giardiasis, the symptoms were unknown for 115 cases, and for six cases the symptoms were listed as not fitting the clinical description.

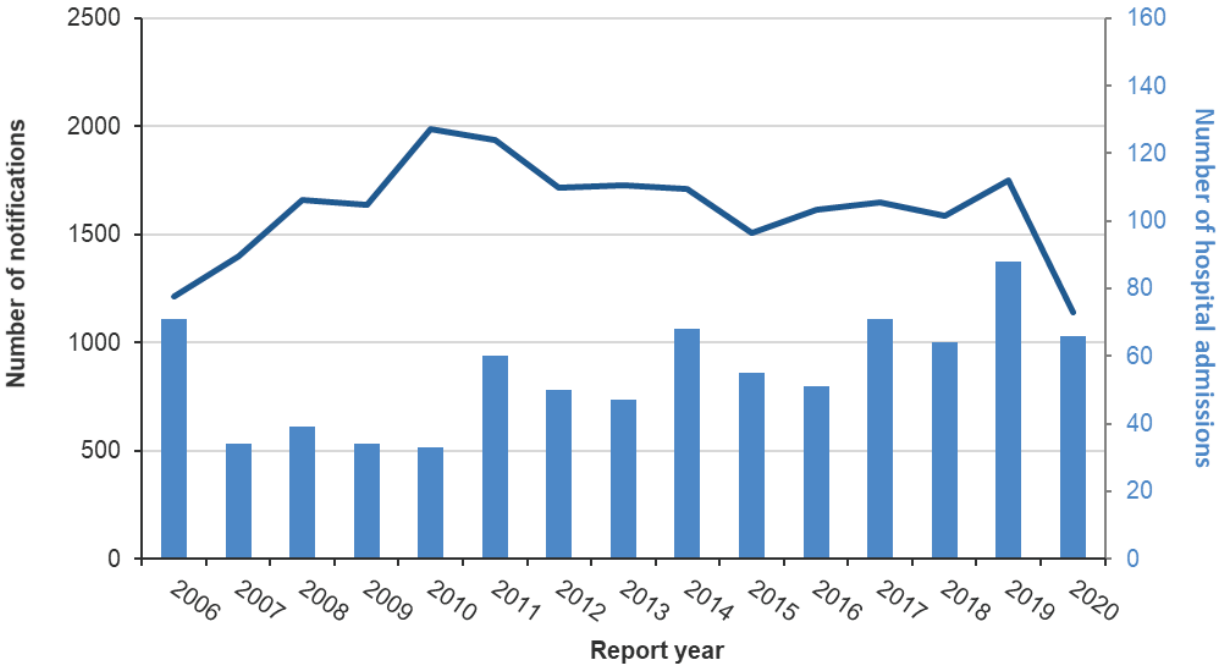
The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 66 hospital admissions (1.3 admissions per 100,000 population) recorded in 2020, 39 cases were reported with giardiasis as the primary diagnosis and 27 were reported with giardiasis as another relevant diagnosis.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

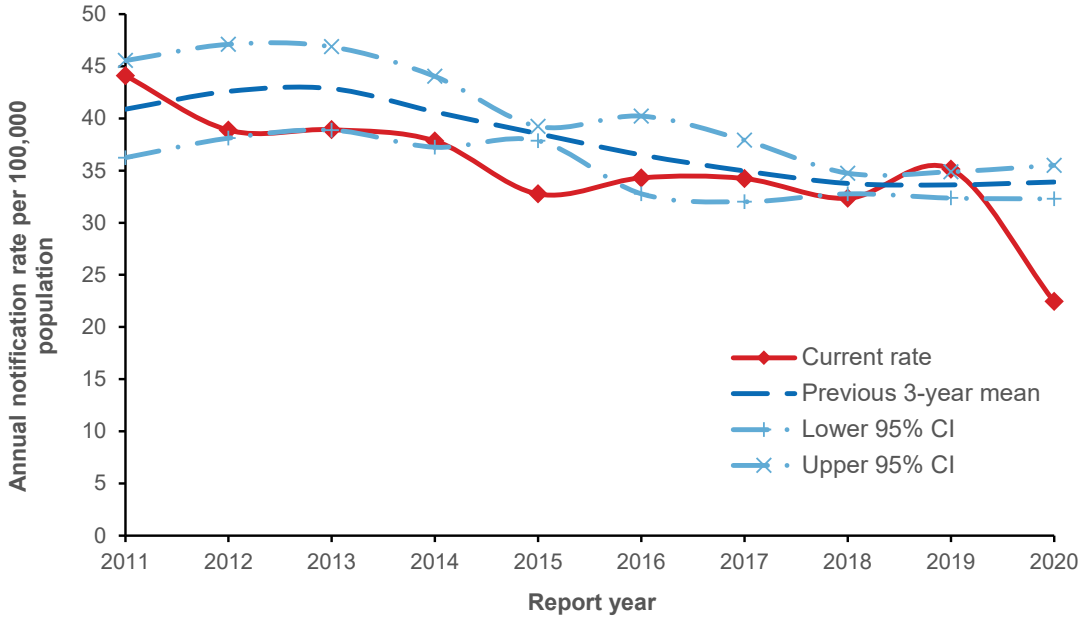
There was a steady decrease in the number of giardiasis cases reported each year until 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 with notification numbers remaining within a similar range since 2012 (range of 1510 to 1749 cases) (Figure 18). There was a pronounced drop in notifications in 2020. The number of hospital admissions with giardiasis as a primary or secondary diagnosis varied year by year and has ranged between 33 (2010) and 88 (2019).

Figure 18. Giardiasis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



The notification rate in 2020 (22.4 cases per 100,000 population) was much lower than the previous three-year average (33.9 cases per 100,000 population) (Figure 19). This drop in notification rates can be attributed to the COVID-19 pandemic*.

Figure 19. Giardiasis notification rate by year, 2011–2020

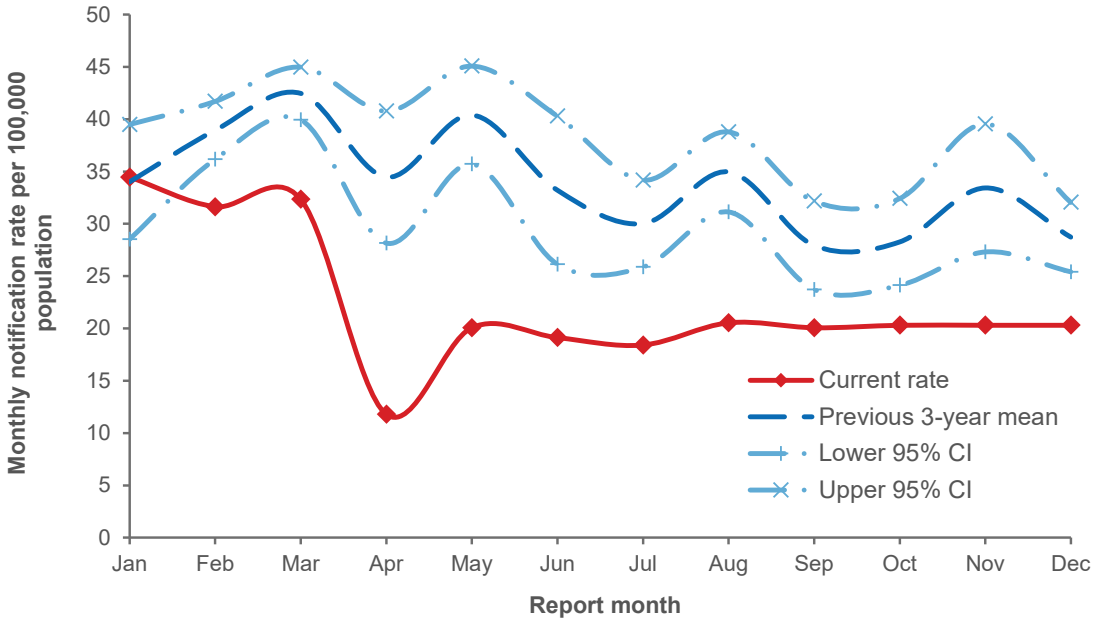


* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 10.

Seasonal data

The number of notified cases of giardiasis reported per 100,000 population by month for 2020 is shown in Figure 20. The monthly number of notifications in 2020 ranged from 50 notifications (April) to 146 notifications (January). There was no distinct seasonal pattern in the population rate of giardiasis notifications reported by month when considering the previous three years (2017–2019). In 2020, a drop in cases was observed in April and May with notification rates well below the previous three-year average for the remainder of the year.

Figure 20. Giardiasis monthly rate (annualised), 2020



Demographics

In 2020, the rate of notifications and hospital admissions for giardiasis was higher for males (23.9 cases, 1.4 admissions per 100,000 population) than females (20.9 cases, 1.2 admissions per 100,000 population) (Table 25).

Table 25. Giardiasis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	604	23.9	36	1.4
Female	536	20.9	30	1.2
Total[c]	**1141**	**22.4**	**66**	**1.3**

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

In 2020, the highest notification rate was for the 0 to 4 years age group (61.2 per 100,000 population, 187 cases), followed by the 30 to 39 years age group (38.6 per 100,000, 273 cases) (Table 26). The highest hospitalisation rate was reported for the 30 to 39 years age group (2.0 admissions per 100,000 population).

Table 26. Giardiasis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	187	61.2	3	-
5 to 9	71	21.6	2	-
10 to 14	27	8.1	5	1.5
15 to 19	18	5.7	0	-
20 to 29	140	19.5	13	1.8
30 to 39	273	38.6	14	2.0
40 to 49	151	23.6	9	1.4
50 to 59	105	16.1	3	-
60 to 69	112	20.8	10	1.9
70+	55	10.1	7	1.3
Total[c]	**1141**	**22.4**	**66**	**1.3**

[a] MoH NMDS data for hospital admissions

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

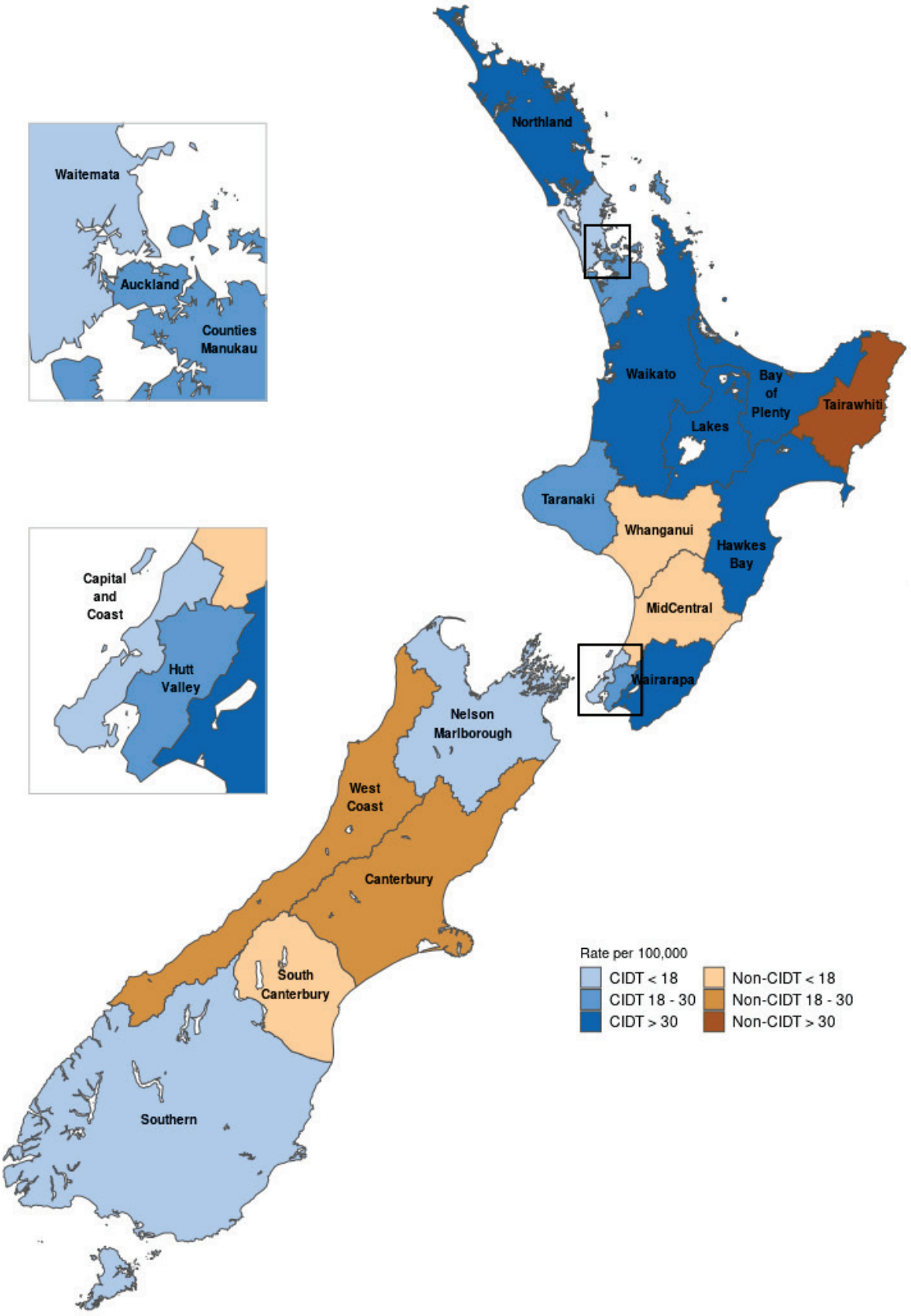
[c] total includes notifications where age is unknown

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 21. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

Notification rates for giardiasis have been variable across New Zealand with Tairawhiti DHB consistently in the highest quantile of notification rates since 2016.

Figure 21. Geographic distribution of giardiasis notifications, 2020



In 2020, the highest notification rates of giardiasis were reported for Tairawhiti DHB (53.3 per 100,000, 27 cases), Hawkes Bay DHB (37.5 per 100,000, 67 cases), Northland DHB (37.0 per 100,000, 72 cases), Waikato DHB (34.9 per 100,000, 153 cases) and Lakes DHB (34.9 per 100,000, 41 cases). All these DHBs, except for Tairawhiti, were serviced by laboratories using CIDT community testing.

Outbreaks reported as caused by *Giardia spp.*

In 2020, there were 11 giardiasis outbreak notifications in EpiSurv, none of which reported food as a possible mode of transmission (Table 27). It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

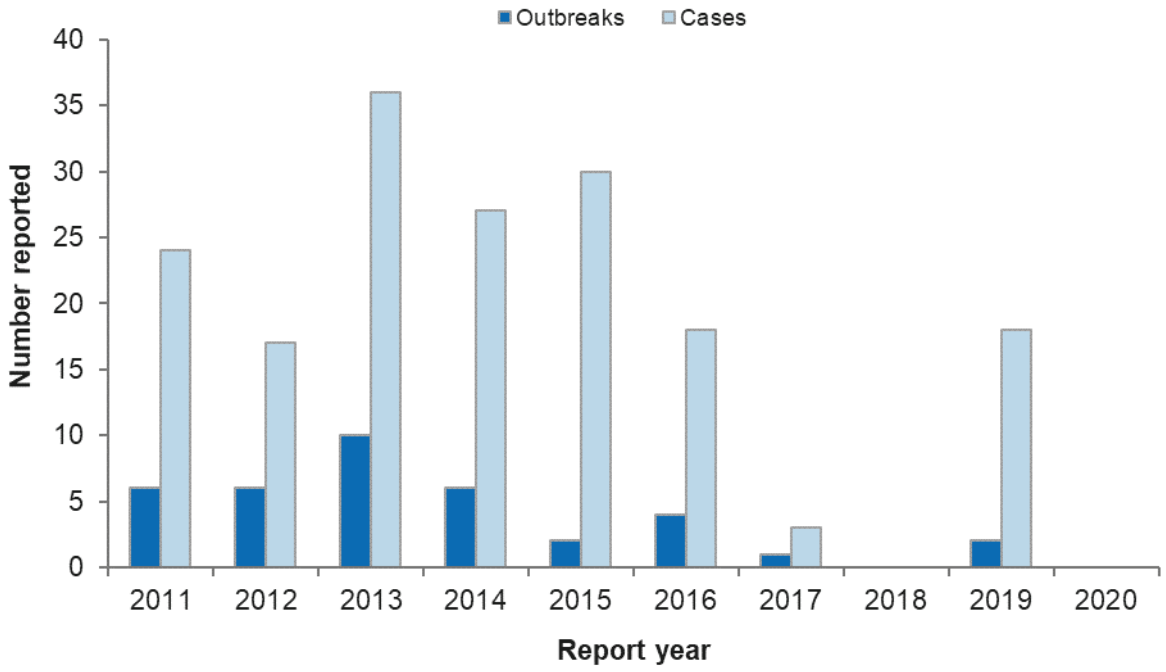
Table 27. Giardiasis outbreaks reported, 2020

	Giardiasis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	0	0	11
Outbreak-associated cases	0	0	79
Hospitalised Cases	0	0	0

[a] All giardiasis outbreaks, including non-foodborne outbreaks

Over the 10-year period 2011 and 2020, between zero and 10 giardiasis outbreaks with food reported as a possible mode of transmission were reported each year with between three and 36 annual outbreak-associated cases (Figure 22).

Figure 22. Giardiasis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2020 are given in Table 28.

Table 28. Summary of surveillance data for hepatitis A, 2020

Parameter	Value in 2020	Source
Number of notified cases	22	EpiSurv
Notification rate (per 100,000)	0.4	EpiSurv
Hospitalisations[a]	17	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b,c]	16 (72%)	EpiSurv
Estimated food-related cases	NE	-

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

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

[b] Percentage of the number of notified cases

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

Case definition

Clinical description:	Following a prodrome of fever, malaise, anorexia, nausea or abdominal discomfort, there is jaundice, elevated serum aminotransferase levels and sometimes an enlarged tender liver. Children are often asymptomatic and occasionally present with atypical symptoms, including diarrhoea, cough, coryza or arthralgia. Jaundice is very unusual in children younger than 4 years, and 90% of cases in the 4–6 years age group are anicteric.
Laboratory test for diagnosis:	Positive hepatitis A virus-specific IgM in serum (in the absence of recent vaccination) OR detection of hepatitis A virus nucleic acid.
Case classification:	
Probable	A clinically compatible illness that is epidemiologically linked to a confirmed case.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Hepatitis A cases reported in 2020 by data source

During 2020, 22 individual cases (0.4 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A with 72% of notified cases recorded as hospitalised in 2020.

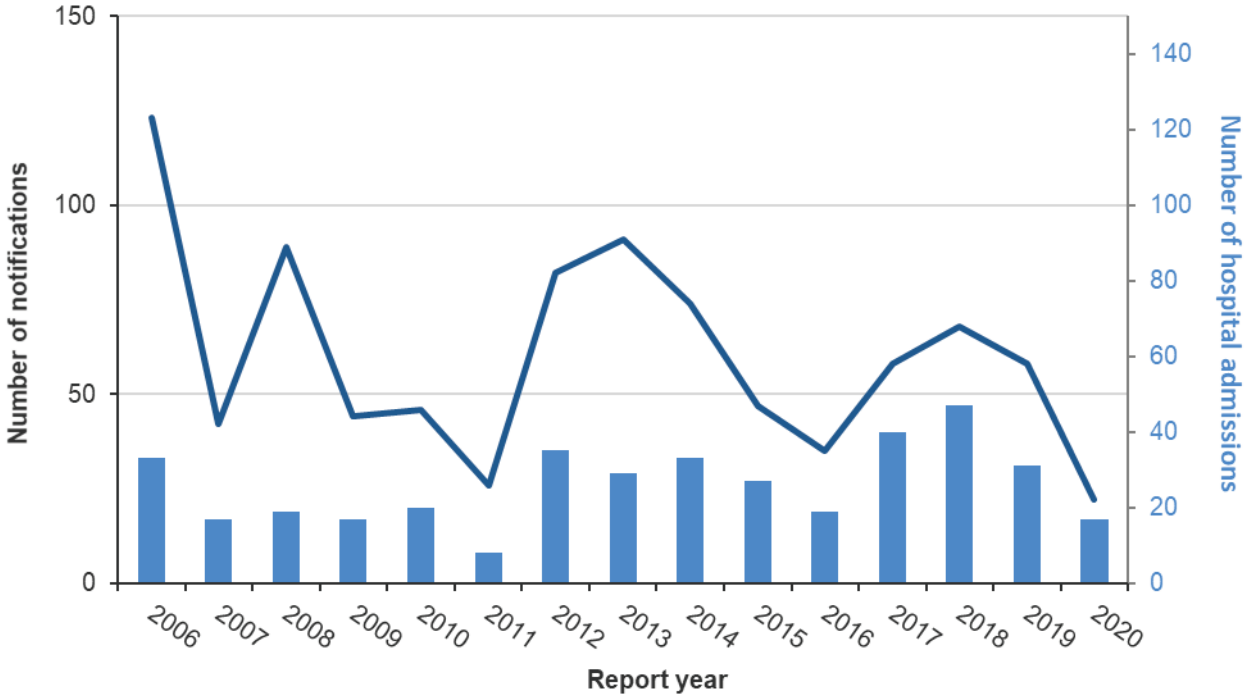
The ICD-10 code B15 was used to extract acute Hepatitis A hospitalisation data from the MoH NMDS database. Of the 57 hospital admissions (1.1 admissions per 100,000 population) recorded in 2020, 17 cases were reported with acute hepatitis A as the primary diagnosis and 40 with acute hepatitis A as another relevant diagnosis.

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

Annual data

Between 2000 and 2020, the annual number of notifications has remained in the range of 22 (2020) to 123 (2006) (Figure 23). Due to the small number of notifications per year, plots of case notification rates by year and month are not presented for hepatitis A.

Figure 23. Hepatitis A EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



Note: Number of hospital admissions include only cases with hepatitis A as a primary diagnosis.

Demographics

In 2020, hepatitis A notification and hospitalisation rates were similar for males and females (Table 29).

Table 29. Hepatitis A cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	12	0.5	10	0.4
Female	10	0.4	7	0.3
Total	**22**	**0.4**	**17**	**0.3**

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

[b] per 100,000 population in this sex group

In 2020, the hepatitis A cases were spread over the age range 5 to 69 years old. The highest number and rate of notifications and hospitalisations were reported in the 20 to 29 years age group (11 cases, 1.5 cases per 100,000 population and 6 hospitalisations, 0.8 hospitalisations per 100,000 population) (Table 30).

Table 30. Hepatitis A cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	0	-	0	-
5 to 9	1	-	1	-
10 to 14	1	-	1	-
15 to 19	1	-	0	-
20 to 29	11	1.5	6	0.8
30 to 39	3	-	2	-
40 to 49	2	-	2	-
50 to 59	0	-	0	-
60 to 69	1	-	2	-
70+	2	-	3	-
Total	**22**	**0.4**	**17**	**0.3**

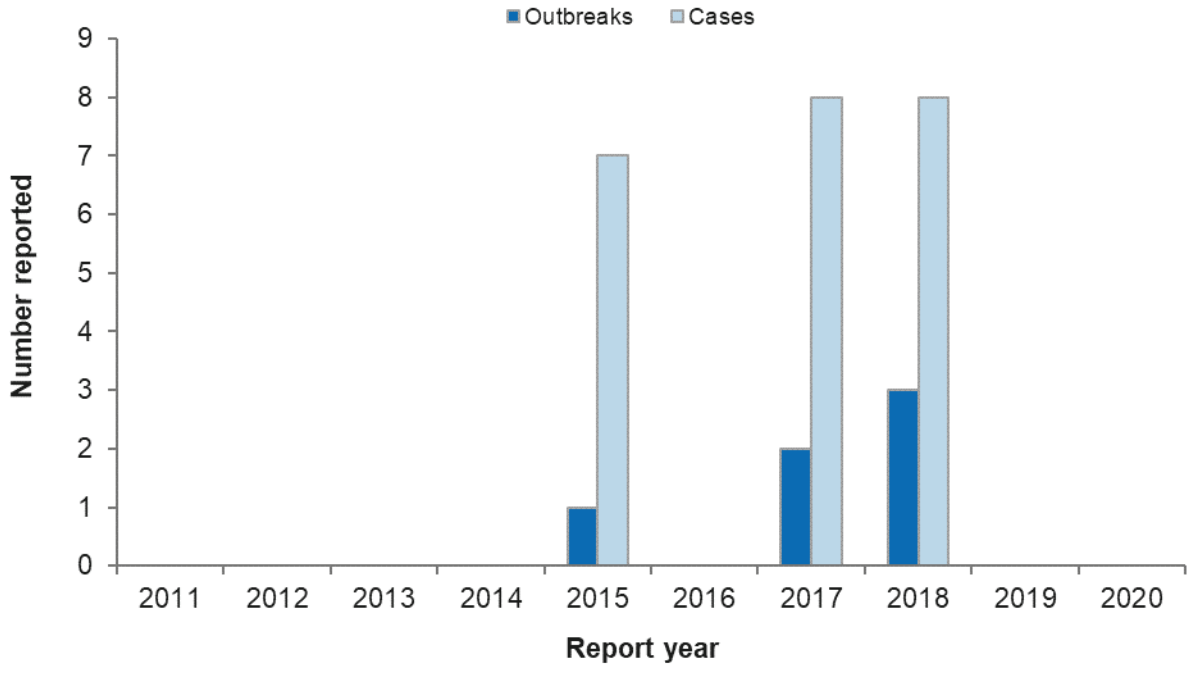
[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis

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

Outbreaks reported as caused by hepatitis A virus

In 2020, no outbreaks of hepatitis A were reported in EpiSurv (Figure 24).

Figure 24. Hepatitis A outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Hepatitis A virus genotypes commonly reported

In 2020, hepatitis A virus typing data from the 16 hepatitus cases were submitted to ESR's Enteric, Environmental and Food Virology Laboratory (Table 31). Samples may be faecal and/or serum/plasma specimens. The data include those cases not associated with foodborne transmission.

Hepatitis A virus IA was the most commonly identified sub-genotype, similar to 2016 to 2019.

Table 31. Hepatitis A genotypes identified by the Enteric, Environmental and Food Virology Laboratory, 2016–2020

Hepatitis A virus genotypes	2016	2017	2018	2019	2020
IA	16	20	20	24	10
IIIA	1	4	14	8	4
IB	0	1	0	1	2
Unable to genotype	0	2	3	1	0
Total	**17**	**27**	**37**	**34**	**16**

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 2020 by data source

During 2020, no individual cases were reported in EpiSurv. Note that not all cases of Histamine (scombroid) fish poisoning are necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code T61.1 was used to extract histamine (scombroid) fish poisoning hospitalisation data from the MoH NMDS database. Of the 10 hospital admissions (0.2 admissions per 100,000 population) recorded in 2020, eight cases were reported with histamine (scombroid) fish poisoning as the primary diagnosis and two cases were reported with histamine (scombroid) fish poisoning as another relevant diagnosis.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with histamine (scombroid) fish poisoning in hospital are reported in EpiSurv.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

One histamine (scombroid) fish poisoning outbreak was reported in 2020 involving 91 cases. No cases were reported as having been hospitalised (Table 32). It should be noted that all cases of histamine (scombroid) fish poisoning will be categorised as foodborne as consumption of contaminated fish is the only recognised transmission route for this disease.

Table 32. Histamine (scombroid) fish poisoning outbreaks reported, 2020

	Histamine (scombroid) fish poisoning outbreaks	
	Foodborne	All
Outbreaks	1	1
Outbreak-associated cases	91	91
Hospitalised Cases	0	0

Table 33 contains details of the histamine (scombroid) fish poisoning outbreak reported in 2020, with 91 associated cases. All 91 cases had consumed fish acquired from a common home delivery food supplier in the same week.

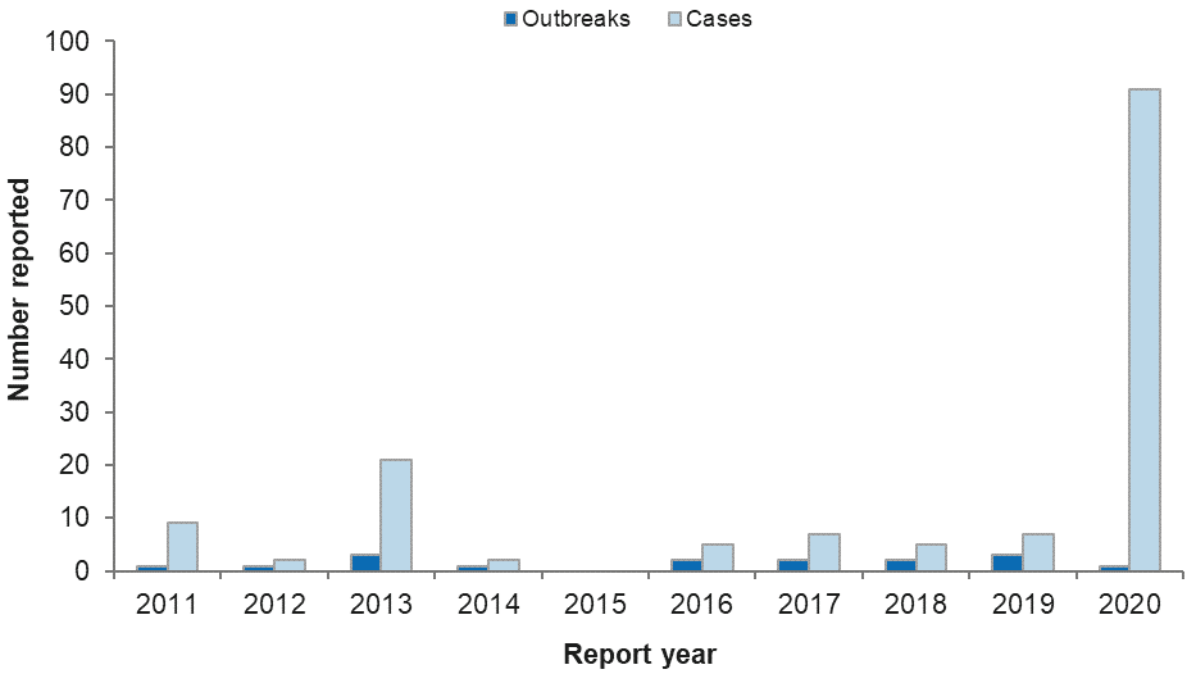
Table 33. Details of histamine (scombroid) fish poisoning outbreaks, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Multiple PHU	Nov	Trevally Fish	Food from a common supplier	Other food outlet, home	91 P

PHU Public health unit, Regional: Regional Public Health
Number ill: C: confirmed, P: probable. Histamine (scombroid) fish poisoning cases are classified as probable if no sample of suspect fish can be analysed

Over the 10-year period 2011 and 2020, the number of histamine (scombroid) fish poisoning outbreaks reported each year ranged from one to four, except for 2015 when no outbreaks were reported (Figure 25). The highest total number of outbreak-associated cases was reported in 2020 (91 cases).

Figure 25. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2020 are given in Table 34.

