Science for Communities

ANNUAL SUMMARY OF OUTBREAKS IN NEW ZEALAND 2017

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ABBREVIATIONS

Abbreviation	Description
DHB	District health board
ESR	Institute of Environmental Science and Research Ltd.
FBVE	Foodborne Viruses in Europe
NRL	Norovirus Reference Laboratory
PHU	Public Health Unit
RSV	Respiratory syncytial virus
STEC	Shiga toxin-producing *Escherichia coli*

SUMMARY

This report summarises data on outbreaks that were reported to the Institute of Environmental Science and Research Limited (ESR) during 2017.

Key findings were:

Outbreaks and associated case rates increased slightly in 2017

There was a non-significant increase in reported outbreaks (▲5.3%, 644 outbreaks) and cases associated with outbreaks (▲8.6%, 11,963 cases) compared with 2016 (610 outbreaks involving 11,012 cases). A total of 195 (3.2%) outbreak-associated cases were hospitalised (194 in 2016, 2.6%) and 21 cases died (10 cases in 2016).

The number of outbreaks per 100,000 population increased to 13.4 outbreaks per 100,000 population from 13.0 in 2016 and 12.2 in 2015, but was the third lowest rate reported since 2008 (10.5 outbreaks). Hawke's Bay, Otago and Wellington reported the highest outbreak rate per 100,000 population (23.7, 22.8 and 22.6 respectively), almost twice the national rate.

The national rate of outbreak-associated cases was higher in 2017 (249.6 per 100,000 population) than in 2016 (234.6) and 2015 (185.3) but remained lower than the rate reported in 2009 (250.4) and 2014 (328.7).

Enteric agents most common cause of outbreaks

As in previous years, enteric agents were implicated as the cause in the vast majority (88.0%) of outbreaks, with the most common causes reported as norovirus (40.5%), *Cryptosporidium* (4.2%) and *Giardia* (3.7%). Over half of the cases associated with all outbreaks in 2017 were caused by norovirus (54.5%).

The most commonly reported non-enteric agents were influenza and influenza-like illness which accounted for 5.3% of outbreaks, 6.4% of associated cases and 10 deaths, followed by *Bordetella pertussis* which accounted for 3.1% of outbreaks.

The non-enteric agent associated with the highest proportion of outbreak-associated cases in 2017 was mumps (9.9%, 1190/11,963).

Hospitalisations and deaths

In 2017, there were 69 outbreaks where cases were hospitalised. A total of 195 hospitalisations were reported among the 1100 associated cases. The largest number of hospitalisations was due to norovirus (91 hospitalisations, 17.0% of cases). The pathogens or conditions with the highest proportion of hospitalised cases were neurotoxin (100.0%, 3/3 cases) and typhoid fever (76.9%, 20/26 cases), followed by paratyphoid fever (72.7%, 8/11 cases).

Twenty-one deaths were associated with 10 different outbreaks in 2017. The deaths were associated with norovirus (10), influenza A (8), influenza-like illness (2) and typhoid fever (1). A pathogen was not identified in two deaths where an influenza-like illness was reported.

Long-term care facilities the most common outbreak setting

Long-term care facilities (42.8%), childcare centres (18.3%) and private homes (11.3%) continued to be the most common settings for outbreaks. The highest numbers of cases associated with outbreaks were reported from long-term care facilities (49.2%), childcare centres (16.2%) and workplaces (10.2%).

Person-to-person the most common mode of transmission

In 2017, 85.2% of outbreaks recorded person-to-person as a mode of transmission, the majority of these as the primary mode, followed by foodborne (9.5%) and environmental (9.2%) transmission. Multiple modes of transmission were implicated in 12.1% of outbreaks.

Norovirus, campylobacter and salmonella the most implicated pathogens in foodborne outbreaks

Norovirus (27.9%), *Campylobacter* and *Salmonella* (6.6% each) were the pathogens most commonly associated with foodborne outbreaks in 2017. Since 2008, norovirus has been the most implicated pathogen in foodborne outbreaks.