Table 34. Summary of surveillance data for listeriosis, 2020

Parameter	Value in 2020	Source
Number of notified cases[a]	34	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalisations [b]	38	MoH NMDS
Deaths	1[e]	EpiSurv
Travel-related cases (%)[c]	0	EpiSurv
Estimated food-related cases (%)[d]	30 (88%)	Expert consultation

[a] Includes non-perinatal (31) and perinatal cases (3)
[b] Cases hospitalised may not be notified on EpiSurv
[c] Percentage of the number of notified cases
[d] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases. It has been estimated by expert consultation that 88% 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. Note: While the 2013 estimate for foodborne transmission of *Listeria monocytogenes* was estimated to be 88%, sources other than food are unlikely.
[e] One case died due to listeriosis. Five other cases notified with listeriosis died, but the primary cause of death was their underlying disease

Case definition

Clinical description: Listeriosis most commonly presents with diarrhoea, often associated with fever, myalgia and vomiting. Bacteraemia most often occurs in pregnant women (usually in the third trimester), the elderly and immunosuppressed. In pregnant women, the foetus may become infected, sometimes leading to miscarriage, stillbirth, premature delivery, new-born septicaemia or meningitis. The elderly and immunosuppressed may present with septicaemia, meningitis or pyogenic foci of infection.

Laboratory test for diagnosis: Isolation of *Listeria monocytogenes* OR detection of *L. monocytogenes* nucleic acid from a normally sterile site, including the foetal gastrointestinal tract.

Case classification:

Probable: Not applicable.

Confirmed: A clinically compatible illness that is laboratory confirmed.

Cases can be further classified, if appropriate, as follows:

Perinatal: Cases are classified as pregnancy-associated if illness occurs in a pregnant woman, foetus, or infant aged ≤ 28 days old; for these cases it is the pregnant woman or mother who is notified as the case but information regarding the foetus or infant should be included on the case form

Listeriosis cases reported in 2020 by data source

During 2020, 34 individual cases (0.7 per 100,000 population) of listeriosis with one resulting death were reported in EpiSurv. Three of those cases were perinatal listeriosis. Hospitalisation rates are usually very high for listeriosis with all 34 notified cases hospitalised in 2020 (100%).

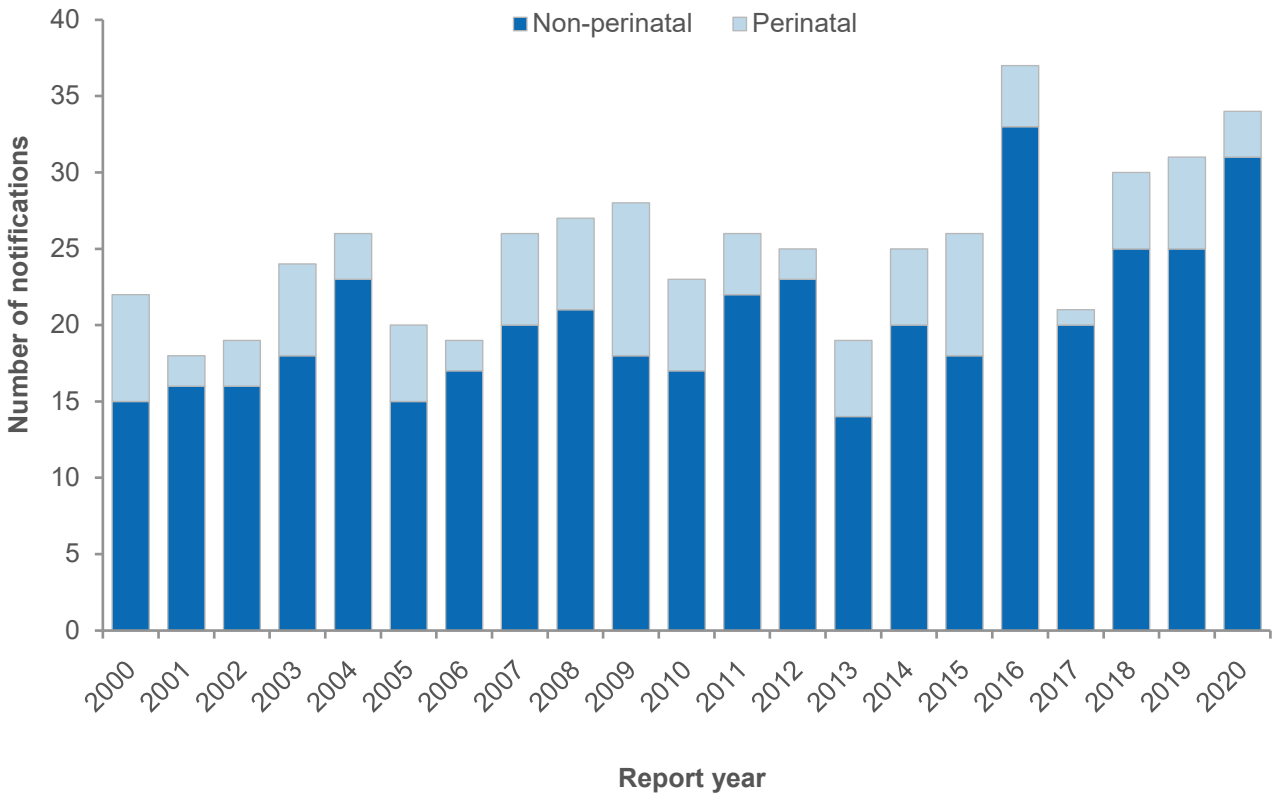
The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 38 hospital admissions (0.7 admissions per 100,000 population) recorded in 2020, 19 were reported with listeriosis as the principal diagnosis and 19 with listeriosis as another relevant diagnosis.

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

Notifiable disease data

Between 2000 and 2020, the annual number of listeriosis notifications has fluctuated between 18 (2001) and 36 (2016) (Figure 26). Because of the low numbers of listeriosis cases, the rates calculated in this report may be highly variable from year to year and it is necessary to interpret trends with caution. The notification rate has been relatively stable for the past 20 years at around 0.6 per 100,000 population.

Figure 26. Listeriosis non-perinatal and perinatal notifications by year, 2000–2020



Demographics

In 2020, the rate and number of notifications for listeriosis was identical for females and males (0.7 per 100,000 population, 17 cases), as well as the number of hospitalisations (19 cases each) (Table 35). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases will include the three perinatal cases.

Table 35. Listeriosis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	17	0.7	19	0.8
Female	17	0.7	19	0.7
Total	**34**	**0.7**	**38**	**0.7**

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

In 2020, rates for listeriosis were highest in the 70 years and over age group for both the notifications (2.9 per 100,000 population, 16 cases) and hospitalisations (2.6 per 100,000, 14 admissions) (Table 36).

Table 36. Listeriosis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
0 to 4	0	-	0	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	0	-	0	-
20 to 29	3	-	4	-
30 to 39	3	-	4	-
40 to 49	3	-	4	-
50 to 59	5	0.8	6	0.9
60 to 69	4	-	6	1.1
70+	16	2.9	14	2.6
Total	**34**	**0.7**	**38**	**0.7**

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

Outbreaks reported as caused by *Listeria* spp.

There were no listeriosis outbreaks reported in 2020. Since 2006 there have been two listeriosis outbreaks reported. There was an outbreak with two associated cases in 2009 and an outbreak with food reported as a possible mode of transmission with six associated cases in 2012. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Listeria monocytogenes types commonly reported

ESR's Special Bacteriology Laboratory reported receiving 32 human isolates of *L. monocytogenes* during 2020. Table 37 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2016 and 2020. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of seven to 20 isolates over the 5-year period.

Table 37. *L. monocytogenes* serotypes identified by the Special Bacteriology Laboratory, 2016–2020

Serotype	2016		2017		2018		2019		2020	
			No.	%	No.	%	No.	%	No.	%
O1/2	17	44.7	13	65.0	12	37.5	14	46.7	14	44
O4	20	52.6	7	35.0	19	59.4	16	53.3	18	56
Untypable	1	2.6	0	-	1	3.1	0	-	0	-
Total	**38**		**20**		**32**		**30**		**32**	**100**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A comparison of Listeria monocytogenes contamination in bagged and unbagged lettuce in supermarkets – Kyere et al. 2020

A study examined the prevalence of *Listeria monocytogenes* in 100 samples of ready-to-eat bagged and non-bagged lettuces sold in supermarkets in New Zealand [25]. Five samples of bagged lettuce tested positive for *L. monocytogenes* and two further bagged lettuce samples tested positive for other *Listeria* species. None of the non-bagged lettuce samples were contaminated with *Listeria*. The results of this survey indicate a higher microbial risk associated with consumption of bagged salads.

Relevant regulatory developments

Nil.

Norovirus infection

Case definition

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

Norovirus infection cases reported in 2020 by data source

During 2020, three individual cases were reported in EpiSurv. It should be noted that not every case of norovirus infection is notifiable; only those that are part of a common source outbreak or from a person in a high-risk category. In contrast to case reports of norovirus, outbreaks of norovirus infection are reported separately and involve significant numbers of cases.

The ICD-10 code A08.1 was used to extract norovirus infection hospitalisation data from the MoH NMDS database. Of the 230 hospital admissions (4.5 admissions per 100,000 population) recorded in 2020, 149 cases were reported with norovirus infection as the primary diagnosis and 81 were reported with norovirus infection as another relevant diagnosis. Of the 230 hospital admissions, 66 were in the 0 to 5 age group and 46 were in the 70+ age group.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Foodborne transmission

It has been estimated by expert consultation that 32.7% (95th percentile credible interval: 10.0% to 66.4%) of norovirus infections are due to foodborne transmission [2]. It was further estimated that approximately 24% of norovirus infections due to foodborne transmission were due to consumption of seafood.

Outbreaks reported as caused by norovirus

In 2020, there were 170 norovirus infection notified outbreaks, 10 (5.9%) of which reported food or a food handler as one of the possible modes of transmission (Table 36). There were no hospitalisations reported for these potentially foodborne norovirus infection outbreaks. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 38. Norovirus infection outbreaks reported in EpiSurv, 2020

	Norovirus infection outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	8	2	170
Outbreak-associated cases	210	27	3786[b]
Hospitalised Cases	0	0	9

[a] All norovirus outbreaks, including non-foodborne outbreaks
[b] One outbreak did not record number of cases

Table 39 contains details of the ten norovirus infection outbreaks with food reported as a possible mode of transmission reported in 2020. In eight of the outbreaks, an infected food handler was the suspected source. One outbreak at a catered conference had strong evidence for a foodborne source. Potato salad was tested at ESR and found to contain *E. coli,* however, case stool samples were positive for norovirus and negative for *E. coli*. Food handler transmission was suspected.

Table 39: Details of norovirus infection outbreaks with food or food handling reported as a possible mode of transmission, 2020

PHU	Month	Suspected source	Evidence	Setting	No. Ill
Auckland	Jan	Potato or orzo salad, food handler	Laboratory testing of food and elevated odds ratio	Conference using caterers	71C 6P
Auckland	Jan	Food handler	Aged care facility outbreak	Long term care facility	10C
South	Jan	Food handler	Common meal in correction facility	Prison	3C 31P
Toi Te Ora	Feb	Unknown	Common meal	Food premises, takeaways	1C 1P
Regional	Aug	Food handler	Common location	Hotel/Motel	4C 16P
MidCentral	Oct	Food handler	Takeaway meal, eaten at home	Home	3C 4P
Auckland	Oct	Food handler	Common event	Childcare centre	3C 4P
Toi Te Ora	Nov	Food handler contaminating marinated fish entrees	Common meal	Restaurant/café/bakery	2C 35P
Auckland	Nov	Food handler	Common meal	Restaurant/café/bakery	3C 15P
Auckland	Dec	Unknown	Common meal	Restaurant/café/bakery	1C 24P

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

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory, faecal specimens relating to eight of the nine outbreaks (Table 39) were received for norovirus testing. Norovirus was detected in faecal samples from all of those outbreaks. For two outbreaks additional pathogens were detected: *Staphyloccocus aureus* intoxication in the August outbreak, and astrovirus in the MidCentral October outbreak.

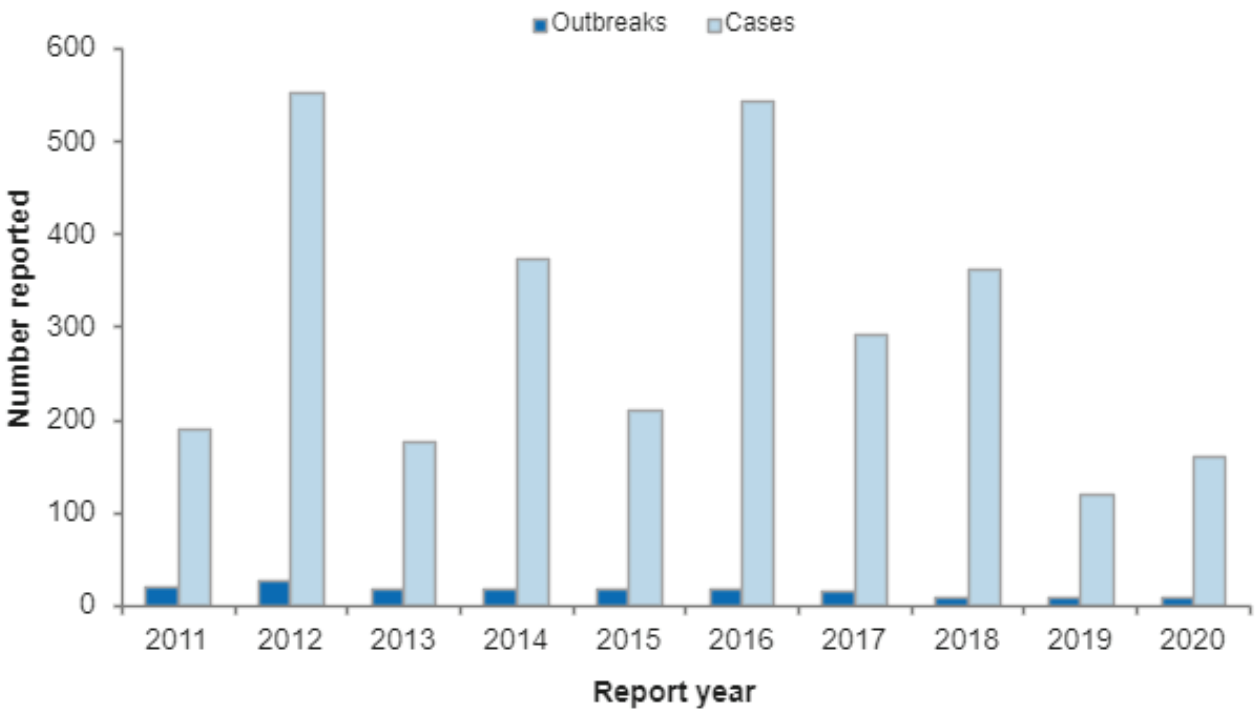
Table 40 shows the total cases by genotype for the eight tested outbreaks. For one outbreak (September, MidCentral), no sample was received for genotyping. The outbreaks are due to a variety of genotypes, with four outbreaks being attributed to one genotype.

Table 40. Norovirus genotypes reported in foodborne outbreaks, 2020

Norovirus genotype	Outbreaks	Total cases
GI.3[P3]	1	34
GII.7[P7]	1	2
GII.2[P16]	4	87
GII.3[P12]	1	10
GI and GII.2[P16]	1	20
Total	**8**	**153**

Over the 10-year period 2011 and 2020, the annual number of norovirus infection outbreaks with food reported as a possible mode of transmission reported each year ranged from 8 (2018) to 27 (2012) (Figure 27). The total number of cases associated with these outbreaks ranged from 159 (2019) to 552 cases (2012) each year.

Figure 27. Norovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Norovirus types commonly reported

Norovirus genotyping data from ESR's Norovirus Reference Laboratory (NRL) are shown in Table 41. The data relate to outbreaks not individual cases and include all outbreaks, including those which are not associated with foodborne transmission. The number of norovirus outbreaks reported to the NRL differs from the number recorded in EpiSurv. Not all specimens from the norovirus outbreaks reported in EpiSurv are sent to ESR for genotyping and not all gastroenteritis outbreaks caused by norovirus are reported as norovirus outbreaks in EpiSurv.

In 2020, 161 norovirus outbreaks were ESR laboratory confirmed. Norovirus genogroup II (GII) was identified in 125/161 (77.6%) outbreaks. In the previous four years, GII was identified in between 77.8% (2017) and 90.8% (2018) of outbreaks. In 2020, norovirus genogroup I (GI) was identified in 33/161 (20.5%) outbreaks. GIX (GIX.1[GII.P15]) was identified in one outbreak. Both GI and GII were identified in 2/161 (1.2%) ESR laboratory-confirmed norovirus outbreaks.

The norovirus genotype was determined for 152/161 (94.4%) of ESR laboratory-confirmed norovirus outbreaks. Unlike previous years, GII.4 variants were not the predominant norovirus genotype identified. The predominant genotype was GII.2[P16] (93/153, 60.1% of outbreaks). For foodborne norovirus outbreaks, predominance of GII.2[P16] (66.7%, 6/9 identified), was also observed (Table 40).

Table 41. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2016–2020

Norovirus genotypes[a]	2016	2017	2018	2019	2020
Genogroup I	**29**	**51**	**15**	**32**	**33**
GI untyped	1	-	-	1	2
GI.1[P1]	2	2	1	-	-
GI.2[P2]	3	-	1	1	-
GI.3[P3]	15	19	4	9	5
GI.3[P13]		10	2	4	8
GI.4[P4]	-	1	3	5	-
GI.5[P4]			2	5	14
GI.5[P5]	-	1	-	1	-
GI.5[P12]	-	-	-	-	1
GI.6[P6]		2	1	4	-
GI.6[P11]	6	13	-	1	3
GI.7[P7]	-	1	-	-	-
GI.8[P8]	-	2	-	-	-
GI.9[P9]	2	-	1	1	-
Genogroup II	**159**	**186**	**158**	**147**	**125**
GII.2[P16]	27	18	38	17	93
GII.3[P12]	19	2	8	20	5
GII.4 Sydney [P16][b]	19	103	70	49	6
GII.4 Sydney[P31][b]	30	13	3	21	-
GII.4 Sydney[P4 New Orleans][b]	35	13	2	13	1
GII.6[P7]	2	1	10	13	3
GII.9[P7]	-	-	-	2	-
GII.10[P16]	-	-	-	3	-
GII.14[P7]	-	4	7	2	1
GII.17[P17]	19	5	4	1	6
Other[c]	8	26	16	6	10
Mixed GI and GII	**-**	**2**	**1**	**3**	**2**
Genogroup GIX[d]	**-**	**1**	**-**	**-**	**1**
Total outbreaks[e]	**188**	**239**	**174**	**182**	**161**

[a] Classification of norovirus changed in 2019, previous year's genotypes have been re-classified accordingly. [b] GII.4 variants

[c] 'Other' includes GII untyped, GII.1[P16], GII.2[P2], GII.3[P3], GII.3[P13], GII.3[P16], GII.3[P21], GII.7[P7], GII.8[P8], GII12[P16], GII.13[P16], GII.13[P21], GII.15[P15]

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

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Salmonellosis

Summary data for salmonellosis in 2020 are given in Table 42. Note that in the following sections the term *Salmonella* refers to non-typhoidal serotypes of *Salmonella enterica* subspecies *enterica*.

Table 42. Summary of surveillance data for salmonellosis, 2020

Parameter	Value in 2020	Source
Number of notified cases	708	EpiSurv
Notification rate (per 100,000)	13.9	EpiSurv
Hospitalisations[a]	165	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	49 (6.9%)	EpiSurv
Estimated food-related cases (%)[d]	409 (62.1%)	Expert consultation

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

Case definition

Clinical description: Salmonellosis presents as gastroenteritis, with abdominal pains, diarrhoea (occasionally bloody), fever, nausea and vomiting. Asymptomatic infections may occur.

Laboratory test for diagnosis: Isolation of *Salmonella* species OR detection of *Salmonella* nucleic acid from a clinical specimen.

Case classification:

Probable: A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source – that is, is part of a common-source outbreak.

Confirmed: A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, all community faecal specimens in all DHBs except for Canterbury, MidCentral, South Canterbury, Tairawhiti, West Coast and Whanganui, were screened by multiplex PCR for a range of pathogens, including *Salmonella* spp. Following the introduction of PCR methods there was no sustained increase in notification rates for salmonellosis. Please refer to the Appendix (page 119) for details.

Effect of COVID-19 on salmonellosis notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, there was a reduction in salmonellosis notifications compared to the previous three years. During April and May 2020, there were 60 notified cases compared to 174 cases in 2019. From June to December 2020, notifications remained lower compared to the previous years (Figure 30).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes

to notification rates to specific COVID -19 related factors. This is discussed in more detail in the Introduction (see page 9).

The frequency of overseas travel has changed due to border restrictions from March 2020. This is reflected in the notifications; in 2020, there were 44 salmonellosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 329 in 2019.

Salmonellosis cases reported in 2020 by data source

During 2020, 708 individual cases (13.9 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. Of the 708 cases, the symptoms of 676 cases (95%) were reported as fitting the clinical description for salmonellosis, the symptoms were unknown for 31 cases, and for one case the symptoms are listed as not fitting the clinical description.

The ICD-10 code A02.0 (*Salmonella* enteritis) was used to extract salmonellosis hospitalisation data from the MoH NMDS database. Of the 165 hospital admissions (3.2 admissions per 100,000 population) recorded in 2020, 138 cases were reported with salmonellosis as the primary diagnosis and 27 were reported with salmonellosis as another relevant diagnosis.

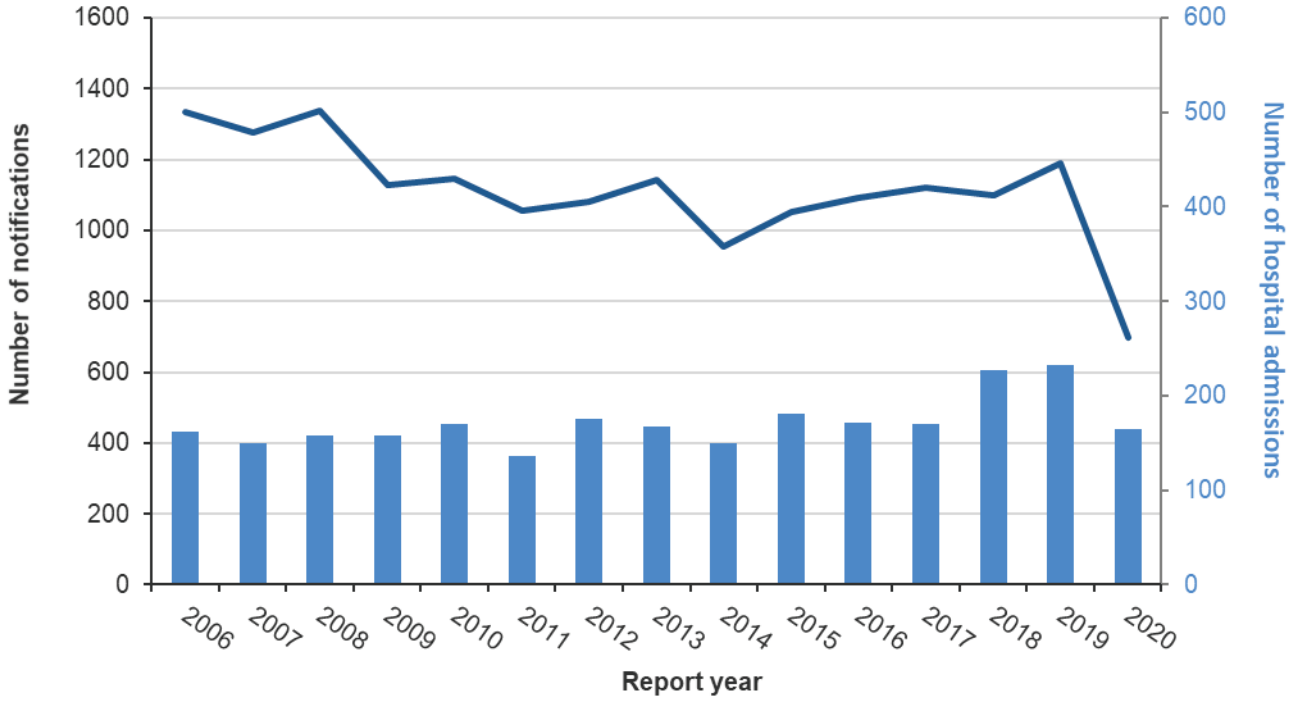
It should be noted that EpiSurv and MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

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.

Annual data

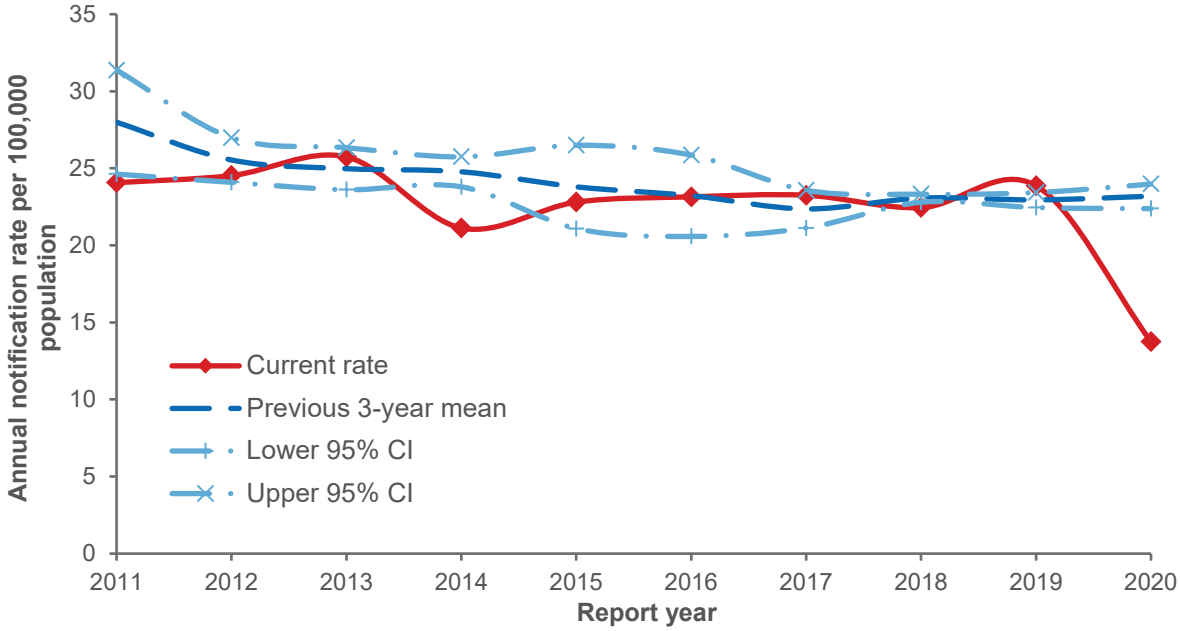
Between 2006 and 2019 the number of salmonellosis notifications has ranged between 955 and 1337 notified cases per year (Figure 28), and between 21.1 and 25.7 cases of salmonellosis per 100,000 population per year (Figure 29). The low number of notifications in 2020 can be attributed to the impact of the COVID-19 public health response. The number of hospital admissions with salmonellosis as a primary or secondary diagnosis varied slightly year by yearbut did not show the same reduction in 2020 as the number of annual notifications.

Figure 28. Salmonellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



The notification rate in 2020 (13.9 cases per 100,000 population) was much lower than the previous three-year average (23.2 cases per 100,000 population) (Figure 29). This drop in notification rates can be attributed to the COVID-19 pandemic*.

Figure 29. Salmonellosis notification rate by year, 2011–2020

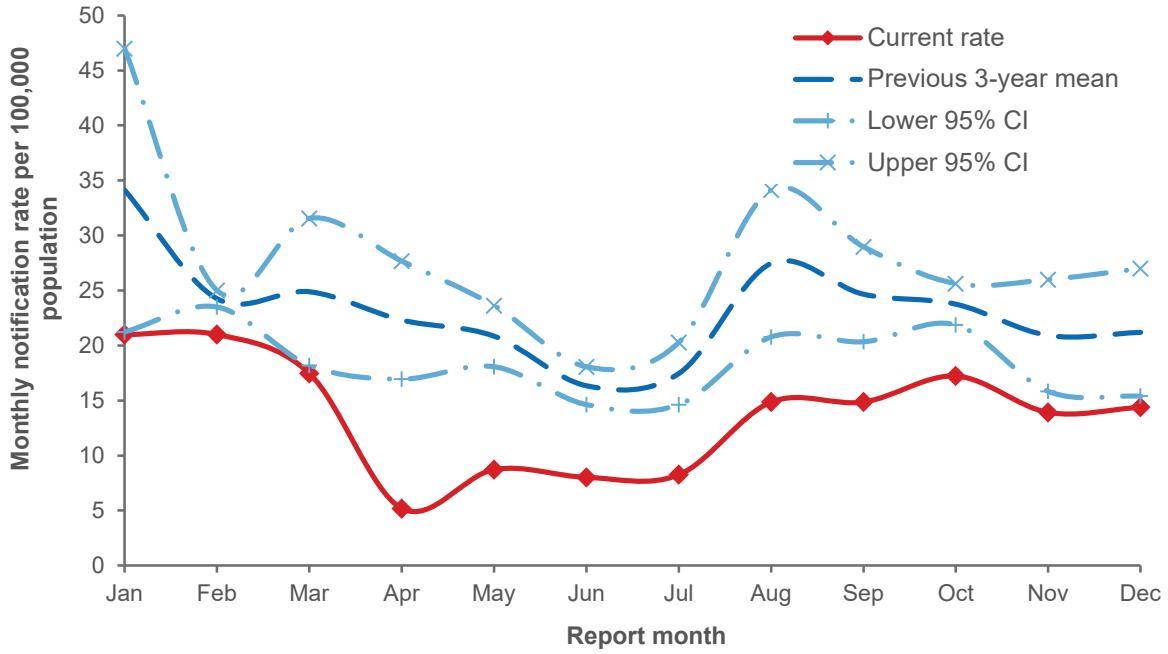


Seasonal data

The number of notified cases of salmonellosis per 100,000 population by month for 2020 is shown in Figure 30. The monthly number of notifications in 2020 ranged from 22 notifications (April) to 92 notifications (January and February). The monthly notification rate in 2020 was generally lower than the previous 3-year mean with a pronounced drop in April (Table 46), related to the impact of the COVID-19 public health response.

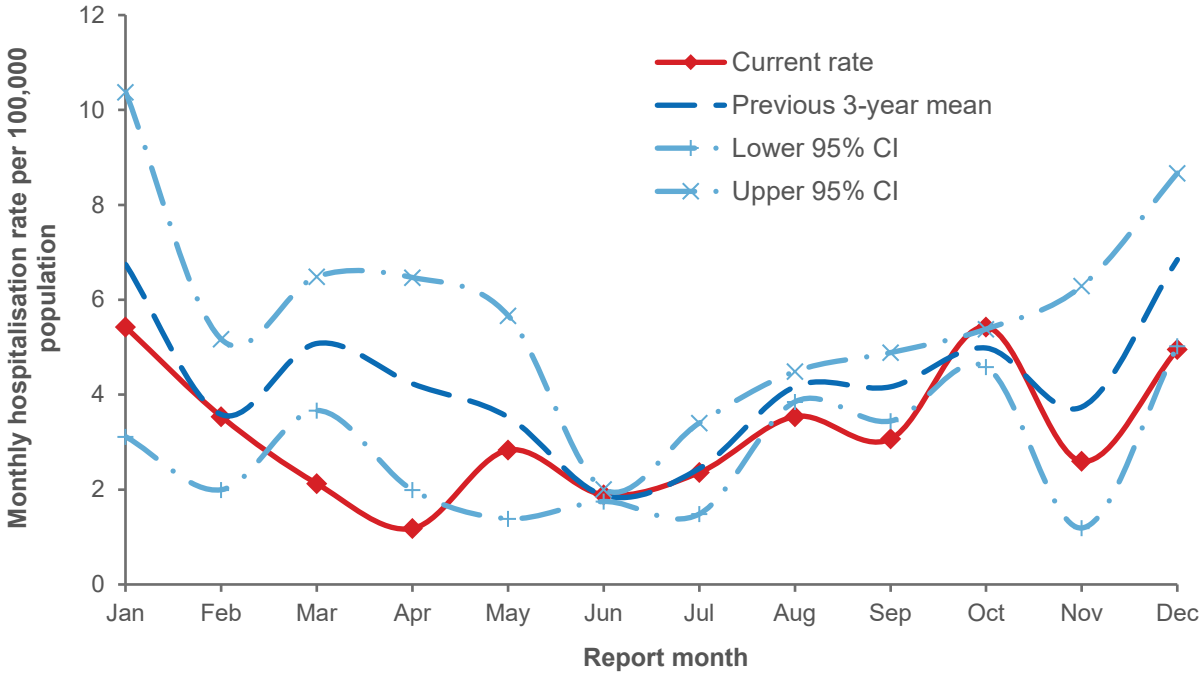
* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 10.

Figure 30. Salmonellosis monthly notification rate (annualised), 2020



In 2020, the monthly hospitalisation rates varied over the year. In March and April, the monthly hospitalisation rate was lower compared to the previous three-year average (Figure 31)

Figure 31. Salmonellosis monthly hospitalisation rate (annualised), 2020



Demographics

In 2020, the rate of notifications and hospital admissions was slightly lower for males compared to females (Table 43).

Table 43. Salmonellosis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	367	14.5	76	3.0
Female	341	13.3	89	3.5
Total	**708**	**13.9**	**165**	**3.2**

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

In 2020, notification rates and hospitalisation rates of salmonellosis were highest for children in the 0 to 4 years age group (55.7 cases and 12.4 admissions per 100,000 population) (Table 44).

Table 44. Salmonellosis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	170	55.7	38	12.4
5 to 9	47	14.3	9	2.7
10 to 14	30	9.0	3	0.9
15 to 19	39	12.3	10	3.1
20 to 29	75	10.4	18	2.5
30 to 39	58	8.2	6	0.8
40 to 49	75	11.7	12	1.9
50 to 59	95	14.6	20	3.1
60 to 69	60	11.2	25	4.7
70+	58	10.7	24	4.4
Total[c]	**708**	**13.9**	**165**	**3.2**

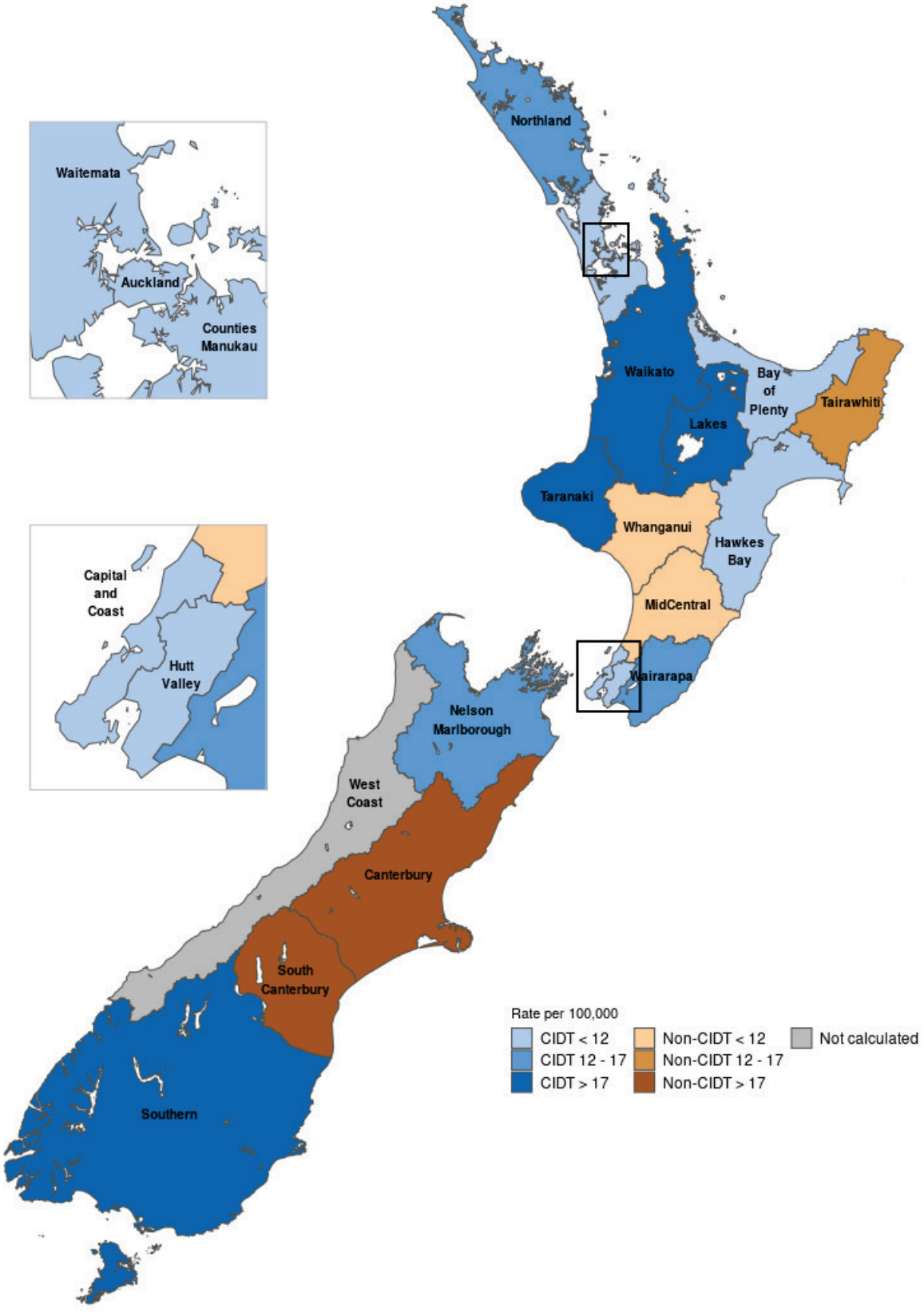
[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this age group
[c] total includes notifications where age is unknown

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 32. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than 5 cases (grey shading): West Coast (2 cases). West Coast DHB is serviced by laboratories using non-CIDT methods.

Notification rates for salmonellosis have been variable across New Zealand with Southern DHB consistently in the highest quantile of notification rates since 2016.

Figure 32. Geographic distribution of salmonellosis notifications, 2020



In 2020, the highest notification rates of salmonellosis were reported for South Canterbury DHB (24.2 per 100,000, 15 cases), Taranaki DHB (24.1 per 100,000, 30 cases), Southern DHB (19.2 per 100,000, 67 cases), Canterbury DHB (18.9 per 100,000, 110 cases) and Waikato DHB (18.7 per 100,000, 82 cases). The DHBs Canterbury and South Canterbury were serviced by laboratories using non-CIDT community testing, while the other three DHBs were using CIDT methods for community testing.

Outbreaks reported as caused by *Salmonella*

In 2020, there were eight salmonellosis notified outbreaks in EpiSurv, two (25%) of which reported food as a possible mode of transmission (Table 45). These two outbreaks included 12 cases, of which no cases were reported to have been hospitalised. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 45. Salmonellosis outbreaks reported, 2020

	Salmonellosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	1	1	8
Outbreak-associated cases	10	2	34
Hospitalised Cases	0	0	0

[a] All salmonellosis outbreaks, including non-foodborne outbreaks

Table 46 contains details of the two salmonellosis outbreaks with food reported as a possible mode of transmission reported in 2020.

Table 46. Details of salmonellosis outbreaks with food reported as a possible mode of transmission, 2020

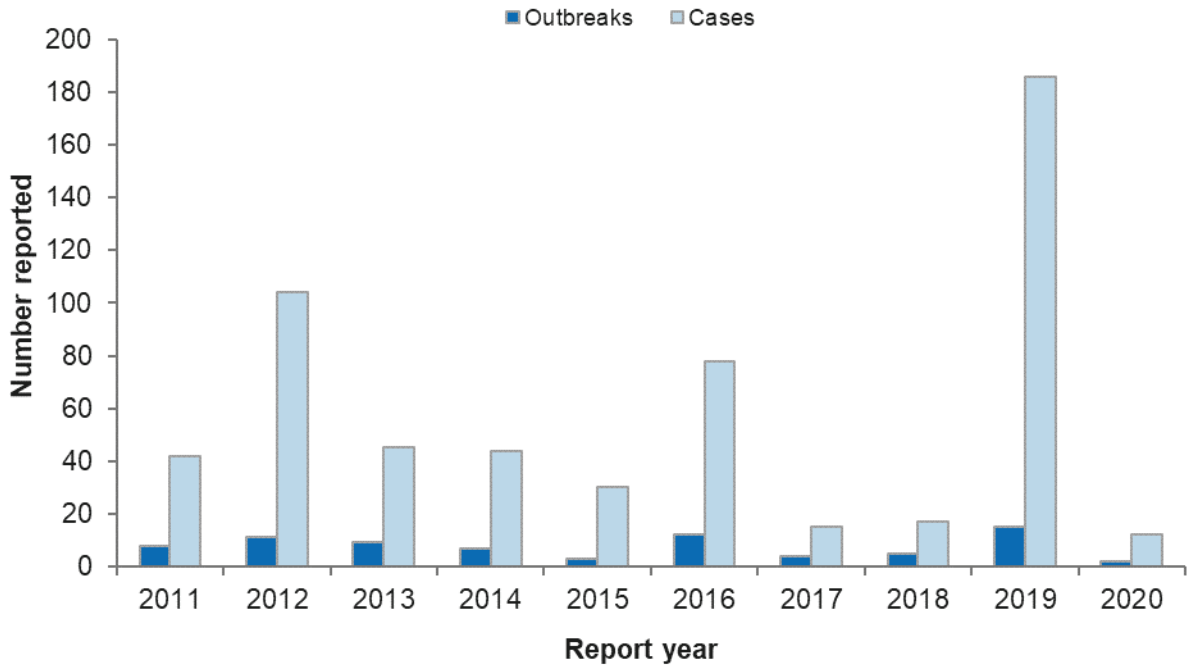
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill	Serotype[a]
Auckland	Jan	Retail raw fish, raw mussels and kina.	Consumption of raw fish from same source	Home, other food outlet	2C	*S.* Typhimurium
Auckland	Oct	Roast pork & chicken	Attendance at common event	Home	3C, 7P	*S.* Typhimurium

PHU: Public health unit, Auckland: Auckland Regional Public Health Service
Number ill: C: confirmed, P: probable
[a] Serotypes were identified in clinical samples from outbreak cases

For both outbreaks the evidence linking the outbreak to a common suspected food source was weak as no specific foods were able to be tested. Cases were genomically linked/clustered through WGS in both outbreaks.

Over the 10-year period 2011 and 2020, the number of salmonellosis outbreaks with food reported as a possible mode of transmission ranged from two (2020) to 15 (2019) (Figure 33). The total number of cases associated with the outbreaks over the same period ranged between 15 (2017) and 186 (2019).

Figure 33. Salmonellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Salmonella types commonly reported

Human isolates

In 2020, isolates from 635 notified cases with non-typhoidal *Salmonella* were typed by the ESR Enteric Reference Laboratory (Table 47). *S.* Typhimurium and *S.* Enteritidis were the most common serotypes identified. Other serotypes commonly reported were *S.* Bovismorbificans (60 cases), *S.* Brandenburg (36 cases) and *S.* Saintpaul (26 cases).

The EpiSurv records for 2020, indicated that for *S.* typhimurium and *S.* Enteritidis cases; 30% of cases with known hospitalisation had been hospitalised and 13% of cases had no hospitalisaion information recorded. For *S.* Bovismorbificans, this proportion increased to 42% (8% no hospital data), but decreased for *S.* Brandenburg (27% cases hospitalised, 17% no hospital data) and *S.* Saintpaul (8% cases, 7% no hospital data).

Table 47. Notified case *Salmonella* isolate serotypes typed by the Enteric Reference Laboratory, 2017–2020

Serotype[a]	2017	2018	2019	2020	% of cases with overseas travel history, 2020[c]	% of cases with unknown travel history, 2020[d]
S. Typhimurium[b]	459	364	484	328	5	24
S. Enteritidis	137	130	153	70	8	31
S. Bovismorbificans	51	81	47	60	0	33
S. Brandenburg	55	42	37	36	0	36
S. Saintpaul	29	37	22	26	14	19
S. Mississippi	15	16	15	17	0	6
S. Stanley	38	34	41	11	22	18
S. Thompson	10	9	11	11	0	46
S. Weltevreden	20	22	19	11	43	36
S. Infantis	20	15	27	7	0	43
S. Give	2	2	1	5	0	60
S. Agona	14	26	13	4	25	0
S. Newport	19	9	10	3	67	0
S. Virchow	7	7	7	3	100	33
S. Javiana	18	5	5	2	0	50
S. Oslo	10	8	7	1	100	0
S. Bareilly	8	8	5	1	0	0
S. Pensacola	5	9	6	1	0	100
S. Kentucky	15	7	9	0	NC	NC
Other[e]	147	150	131	38	25	26
Unknown	**36**	**89**	**112**	**64**	13	27
Total	**1115**	**1070**	**1162**	**699**	**8.6**	**26.5**

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

[a] Excludes *S.* Paratyphi and *S.* Typhi. Table lists the serotypes which had four or more associated cases in 2020 or had higher rates of cases in the previous three years.

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

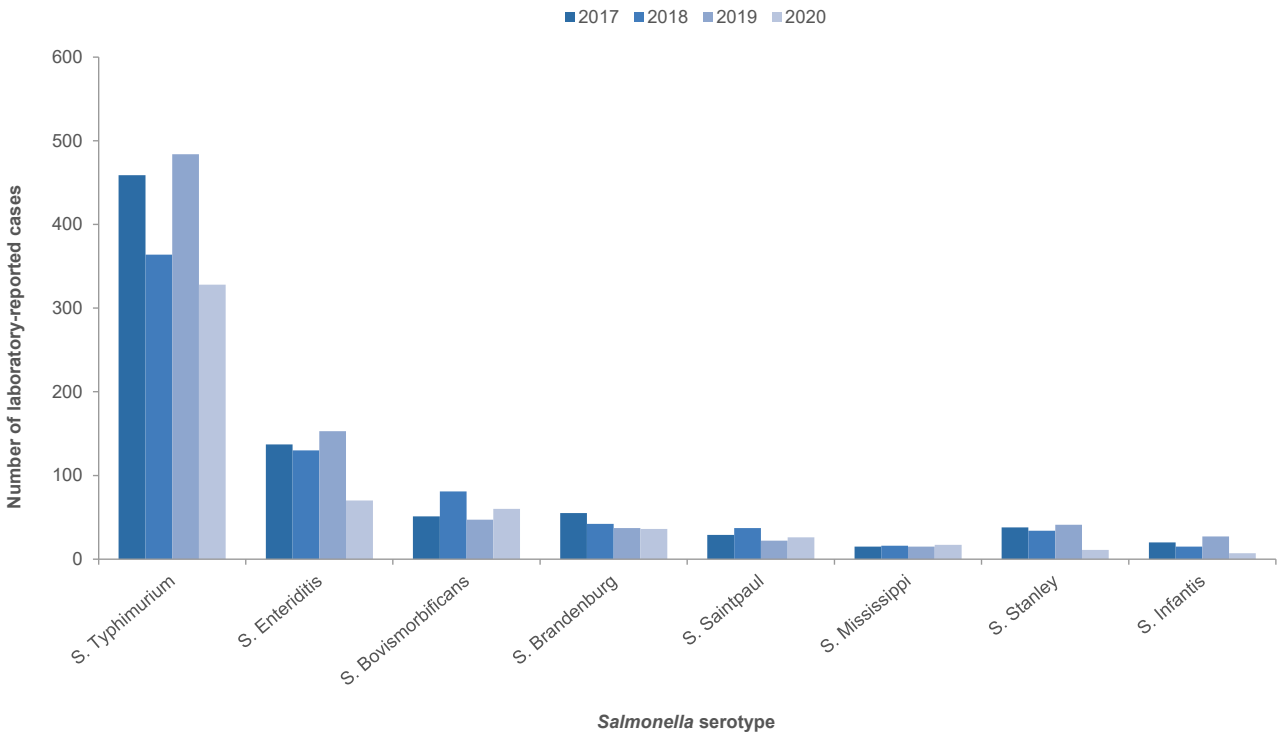
[c] Percentage refers to the number of cases that answered "yes" for overseas travel during the incubation period out of the total number of cases for which travel information was recorded. However, even if a person has travelled within the incubation period it does not necessarily imply the infection has been acquired in the respective country. Incubation periods for salmonellosis typically range between 6-72 hours [12], for atypical cases incubation periods of up to 16 days have been reported

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

[e] Serotypes where able to be determined, but there were 3 or less associated notified cases in 2020.

Figure 34 shows the annual trend for selected *Salmonella* serotypes during 2017 to 2020. For the types shown, there is within type variation year to year. *S.* Typhimurium was the most prevalent serotype isolated from notified cases in the years shown.

Figure 34. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2017–2020



Non-human isolates

A total of 833 non-human *Salmonella* isolates were serotyped by the Enteric Reference Laboratory during 2020. *S.* Typhimurium and *S.* Bovismorbificans were the most commonly isolated serotypes in non-human samples in 2020. The most common of the other serotypes were *S.* Brandenburg and *S.* Give with 91 and 78 isolates, respectively (Table 48). 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 48. *Salmonella* serotypes from non-human sources identified by the Enteric Reference Laboratory, 2016–2020

Serotype	2016	2017	2018	2019	2020	Major sources, 2020
S. Typhimurium	**249**	**372**	**282**	**320**	**336**	Bovine (265), equine (16), poultry environmental (12), canine (11), feline (11)
S. Enteritidis	**13**	**11**	**5**	**8**	**5**	Bovine (3)
Other serotypes	**422**	**589**	**561**	**598**	**492**	
S. Agona	10	17	18	9	9	Food[a] (3), meat/bone meal (3)
S. Bovismorbificans	135	292	297	309	247	Bovine (228), canine (10), feline (7)
S. Brandenburg	127	137	106	133	91	Bovine (53), ovine (24)
S. Hindmarsh	48	27	26	28	8	Ovine (8)
S. Mbandaka	6	9	4	16	7	Poultry environmental (4)
S. Saintpaul	9	12	12	14	8	Bovine (2), feline (2)
S. Give	0	0	0	12	78	Bovine (65), canine (5), food[b] (5)
Other or unknown serotypes	87	95	98	77	44	-
Total	**684**	**972**	**848**	**926**	**833**	

[a] Includes animal carcasses from meat works

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Persistent contamination of Salmonella, Campylobacter, Escherichia coli, and Staphylococcus aureus at a broiler farm in New Zealand. Castaneda-Gulla et al. 2020.

In a study conducted in 2016, broiler shed surfaces (annex, crevices, drinkers, fans, feed loaders, feeders and vents) were swabbed and tested for *Salmonella* before cleaning and after disinfection across three 6-week growth cycles [17]. While the prevalence of positive swabs decreased following cleaning and disinfection, *Salmonella* contamination persisted. Microbial counts were enumerated using a correlation between qPCR C_t values and conventional plate counts. There were minimal decreases (<0.5 $\log_{10}$ CFU/mL) in *Salmonella* concentrations on most surface types across the cleaning/disinfection cycles. The exception was for fans, where the *Salmonella* concentrations were reduced to a non-detectable level. This study demonstrates the ability of *Salmonella* to persist in broiler sheds. It should be noted that isolates were not typed, and it was not confirmed that the same strains were present in broiler sheds across multiple growth cycles.

Relevant regulatory developments

Nil.

Sapovirus infection

Case definition

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

Sapovirus infection cases reported in 2020 by data source

During 2020, no individual cases of sapovirus infection were reported in EpiSurv. Note that not every case of sapovirus infection is necessarily notifiable; only those that are part of a common source outbreak or from a person in a high-risk category.

Outbreaks reported as caused by sapovirus

In 2020, three sapovirus infection outbreaks were reported in EpiSurv. One of the outbreaks reported food as a possible mode of transmission with three associated cases (Table 49). The suspected source of infection was takeaway food, consumed at home (Table 54). 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 49. Sapovirus infection outbreaks reported, 2020

	Sapovirus infection outbreaks	
	Possible foodborne transmission with a suspected or confirmed source	All [a]
Outbreaks	1	3
Outbreak-associated cases	3	43
Hospitalised Cases	0	0

[a] All sapovirus infection outbreaks, including non-foodborne outbreaks

Table 50. Details of sapovirus infection outbreak with food reported as a possible mode of transmission, 2020

PHU	Month	Suspected source	Evidence	Setting	No. ill
Auckland	Feb	Takeaway food / Food Handler	Common meal	Household exposure	2C 1P

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

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

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2020 are given in Table 51.

Table 51. Summary of surveillance data for shigellosis, 2020

Parameter	Value in 2020	Source
Number of notified cases	76	EpiSurv
Notification rate (per 100,000)	1.5	EpiSurv
Hospitalisations[a]	39	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	30 (39%)	EpiSurv
Estimated food-related cases (%)	NE	-

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

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

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

Case definition

Clinical description: Acute diarrhoea with fever, abdominal cramps, blood or mucus in the stools and a high secondary attack rate among contacts.

Laboratory test for diagnosis: Requires isolation of any *Shigella* spp. from a stool sample or rectal swab and confirmation of genus. Nucleic acid testing may be used for screening only.

Case classification:

Probable: A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source i.e., is part of an identified common source outbreak.

Confirmed: A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, all community faecal specimens in all DHBs except for Canterbury, MidCentral, South Canterbury, Tairawhiti, West Coast and Whanganui, were screened by culture-independent diagnostic tests (CIDT) for a range of pathogens, including *Shigella* spp.. Following the introduction of CIDT there was no sustained increase in notification rates for shigellosis. Please refer to the Appendix (page 119) for details.

Effect of COVID-19 on shigellosis notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, there was a pronounced reduction in shigellosis notifications compared to the previous three years. During April and May 2020, there were 4 notified cases compared to 30 cases in 2019. From June to December 2020, notifications remained very low compared to the previous years (Figure 37).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9).

The frequency of overseas travel has changed due to border restrictions from March 2020. This is reflected in the notifications; in 2020, there were 2 shigellosis notifications in EpiSurv listing overseas travel as a risk factor during April to December, compared to 82 in 2019.

Shigellosis cases reported in 2020 by data source

In 2020, 76 individual cases (1.5 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. Of the 76 cases, the symptoms of 67 cases (88%) were reported as fitting the clinical description for shigellosis and the symptoms were unknown for nine cases.

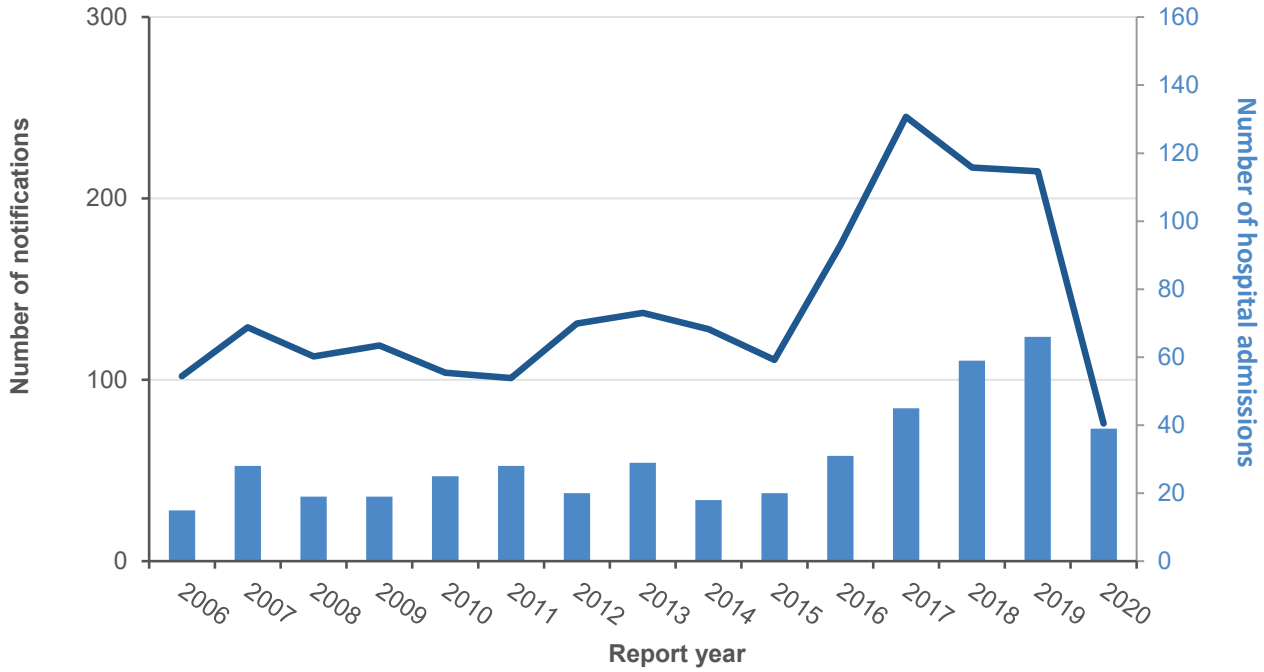
The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 39 hospital admissions (0.8 admissions per 100,000 population) recorded in 2020, 15 were reported with shigellosis as the principal diagnosis and 24 with shigellosis as another relevant diagnosis.

It should be noted that EpiSurv and MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

Between 2006 and 2015 the number of notifications has been in the range of 101 to 137 cases. In 2016 to 2017 there was an increase in notifications and the notification rate per 100,000 population, which has been sustained in 2018 (217 cases) and 2019 (215 cases) (Figure 35 and Figure 36). The drop in 2020 can be attributed to travel restrictions due to the COVID-19 pandemic. The number of hospital admissions with shigellosis as a primary or secondary diagnosis varied year by year, similar to the number of annual notifications.

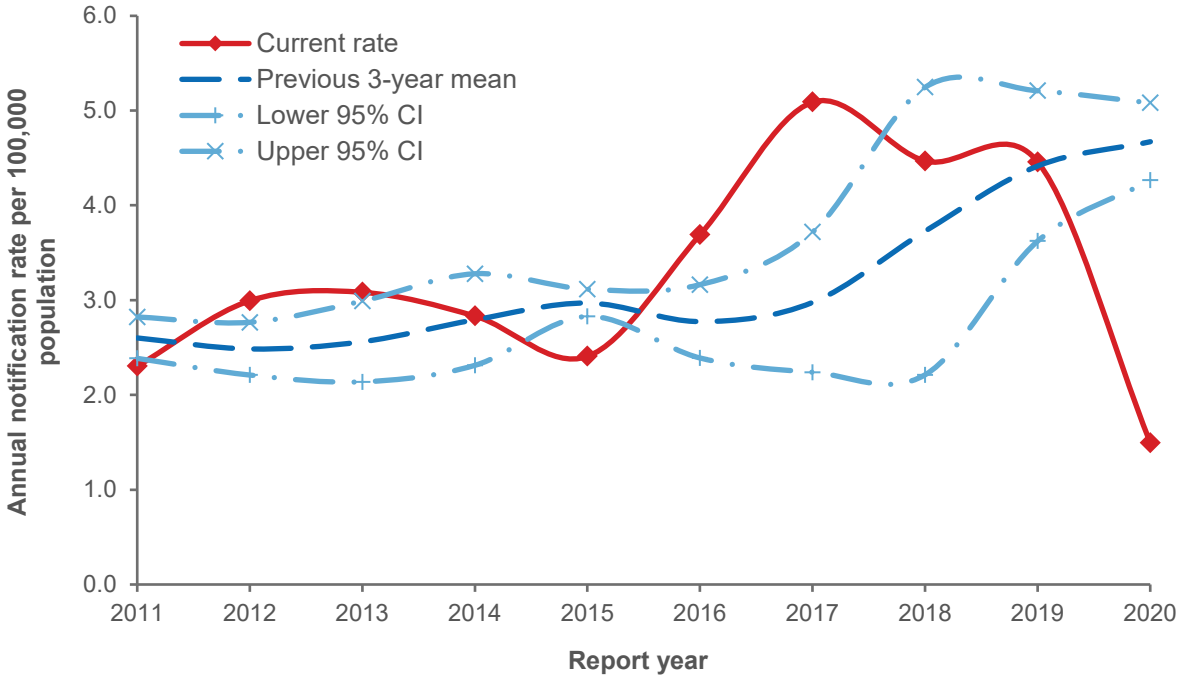
Figure 35. Shigellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



The notification rate in 2020 (1.5 cases per 100,000 population) was much lower than the previous three-year average (4.7 cases per 100,000 population) (Figure 36). This drop in notification rates can be attributed to the COVID-19 pandemic*.

* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 10.

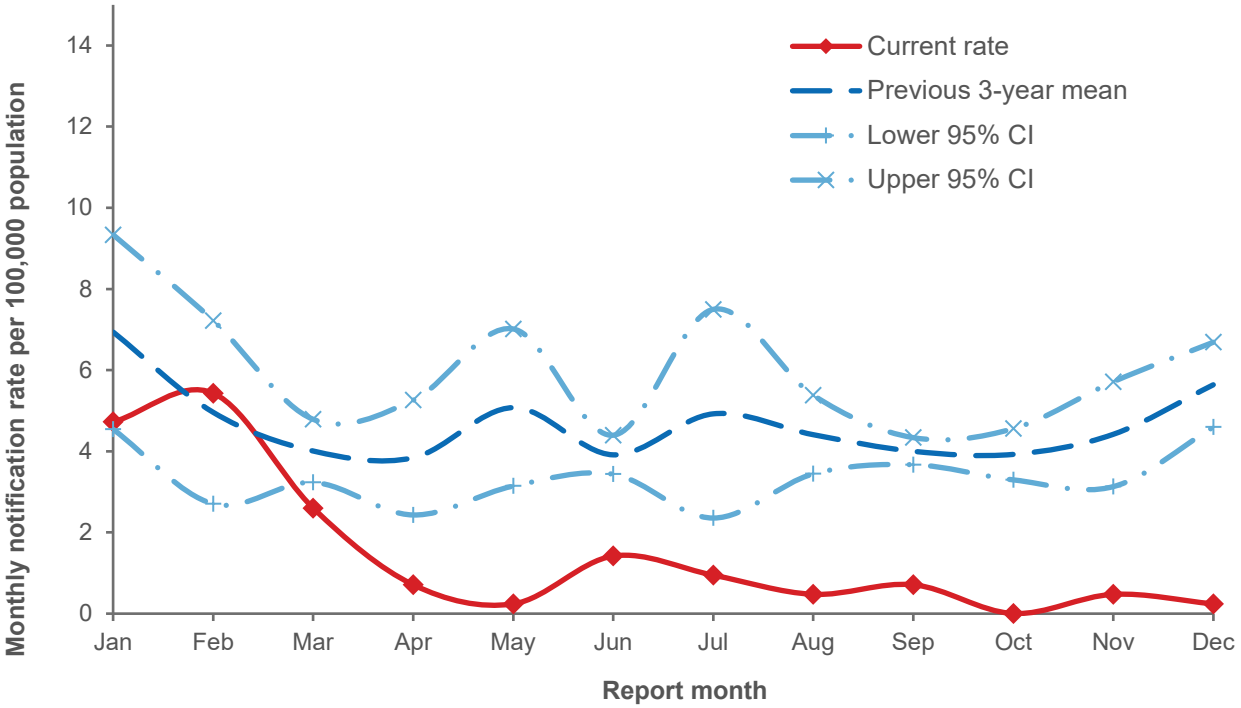
Figure 36. Shigellosis notification rate by year, 2011–2020



Seasonal data

The number of notified cases of shigellosis per 100,000 population by month for 2020 is shown in Figure 37. The number of notifications per month for the first three months of the year was in the range of the previous 3-year average. From April onwards the monthly notification rates were very small, which can be attributed to travel restrictions due to the COVID-19 border restrictions.