Trends remain the same as previous years

The 2017 outbreaks showed continuing trends:

1. an increase in outbreaks in institutional settings and decrease in outbreaks linked to commercial food operators

More than three-quarters of reported outbreaks (75.6%) in 2017 were in institutions, a further increase from previous years. Since 2007, institutional outbreaks have accounted for around half of the outbreaks reported each year. Prior to 2007, commercial food operators and private homes were the most commonly reported settings

The proportion of outbreaks set in childcare centres and schools increased in 2017 compared with 2008–2017.

2. an increase in outbreaks associated with person-to-person transmission.

Over the 2008–2017 period an increase in outbreaks involving person-to-person transmission has been reported. This increase could be partly explained by:

- increasing numbers of people living in long-term care facilities due to the ageing population, and increasing numbers of children attending early childhood education facilities due to the funded 20 hours of early childcare introduced in 2007; and
- the introduction of national guidelines for the management of norovirus outbreaks in hospitals and elderly care institutions [1] in early 2009, which may have led to increased reporting of outbreaks.

Foodborne transmission was the most commonly reported mode of transmission prior to 2007.

INTRODUCTION

This report summarises data on outbreaks that were reported to the Institute of Environmental Science and Research Limited (ESR) during 2017.

Outbreak surveillance in New Zealand has been conducted by ESR on behalf of the Ministry of Health since 1996. The outbreak surveillance system collects data on disease outbreaks reported by public health units (PHUs). Since 1997, the outbreak surveillance system has been incorporated as a module within EpiSurv, the national notifiable disease database.

Investigating outbreaks provides information to [2]:

- halt an outbreak and prevent further illness;
- prevent further outbreaks from the immediate source;
- prevent further outbreaks from other similar sources;
- address public concerns;
- involve the public in disease control;
- reduce direct and indirect costs;
- identify new mechanisms of transmission of known illnesses;
- identify new or emerging disease agents;
- satisfy legal and international obligations;
- improve investigation methods; and
- improve public health training.

METHODS

OUTBREAK DEFINITION

The Guidelines for the Investigation and Control of Disease Outbreaks [2] state that the following types of outbreaks should be reported:

- two or more cases linked to a common source, in particular where the common source is exposure at a common event, food or water dispersed in the community, an environmental source, or a source in an institutional setting;
- a community-wide or person-to-person outbreak (except when the source has become well-established as a national epidemic and reporting it as a discrete event no longer serves a useful purpose);
- any other situation where outbreak investigation or control measures are being used or considered. This situation would include a single detected case of an illness that is exotic to New Zealand or has been eradicated (eg, a locally acquired case of dengue fever, poliomyelitis).

Outbreak reporting is encouraged for:

- a secondary case in an institution;
- household outbreaks—if there is a reasonable possibility that the outbreak resulted from a common source exposure for that household group.

Outbreak reporting is not usually required for:

- most secondary cases— with a few exceptions to this (eg measles, pertussis), and where person-to-person spread of a foodborne illness originating from a common source has occurred; Secondary cases should be identified on the outbreak report form.
- single cases where a specific contaminated source is identified.

DATA SOURCES

Outbreaks are reported to, or identified by, local PHUs. Each PHU records data on outbreaks on a standardised outbreak report form within EpiSurv. PHUs are encouraged to enter data initially as an interim report that can be finalised when further data becomes available. Data is collated and analysed by ESR on behalf of the Ministry of Health. National data is supplemented by data from ESR's Enteric Reference Laboratory, and Virology and Public Health Laboratories. If an outbreak is first identified by these laboratories, the appropriate PHU is asked to complete an outbreak report form.

The outbreak report form has the following sections:

- reporting authority (outbreak report date and interim or final report);
- condition and implicated pathogen, toxin or chemical (name of implicated agent and case definitions);
- outbreak demographics (number of cases, outbreak dates, age/sex of cases, incubation period and duration of illness);

- circumstances of exposure/transmission (means of outbreak recognition, setting, geographic location, mode of transmission and vehicle/source evidence);
- factors contributing to the outbreak (specific factors relating to foodborne, waterborne, person-to-person contact and environmental outbreaks);
- management of the outbreak (control measures undertaken).

The terms used in the outbreak report form are defined in a glossary at the end of this report. The form can be found at: https://surv.esr.cri.nz/episurv/CaseReportForms/Outbreak-Oct2010.pdf and in the appendix of this report.