Figure 37. Shigellosis monthly rate (annualised), 2020



Demographics

In 2020, notification rates for males were higher than for females (1.8 and 1.2 per 100,000 population, respectively). Hospitalisation rates were similar for both genders (Table 52).

Table 52. Shigellosis cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	45	1.8	17	0.7
Female	31	1.2	22	0.9
Total	**76**	**1.5**	**39**	**0.8**

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

In 2020, the highest shigellosis notification rate was in the 0 to 4-years age group (4.6 cases per 100,000 population). The hospital admissions rate was also highest for the 0 to 4 years of age group (2.3 admissions per 100,000 population) (Table 53).

Table 53. Shigellosis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	14	4.6	7	2.3
5 to 9	6	1.8	3	-
10 to 14	2	-	2	-
15 to 19	2	-	1	-
20 to 29	14	1.9	5	0.7
30 to 39	14	2.0	5	0.7
40 to 49	8	1.2	0	-
50 to 59	7	1.1	0	-
60 to 69	2	-	10	1.9
70+	7	1.3	6	1.1
Total	**76**	**1.5**	**39**	**0.8**

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

Outbreaks reported as caused by *Shigella spp.*

In 2020, there were five shigellosis outbreaks reported in EpiSurv, one (20%) of which reported food as a possible mode of transmission (Table 54). It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 54. Shigellosis outbreaks reported, 2020

	Shigellosis outbreaks	
	Possible foodborne transmission but no suspected source	All [b]
Outbreaks	1[a]	5
Outbreak-associated cases	2	15
Hospitalised Cases	0	0

[a] Outbreak associated with overseas travel
[b] All shigellosis outbreaks, including non-foodborne outbreaks

Table 55 contains details of the shigellosis outbreak with food reported as a possible mode of transmission. This outbreak was associated with overseas travel and no suspected food was recorded.

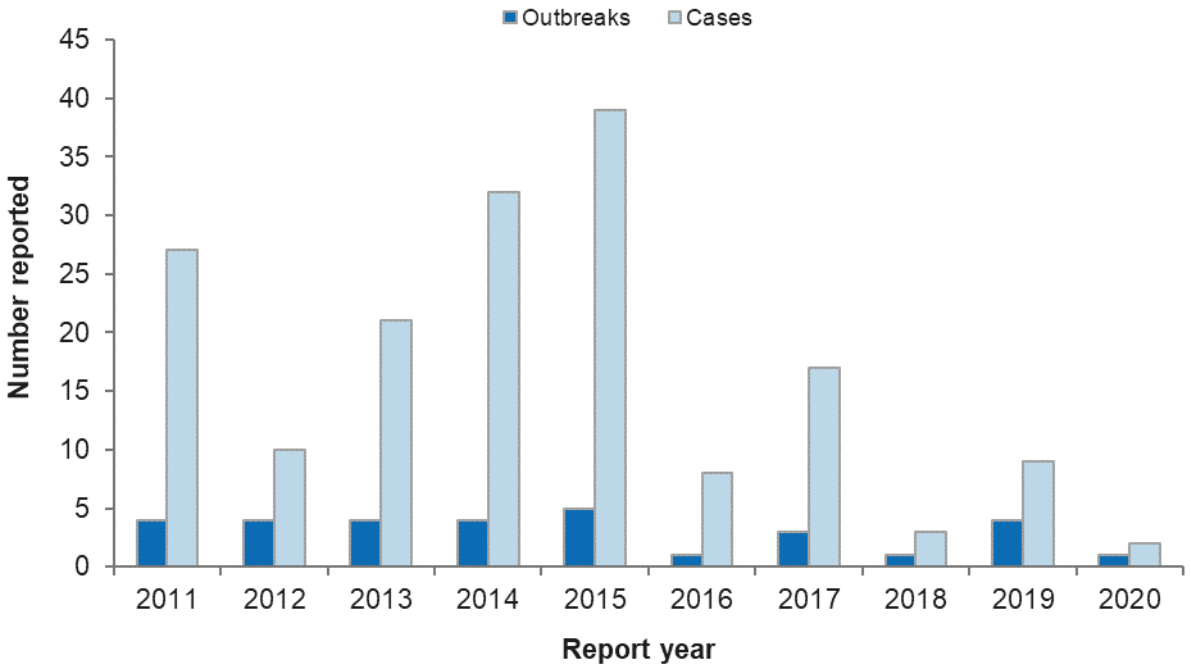
Table 55. Details of shigellosis outbreak with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland	Jan	Unknown	Household cluster	Other setting, overseas (Indonesia)	1C 1P

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

Over the 10-year period 2011–2020, the number of shigellosis outbreaks with food reported as a possible mode of transmission has ranged between one and five outbreaks each year, with between two and 39 associated cases (Figure 38).

Figure 38. Shigellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Shigella species commonly reported

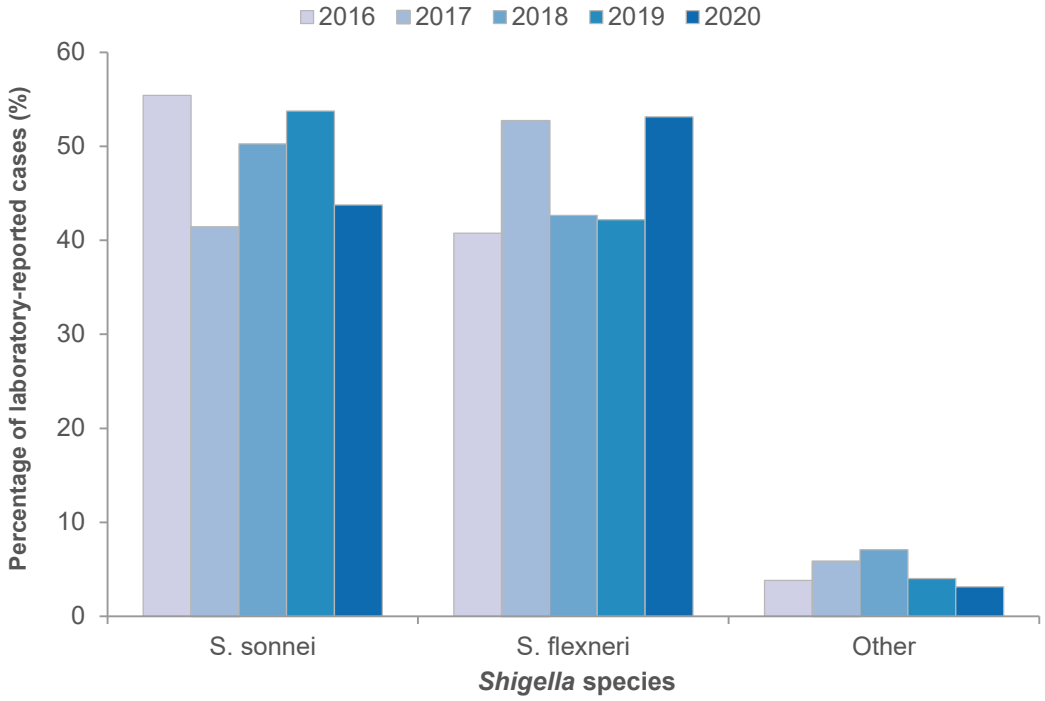
In 2020, isolates from 64 cases infected with *Shigella* spp. were typed by the Enteric Reference Laboratory at ESR. *S. sonnei* and *S. flexneri* were the species most often identified. Of these, *S. sonnei* biotype g was most common in 2020 (Table 56).

Table 56. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2016–2020

Species	2016	2017	2018	2019	2020
S. sonnei	**87**	**99**	**99**	**107**	**28**
biotype a	31	30	37	33	9
biotype f	1	1	1	1	2
biotype g	55	68	61	73	17
S. flexneri	**64**	**126**	**84**	**84**	**34**
1b	16	31	36	14	2
2a	18	18	15	19	12
6 biotype Boyd 88	10	43	13	12	1
Other	20	34	20	39	19
Other	**6**	**14**	**14**	**8**	**2**
S. boydii	3	13	10	3	2
S. dysenteriae	2	1	4	4	0
Shigella species not identified	1	0	0	1	0
Total	**157**	**239**	**197**	**199**	**64**

The percentage of shigellosis cases infected with *S. sonnei* in 2020 (43.8%) was within the range of values observed between 2016 and 2019 (between 41.4% and 55.4%). The percentage of shigellosis cases with *S. flexneri* in 2020 (53.1%) was only slightly above the range of values observed between 2016 and 2019 (between 40.8% and 52.7%) (Figure 39).

Figure 39. Percentage of laboratory-reported cases by *Shigella* species and year, 2016–2020



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 2020 by data source

During 2020, no individual cases of *S. aureus* intoxication were reported in EpiSurv. Note that not every case of *S. aureus* intoxication is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.0 was used to extract foodborne staphylococcal intoxication hospitalisation data from the MoH NMDS database. Two hospital admissions were recorded in 2020 with *S. aureus* intoxication as the primary diagnosis and no cases were reported with *S. aureus* intoxication as another relevant diagnosis.

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

Outbreaks reported as caused by *Staphylococcus aureus*

During 2020, one outbreak of *S. aureus* intoxication was reported in EpiSurv. This outbreak was associated with foodborne transmission. There were four lab confirmed cases, and 16 probable cases associated with this outbreak. No hospitalisations were reported. 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 57. *S. aureus* intoxication outbreaks reported, 2020

	S. aureus intoxication outbreaks	
	Possible foodborne transmission with suspected source	All [a]
Outbreaks	1	1
Outbreak-associated cases	20	20
Hospitalised Cases	0	0

[a] All *S. aureus* intoxication outbreaks, including non-foodborne outbreaks

Table 58 contains details of the foodborne *S. aureus* intoxication outbreak reported in 2020. The specific food vehicle was unknown. Clinical samples from cases tested by ESR, contained staphylococcal enterotoxin.

Table 58. Details of *S. aureus* intoxication outbreak with food reported as a possible mode of transmission, 2020

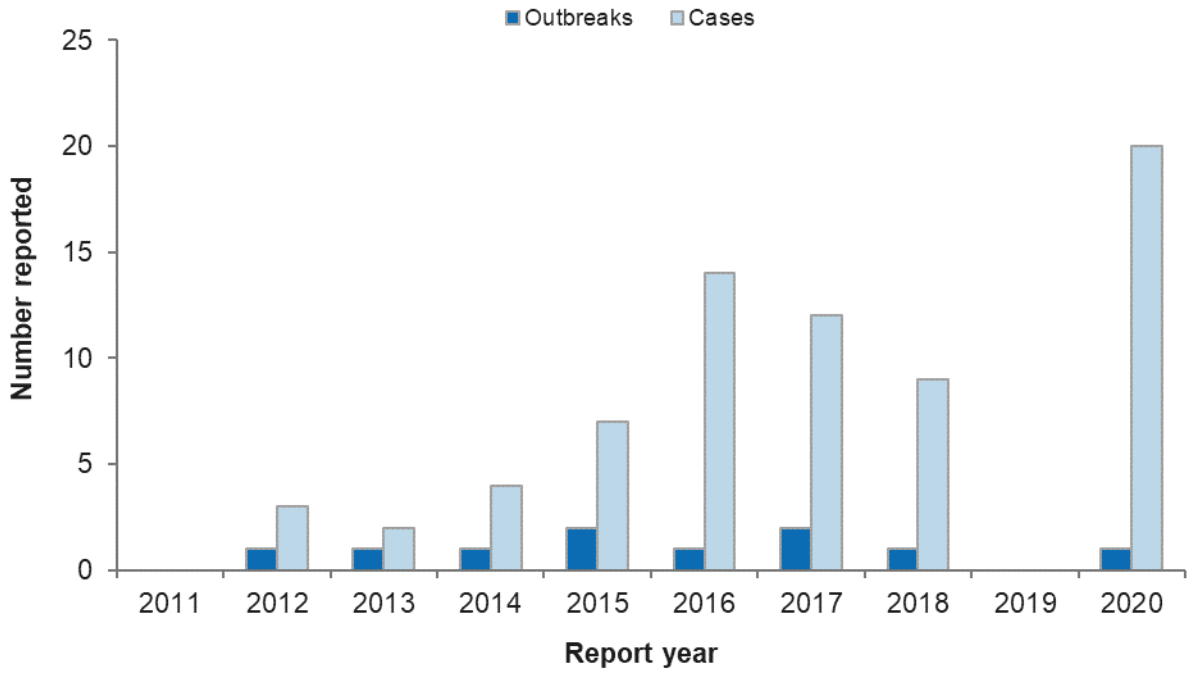
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Regional	Aug	Infected food handler, mashed egg	Common meal	Hotel/Motel	4C 16P

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

Cases from this outbreak were also suspected to be infected with norovirus.

Over the 10-year period 2011 to 2020, the number of *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission ranged from zero to two, with between two and 20 associated cases (Figure 40).

Figure 40. *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Persistent contamination of Salmonella Campylobacter, Escherichia coli, and Staphylococcus aureus at a broiler farm in New Zealand – Castaneda-Gulla et al. 2020

In a study conducted in 2016, broiler shed surfaces (annex, crevices, drinkers, fans, feed loaders, feeders and vents) were swabbed and tested for *S. aureus* before cleaning and after disinfection across three 6-week growth cycles [17]. *S. aureus* was detected on all surfaces, with pre-cleaning concentrations up to 6.8 $\log_{10}$ CFU/mL. Decreases in *S. aureus* concentrations on surface types across the cleaning/disinfection cycles were highly variable, ranging from 0.6 to 3.4 $\log_{10}$ CFU/mL.

Relevant regulatory developments

Nil.

STEC infection

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

Summary data for STEC infection in 2020 are given in Table 59.

Table 59. Summary of surveillance data for STEC infection, 2020

Parameter	Value in 2020	Source
Number of notified cases	844	EpiSurv
Notification rate (per 100,000)	16.6	EpiSurv
Hospitalisations[a]	39	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b,c]	18 (2.1%)	EpiSurv
Estimated food-related cases (%)[b,d]	330 (40%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases.

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

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

Case definition

Clinical description: An acute onset diarrhoeal illness (with or without blood or mucus in stool) OR Any case with Haemolytic Uraemic Syndrome (HUS) or Thrombotic Thrombocytopenic Purpura (TTP) with or without a history of an acute onset diarrhoeal illness. In the absence of HUS/TTP, asymptomatic infection or presentations with milder bowel symptoms (e.g., occasional loose stools) and/or non-diarrhoeal abdominal symptoms do not meet the case definition.

Laboratory test for diagnosis: Isolation of Shiga toxin (verotoxin)-producing *Escherichia coli* OR detection of the genes associated with the production of Shiga toxin in *E. coli.* Isolates producing Shiga toxin 2 (stx2) are more likely to cause serious human disease than isolates producing Shiga toxin 1 (stx1) or both toxins together. Any positive toxin test should be reported as a confirmed case of STEC.

Case classification:

Probable A clinically compatible illness that is either epidemiologically linked to a confirmed case or has had contact with the same common source as a confirmed case, i.e., is part of a common-source outbreak.

Confirmed A clinically compatible illness that is laboratory confirmed.

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, community faecal specimens in all DHBs apart from Canterbury, Mid Central, South Canterbury, Tairawhiti, West Coast and Whanganui, were screened by multiplex PCR for a range of pathogens, including STEC.

Prior to the changes in methodology only specimens from patients with certain epidemiological or clinical criteria, e.g., aged less than 5 years, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea were tested for STEC infection. With multiplex PCR testing all faecal samples are screened for STEC. This has led to an increase in the number of faecal samples tested for STEC, with some cases with a non-O157 infection being diagnosed which previously would not have been diagnosed with STEC infection. Where STEC is detected by screening PCR, specimens are referred to the Enteric Reference Laboratory at ESR to obtain a STEC culture for serotyping.

The community laboratory covering most of Canterbury, South Canterbury and some West Coast samples have not changed to CIDT but changed their culture-based testing approach for STEC infection to include more non-O157 STEC serotypes. Since September 2018 all faecal samples are being tested for STEC, with this new, still culture-based approach which will identify some non-O157 serotypes but not as many as PCR (plating to CHROMagar STEC, followed up with EIA stx testing).

Effect of COVID-19 on STEC notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, there was a reduction in STEC infection notifications compared to the previous three years. During April and May 2020, there were 70 notified cases compared to 182 cases in 2019. From June to December 2020, notification rates are similar to the previous year.

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID -19 related factors. This is discussed in more detail in the Introduction (Page 9).

The frequency of exposure to overseas travel changed in 2020 compared to previous years due to border restrictions from March 2020. This is reflected in the notifications; in 2020, there were 18 STEC infection notifications in EpiSurv listing overseas travel as a risk factor, compared to 113 in 2019.

STEC infection cases reported in 2020 by data source

During 2020, 844 individual cases (16.6 cases per 100,000 population) of STEC infection and no resulting deaths were reported in EpiSurv. Of the 844 cases, the symptoms of 810 cases (96%) were reported as fitting the clinical description for STEC infection, the symptoms were unknown for 28 cases, and for 6 cases the symptoms are listed as not fitting the clinical description.

The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E. coli* infection hospitalisation data from the MoH NMDS database. Of the 39 hospital admissions (0.8 admissions per 100,000 population) recorded in 2020, 17 cases were reported with enterohaemorrhagic *E. coli* infection as the primary diagnosis and 22 were reported with enterohaemorrhagic *E. coli* infection as another relevant diagnosis.

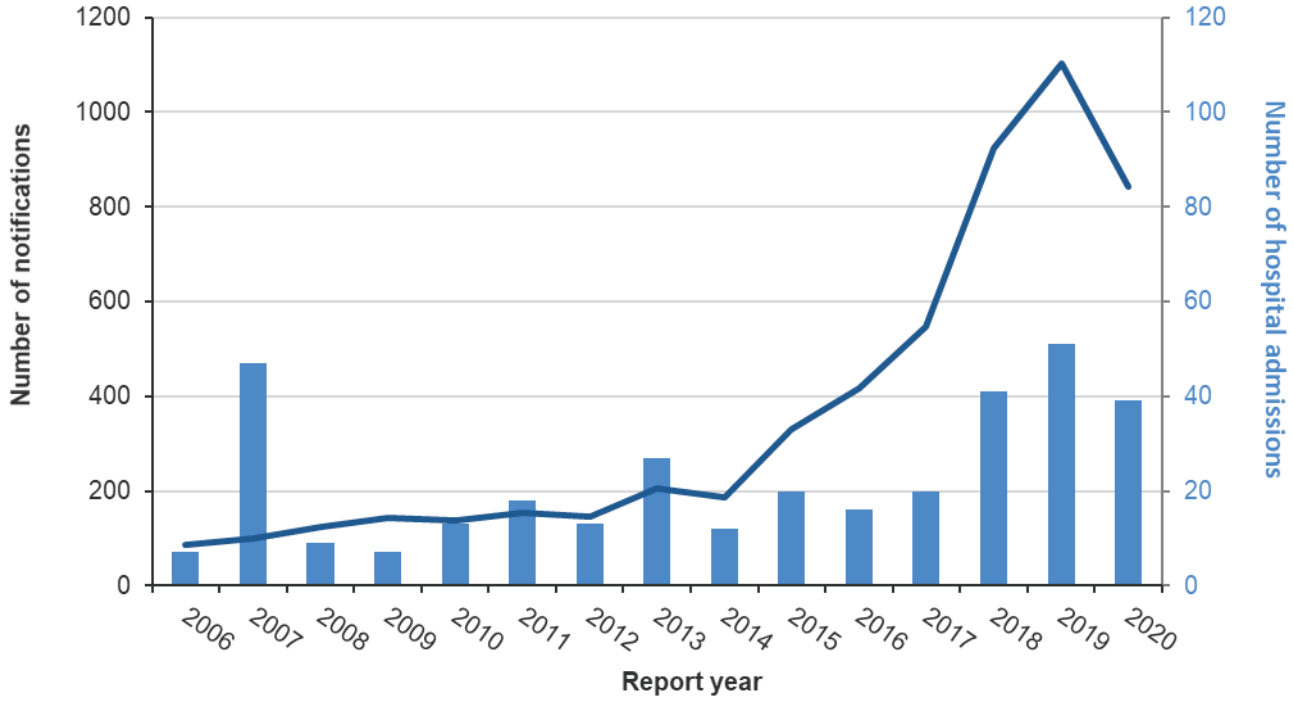
It should be noted that EpiSurv and MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

Until 2014 the number of STEC notifications was below 210 cases per year. From 2015 there has been a steady increase until 2019, with a small drop in 2020 when the number of notifications was less than the previous two years (Figure 41). This annual decrease in 2020 is consistent with the reduction in monthly cases reported during the COVID-19 lockdown period months compared to 2019 data (Figure 44).

The number of hospital admissions with STEC infection as a primary or secondary diagnosis varies year to year. The last three years (2018-2020) has seen hospital admission numbers consistently higher than the previous 10 years. Of the hospitalisations in 2020, ~30% were identified with the O157:H7 serotype, ~40% with non-O157:H7 serotypes and ~30% of cases did not have samples typed. Before the introduction of CIDT, non-O157:H7 hospital admissions with gastrointestinal infection symptoms may not have been diagnosed with an STEC infection.

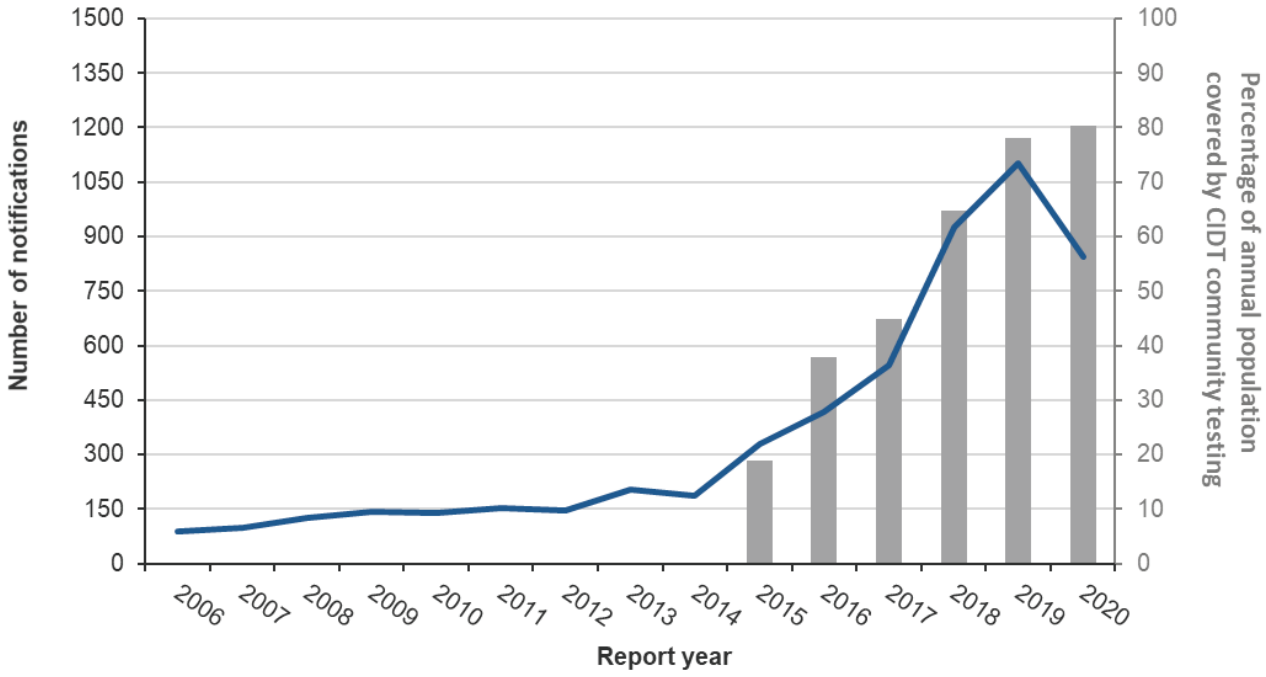
Figure 41. STEC infection EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



Between 2015 and 2019, the annual increases in STEC infection notifications correspond to the increase in the population being tested by community laboratory CIDT (Figure 42). The increased sensitivity of CIDT to detect non-O157 STEC serotypes (Table 65) and the increased number of samples being routinely tested for STEC appears to be causing the majority of the increase in STEC notifications [26] (Appendix page119). Areas and time periods that have not used CIDT and increased screening for STEC, show no indication of an increase in notification rates for STEC.

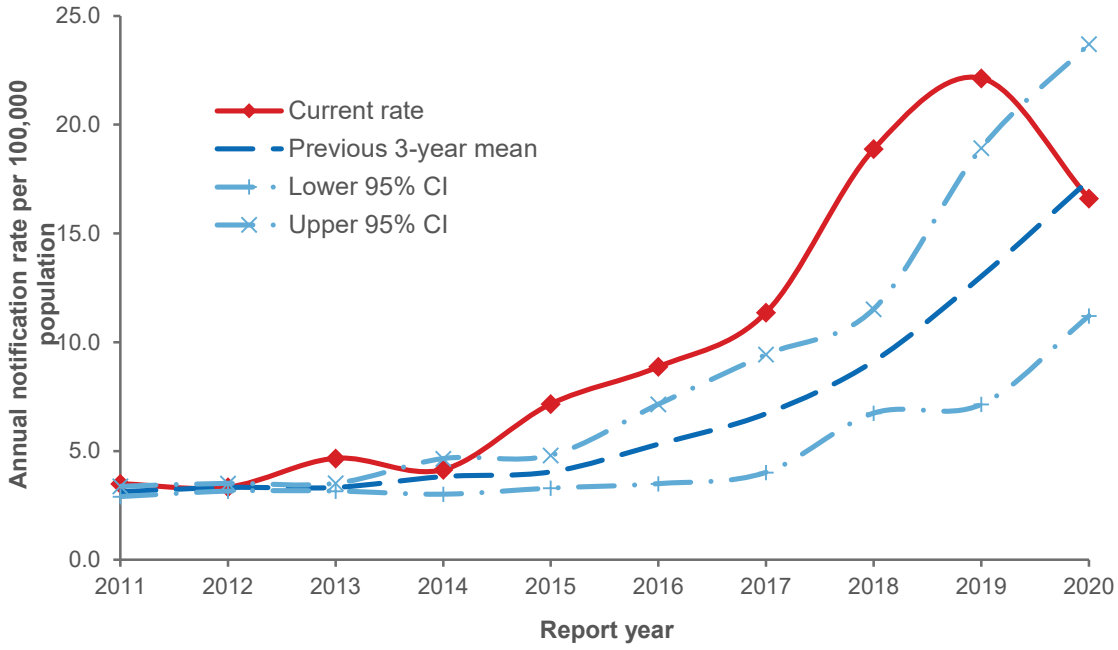
In 2020, approximately 80% of the New Zealand population were covered by community laboratories using CIDT for STEC testing.

Figure 42. STEC infection EpiSurv notifications (line) and proportion of the NZ population covered by community CIDT (bar) by year, 2006–2020



Between 2011 and 2014, the notification rate of STEC infection was in the range of 3.5 to 4.7 notifications per 100,000 population (Figure 43). Increasing rates have been noted every year from 2015 to 2019 (22.1 cases per 100,000 population), followed by a drop in 2020, attributed to the COVID-19 pandemic* (16.6 cases per 100,000 population). The previous three-year average was 17.5 cases per 100,000 population.

Figure 43. STEC infection notification rate by year, 2011–2020



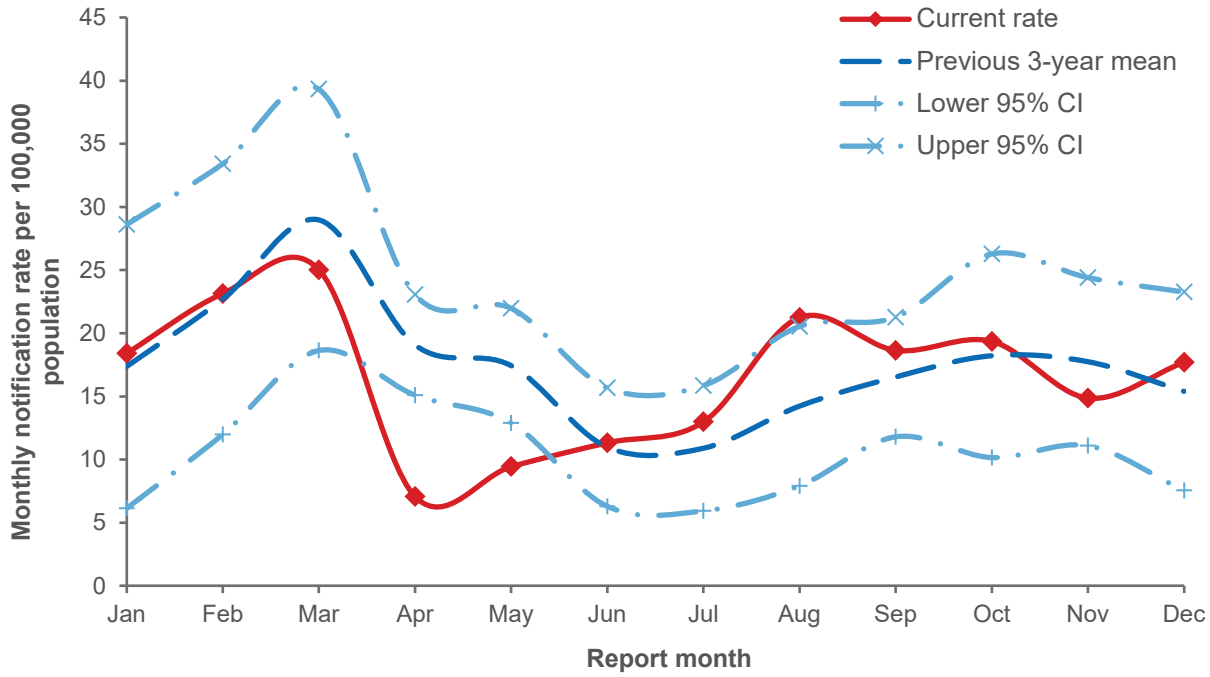
* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 10.

Seasonal data

The rate of notified cases of STEC infection per 100,000 population by month for 2020 is shown in Figure 44. In 2020, monthly notification rates were similar to the previous three-year period with the exception of much lower rates in April and May related to the impact of the COVID-19 public health response.

The monthly number of notifications in 2020 ranged from 30 notifications (April) to a peak of 106 notifications (March). The seasonal trend in monthly notification rates in 2020, excluding the COVID-19 level 3 and 4 period (22nd March to 14th May) was similar to recent years (2017-2019) with a small increase in spring (August), and a higher peak centred in March.

Figure 44. STEC infection monthly notification rate (annualised), 2020



In 2020, the monthly hospitalisation rates varied over the year and the numbers were within the range observed in the previous three years (Table 60) except for the lockdown month of April 2020, during which zero hospital admissions were attributable to STEC infection in the NMDS database.

Table 60. STEC infection monthly NMDS hospitalisation admissions 2017-2020

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

Demographics

In 2020 notification rates and hospitalisation rates were similar for both males and females (Table 61).

Table 61. STEC cases by sex, 2020

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	419	16.6	18	0.7
Female	425	16.6	21	0.8
Total	**844**	**16.6**	**39**	**0.8**

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

In 2020, the STEC infection notification rate was highest for 0 to 4-year age group (58.3 per 100,000 population, 178 cases). The hospital admission rate was also highest for the 0 to 4 years age group, followed by the 60 to 69-years age group (2.6 and 2.0 hospital admissions per 100,000 population) (Table 62).

Table 62. STEC cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	178	58.3	8	2.6
5 to 9	53	16.1	0	-
10 to 14	34	10.2	1	-
15 to 19	39	12.3	1	-
20 to 29	89	12.4	4	-
30 to 39	72	10.2	1	-
40 to 49	67	10.5	1	-
50 to 59	85	13.0	2	-
60 to 69	101	18.8	11	2.0
70+	126	23.2	10	1.8
Total	**844**	**16.6**	**39**	**0.8**

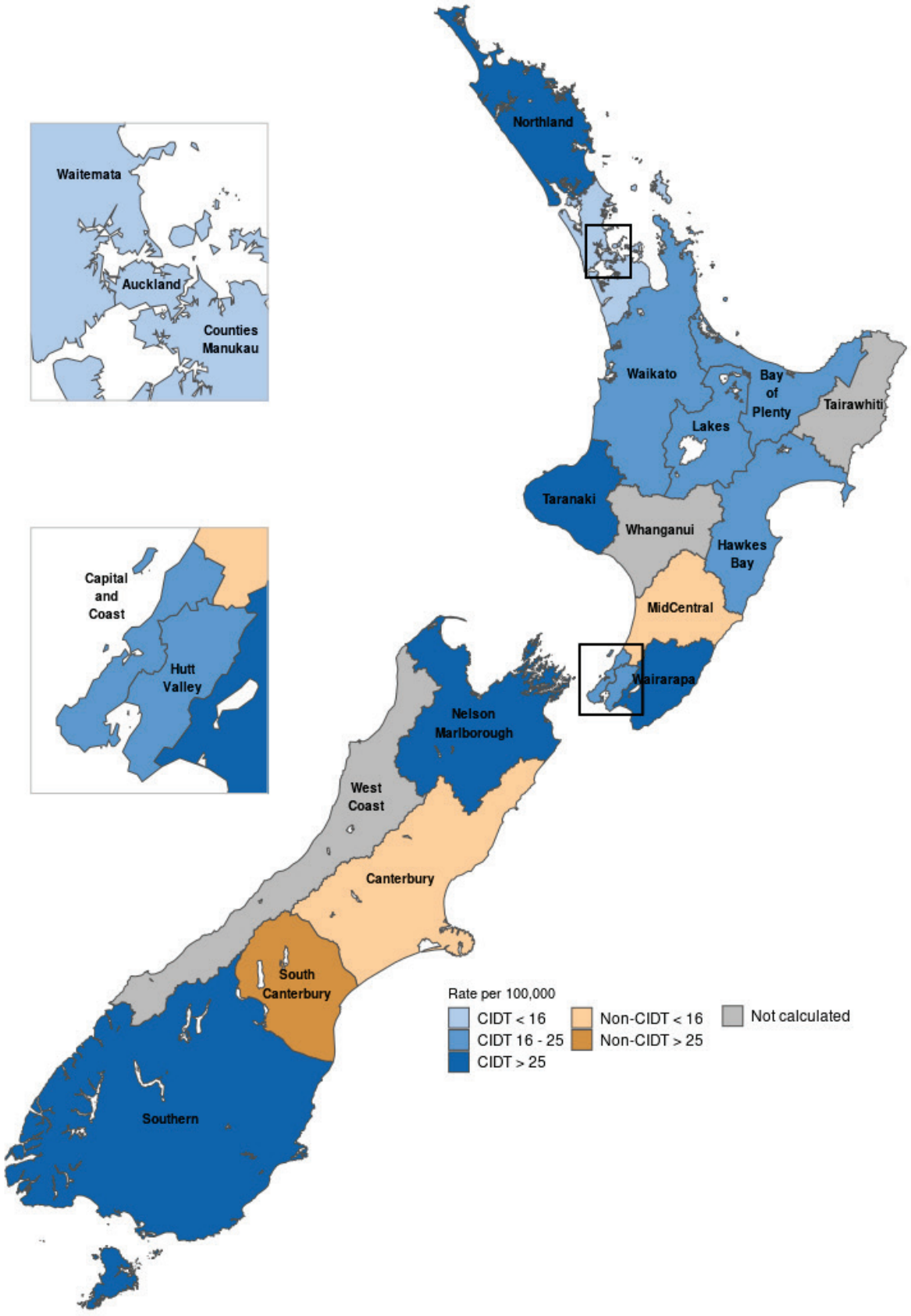
[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 45. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than 5 cases (grey shading): Tairawhiti (1 case), Whanganui (4 cases) and West Coast (1 case). These three DHBs all use culture-based testing for STEC.

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

Figure 45. Geographic distribution of STEC infection notifications, 2020



The highest rates of STEC notification in 2020 were reported in Southern DHB (41.8 per 100,000, 146 cases), Wairarapa DHB (40.9 per 100,000, 20 cases), Taranaki DHB (36.9 per 100,000, 46 cases) and Northland DHB (33.9 per 100,000, 66 cases). These four DHBs are using CIDT for community testing. The highest rates observed in DHB's using culture based tested were reported in South Canterbury (27.4 per 100,000, 17 cases) and Canterbury (14.1 per 100,000, 82 cases) DHBs.

Outbreaks reported as caused by STEC

Of the 8 outbreaks (44 cases) of STEC infection during 2020, four outbreaks (14 cases) were reported with food as a possible mode of transmission (Table 63). 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 63. STEC infection outbreaks reported, 2020

	STEC infection outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All [a]
Outbreaks	1	3	8
Outbreak-associated cases	3	11	44
Hospitalised Cases	0	0	0

[a] All STEC infection outbreaks, including non-foodborne outbreaks

Table 64 gives the details of the four outbreaks of STEC infection with food reported as a possible mode of transmission. No suspected foods were recorded for three of the outbreaks and the level of evidence that the outbreaks were foodborne was weak.

Table 64. Details of STEC infection outbreaks with food reported as a possible mode of transmission, 2020

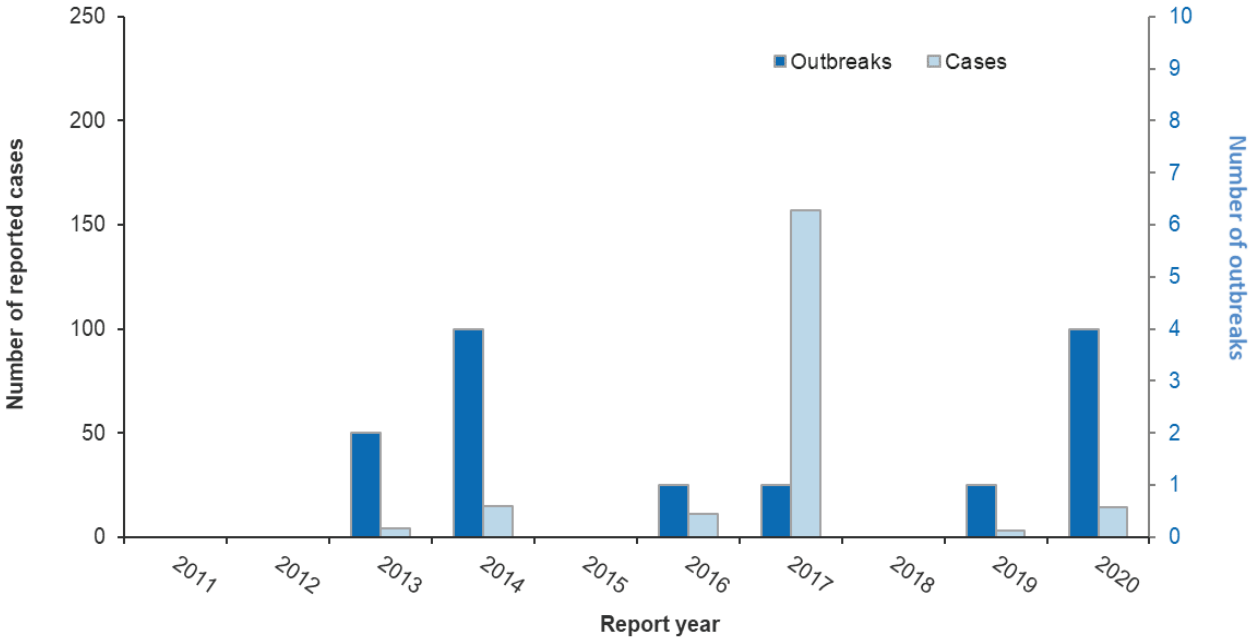
PHU	Month	Suspected Source	Evidence	Setting	No. Ill
Auckland	Jan	Chicken bun	Household cluster	Overseas, home	1C 2P
Auckland	Feb	Unknown	Household cluster	Home	1C 4P
Auckland	Feb	Unknown	Household cluster	Home	2C
Auckland	Sep	Unknown	Increase in disease incidence	Long-term care facility	4C

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

Cases in the September outbreak at a long-term care facility were also found to be infected with *Campylobacter*.

Over the 10-year period 2011 to 2020, the number of STEC outbreaks with food reported as a possible mode of transmission ranged from one to four per year, with no outbreaks reported for four of the ten years (Figure 46). The total number of cases associated with outbreaks has varied over the same period with a peak in 2017 (157 cases). The 2017 outbreak took place on a cruise ship and no specific food was recorded as a suspected source for the outbreak.

Figure 46. STEC infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020

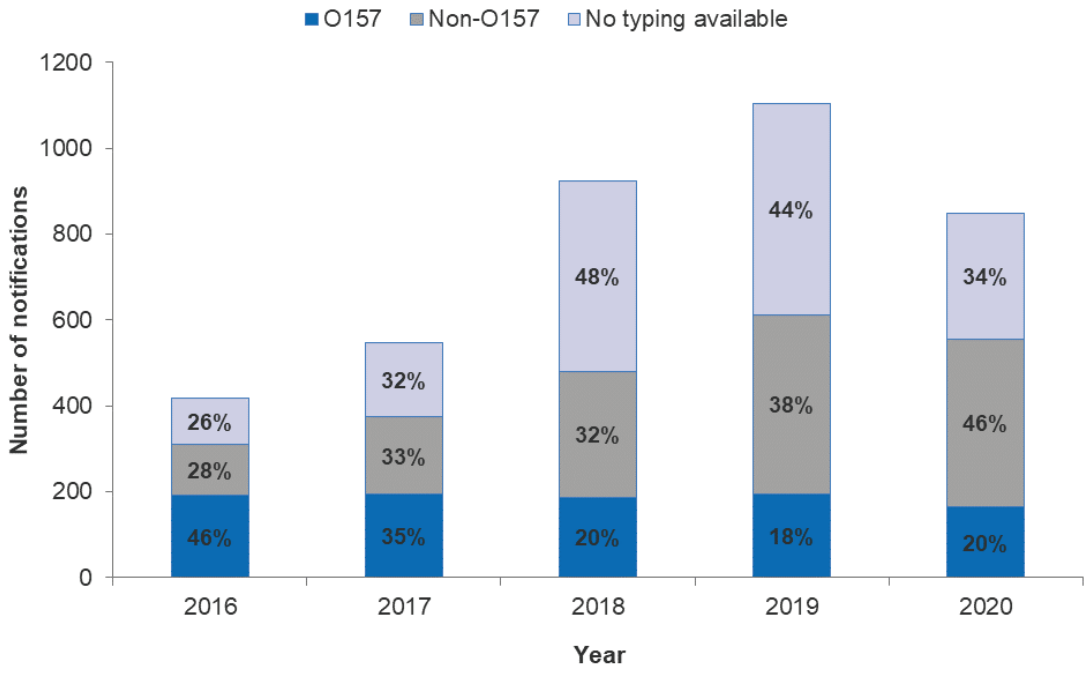


STEC types reported for notified cases

Isolates from 552 notified cases infected with STEC were typed by the ESR Enteric Reference Laboratory (ERL) in 2020. A single STEC was confirmed from 548 cases but two different STEC serotypes were isolated and serotyped from each of the remaining four cases giving a total of 556 isolates.

Of the 556 typed isolates, 165 (29.7%) were identified as *E. coli* O157:H7 and 391 (70.3%) as other serotypes. For 292 (34%) of the STEC notifications in 2020 no typing information was available (Figure 47). Notifications may not have typing information, e. g. due to ERL not receiving culture samples from diagnostic laboratories or if the culture was no longer viable. All isolates confirmed as STEC were whole genome sequenced in 2020, which has increased the proportion of STEC isolates that can be assigned a serotype.

Figure 47. *E. coli* O157 and non-O157 associated notifications by year, 2016–2020



The number of notified cases associated with *E. coli* O157:H7 infections was similar from 2016 to 2019, followed by a slight decrease in 2020 (Table 65).

The EpiSurv records indicated that for *E. coli* O157:H7, 35% of cases with known hospitalisation status had been hospitalised and 6% of cases had no hospitalisaion information recorded. The proportion hospitalised was less for *E. coli* O26:H11 (28% cases hospitalised, 10% no hospital data recorded) and *E. coli* O128:H2 (15% cases hositalised, 10% no hospital data).

Table 65. Annual number of notifications with different STEC serotypes identified by the Enteric Reference Laboratory, 2017–2020

Serotype	2017	2018	2019	2020
O157	**194**	**188**	**196**	**165**
O157:H7[a]	194	184	191	164
Non-O157	**180**	**292**	**417**	**391**
O26:H11	42	70	113	112
O128:H2	4	17	45	61
O38:H26	5	18	22	27
O146:H21	11	11	12	18
O176:H4	-	-	10	14
O5:HNT[b]	-	-	6	12
O84:H2	-	-	2	10
O91:H14	-	-	11	10
O103:H2	3	6	6	9
O174:H8	1	1	7	9
O88:H8	-	-	5	8
O123:H10	-	-	2	8
O130:H11	1	1	6	7
O182:H25	-	1	2	7
Other Types[c]	113	167	172	79

Serotype	2017	2018	2019	2020
Cases without typing information[d]	173	445	491	292

[a] Whole genome sequencing of human O157:H7 isolates from 2017 to 2020 revealed a wide diversity of genotypes present, with most of the isolates quite distinct to each other.

[b] HNT: Non-typable

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

[d] Some cases have been identified with dual serotypes. The sum of the total rows will not equal the number of notifications in a year.

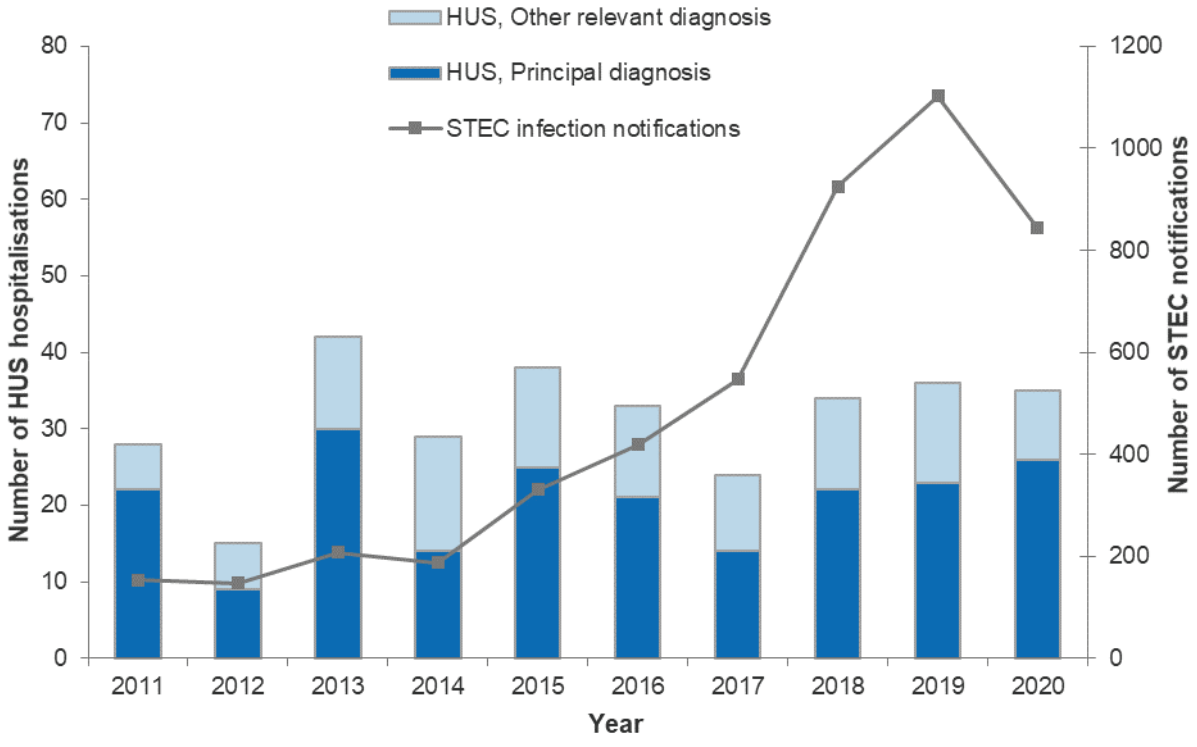
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from a STEC infection. HUS is usually preceded by a STEC infection [27]. It is not clear which STEC genotypes are most commonly associated with HUS cases. While it has been reported that two-thirds of HUS cases are associated with *E. coli* O157 infections [28], the most recent European data report that *E. coli* O26 was most frequently associated with HUS cases [29]. In 2020, 21 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O157:H7 (11), O26:H11 (3), O38:H25 (1), O88:H8 (1) while for five cases the serotype was not reported.

The ICD-10 code D59.3 was used to extract HUS hospitalisation data from the MoH NMDS database. Only HUS cases that were incident in the 2020 year were considered, rather than all cases that were hospitalised in that year. That is, if a HUS case hospitalised in 2020 had been hospitalised with HUS in a previous year, the 2020 admission was considered to be a re-admission, rather than an incident case. Of the 35 incident hospital admissions recorded in 2020 (0.7 per 100,000 population), 26 were reported with HUS as the primary diagnosis and 9 with HUS as another relevant diagnosis.

Between 2011 and 2020, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 38 (Figure 48). In 2020, the number of incident hospitalised cases (35) was similar to 2019 (36). STEC notifications have increased steadily over this period (Figure 41). However annual numbers of HUS cases remain similar over the last decade.

Figure 48. Haemolytic uraemic syndrome (HUS) hospitalised cases, 2011–2020



In 2020, the number of female cases hospitalised due to HUS was greater than the number of male cases (Table 66). This is the same as the pattern seen in most years other than 2017, when more males were hospitalised with HUS than females.

Table 66. Haemolytic uraemic syndrome hospitalised cases by sex, 2020

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	15	0.6
Female	20	0.8
Total	**35**	**0.7**

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

In 2020, the highest age-specific rates of incident hospitalised cases due to HUS were for children less than 5 years old. (Table 67).

Table 67. Haemolytic uraemic syndrome hospitalised cases by age group, 2020

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
0 to 4	18	5.9
5 to 9	1	-
10 to 14	2	-
15 to 19	1	-
20 to 29	2	-
30 to 39	1	-
40 to 49	1	-
50 to 59	3	-
60 to 69	4	-
70+	2	-
Total	**35**	**0.7**

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

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

During 2020, 17 cases of HUS were reported to the NZPSU, of which 16 had a diarrhoeal prodrome. The median age of cases was 1.5 years (range 0.7-10.8 years). Of the 16 diarrhoea-associated cases, 8 had STEC isolated from their stools. No fatalities were reported.

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

Whole genome sequencing of STEC and O26 and O157 isolates from ovine enrichments – Wright 2020

During 2016 – 2017, MPI undertook a Microbiological Baseline Survey to ascertain the prevalence of STEC, particularly the United States Department of Agriculture (USDA) Top 7 STEC (O157:H7, O26, O45, O103, O111, O121, O145), in sheep meat. A study was conducted to isolate STEC from enrichment cultures that had been stored from the above ovine baseline survey for either *E. coli* O157:H7 (n=14), or STEC O26 (n=7) and to genotype the isolates, in order to compare STEC O157 and O26 isolates from ovine with each other and with other relevant and available bovine/clinical isolates within ESR's database [30]. Fourteen broth cultures were available, consisting of *E. coli* O157:H7 (n=7), and STEC O26 (n=7). No viable *E. coli* O157:H7 or STEC O26 were recovered from the 14 broths that were received, despite the use of a resuscitation culture process.

The enrichment broths were screened by Real Time PCR (RT-PCR) for genes associated with the USDA Top 7 serotypes and whole genome sequencing analysis was carried out for two *E. coli* O157:H7 isolates which had been isolated during the baseline study. Thirteen of the 14 resuscitated broths had cycle threshold values (Ct) indicative of a positive detection for O26 and/or O157, which correlated to the NeoSEEK™ results previously determined. One sample (P12) which was previously STEC O157 positive via NeoSEEK™ was negative for the O157 antigen target using RT-PCR. This lack of detection may be due to the dilution effects of the resuscitation step.

Using single nucleotide polymorphism (SNP) analysis, it was observed that the two ovine *E. coli* O157:H7 isolates were genetically indistinguishable, showing no SNP differences between them. This supports the suspicion of the referring laboratory that they were from the same original sample. Further SNP analysis showed that these two ovine isolates were between 50 and 100 SNP differences from any of the bovine and human isolates in the ESR *E. coli* O157:H7 data set.

Analysis using whole genome multi-locus sequence typing (wgMLST) including 82 bovine isolates from 2016-2019 demonstrated that the ovine *E. coli* O157 isolates were genetically distinct, with at least 48 allele differences from the *E. coli* O157 bovine isolates.

Journal papers

Nil.

Relevant regulatory developments

Nil.

Toxic shellfish poisoning

Case definition

Due to the diverse nature of toxins that may cause toxic shellfish poisoning, no consistent clinical description is provided for this condition. Depending on the toxin involved, toxic shellfish poisoning may result in various combinations of gastrointestinal, neurosensory, neurocerebellar/neuromotor, general neurological and other symptoms.

Suspected:

Amnesic shellfish poisoning (ASP): Vomiting or diarrhoea occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food AND/OR one or more of the neurological symptoms from group C (see below) occurring within 48 hours of consuming shellfish.

Diarrhoeic shellfish poisoning (DSP): Vomiting or diarrhoea occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food.

Neurotoxic shellfish poisoning (NSP): Two or more of the neurological symptoms from groups A and B (see below) occurring within 24 hours of consuming shellfish.

Paralytic shellfish poisoning (PSP): Paraesthesia occurring within 12 hours of consuming shellfish AND one of the neurological symptoms from group B (see below).

Toxic shellfish poisoning type unspecified (TSP): Vomiting or diarrhoea occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food OR any of the neurological symptoms from groups A and B (see below) occurring within 24 hours of consuming shellfish OR one or more of the neurological signs/symptoms from group C (see below) occurring within 48 hours of consuming shellfish.

Clinical symptoms for assigning status

Group A

- paraesthesia - i.e. numbness or tingling around the mouth, face or extremities
- alteration of temperature sensation

Group B

- weakness such as trouble rising from seat or bed
- difficulty swallowing
- difficulty breathing
- paralysis
- clumsiness
- unsteady walking
- dizziness/vertigo
- slurred/unclear speech
- double vision

Group C

- confusion
- memory loss
- disorientation
- seizure
- coma

Probable:

Meets case definition for suspect case AND detection of relevant biotoxin at or above the regulatory limit in shellfish obtained from near or same site (not leftovers) within seven days of collection of shellfish consumed by case. Current levels are as follows:

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

Confirmed:

Meets case definition for suspect case AND detection of TSP biotoxin in leftover shellfish at a level resulting in the case consuming a dose likely to cause illness. Current dose levels are as follows:

ASP: 0.05 mg/kg body weight	NSP: 0.3 MU/kg body weight
DSP: ingestion of 48 µg or 12 MU	PSP: 10 MU/kg body weight (≅ 2µg/kg body weight)

Toxic shellfish poisoning cases reported in 2020 by data source

During 2020, no individual cases of toxic shellfish poisoning were reported in EpiSurv.

The ICD-10 code T61.2 was used to extract hospitalisation data for 'other fish and shellfish poisoning' from the MoH NMDS database. Of the 11 hospital admissions (0.2 admissions per 100,000 population) recorded in 2020, nine cases were reported with 'other fish and shellfish poisoning' as the primary diagnosis and two cases were reported with 'other fish and shellfish poisoning' as another relevant diagnosis. Note that this ICD-10 code includes shellfish and other fish.

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

Outbreaks reported as caused by toxic shellfish poisoning

In 2020, no toxic shellfish poisoning outbreaks were reported in which cases had symptoms consistent with PSP. It should be noted that all cases of toxic shellfish poisoning will be categorised as foodborne as consumption of contaminated fish is the only recognised transmission route for this disease.

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Risk assessment of pectenotoxins in New Zealand bivalve molluscan shellfish, 2009 – 2019 – Boundy et al, 2020

Pectenotoxins (PTXs) are produced by *Dinophysis* spp., along with okadaic acid, dinophysistoxin 1, and dinophysistoxin 2 [31]. The okadaic acid group toxins cause diarrhetic shellfish poisoning (DSP). New Zealand regulations currently include pectenotoxins within the DSP regulations. Shellfish biotoxin data collected between 2009 and 2019 showed that 85 samples exceeded the DSP regulatory limit (0.45%) and that excluding pectenotoxins would have reduced this by 10% to 76 samples. The incidence (1.3%) and maximum concentrations of pectenotoxins (0.079 mg/kg) were also found to be low, well below the current European Food Safety Authority (EFSA) safe limit of 0.12 mg/kg. However, pectenotoxins and okadaic acid have different mechanisms of action, meaning that their toxicities are not additive. Evaluation of the available toxicity data suggests that pectenotoxins have very low oral toxicity, with recent studies showing no oral toxicity in mice dosed with the PTX analogue PTX2 at 5000 µg/kg. No known human illnesses have been reported due to exposure to pectenotoxins in shellfish, a fact which combined with the toxicity data indicates that they pose negligible risk to humans.

Relevant regulatory developments

Nil.

Vibrio parahaemolyticus infection

Case definition

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

Vibrio parahaemolyticus infection cases reported in 2020 by data source

During 2020, eight individual cases were reported in EpiSurv. Note that not all cases of *V. parahaemolyticus* infection are necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.3 was used to extract foodborne *V. parahaemolyticus* infection hospitalisation data from the MoH NMDS database. Of the five hospital admissions (0.1 admissions per 100,000 population) recorded in 2020, three cases were reported with *V. parahaemolyticus* infection as the primary diagnosis and two were reported with *V. parahaemolyticus* infection as another relevant diagnosis.

It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Outbreaks reported as caused by *Vibrio parahaemolyticus*

One outbreak of *V. parahaemolyticus* infection with food as a possible mode of transmission was reported in 2020 involving 16 associated cases, seven of whom were hospitalised (Table 68).

Table 68. *V. parahaemolyticus* infection outbreaks reported, 2020

	V. parahaemolyticus infection outbreaks	
	Possible foodborne transmission with suspected source	All [a]
Outbreaks	1	1
Outbreak-associated cases	16	16
Hospitalised cases	7	7

[a] All *V. parahaemolyticus* infection outbreaks, including non-foodborne outbreaks

Table 69 provides details of the *V. parahaemolyticus* outbreak with food reported as a possible mode of transmission reported in 2020.

Table 69. Details of *V. parahaemolyticus* infection outbreak with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Toi Te Ora	June	Raw mussels	Common food type eaten by cases	Home consumption of commercially grown mussels	16C

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Influence of farming methods and seawater depth on Vibrio species in New Zealand pacific oysters – Cruz et al. 2020

Pacific oysters (*Crassostrea gigas*) were grown in the Kaipara and Mahurangi Harbours in New Zealand at different heights from the seafloor in different ways: fixed positions intertidally and subtidal, and as floating long lines over the 2013 and 2014 summer periods [32]. Two geographically distinct commercial harvest areas: Coromandel Harbour (North Island) and Croisilles Harbour (South Island) in New Zealand were also compared in 2015 where oysters are grown under different methods. Detection and enumeration of *Vibrio* spp. was performed according to the Bacteriological Analytical Manual using the Most Probable Number approach and real-time polymerase chain reaction technique. The only significant growing method effect was observed in Mahurangi Harbour, where intertidal oysters at 1.5 m from the seafloor had higher numbers of trh+ *Vibrio parahaemolyticus* than other intertidal samples from Kaipara Harbour and Coromandel Harbour. All other samples showed a relationship with surface seawater temperature, but not with distance from seafloor or farming method. Overall, there is no clear evidence that different oyster farming methods (floating, subtidal or intertidal at different depths) affect *Vibrio* spp. population sizes, which were dominated by seasonal changes and environmental parameters.

Correlations between environmental conditions and Vibrio parahaemolyticus or Vibrio vulnificus in Pacific oysters from New Zealand coastal waters – King et al. 2020

Correlations between concentrations of *Vibrio parahaemolyticus* and *V. vulnificus* in Pacific oysters from eight New Zealand coastal regions (2008–2017), and seawater surface temperature (SST), salinity and rainfall were investigated [33]. Most (88%) of the oyster samples were collected during summer and autumn. The prevalence of *V. parahaemolyticus* and *V. vulnificus* was 85% and 15%, respectively. *Vibrio vulnificus* was always detected in the presence of *V. parahaemolyticus*. Across all regions, *V. parahaemolyticus* concentration positively correlated with SST (r = 0.60), but not with salinity (r = −0.01). *Vibrio vulnificus* concentration weakly correlated with SST (r = 0.26) and salinity (r = −0.21). Linear and generalised additive models were investigated but none were satisfactory for prediction. Salinity and SST explained < 50% of the variability in *V. parahaemolyticus* concentrations, indicating that other environmental or biological factors contributed. When SST, salinity and rainfall 15 days prior to harvesting were investigated for one region, SST was the best pre-harvest indicator for elevated concentrations of both *Vibrio* species.

Relevant regulatory developments

Nil.

Yersiniosis

Summary data for yersiniosis in 2020 are given in Table 70.

Table 70. Summary of surveillance data for yersiniosis, 2020

Parameter	Value in 2020	Source
Number of notified cases (Total)	1261	EpiSurv
Notification rate (per 100,000)	24.8	EpiSurv
Hospitalisations[a]	164	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b]	11 (0.9%)	EpiSurv
Estimated food-related cases (%)[c]	937 (75%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] For estimation of food-related cases the proportions derived from expert consultation [3] exclude travel-related cases

Case definition

Clinical description:	In children under five years old, *Yersinia enterocolitica* infection typically causes diarrhoea, vomiting, fever and occasionally abdominal pain. In contrast, older children and adults are more likely to experience abdominal pain as the prominent symptom. Bacteraemia and sepsis may occur in immunocompromised individuals. *Y. pseudotuberculosis* is more likely to cause mesenteric adenitis and septicaemia than *Y. enterocolitica*.
Laboratory test for diagnosis:	Isolation of *Y. enterocolitica* or *Y. pseudotuberculosis* from blood or faeces OR detection of *Yersinia* spp. nucleic acid from faeces*.
Case classification:	
Probable	A clinically compatible illness that is epidemiologically linked to a confirmed case or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

* Note that presently PCR testing may not detect *Y. pseudotuberculosis* and the ability of the assays to adequately detect *Y. enterocolitica* biotype 1A is uncertain [12].