NOROVIRUS OUTBREAKS

Norovirus genotyping is carried out in the Norovirus Reference Laboratory (NRL) at ESR. Phylogenetic analysis is used for genotyping. The Norovirus Automated Genotyping Tool is used to identify the norovirus genotype using sequences from the GenBank database and the Foodborne viruses in Europe network [3].

The number of outbreaks reported to the NRL differs from the number recorded in EpiSurv (and therefore reported elsewhere in this report), because 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.

DATA ANALYSIS

This report contains an analysis of outbreak data reported between 1 January and 31 December 2017, and recorded on the EpiSurv database as at 16 April 2018. Any amendments made to outbreak data after 16 April 2018 are not reflected in this report. Outbreaks reported at the end of the period may not have been finalised by the cut-off date. This means that the number of cases reported here may differ from that reported in the Notifiable Diseases in New Zealand Annual Report 2017 [4].

Rates were calculated using national and PHU population figures based on Statistics New Zealand mid-year population estimates for 2017. Tests for statistical significance were calculated using the two-tailed test for difference in proportions (Fisher's exact).

DATA LIMITATIONS

The data is restricted to outbreaks recorded in EpiSurv. Outbreaks are more likely to be reported if they involve unusual pathogens, notifiable diseases, a large number of cases or a well-defined setting. The differing availability of resources among PHUs may also impact on outbreak investigation and reporting at a regional level. The source of many reported outbreaks remains in the suspected category, as no confirmatory evidence has been found. For these reasons, caution is advised when interpreting the information contained in this report.

This report does not include details about outbreaks of lead absorption (2 outbreaks) reported into EpiSurv in 2017. Responsibility for the collection and reporting of lead absorption, chemical poisoning from the environment and hazardous substance notifications transferred from ESR to the Centre for Public Health Research, Massey University, in January 2013.

RESULTS

CHARACTERISTICS OF OUTBREAKS

There were 644 reported outbreaks (13.4 outbreaks per 100,000 population) in 2017, an increase from the 610 (13.0 outbreaks per 100,000 population) reported in 2016. All but two of the outbreaks were recorded as final reports. A total of 11,963 cases were associated with outbreaks; 36.6% (4377/11,963) of the cases were either clinically or laboratory confirmed and 63.4% (7586/11,963) were probable cases. In 2017, the national rate was 249.6 outbreak-associated cases per 100,000 population, higher than the rate in 2016 (235.1 cases per 100,000 population).

DISTRIBUTION OF OUTBREAKS BY PUBLIC HEALTH UNIT

In 2017, Auckland PHU had the highest proportion of outbreaks (22.7%, 146/644) and cases (22.8%, 2727/11,963) reported followed by Wellington PHU (18.0%, 116/644 and 18.6%, 2230/11,963 respectively) (Table 1). Hawke's Bay PHU reported the highest outbreak rate (23.7 per 100,000 population) and Whanganui reported the highest outbreak-associated case rate (535.4 per 100,000 population) (Table 1, Figure 1).

Table 1. Number and rate of outbreaks and associated cases by PHU Office, 2017

PHU Office	Outbreaks			Cases		
	Total	% of outbreaks (n=644)	Outbreak rate[1]	Total	% of cases (n=11,963)	Case rate[1]
Northland	17	2.6	9.7	391	3.3	223.1
Auckland[2]	146	22.7	8.7	2727	22.8	162.8
Waikato	50	7.8	12.2	1026	8.6	250.6
Bay of Plenty	26	4.0	11.2	308	2.6	133.0
Rotorua	18	2.8	16.4	203	1.7	185.0
Taranaki	17	2.6	14.4	220	1.8	186.3
Hawke's Bay	39	6.1	23.7	833	7.0	506.2
Gisborne	6	0.9	12.4	144	1.2	296.9
Whanganui	8	1.2	12.8	335	2.8	535.4
Manawatu	31	4.8	18.5	677	5.7	403.1
Wellington[3]	116	18.0	22.6	2230	18.6	433.9
Nelson Marlborough[4]	26	4.0	17.4	390	3.3	261.7
West Coast	6	0.9	18.5	81	0.7	250.2
Canterbury	73	11.3	14.1	1341	11.2	259.9
South Canterbury	2	0.3	2.1	36	0.3	38.4
Otago	43	6.7	22.8	796	6.7	421.9
Southland	20	3.1	14.8	225	1.9	166.0
Total	**644**	**100**	**13.4**	**11963**	**100**	**249.6**