Changes to laboratory methods

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2020, all community faecal specimens in all DHBs except for Canterbury, MidCentral, South Canterbury, Tairawhiti, West Coast and Whanganui, were screened by culture-independent diagnostic tests (CIDT) for a range of pathogens, including *Yersinia.*

Of the DHBs who have moved to CIDT, all faecal specimens in the Capital & Coast, Hawke's Bay, Hutt Valley, Nelson Marlborough, Southern, Taranaki, and Wairarapa DHBs are routinely tested for *Y. enterocolitica and Y. pseudotuberculosis.* Faecal specimens in Northland, Counties Manukau, Auckland, Waitemata, Waikato, Lakes and Bay of Plenty DHBs are only being screened for *Y. enterocolitica*. [34].

The introduction of CIDT methods has had no significant impact on notifications for yersiniosis. Please refer to the Appendix (page 119) for details.

Due to these ongoing changes to laboratory testing methods faecal samples from some DHB areas are no longer tested for *Yersinia pseudotuberculosis.* In 2020, clinical samples from the top half of the North Island, including Northland, Auckland, Counties Manukau, Waitemata, Waikato, Lakes and Bay of Plenty DHB areas, which corresponds to 54% of the population, are now only being screened for *Yersinia enterocolitica*. Cases of *Y. pseudotuberculosis* in these DHBs may be notified as acute gastroenteritis cases or not be notified. In the last 10 years, *Y. pseudotuberculosis* has been associated with less than 3% of sporadic cases in each reporting year.

Effect of COVID-19 on yersiniosis notification rates

During the level 3 and 4 lockdown period, from the end of March to middle of May 2020, yersiniosis notifications were similar compared to the previous three years. During April and May 2020, there were 141 notified cases compared to 180 cases in 2019. Compared to the previous three-year mean notifications remained similar for the months June to August 2020 but were higher from September to December (Figure 51).

Public health and social measures introduced in 2020 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 9).

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

Yersiniosis cases reported in 2020 by data source

During 2020, 1261 individual cases (24.8 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv. Of the 1261 cases, the symptoms of 1127 cases (89%) were reported as fitting the clinical description for yersiniosis infection, the symptoms were unknown for 132 cases, and for two cases the symptoms are listed as not fitting the clinical description.

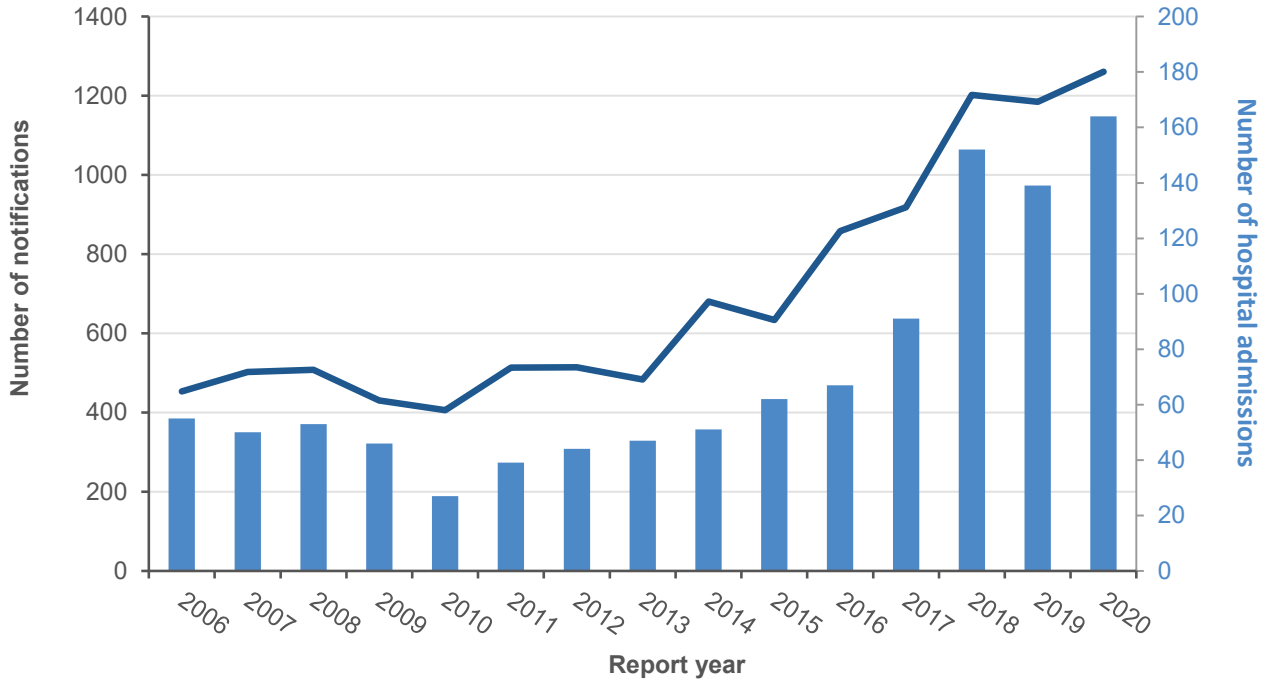
The ICD-10 code A04.6 was used to extract yersiniosis (enteritis due to *Y. enterocolitica)* hospitalisation data from the MoH NMDS database. Of the 164 hospital admissions (3.2 admissions per 100,000 population) recorded in 2020, 98 cases were reported with yersiniosis as the primary diagnosis and 66 were reported with yersiniosis as another relevant diagnosis.

It should be noted that EpiSurv and MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

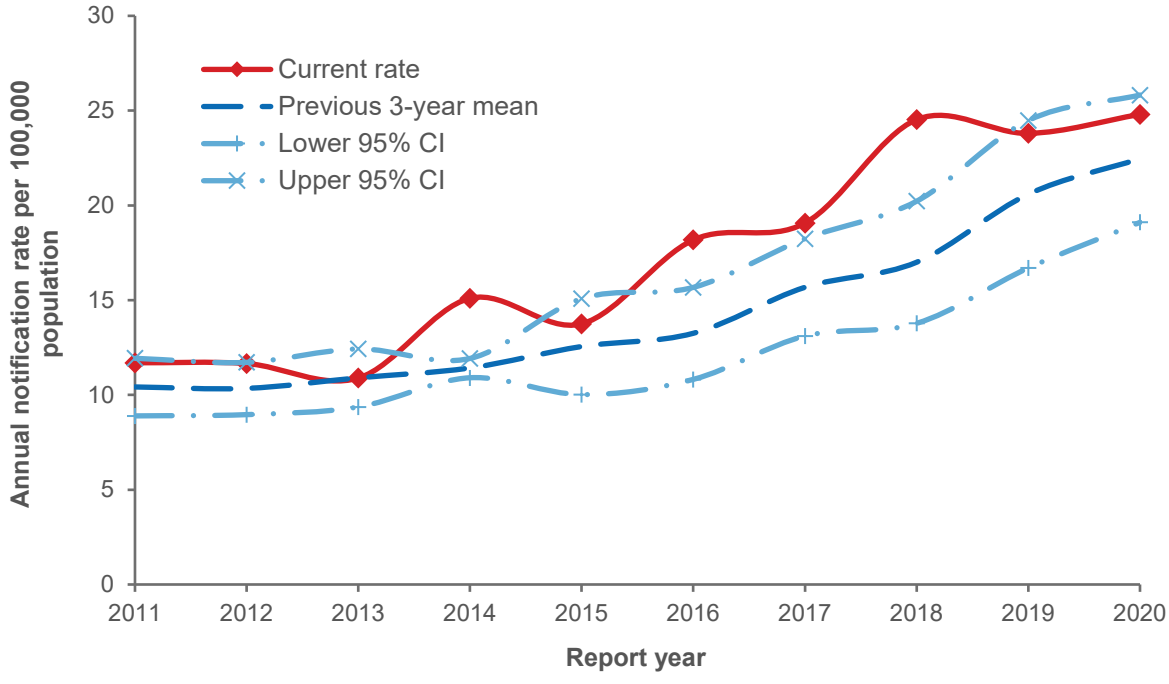
Between 2001 and 2013 the annual number of notifications reported ranged between 383 and 514. Since 2013, the number of notifications for yersiniosis and the rate of yersiniosis notifications per 100,000 population has been increasing, with the highest number of cases reported in 2018 (1201 cases) and 2020 (1261) (Figure 49 and Figure 50). The number of hospital admissions with yersiniosis as a primary or secondary diagnosis has been increasing since 2013.

Figure 49. Yersiniosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2006–2020



The yersiniosis annual notification rate has been generally increasing since 2013 (Figure 50). The 2020 notification rate was 24.8 per 100,000 population, higher than the previous three-year average (22.5 cases per 100,000), but within the three-year confidence interval.

Figure 50. Yersiniosis notification rate by year, 2011–2020

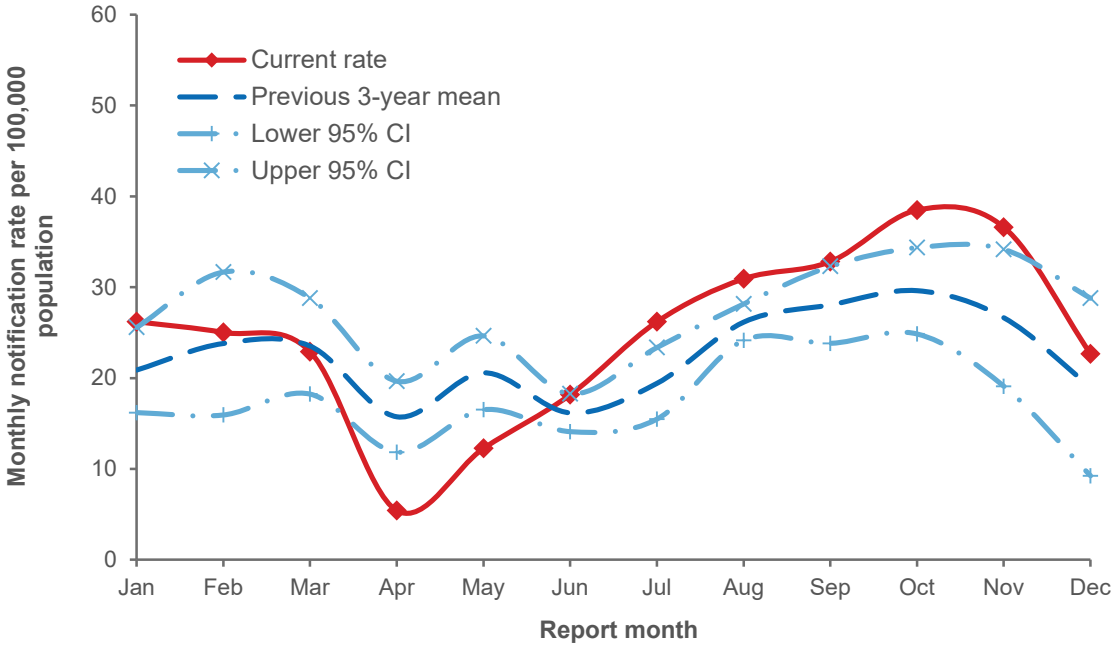


Seasonal data

The number of notified cases of yersiniosis per 100,000 population by month for 2020 is shown in Figure 51. In 2020, monthly notification rates were generally higher or similar to the previous three-year average. Much lower rates of notified cases occurred in April and May, related to the impact of the COVID-19 public health response.

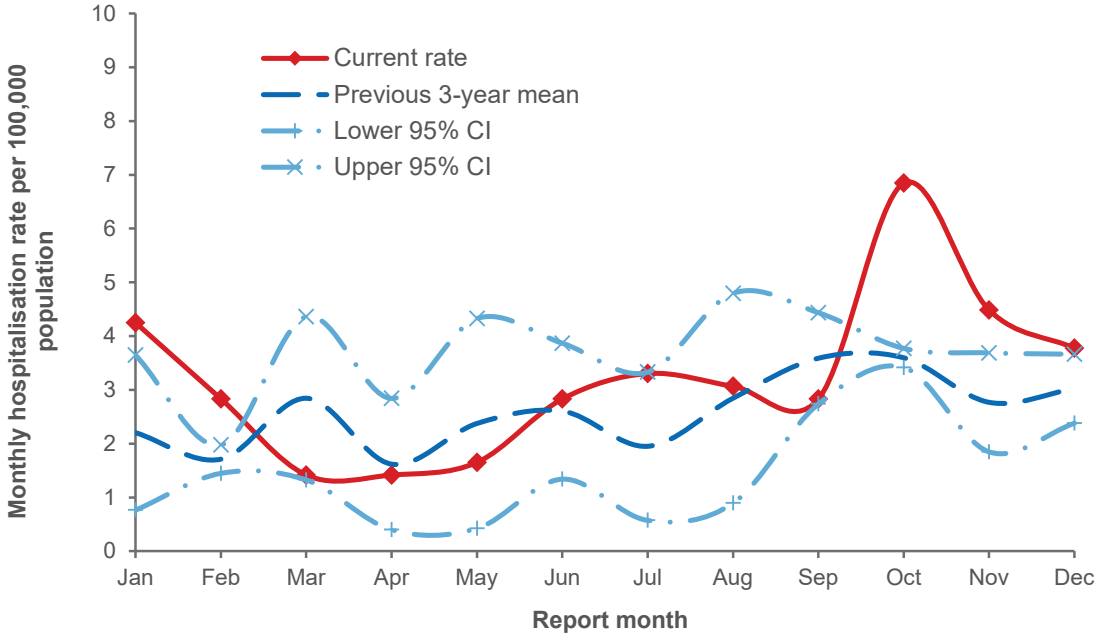
The monthly number of notifications in 2020 ranged from 23 notifications (April) to a peak of 163 notifications (October). The seasonal trend in monthly notification rates in 2020, excluding the COVID-19 level 3 and 4 period (22 March to 14 May) was similar to recent years (2017–2019) with increasing rates in spring.

Figure 51. Yersiniosis monthly notification rate (annualised), 2020



In 2020, the monthly hospitalisation rates were generally within the previous three-year average range, apart from a peak in October. (Figure 52).

Figure 52. Yersiniosis monthly hospitalisation rate (annualised), 2020



Demographics

In 2020, the yersiniosis notification and hospitalisation rates were similar for males and females (Table 71).

Table 71. Yersiniosis cases by sex, 2020

Gender	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	610	24.2	78	3.1
Female	651	25.4	86	3.4
Total	**1261**	**24.8**	**164**	**3.2**

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

In 2020, the highest yersiniosis notification rates were for the 0 to 4 years age group (78.6 per 100,000, 240 cases) (Table 72). The highest hospitalisation rates were reported for the 0 to 4 years age group (7.9 per 100,000 population, 24 cases) and for the 70+ years age group (7.9 per 100,000 population, 43 cases).

Table 72. Yersiniosis cases by age group, 2020

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	240	78.6	24	7.9
5 to 9	43	13.1	2	0.6
10 to 14	44	13.2	3	0.9
15 to 19	43	13.5	4	1.3
20 to 29	154	21.4	14	1.9
30 to 39	174	24.6	15	2.1
40 to 49	129	20.1	16	2.5
50 to 59	140	21.5	24	3.7
60 to 69	137	25.5	19	3.5
70+	157	28.9	43	7.9
Total	**1261**	**24.8**	**164**	**3.2**

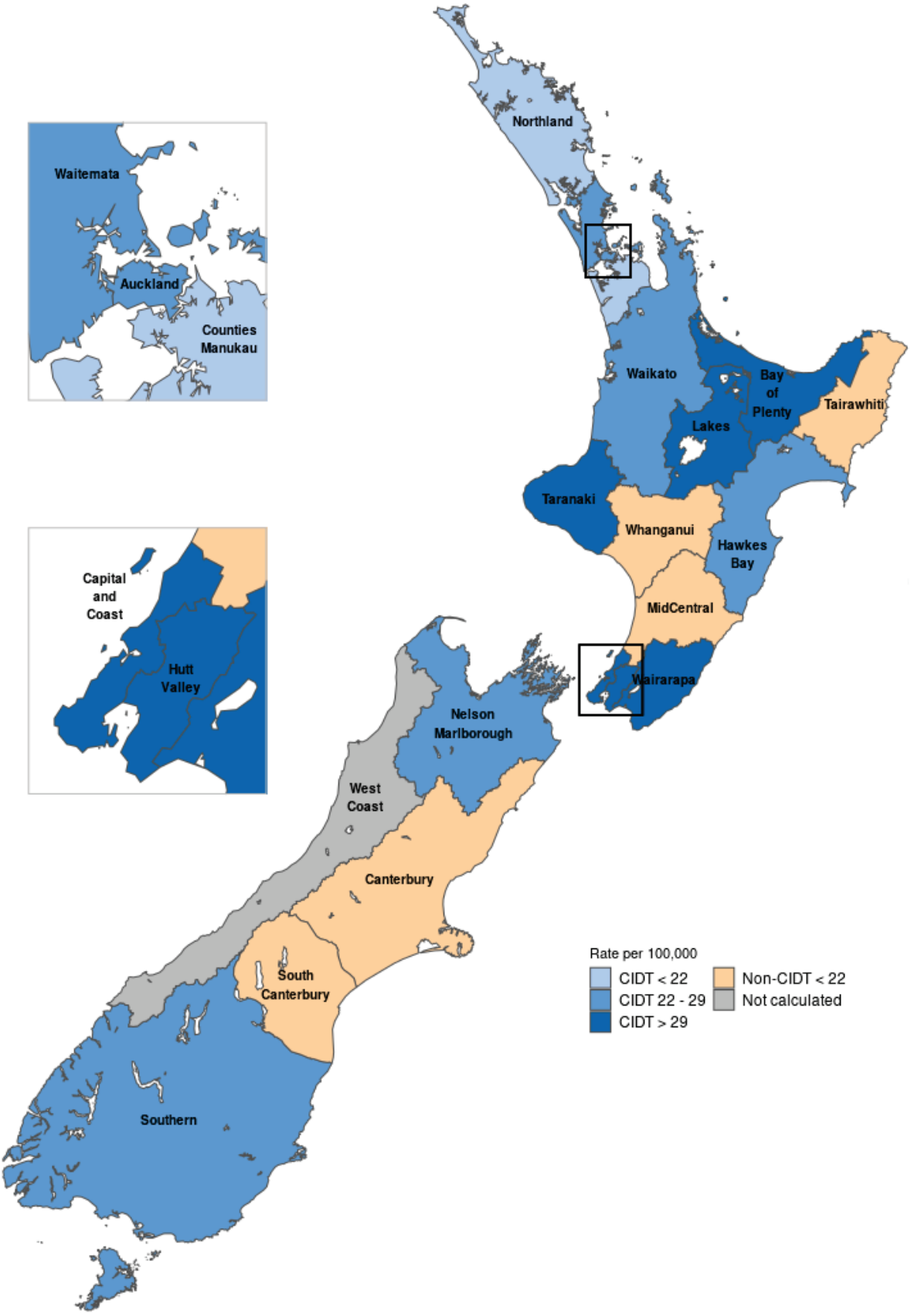
[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported)

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 53. Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than 5 cases (grey shading): West Coast (3 cases). West Coast DHB is serviced by laboratories using non-CIDT methods.

Notification rates for yersiniosis have been variable across New Zealand with Wairarapa DHB consistently in the highest quantile of notification rates since 2017.

Figure 53. Geographic distribution of yersiniosis notifications, 2020



In 2020, the highest notification rates of yersiniosis were reported for Wairarapa DHB (45.0 per 100,000, 22 cases), Hutt Valley DHB (36.5 per 100,000, 58 cases), Capital and Coast DHB (36.4 per 100,000, 118 cases), Taranaki DHB (34.5 per 100,000, 44 cases) and Lakes DHB (29.8 per 100,000, 35 cases). All these five DHBs were serviced by laboratories using CIDT community testing.

Outbreaks reported as caused by *Yersinia* spp.

In 2020, there was one yersiniosis outbreak reported in EpiSurv, for which food was reported as a possible mode of transmission (Table 73). 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 73. Yersiniosis outbreaks reported, 2020

	Possible foodborne transmission but no suspected source	All yersiniosis outbreaks [a]
Outbreaks	1	1
Outbreak-associated cases	2	2
Hospitalised cases	0	0

[a] All yersiniosis outbreaks, including non-foodborne outbreaks

Table 74 contains details of the yersiniosis outbreak with food reported as a possible mode of transmission reported in 2020. The evidence for foodborne transmission was weak with no suspected food source recorded for this outbreak.

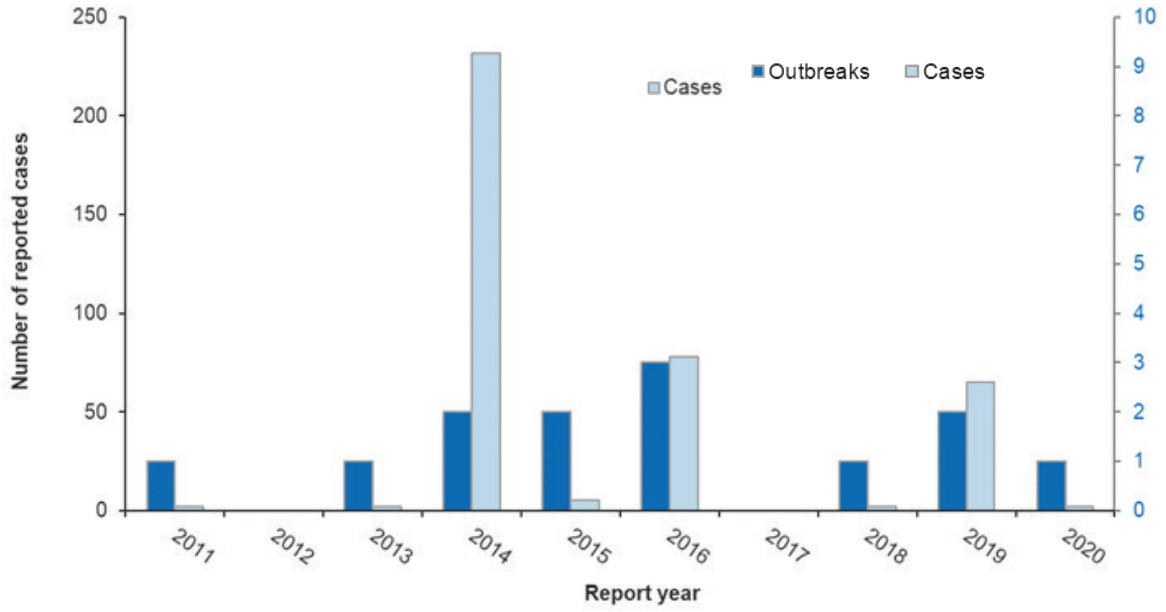
Table 74. Details of yersiniosis outbreak with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected Vehicle	Evidence	Setting	No. Ill
Toi Te Ora	Aug	Unknown	Attendance at common event	Home	1C 1P

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

Over the 10-year period 2011 to 2020, very few yersiniosis outbreaks with food reported as a possible mode of transmission were reported in EpiSurv; three or fewer each year, with a total number of associated cases ranging from two to 232 (Figure 54). The number of outbreaks in 2014 (2 outbreaks) and 2016 (3 outbreaks) was not unusual, but the number of cases involved (232 and 78, respectively) was higher than has been previously seen in New Zealand. The increased number of outbreak cases in 2019 was due to an outbreak in a prison setting.

Figure 54. Yersiniosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2011–2020



Yersinia species commonly reported

In 2020, the isolates from 888 (71%) cases of notifiable *Yersinia* spp. (i.e. *Y. enterocolitica* (YE) and *Y. pseudotuberculosis* (YTB) were able to be typed by the Enteric Reference Laboratory (ERL).

The number of notifiable *Yersinia* spp. cases identified by the Enteric Reference Laboratory at ESR each year is shown in Table 75 and the percentage of cases of each type is shown in Figure 55. The table and figure need to be interpreted with some caution as:

a) not all clinical laboratories forward all Yersinia isolates to ERL for confirmation and typing,

b) the number of isolates forwarded for confirmation and typing, as a percentage of all notifications, has changed during this period and

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

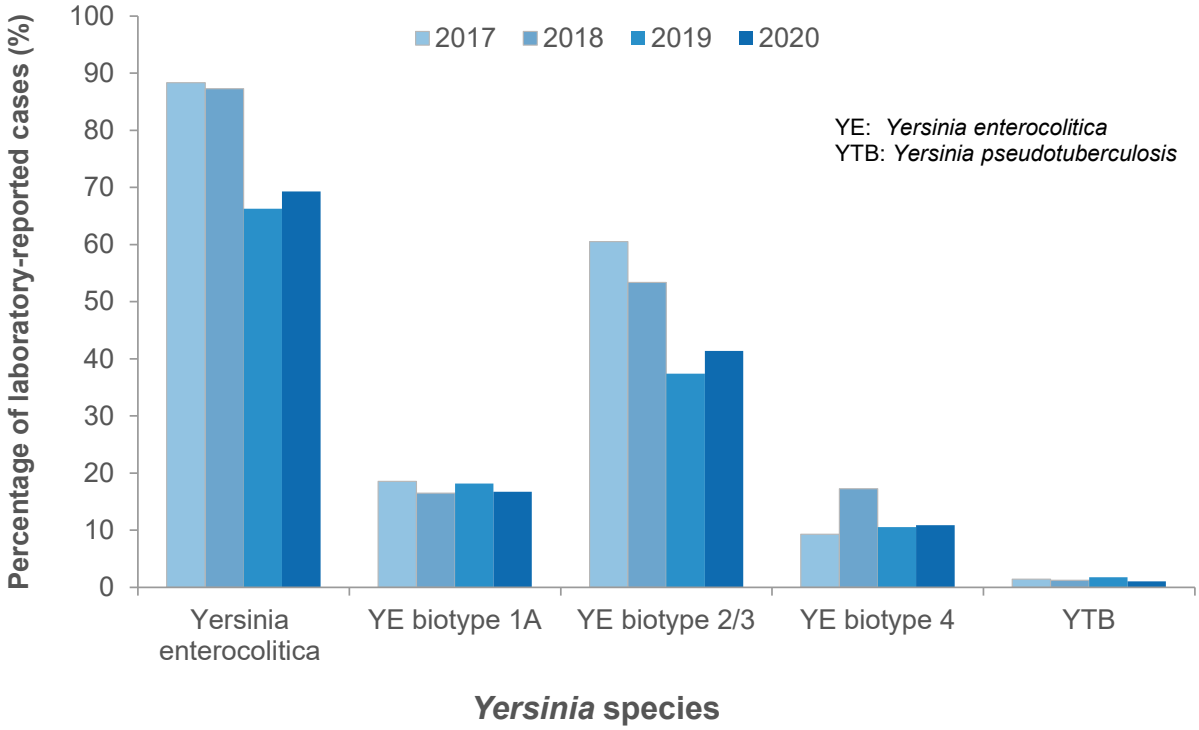
Between 2017 and 2020, each year the largest proportion of cases was due to *Y. enterocolitica* (Table 75 and Figure 55). In 2019 and 2020 approximately 30% of notified cased were not typed by the Enteric Reference Laboratory.

The most prevalent type of *Y. enterocolitica* has been biotype 2/3, serotype O:9, the type associated with just over 50% of the notified cases with typing information, in each year 2018 to 2020.
Y. enterocolitica biotype 1A accounts for approximately 25% of notified cases with typing information in 2019 and 2020.

Table 75. Notifiable case *Yersinia* spp. identified by the Enteric Reference Laboratory, 2017–2020

Species	2017	2018	2019	2020
Yersinia enterocolitica	**810**	**1048**	**785**	**874**
biotype 1A	**170**	**198**	**215**	**211**
serotype O:5	-	-	18	38
serotype O:8	-	-	18	38
biotype 2/3[a]	**555**	**641**	**443**	**522**
serotype O:5, 27	2	43	16	40
serotype O:9	110	598	425	482
biotype 4	**85**	**207**	**125**	**137**
serotype O:3	12	207	125	137
biotype not identified	**-**	**2**	**2**	**4**
Yersinia pseudotuberculosis	**13**	**15**	**21**	**13**
Yersinia hibernica	**-**	**-**	**-**	**1**
Cases without typing information	**94**	**138**	**379**	**373**

Figure 55. Percentage cases of notifiable *Yersinia* spp. by species and year, 2017–2020



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Other foodborne outbreaks

This section contains any footborne outbreaks caused by pathogens not covered in the previous sections of this report.

Outbreak reported as caused by *Clostridium botulinum*

During 2020 there was one botulism outbreak reported in EpiSurv with four associated cases. This was the first outbreak of botulism reported in EpiSurv. All four cases were hospitalised with botulism as the primary diagnosis.

Table 76 contains details of the foodborne botulism outbreak reported in 2020. The suspected vehicle of this outbreak was improperly home-preserved seafood. The level of evidence for the outbreak being foodborne was strong.

Table 76. Details of botulism outbreak with food reported as a possible mode of transmission, 2020

PHU	Report Month	Suspected source	Evidence	Setting	No. ill
Toi Te Ora	May	Marinated seafood	Botulinum toxin detected in both case and vehicle	Home	1C 3P

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

Following the outbreak, in July 2021, MPI collected and analysed a total of 100 samples of shellfish and sediments from the same area where the shellfish consumed by the cases were harvested.

Several samples were found positive by PCR for the gene encoding the neurotoxin type A and one sample was found positive for the neurotoxin type A and the Non-Toxin Non-Hemagglutinin protein, confirming the presence of C. botulinum type A in the New Zealand environment*.

* https://www.mpi.govt.nz/dmsdocument/45799-Isolation-of-Clostridium-botulinum-type-A-from-seafood-and-from-a-recreational-area-associated-with-an-outbreak-of-botulism-Technical-paper

APPENDIX A - METHODS

This section includes descriptions of the data sources, analytical methods used and comments on quality of data, including known limitations.

The report uses the calendar year, 1 January to 31 December 2020, for the reporting period.

Data sources

The key sources of data used in this report are detailed in the following sections. The data sources have been selected on the basis of availability of data for the specified reporting period and their accessibility within the timeframe required for the report.

Some data, such as official cause of death, are not published until several years after the end of the year in which the event occurred (although deaths may be reported as part of the case notification data recorded in EpiSurv). For this reason, these data are not available for inclusion in a report published soon after the end of the calendar year.

EpiSurv - the New Zealand notifiable disease surveillance system

Under the Health Act 1956 health professionals are required to inform their local Medical Officer of Health of any suspected or diagnosed notifiable disease. Since December 2007, laboratories have also been required to report notifiable disease cases to their local Medical Officer of Health.

Notification data are recorded using a web-based application (EpiSurv) available to staff at each of the 12 Public Health Units (PHUs) in New Zealand. The EpiSurv database is maintained and developed by the Institute of Environmental Science and Research (ESR) Ltd., which is also responsible for the collation, analysis and reporting of disease notifications on behalf of the Ministry of Health (MoH).

Data collected by PHUs depends on the specific disease, but usually includes demography, outcome, basis of diagnosis, risk factors and some clinical management information. Data on risk factors reflect the frequency of exposure in the incubation period for illness and are not a measure of association with illness in comparison with the general population. For the purpose of this report, only the overseas travel risk factor is reported.

Further information about notifiable diseases can be found in the *Notifiable Diseases in New Zealand: Annual Report* [15].

Laboratory-based surveillance

For a number of organisms (e.g. *Salmonella*, *Escherichia coli*), clinical laboratory isolates are forwarded to reference laboratories at ESR for confirmation and typing. The number of isolates forwarded differs by DHB and organism (e.g. almost all isolates are forwarded for *Salmonella* typing but not all *Yersinia* isolates are forwarded).

Ministry of Health

The Ministry of Health collates national data on patients admitted and discharged from publicly funded hospitals. These data are stored as part of the National Minimum Dataset (NMDS). Cases are assigned disease codes using the tenth revision of the International Classification of Diseases (ICD-10) coding system [13]. Up to 99 diagnostic, procedure, and accident codes may be assigned to each admission. The first of these is the principal or primary diagnosis, which is the condition that led to admission. This may differ from the underlying diagnosis.

Hospital admission data are only added to the NMDS after the patient is discharged. The number of hospitalisations presented for the reported year may be under-reported due to the delay in receiving discharge summaries.

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

In this report all hospitalisations, including re-admissions, have been reported for all primary diseases. For the disease sequelae (GBS and HUS) re-admissions of cases within the calendar year were removed. For GBS and HUS reported case numbers represent unique cases that have been hospitalised during the calendar year, not the total number of admissions due to the sequelae.

Outbreak surveillance

ESR has operated an outbreak surveillance system as an additional module in EpiSurv since mid-1997. This enables Public Health Units (PHUs) to record and report outbreaks for national reporting and analysis. It should be noted that, due to the practicalities of collecting information and laboratory resource constraints, not all cases associated with outbreaks are recorded as individual cases of notifiable disease in EpiSurv. The terms 'setting' and 'suspected vehicle' are both used in outbreak reporting to describe likely implicated sources of exposure found in epidemiological or environmental investigations.

An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. More information about the outbreak reporting system can be found in the *Guidelines for the Investigation and Control of Disease Outbreaks* [35].

Laboratory investigation of outbreaks

PHUs may submit clinical, food or environmental samples associated with single cases or outbreaks of suspected food poisoning to ESR's Public Health Laboratory (PHL). While faeces are the most common human clinical sample, on occasions other clinical samples, such as vomit, urine or breast milk, may be submitted. Wherever possible, samples are linked to associated EpiSurv records. Samples are analysed for possible causative agents, based on information on symptoms and incubation period. In this report, laboratory investigations are reported only for outbreaks classified as foodborne in EpiSurv.

The present report only includes information on samples submitted to ESR's PHL. It should be noted that human faecal samples associated with outbreaks and sporadic cases may be tested by community laboratories, following submission by general practitioners or PHUs. If the pathogen identified is a notifiable disease, a notification will be generated, and a case reported in EpiSurv. No information is available from community laboratories on the number of samples submitted for which no pathogen is detected.

Level of evidence for outbreaks

Foodborne outbreaks have been classified as having weak or strong evidence for any given suspected vehicle. Outbreaks with strong evidence included those with a statistically significant elevated risk ratio or odds ratio (95% confidence) from an epidemiological investigation and/or laboratory evidence with the same organism and strain detected in both disease cases and vehicle (to the highest available level of identification).

Outbreaks were classified as having weak evidence when they met one or more of the following criteria:

- compelling evidence with symptoms attributable to specific organism, e.g. scombrotoxin, ciguatoxin, etc.,
- other association but no microbial evidence for causal link, i.e. organism detected at source but not linked directly to the cases by indistinguishable DNA profiles,
- raised but not statistically significant relative risk or odds ratio,
- no evidence found but logical deduction given circumstances.

Statistics New Zealand

Population data from the Statistics New Zealand website www.stats.govt.nz were used to calculate notification and hospitalisation population rates of disease. See analytical methods section for further details.

New Zealand Food Safety project reports and other publications

New Zealand Food Safety project reports, prepared by ESR or other providers, and publications from the general literature were used to provide specific contextual information on the prevalence of selected pathogens in specific food types.

Relevant regulatory developments

Organism-specific regulatory developments, such as legislation (Australia New Zealand Food Standards Code, New Zealand Food Standards), notices, guidelines or other guidance documents, or instructional material produced by New Zealand Food Safety or Food Standards Australia New Zealand (FSANZ) were briefly summarized to provide contextual information and a single point of reference for developments in the control of pathogens in food. It should be noted that New Zealand Food Safety are the authority and experts in this area and the regulatory developments summarised in this report were confirmed with New Zealand Food Safety.

Analytical methods

Key analytical methods used include:

Dates

Notification data contained in this report are based on information recorded in EpiSurv for individual cases as at 22 February 2021. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 5 May 2021. Changes made to EpiSurv data by PHU staff after these dates will not be reflected in this report. Consequently, future analyses of these data may produce revised results. Disease numbers are reported according to the date of notification.

Case status for notifications

All notifications recorded in EpiSurv that meet the case definitions [12] are included for analysis in this report with the exception of cases classified as ‘not a case’. In some instances, the investigation of a case may not be complete, and the status may be set to ‘under investigation’. These cases are included in this report. Any changes will be reflected in future surveillance reports.

Data used for calculating rates of disease

All population rates use Statistics New Zealand 2020 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2020, the New Zealand population was estimated to be 5,084,300. The population estimates for 2014 to 2019 have been revised by Statistics New Zealand, considering new migration measures and 2018 Census distributions. Any cases rates given in this report for 2014 to 2019 will be based on the revised population estimates.

Rates have not been calculated where there were fewer than five notified cases or hospitalisations in any category. Calculating rates from fewer than five cases produces unstable rates.

Geographical breakdown

This report provides rates for current district health boards (DHBs). The DHB populations have been derived from the Statistics New Zealand mid-year population estimates for territorial authorities in New Zealand incorporating the Census 2018 base data.

Map classification scheme

The map classification break points for the disease have been selected to divide the DHB rates into three bands. The darkest colour represents the highest rates in New Zealand and the lightest colour the lowest rates. The grey speckled colour shows where there are insufficient data to calculate a rate (fewer than five cases). DHB populations being covered by CIDT community testing for a pathogen is shown by a blue colour scale and DHBs where the community diagnostic testing is culture based is shown by a brown colour scale.

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 (2017−2019).

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

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

An overview of when laboratories servicing different DHBs moved to PCR-based detection methods and which pathogens are included in the respective PCR panels is summarised in Table 77 below. In 2020 there were three different commercial panels being used across NZ.

Some DHBs continue to use separate hospital and community laboratories, with differing testing methods for enteric pathogens. In 2020, the following DHBs were served by separate hospital and community laboratories:

- Hawke's Bay
- Northland
- Waikato
- Waitemata

Table 77. Timeline when DHBs changed to PCR detection methods for enteric pathogens (X: no change to PCR-based methods, NS: Not screened for)

District Health Board		*Campylobacter*	*Salmonella*	*Shigella*	*STEC*	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
Auckland	Hospital	Jul 2017	Jul 2017	Jul 2017	Jul 2017	Jul 2017	X	Jul 2017	Jul 2017	Jul 2017
Auckland	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
Bay of Plenty	Hospital	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Bay of Plenty	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Canterbury	Hospital	X	X	X	X	X	X	X	X	X
Canterbury	Community	X	X	X	X	X	X	X	X	X
Capital & Coast	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Capital & Coast	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Counties Manukau	Hospital	Nov 2015	Nov 2015	Nov 2015	Nov 2015	Nov 2015	X	Nov 2016	Nov 2016	Dec 2017
Counties Manukau	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
Hawke's Bay	Hospital	X	X	X	X	X	X	X	X	X
Hawke's Bay	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Hutt Valley	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Hutt Valley	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Lakes	Hospital	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018

District Health Board		*Campylobacter*	*Salmonella*	*Shigella*	*STEC*	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
Lakes	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
MidCentral	Hospital	X	X	X	X	X	X	X	X	X
MidCentral	Community	X	X	X	X	X	X	X	X	X
Nelson Marlborough	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Nelson Marlborough	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Northland	Hospital	X	X	X	X	X	X	X	X	X
Northland	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
South Canterbury	Hospital	X	X	X	X	X	X	X	X	X
South Canterbury	Community	X	X	X	X	X	X	X	X	X
Southern	Hospital	Jan 2017	Jan 2017	Jan 2017	Jan 2017	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Southern	Community	Jan 2017	Jan 2017	Jan 2017	Jan 2017	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Tairawhiti	Hospital	X	X	X	X	X	X	X	X	X
Tairawhiti	Community	X	X	X	X	X	X	X	X	X
Taranaki	Hospital	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	X
Taranaki	Community	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	X
Waikato	Hospital	X	X	X	X	X	X	X	X	X
Waikato	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Wairarapa	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Wairarapa	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Waitemata	Hospital	X	X	X	Dec 2016	X	X	X	X	X
Waitemata	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
West Coast	Hospital	X	X	X	X	X	X	X	X	X
West Coast	Community	X	X	X	X	X	X	X	X	X
Whanganui	Hospital	X	X	X	X	X	X	X	X	X
Whanganui	Community	X	X	X	X	X	X	X	X	X

Data source: New Zealand Microbiology Network CIDT survey, personal communication, Dec 2021

[a] Until 2018 only faecal specimens where parasite screening was requested were tested by PCR for *Giardia* and *Cryptosporidium*.

Changes in culture-based testing methods

The community laboratory covering most of Canterbury, South Canterbury and some West Coast samples have not changed to CIDT but changed their culture-based testing approach for STEC infection to include more non-O157 STEC serotypes. Since September 2018 all faecal samples are being tested for STEC with this new, still culture-based approach (plating to CHROMagar STEC, followed up with EIA stx testing), which explains the slight increase in STEC notifications in these regions (see Figure 60).

How does moving to PCR-based detection methods affect notification rates?

Introduction

Since 2015, NZ diagnostic laboratories gradually introduced changes in enteric testing methods and screening criteria. Traditional culture-based methods for enteric pathogens are gradually being replaced by diagnostic tests such as multiplex Polymerase Chain Reaction (PCR).

This section compares the notification rates obtained by PCR methods and associated screening frequencies, with those obtained using culture-based methods for a range of bacterial pathogens.

Methods

The following approach has been taken:

- Diseases considered: *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., STEC infection, and *Yersinia enterocolitica*.
- Notifications associated with an outbreak have been excluded from the analyses.
- Report dates grouped by quarter (January-March, April-June, July-September and October to December).
- Data grouped by DHB clusters based on testing laboratory and location. The data have been checked at the DHB level and the results are consistent across DHBs within a cluster, unless stated otherwise.
- Data are presented for notifications with reporting dates in 2014 to 2019, to allow any step changes due to testing changes to be identified. The data for 2020 are excluded, due to the impact of COVID-19 on notification rates.
- The quarterly notification rates are calculated using quarterly population estimates which are linearly interpolated between mid-year population estimates based on the 2018 Census.

Notification Rates

Figure 56 to Figure 59 show the quarterly rates of notifications per 100,000 population by region for the years 2014 to 2019 for *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., and *Yersinia* spp. infections.

The time periods when area populations were covered by community culture independent diagnostic testing methods (CIDT) using PCR are highlighted by green shading. For the time periods and areas indicated by the green shading, the hospital laboratories were also using PCR testing, with the exception of Northland, Waitemata (only STEC screened by PCR methods from December 2016), Waikato and Hawke's Bay hospitals.

These figures indicate there is no step with sustained increase in notification rates following the introduction of PCR testing for *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., and *Yersinia* spp..

There is a definite step increase in the number of notifications of STEC infection following the introduction of PCR testing and the subsequent screening of all samples for STEC (Figure 59). For time periods of consistent testing methodology, there is no evidence of increasing STEC notification rates over time. This suggests the national increase in STEC notifications observed since 2015 is due to diagnosing more people with STEC infection, rather than an underlying increase in STEC infections in New Zealand. This increase can be attributed to the higher number of faecal samples tested for STEC, which has resulted in far more cases diagnosed with a non-O157 infection. Many of these cases would not previously have been diagnosed with STEC infection.

Figure 56. Quarterly rates of campylobacteriosis notifications by region, 2014 – 2019

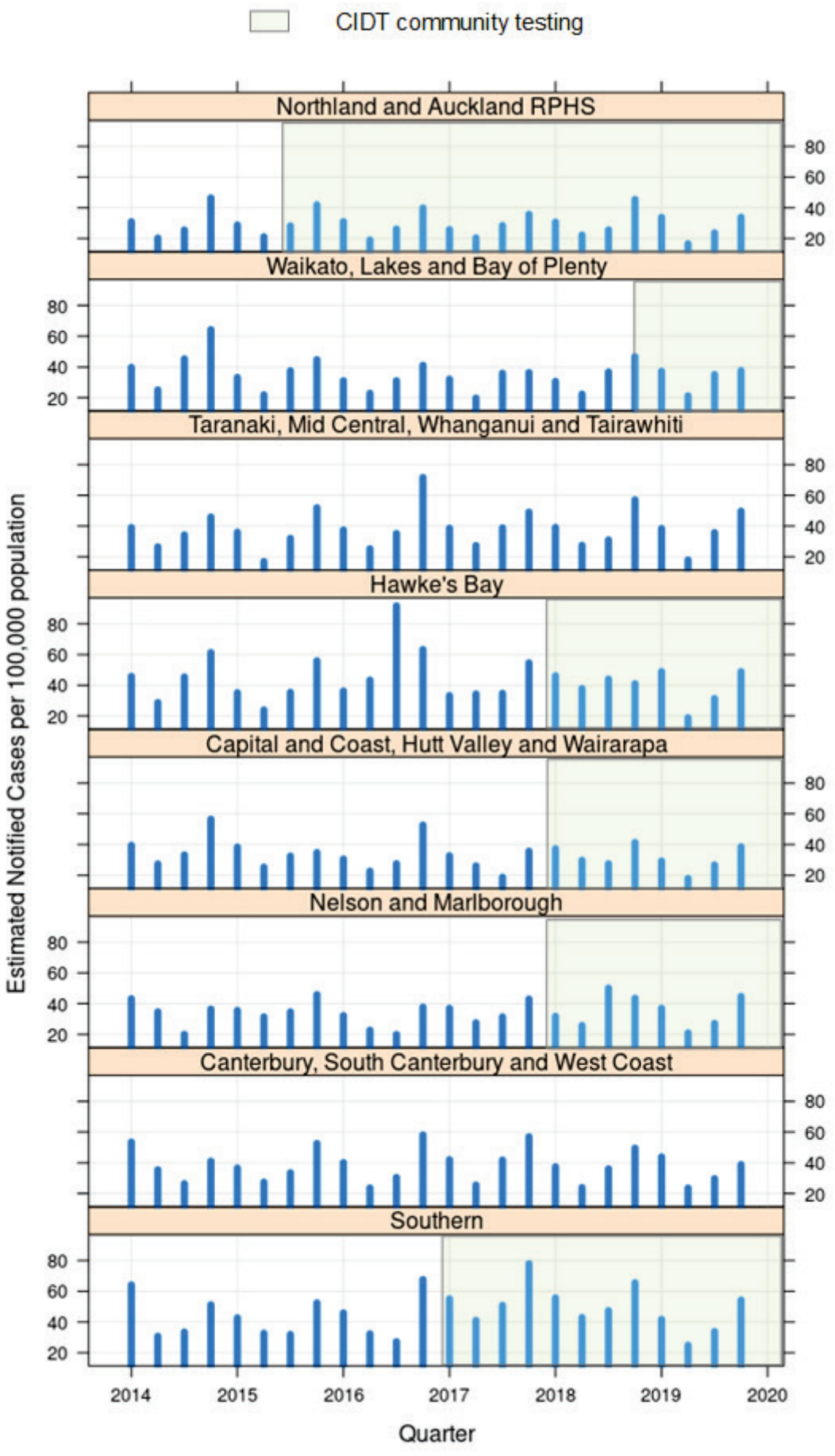


Figure 57. Quarterly rates of salmonellosis notifications by region, 2014 – 2019

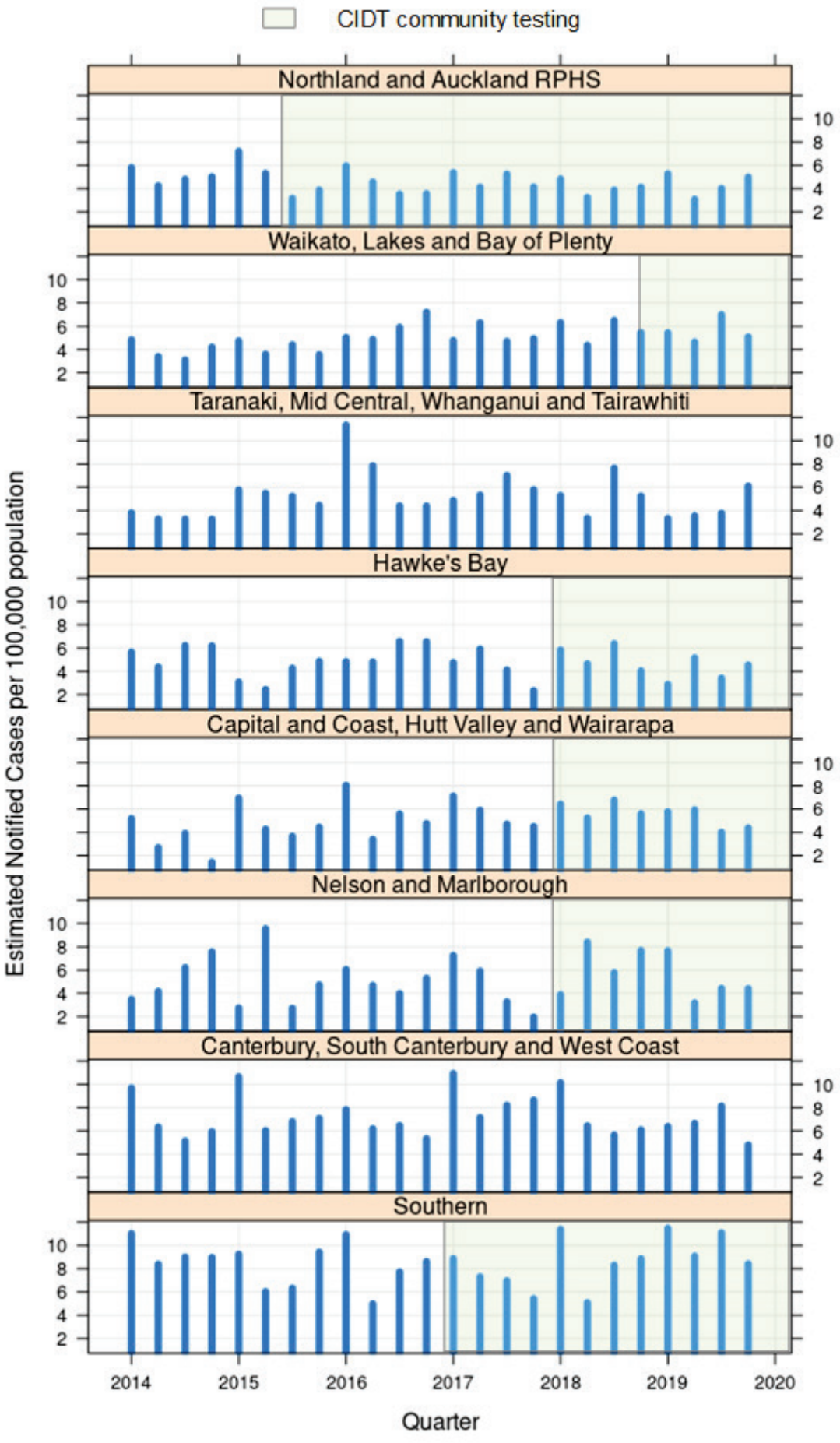


Figure 58. Quarterly rates of shigellosis notifications by region, 2014 – 2019

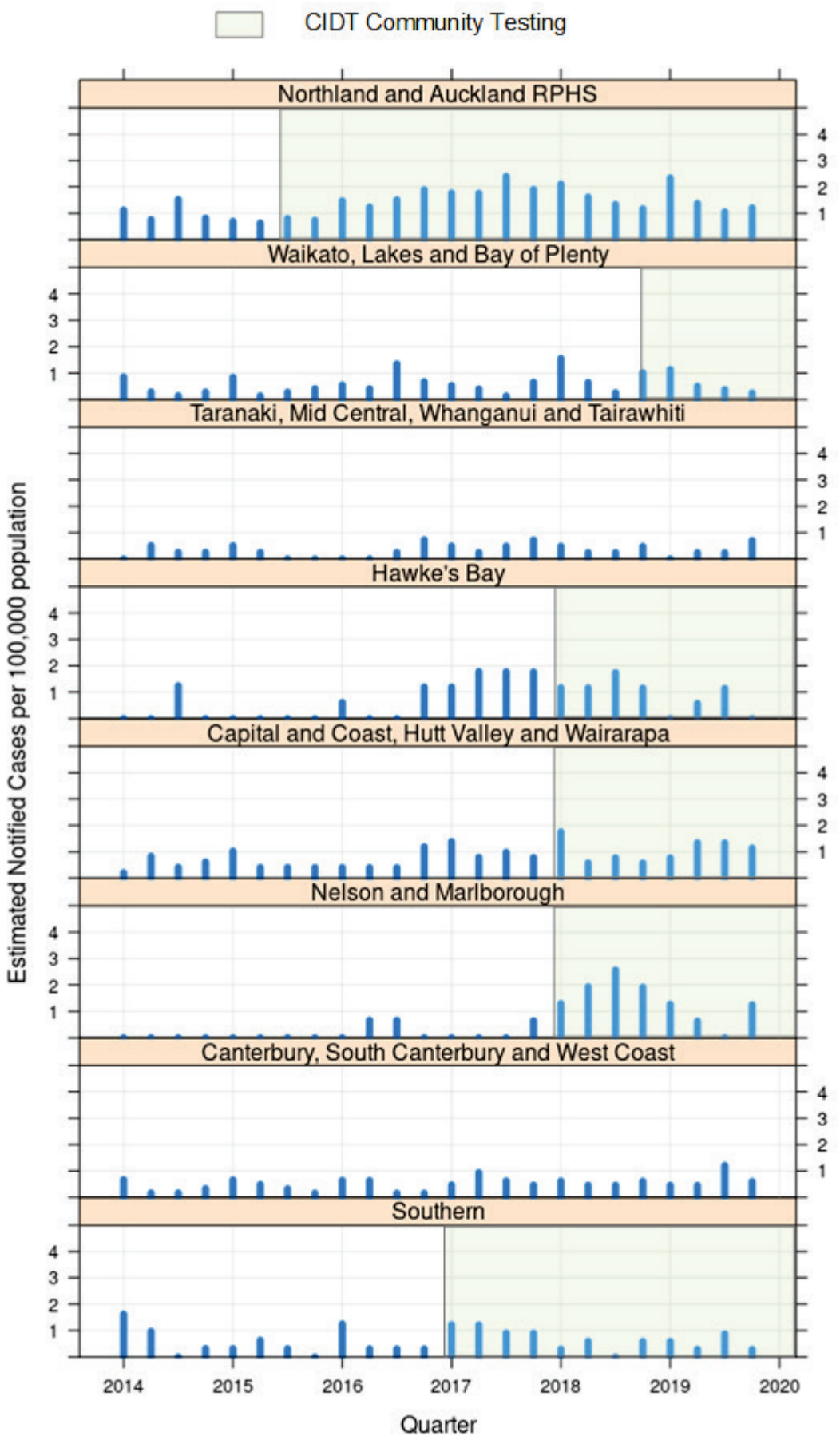


Figure 59. Quarterly rates of yersiniosis notifications by region, 2014 - 2019

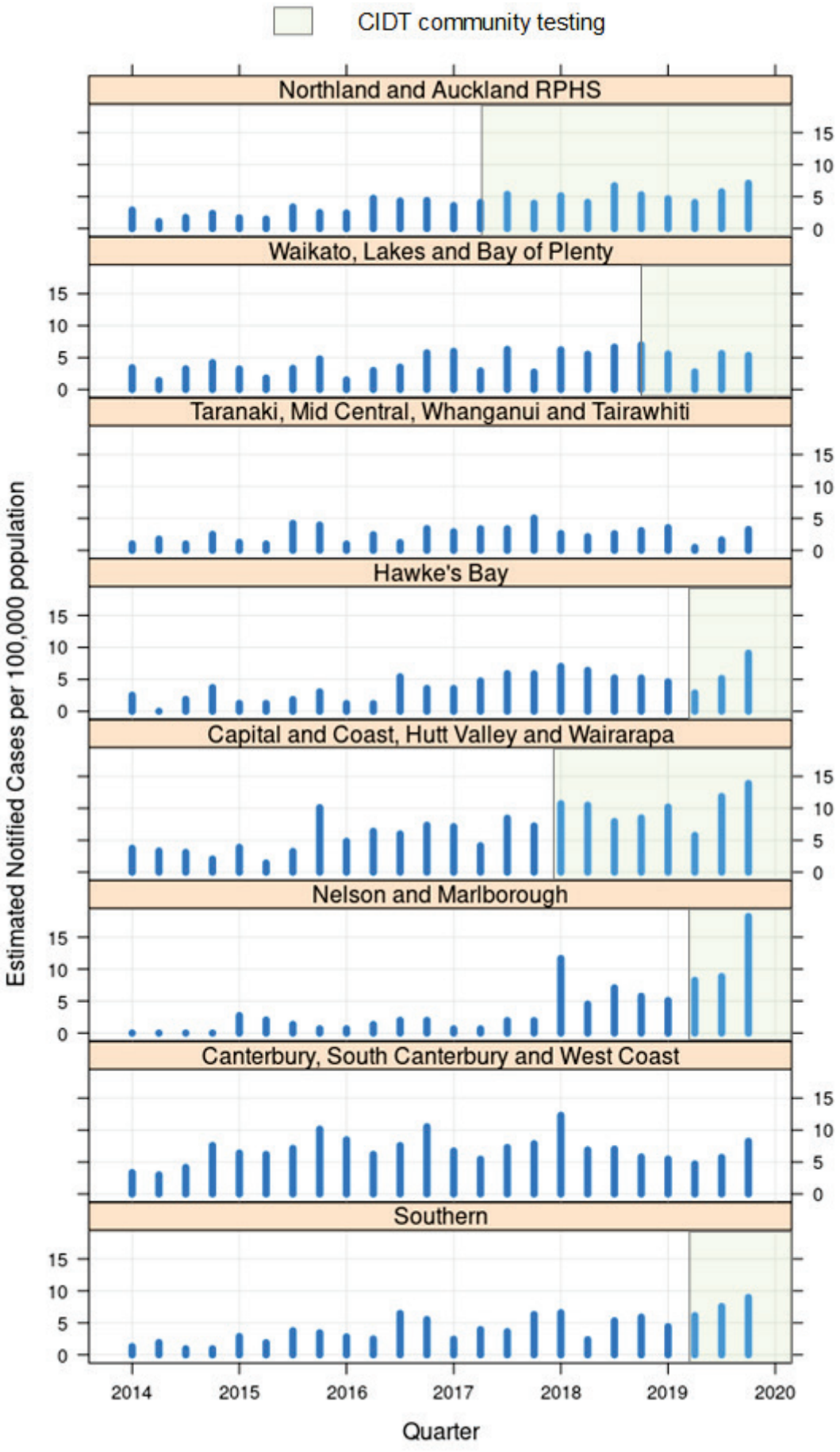
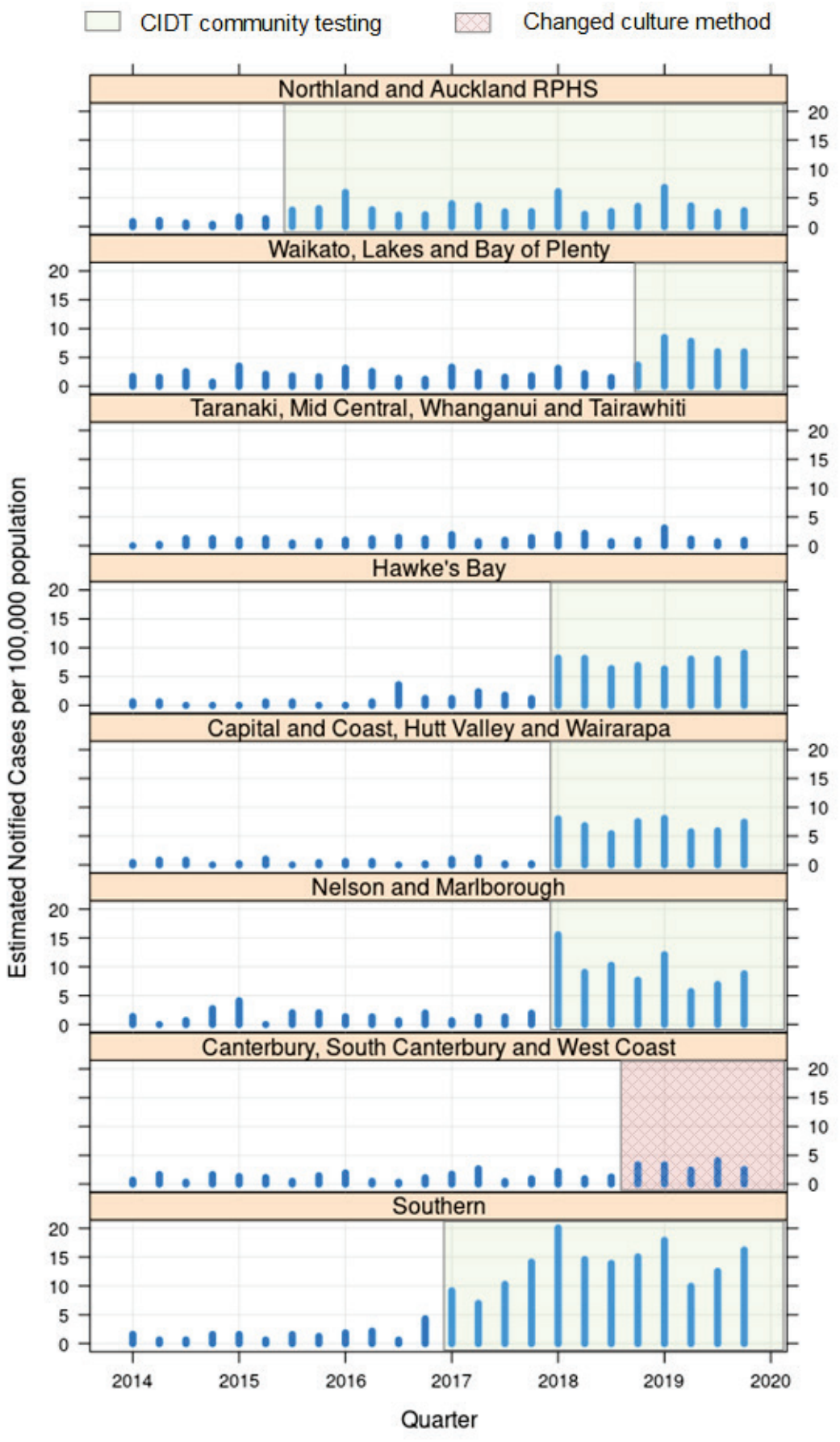


Figure 60. Quarterly rates of STEC infection notifications by region, 2014 – 2019



Note: In July 2018, Canterbury, South Canterbury and West Coast DHBs community testing moved to a different culture testing methodology (Brown hashed box), see page 121 for more information.

Age profile of STEC notified cases

The move to wide-screen PCR-based testing led to more samples being routinely tested for STEC. When culture methods were used, only specimens from patients with certain epidemiological or clinical criteria, e.g., aged less than 5 years, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea were tested for STEC infection.

Table 78 shows how the change in frequency of screening of fecal samples for STEC has changed the age profile of notified cases. The under 5-year olds remain a higher risk age group under the CIDT regime, but the proportion of notified cases in this age group has approximately halved compared to notifications associated with non-CIDT.

Most other age groups have increased as a proportion of total cases following introduction of CIDT compared to non-CIDT. The 70+ age group has the greatest proportional increase.

Table 78. Percentage of cases by age for PCR and non-PCR screened notifications (excluding outbreaks) during 2014 to 2019

Age Group	PCR (N=2346)	Non-PCR (N=1006)
<1	4.4	7.1
1 to 4	14.5	30.3
5 to 9	5.1	7.1
10 to 19	9.1	8.6
20 to 29	11.5	9.5
30 to 39	8.4	5.7
40 to 49	8.1	5.9
50 to 59	10.1	7.7
60 to 69	12.7	8.2
70+	16.0	10.0

APPENDIX C - SUMMARY TABLES

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

Table 79. Number of cases and rate per 100,000 population of selected notifiable diseases in New Zealand, 2019–2020

Disease	2019		2020		Change[b]
	Cases	Rate	Cases	Rate	
Campylobacteriosis	6203	124.6	5289	104.0	🡻
Cryptosporidiosis	1035	20.8	735	14.5	🡻
Gastroenteritis[a]	486	9.8	362	7.1	🡻
Giardiasis	1749	35.1	1141	22.4	🡻
Hepatitis A	58	1.2	22	0.4	🡻
Listeriosis	31	0.6	34	0.7	⇧
Salmonellosis	1188	23.9	708	13.9	🡻
Shigellosis	215	4.3	76	1.5	🡻
STEC infection	1103	22.2	844	16.6	🡻
Yersiniosis	1185	23.8	1261	24.8	⇧

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

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

🡻 = Significant decrease, 🡹 = Significant increase, ⇩ = Not significant decrease, ⇧ = Not significant increase, - = No change

Note: Annual decreases of many enteric diseases may be due to COVID-19 related lockdown periods (page 9). Please refer to individual sections for details.

Table 80. Deaths due to selected notifiable diseases recorded in EpiSurv, 2001–2020

Disease	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Campylobacteriosis	1	1	0	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Gastroenteritis[a]	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	1
Giardiasis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Listeriosis - non-perinatal	1	0	2	3	1	0	2	3	2	3	1	4	2	3	1	0	0	2	0	1
Listeriosis - perinatal	1	2	2	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0	4	0
Salmonellosis	2	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0
Shigellosis	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
STEC infection	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2	0	0
Yersiniosis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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

Note: The numbers in this table are those recorded in EpiSurv where the notifiable disease was the primary cause of death. Information on deaths is most likely to be reported by Public Health Services when it occurs close to the time of notification and investigation

Table 81. Ministry of Health hospitalisations data for selected notifiable diseases, 2018–2020

Disease	ICD 10 Codes	2018		2019		2020	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	630	150	588	123	609	109
Cryptosporidiosis	A07.2	82	53	43	24	49	15
Giardiasis	A07.1	38	26	42	46	39	27
Hepatitis A	B15	47	49	31	44	17	40
Listeriosis	A32	17	24	22	24	19	19
Salmonellosis[a]	A02.0	183	44	206	27	138	27
Shigellosis	A03	37	22	45	21	15	24
STEC infection[b]	A04.3	19	22	28	23	17	22
Yersiniosis	A04.6	85	67	69	70	98	66

[a] *Salmonella* enterocolitis.

[b] Enterohaemorrhagic *Escherichia coli* infection.

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years.

Table 82. Number of cases and rate per 100,000 population of selected notifiable diseases by ethnic group, 2020

Disease	Ethnic group									
	Maori		Pacific peoples		Asian		European or Other[a]		Total[b]	
	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	557	64.6	135	37.9	361	42.0	4201	137.8	5289	104.0
Cryptosporidiosis	91	10.7	16	4.7	28	3.3	593	19.5	735	14.5
Gastroenteritis[c]	53	6.2	10	2.9	31	3.7	263	8.6	362	7.1
Giardiasis	149	17.5	15	4.4	71	8.4	901	29.6	1141	22.4
Hepatitis A	0	-	6	1.7	8	0.9	8	0.3	22	0.4
Listeriosis	1	-	1	-	7	0.8	25	0.8	34	0.7
Salmonellosis	113	13.0	38	11.1	70	8.2	479	15.7	708	13.7
Shigellosis	5	0.6	11	3.2	21	2.5	39	1.3	76	1.5
STEC infection	113	13.3	17	4.8	51	5.9	662	21.7	844	16.6
Yersiniosis	112	13.2	52	14.6	294	34.8	798	26.2	1261	24.8

In the data analyses ethnicity is prioritised in the following order: Maori, Pacific Peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander).

[a] European/Middle Eastern/Latin America/African/Other, European is grouped with MELAA for this year's report due to population estimation availability.

[b] Total includes cases where ethnicity was unknown

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

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

Table 83. Number of cases and rate per 100,000 population of selected notifiable diseases by sex, 2020

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	2980	118.0	2305	90.1	5289	104.0
Cryptosporidiosis	323	12.8	412	16.1	735	14.5
Gastroenteritis[b]	156	6.2	205	8.0	362	7.1
Giardiasis	604	23.9	536	20.9	1141	22.4
Hepatitis A	12	0.5	10	0.4	22	0.4
Listeriosis[c]	17	0.7	17	0.7	34	0.7
Salmonellosis	367	14.5	341	13.3	708	13.9
Shigellosis	45	1.8	31	1.2	76	1.5
STEC infection	419	16.6	425	16.6	844	16.6
Yersiniosis	610	24.2	651	25.4	1261	24.8

[a] Total includes cases where sex was unknown

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

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

Table 84. Number of cases of selected notifiable diseases by age group, 2020

Disease	Age Group										
	0 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total[a]
Campylobacteriosis	672	225	179	285	790	568	526	660	656	722	5289
Cryptosporidiosis	185	71	41	59	153	97	56	32	24	17	735
Gastroenteritis[b]	32	13	8	15	47	53	54	57	35	40	362
Giardiasis	187	71	27	18	140	273	151	105	112	55	1141
Hepatitis A	0	1	1	1	11	3	2	0	1	2	22
Listeriosis[c]	0	0	0	0	3	3	3	5	4	16	34
Salmonellosis	170	47	30	39	75	58	75	95	60	58	708
Shigellosis	14	6	2	2	14	14	8	7	2	7	76
STEC infection	178	53	34	39	89	72	67	85	101	126	844
Yersiniosis	240	43	44	43	154	174	129	140	137	157	1261

[a] Total includes cases where age was unknown

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

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

Table 85. Rate per 100,000 population of selected notifiable diseases by age group, 2020

Disease	Age Group										
	0 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total[b]
Campylobacteriosis	220.1	68.4	53.9	89.7	109.9	80.2	82.1	101.3	122.1	132.8	104.0
Cryptosporidiosis	60.6	21.6	12.3	18.6	21.3	13.7	8.7	4.9	4.5	3.1	14.5
Gastroenteritis[a]	10.5	4.0	2.4	4.7	6.5	7.5	8.4	8.7	6.5	7.4	7.1
Giardiasis	61.2	21.6	8.1	5.7	19.5	38.6	23.6	16.1	20.8	10.1	22.4
Hepatitis A	-	-	-	-	1.5	-	-	-	-	-	0.4
Listeriosis[c]	-	-	-	-	-	-	-	-	-	2.9	0.7
Salmonellosis	55.7	14.3	9.0	12.3	10.4	8.2	11.7	14.6	11.2	10.7	13.9
Shigellosis	4.6	1.8	-	-	1.9	2.0	1.2	1.1	-	1.3	1.5
STEC infection	58.3	16.1	10.2	12.3	12.4	10.2	10.5	13.0	18.8	23.2	16.6
Yersiniosis	78.6	13.1	13.2	13.5	21.4	24.6	20.1	21.5	25.5	28.9	24.8

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

[b] Total includes cases where age was unknown

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

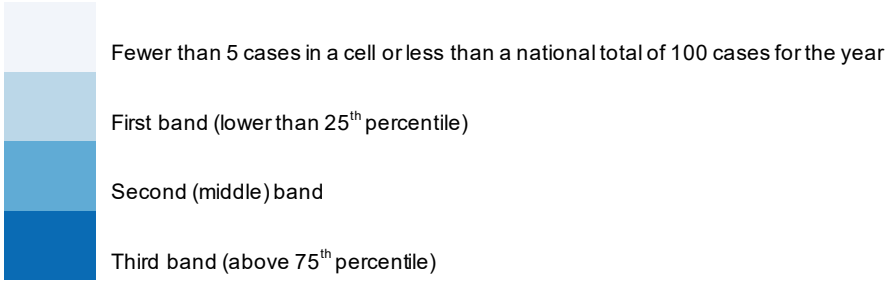


Table 86. Number of cases of selected notifiable diseases by District Health Board, 2020

Disease	District Health Board																			
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawkes Bay	Whanganui	MidCentral	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	207	594	389	420	596	136	262	63	194	232	81	249	116	241	85	174	54	548	129	519	5289
Cryptosporidiosis	24	63	47	66	110	14	31	7	36	23	6	37	17	26	6	16	4	56	30	116	735
Gastroenteritis[a]	14	23	20	16	39	22	64	6	1	2	6	5	31	41	2	8	5	46	2	9	362
Giardiasis	72	96	98	120	153	41	91	27	33	67	8	33	31	44	16	29	7	106	11	58	1141
Hepatitis A	0	4	2	6	1	0	0	0	0	1	0	0	2	2	0	0	0	4	0	0	22
Listeriosis	0	3	5	6	3	0	5	0	0	0	0	1	0	3	1	3	1	1	0	2	34
Salmonellosis	30	76	57	67	82	21	22	8	30	23	9	16	16	23	7	27	2	110	15	67	708
Shigellosis	0	10	14	16	8	0	3	0	2	3	0	1	3	8	0	1	0	2	2	3	76
STEC infection	66	45	46	33	85	24	55	1	46	40	4	5	26	52	20	50	1	82	17	146	844
Yersiniosis	22	152	146	108	109	35	78	7	44	50	8	19	58	118	22	43	3	128	11	100	1261

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

Table 87. Rate per 100,000 population of selected notifiable diseases by District Health Board, 2020

Disease	District Health Board																			
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawkes Bay	Whanganui	MidCentral	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	106.4	92.9	77.0	70.6	136.0	115.8	99.3	124.3	155.6	130.0	118.2	132.9	73.0	74.3	173.8	107.9	166.7	94.0	208.1	148.4	104.10
Cryptosporidiosis	12.3	9.9	9.3	11.1	25.1	11.9	11.7	13.8	28.9	12.9	8.8	19.8	10.7	8.0	12.3	9.9	-	9.6	48.4	33.2	14.5
Gastroenteritis[a]	7.2	3.6	4.0	2.7	8.9	18.7	24.3	11.8	-	-	8.8	2.7	19.5	12.6	-	5.0	15.4	7.9	-	2.6	7.1
Giardiasis	37.0	15.0	19.4	20.2	34.9	34.9	34.5	53.3	26.5	37.5	11.7	17.6	19.5	13.6	32.7	18.0	21.6	18.2	17.7	16.6	22.4
Hepatitis A	-	-	-	1.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.4
Listeriosis	-	-	1.0	1.0	-	-	1.9	-	-	-	-	-	-	-	-	-	-	-	-	-	0.7
Salmonellosis	15.4	11.9	11.3	11.3	18.7	17.9	8.3	15.8	24.1	12.9	13.1	8.5	10.1	7.1	14.3	16.7	-	18.9	24.2	19.2	13.9
Shigellosis	-	1.6	2.8	2.7	1.8	-	-	-	-	-	-	-	-	2.52.5	-	-	-	-	-	-	1.5
STEC infection	33.9	7.0	9.1	5.5	19.4	20.4	20.8	-	36.9	22.4	-	2.7	16.4	16.0	40.9	31.0	-	14.1	27.4	41.8	16.6
Yersiniosis	11.3	23.8	28.9	18.1	24.9	29.8	29.6	13.8	35.3	28.0	11.7	10.1	36.5	36.4	45.0	26.7	-	22.0	17.7	28.6	24.8

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

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

First band (lower than 25th percentile)

Second (middle) band

Third band (above 75th percentile)

Table 88. Number of cases of selected notifiable diseases by year, 1991–2020

Disease	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
Campylobacteriosis	4148	5144	8101	7714	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215	13,836
Cryptosporidiosis[a]	-	-	-	-	-	119	357	866	977	775	1208	975	817	611	888
Gastroenteritis[a b]	-	-	-	-	-	555	316	493	608	730	942	1088	1030	1362	559
Giardiasis[a]	-	-	-	-	-	1235	2127	2183	1792	1688	1604	1547	1570	1514	1231
Hepatitis A	224	288	257	179	338	311	347	144	119	107	61	106	70	49	51
Listeriosis	26	16	11	8	13	10	35	17	19	22	18	19	24	26	20
Salmonellosis	1244	1239	1340	1522	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081	1382
Shigellosis	152	124	128	185	191	167	117	122	147	115	157	112	87	140	183
STEC infection[c]	-	-	3	3	6	7	13	48	64	67	76	73	104	89	92
Yersiniosis[a]	-	-	-	-	-	330	488	546	503	396	429	472	436	407	383

Disease	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Campylobacteriosis	15,873	12,778	6692	7177	7346	6686	7016	6837	6782	6218	7457	6482	6957	6203	5289
Cryptosporidiosis	737	924	765	854	954	610	877	1348	584	696	1062	1192	1613	1035	735
Gastroenteritis[a]	926	617	676	713	502	570	765	558	774	506	513	324	231	486	362
Giardiasis	1214	1402	1660	1639	1985	1934	1714	1729	1709	1510	1616	1648	1585	1749	1141
Hepatitis A	123	42	89	44	46	26	82	91	74	47	35	58	68	58	22
Listeriosis	19	26	27	28	23	26	25	19	25	26	36	21	30	31	34
Salmonellosis	1335	1275	1337	1128	1146	1055	1081	1143	955	1051	1091	1127	1100	1188	708
Shigellosis	102	129	113	119	104	101	131	137	128	111	174	244	217	215	76
STEC infection	87	100	122	143	138	153	147	205	187	330	417	547	925	1103	844
Yersiniosis	453	502	508	430	406	513	514	483	680	634	858	917	1201	1185	1261

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

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

[c] The first case of STEC infection confirmed in New Zealand was reported in October 1993 [36]. Note: cell marked "-" where data are unavailable

Table 89. Rate per 100,000 population of selected notifiable diseases in New Zealand and other selected countries

Disease	Country/Region (year data relate to)						
	New Zealand (2020)	Australia[a] (2020)	USA[b] (2019)	Canada[d] (2018)	UK[e] (2019)	EU Total[e] (2019)	Other high
Campylobacteriosis	104.0	124.6	19.5	27.6	88.1	59.7	215.0 (Czech Republic)[e] 141.1 (Slovakia)[e]
Cryptosporidiosis	14.5	9.6	3.8[c]	3.5	7.7[f]	3.2[f]	12.0 (Ireland)[f] 7.8 (Sweden)[f]
Giardiasis	22.4	NN	6.1[c]	10.5	7.9[f]	5.5[f]	17.6 (Belgium)[f] 12.2 (Estonia)[f]
Hepatitis A	0.4	0.3	3.8[c]	1.0	0.8[f]	2.4[f]	25.0 (Slovakia)[f] 22.7 (Bulgaria)[f]
Listeriosis	0.7	0.2	0.3	0.43	0.23	0.46	1.59 (Estonia)[e] 1.12 (Iceland)[e]
Salmonellosis	13.9	47.5	17.1	19.2	14.6	20.0	122.2 (Czech Republic)[e] 91.6 (Slovakia)[e]
Shigellosis	1.5	6.3	4.8	2.3	3.1[f]	1.7[f]	4.7 (Slovakia)[f] 4.3 (Bulgaria)[f]
STEC infection	16.6	2.3	6.3	2.9	2.4	2.2	16.3 (Ireland)[e] 11.5 (Switzerland)[e]
Yersiniosis	24.8	NN	1.4	NN	0.2[f]	1.7[f]	7.4 (Finland)[f] 6.5 (Lithuania)[f]

NN: Not notifiable

[a] National Notifiable Diseases Surveillance System (NNDSS) http://www9.health.gov.au/cda/source/CDA-index.cfm (data downloaded on 22 April 2021)

[b] FoodNet – Foodborne Diseases Active Surveillance Network http://www.cdc.gov/foodnet/. From 2017, FoodNet incidence rates are made up of a mixture of culture positive and culture-independent diagnostic test positive detections (data downloaded on 22 April 2021)

[c] Centers for Disease Control and Prevention. Summary of notifiable disease https://wwwn.cdc.gov/nndss/infectious-tables.html (CDC data presented here relate to the 2018 year, data downloaded on 22 April 2021)

[d] Canadian Notifiable Disease Surveillance System (CNDSS) http://dsol-smed.phac-aspc.gc.ca/dsol-smed/ndis/index-eng.php (data downloaded on 22 April 2021)

[e] European Food Safety Authority and European Centre for Disease Prevention and Control (ECDC). The European Union One Health 2019 Zoonoses Report https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2021.6406 (data downloaded on 22 April 2021)

[f] European Centre for Disease Prevention and Control (ECDC). Annual epidemiological reports http://ecdc.europa.eu/en/publications/surveillance_reports/annual_epidemiological_report/Pages/epi_index.aspx (ECDC data presented here relate to the 2019 year for yersiniosis, the 2017 year for cryptosporidiosis, giardiasis and shigellosis and the 2016 year for hepatitis A, data downloaded 22 April 2021)

Table 90. Foodborne outbreaks and associated cases by pathogen/condition as reported in EpiSurv, 2020

Pathogen/Condition	Outbreaks (n = 41)		Cases (n = 490)	
	No.	%[d]	No.	%[e]
Norovirus infection [a,b]	9	22.0	160	32.7
Campylobacteriosis [c]	6	14.6	30	6.1
STEC infection [c]	5	12.2	91	18.6
Salmonellosis	2	4.9	12	2.4
Histamine (scombroid) fish poisoning	1	2.4	91	18.6
Staphylococcus aureus intoxication [a]	1	2.4	20	4.1
V. parahaemolyticus infection	1	2.4	16	3.3
Clostridium perfringens intoxication	1	2.4	14	2.9
Astrovirus infection [b]	1	2.4	7	1.7
Ciguatera poisoning	1	2.4	4	0.8
Clostridium botulinum intoxication	1	2.4	4	0.8
Sapovirus infection	1	2.4	3	0.6
Bacillus cereus intoxication	1	2.4	2	0.4
Shigellosis	1	2.4	2	0.4
Yersiniosis	1	2.4	2	0.4
Pathogen not identified[f]	11	26.8	63	12.9

Note: Two agents were reported in three outbreaks (4, 7 and 20 cases), therefore percentage totals add to more than 100%.

[a] For one norovirus outbreak *Staphyloccocus aureus* intoxication was also reported (20 cases).

[b] For a second norovirus outbreak, astrovirus was also detected (7 cases).

[c] For one *Campylobacter* outbreak STEC was implicated as an additional pathogen (4 cases).

[d] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (41). 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

[e] Percentage of cases for each pathogen/condition, calculated using the total number of associated cases (490)

[f] All enteric outbreaks with no pathogen identified in 2020 were recorded as gastroenteritis

Table 91. Foodborne outbreaks and associated cases by exposure setting as reported in EpiSurv 2020

Exposure setting	Outbreaks (n = 41)		Cases (n = 490)	
	No.	%[a]	No.	%[b]
Commerical food operators	**15**	**36.6**	**228**	**46.5**
Restaurant/cafe/bakery	7	17.1	117	23.9
Takeaway	4	9.8	9	1.8
Other food outlet	4	9.8	102	20.8
Fast food restaurant	1	2.4	5	1.0
Institutions	**7**	**17.1**	**91**	**18.6**
Long term care facility	4	9.8	30	6.1
Prison	1	2.4	34	6.9
Hotel/motel	1	2.4	20	4.1
Childcare centre	1	2.4	7	1.4
Other	**21**	**51.2**	**265**	**54.1**
Home	16	39	161	32.9
Community, church, sports gathering	2	4.9	91	18.6
Overseas	2	4.9	5	1.0
Workplace	1	2.4	8	1.6
Unknown	**1**	**2.5**	**3**	**0.6**

Note: Four outbreaks had two exposure settings each (2, 4, 5, and 91 cases).

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (41). 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 (490)

Table 92. Foodborne outbreaks and associated cases by preparation setting as reported in EpiSurv, 2020

Preparation setting	Outbreaks (n = 41)		Cases (n = 490)	
	No.	%[a]	No.	%[b]
Commerical food operators	**21**	**51.2**	**325**	**66.3**
Restaurant/cafe/bakery	10	24.4	124	25.3
Takeaway	6	14.6	21	4.3
Other food outlet	3	7.3	101	20.6
Caterers	1	2.4	77	15.7
Fast food restaurant	1	2.4	2	0.4
Institutions	**7**	**17.1**	**91**	**18.6**
Long Term Care Facility	4	9.8	30	6.1
Prison	1	2.4	34	6.9
Hotel/motel	1	2.4	20	4.1
Childcare Centre	1	2.4	7	1.4
Other	**12**	**31.7**	**68**	**13.9**
Home	9	22	49	10
Community, church, sports gathering	1	2.4	14	2.9
Overseas	3	7.3	9	1.0
Unknown	**2**	**4.9**	**8**	**1.6**

Note: Two outbreaks had two preparation settings each (2 and 4 cases)

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (41). 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 (490)

Table 93. All Non-O157 STEC serotypes identified from human isolates by the Enteric Reference Laboratory, 2016–2020

Serotype	2016	2017	2018	2019	2020
O2:H6	0	0	0	0	1
O3:H21	0	0	0	1	0
O5:H19	0	0	0	0	3
O5:HNT	0	0	0	8	13
O5:HNM	4	1	4	0	0
O6:H10	0	0	0	0	1
O6:H34	0	0	0	1	0
O6:HNM	0	0	1	0	0
O8:H7	0	1	0	0	0
O8:H9	0	0	1	0	1
O8:H16	0	0	0	0	2
O8:H28	0	0	0	0	0
O8:HNM	1	1	1	0	0
O9:H2	0	1	0	0	0
O11:H25	0	0	0	0	1
O15:H2	1	0	1	2	3
O15:H14	0	1	0	0	0
O15:H16	0	0	0	1	0
O15:H21	0	1	0	0	0
O15:H27	0	0	0	1	1
O17:H18	0	0	0	2	1
O18:H7	0	1	0	0	0
O20:HNM	0	1	0	0	0
O22:H16	0	1	0	1	0
O23:H8	0	0	0	1	0
O23:H39	0	1	0	0	0
O25:H4	0	0	0	1	0
O26:H8	0	0	0	1	0
O26:H11	46	44	76	119	121
O26:HNT	0	2	1	7	0
O26:HNM	5	4	1	0	0
O29:H4	0	0	1	0	0
O38:H26	10	7	19	27	33
O38:HNT	0	1	0	2	0
O38:HNM	1	0	0	0	0
O41:H21	0	0	0	2	0
O43:H2	0	0	0	1	0
O45:H2	0	0	1	0	1
O51:H24	0	0	0	1	2
O53:H45	0	0	0	0	1
O55:H12	1	0	0	1	2
O55:HNT	0	0	0	0	0
O60:HNM	0	1	0	0	0
O61:H2	0	0	0	1	0
O63:H6	1	0	0	0	0
O64:H20	3	2	4	7	5
O65:H2	1	0	1	1	0

Serotype	2016	2017	2018	2019	2020
O69:H11	0	0	0	1	0
O71:H2	0	0	0	1	0
O74:H20	0	0	0	1	1
O75:H5	0	0	0	0	1
O75:H7	1	0	0	0	2
O75:H8	0	2	1	1	0
O75:HNT	0	0	1	0	0
O76:H19	2	1	0	1	0
O76:H20	1	0	0	0	0
O76:H21	0	0	1	0	0
O77:HNM	0	0	1	0	0
O78:H4	0	0	0	0	1
O78:HNT	0	1	0	0	0
O80:H2	1	1	0	0	0
O80:HNM	0	0	1	0	0
O81:H6	1	0	0	0	0
O81:H21	0	0	1	0	0
O82:H8	0	0	0	1	0
O83:H27	0	0	0	0	1
O84:H2	0	0	0	4	10
O84:HNM	2	6	2	0	0
O84:HNT	0	0	0	3	0
O85:H49	0	0	0	2	1
O87:H2	0	0	1	0	0
O88:H8	0	0	0	7	7
O88:HNT	0	1	2	2	0
O88:HNM	0	1	2	0	0
O91:H14	0	0	0	12	12
O91:H21	2	0	2	1	1
O91:HNM	2	2	5	0	0
O91:HNT	0	0	1	1	0
O93:H46	0	0	0	0	1
O95:H16	1	0	0	0	0
O96:H5	1	0	0	0	0
O99:H11, H35	0	0	0	1	0
O100:H20	0	0	0	1	0
O101:H2	1	0	0	0	0
O101:H19	0	0	1	0	0
O101:HNM	1	0	0	0	0
O103:H2	2	3	7	11	0
O103:H25	1	1	4	12	1
O103:HNT	0	0	1	1	0
O103:HRough	0	0	1	0	0
O104:H7	1	0	1	1	1
O107:H7	0	1	0	0	0
O108:H9	0	0	0	1	0
O108:H25	0	0	1	0	0

Serotype	2016	2017	2018	2019	2020
O111:H2	0	0	0	0	1
O111:H21	0	0	1	0	0
O111:HNM	1	2	3	0	0
O112:H8	0	0	0	1	0
O112:H9	0	0	0	4	5
O112:H19	0	0	0	1	0
O112:HNM	0	0	2	0	0
O113:H4	1	0	0	1	1
O113:H21	0	2	0	1	1
O114:HNT	0	0	0	1	0
O117:H4	0	0	2	3	1
O117:H7	0	1	2	7	4
O117:HNM	0	0	1	0	0
O118:H2	0	0	0	1	0
O119:H4	0	0	1	0	0
O121:H19	0	0	0	1	0
O123:H2	0	1	0	3	1
O123:H10	0	0	0	2	11
O128:H2	25	7	22	55	79
O128:H8	0	0	0	1	0
O128:H45	0	0	1	0	0
O128:HNM	5	1	6	0	0
O128:HNT	0	1	1	3	0
O130:H11	2	1	1	4	11
O130:H23	0	1	0	0	0
O136:H16	0	0	1	0	0
O136:H20	0	0	0	0	1
O141:H2	0	0	0	1	0
O141:HNT	0	0	0	1	0
O144:H2	0	0	0	1	0
O145:H2	3	0	1	0	0
O145:HNM	0	1	0	0	0
O146:H8	1	0	0	0	0
O146:H11	0	1	0	0	0
O146:H21	4	13	17	15	28
O146:H28	0	0	0	1	4
O146:HNM	0	3	2	0	0
O146:HNT	0	1	0	0	0
O148:H7	0	0	0	1	0
O148:H21	0	1	0	0	0
O149:H2	2	0	2	2	0
O149:H18	0	0	0	0	0
O152:H10	0	0	1	0	0
O152:H38	0	0	1	0	0
O153:H2	2	0	3	10	8
O153:H7	0	0	0	0	1
O153:H21	0	0	0	0	1
O153:HNT	0	2	0	1	0
O156:H19	0	1	0	0	0
O156:H25	0	0	0	2	0

Serotype	2016	2017	2018	2019	2020
O158:HNM	0	0	1	0	0
O159:HNT	0	0	0	1	0
O162:H7	1	0	0	0	0
O162:H10	0	0	1	0	0
O163:H19	0	0	1	7	1
O165:H7	0	0	0	0	2
O165:H25	0	0	0	0	1
O165:HNM	0	3	0	0	0
O165:HNT	0	0	0	2	0
O166:H15	0	0	0	1	0
O171:H2	0	0	1	1	1
O172:H25	0	0	0	0	1
O172:HNM	1	0	0	0	0
O174:H8	0	1	4	10	10
O174:H21	0	0	1	5	7
O174:HNM	1	0	3	0	0
O174:HNT	0	0	2	1	0
O176:H4	0	0	0	12	16
O176:HNM	2	4	9	0	0
O176:HNT	0	0	0	4	0
O176:HRough	0	1	0	0	0
O177:H2	0	0	0	0	1
O177:H25	0	0	0	2	3
O177:HNM	0	1	1	0	0
O177:HNT	0	0	0	1	0
O178:H7	1	0	1	0	0
O179:H8	0	2	0	0	0
O179:H26	0	0	0	1	0
O181:H16	0	0	1	1	0
O182:H25	0	0	0	3	7
O182:HNM	1	2	2	0	0
O183:H18	3	0	0	3	1
O183:HNM	1	0	0	0	0
O186:H10	0	2	0	2	0
O186:HNM	0	4	0	0	0
O186:HNT	0	0	0	4	0
O187:H7	0	0	1	0	0
O188:H7	0	0	1	0	0
O188:H14	0	0	5	0	0
ONT:H1	0	0	0	1	0
ONT:H2	3	22	17	11	0
ORough:H2	6	4	7	0	0
O123/O186:H2	0	0	2	0	0
ONT:H4	0	0	2	0	0
ORough:H5	0	0	1	0	0
ONT:H5	1	0	0	0	0
ONT:H6	0	0	0	1	0
ONT:H7	3	7	6	6	0
ORough:H7	1	0	0	0	0

Serotype	2016	2017	2018	2019	2020
ONT:H8	0	1	2	4	0
ONT:H9	0	1	2	1	0
ONT:H10	1	0	1	2	0
O123/O186:H10	0	0	2	0	0
ORough:H10	0	0	1	0	0
Onovel32:H10	0	0	0	1	0
ONT:H11	0	1	2	0	0
ONT:H12	0	0	1	0	0
ONT:H13	1	0	0	0	0
ONT:H14	1	2	1	1	0
Onovel21:H14	0	0	0	2	0
ONT:H15	0	0	1	0	0
Onovel1:H16	0	0	0	0	1
ONovel27:H16	0	0	0	0	1
ORough:H16	0	0	0	0	0
ONT:H18	0	0	0	2	0
ONT:H19	0	2	1	1	0
ORough:H19	0	0	2	0	0
ONT:H20	0	0	2	0	0
ONT:H21	1	4	4	5	0
ORough:H21	1	0	1	0	0
Onovel5:H21	0	0	0	0	1
Onovel27:H21	0	0	0	1	0
O153/O178:H23	0	0	0	0	1
ONT:H25	0	0	0	4	1
ORough:H25	0	1	0	0	0
ONT:H26	0	4	0	0	0
ORough:H26	0	0	1	0	0
ONT:H27	0	1	1	0	0
ONT:H28	1	0	0	0	0
ONT:H30	0	0	1	0	0
ONT:H31	0	1	1	0	0
O17/O106:H45	0	0	0	0	1
ORough:H45	0	0	1	0	0
ONT:H45	0	1	0	0	0
ONT:H49	0	0	0	1	0
O123/O186:HNM	0	0	13	0	0

NM: Non-Motile. NT: Non-typable

Note: This tables gives the frequency of types from all human isolates typed by the Enteric Reference Laboratory in a calendar year. These frequencies may be different to the frequency of types only associated with notified cases, which are reported in the calendar year of their report date (Table 65).

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