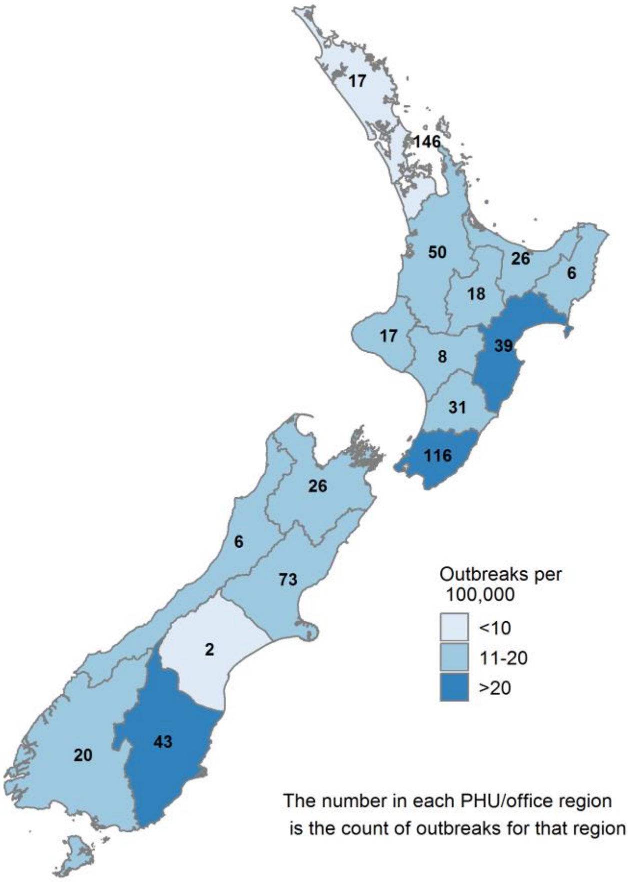
[1] Crude rate of outbreaks per 100,000 population is calculated using Statistics New Zealand population estimates for 2017.

[2] Auckland PHU covers the Tāmaki Makaurau-Auckland health district.

[3] Includes Wellington, Hutt and Wairarapa health districts.

[4] Includes both Nelson and Blenheim offices.

Figure 1. Number and rate of outbreaks per 100,000 population by PHU, 2017



MULTI-REGIONAL GASTROINTESTINAL OUTBREAKS AND OTHER OUTBREAKS OF NATIONAL SIGNIFICANCE

Monitoring of gastrointestinal outbreaks is undertaken at a national and local level. Where a multi-regional outbreak is suspected, ESR conducts epidemiological and microbiological investigations in conjunction with affected PHUs. The Ministry of Health is also involved in the investigation and response and, if the outbreak is likely to be foodborne, the Ministry for Primary Industries is also involved.

In 2017, there were no multi-regional gastrointestinal outbreaks investigated at the national level. However, a national outbreak of pertussis began in October 2017 and an outbreak of mumps involving multiple DHBs which began in September 2016 continued throughout 2017.

CAUSAL AGENTS

A causal agent or condition* was identified in 70.3% (453/644) of outbreaks, involving 79.6% (9525/11,963) of all outbreak-associated cases. In 16 of these outbreaks, two or more causal agents were identified. No specific pathogen or condition was identified in the remaining 191 outbreaks, all of which were recorded as gastroenteritis.

As with previous years, enteric agents were implicated in the majority of outbreaks (88.0%, 567/644) and accounted for the majority of associated cases (82.1%, 9816/11,963) (Table 2). Norovirus (40.5%, 261/644) was the most common causal agent implicated in outbreaks in 2017. Norovirus outbreaks also had the highest proportion of associated cases (54.5%, 6517/11,963). For the enteric pathogens with more than one outbreak-associated, rotavirus had the highest median number of cases associated with each outbreak (20.5 cases).

Non-enteric agents accounted for 12.0% (77/644) of outbreaks and 17.9% (2147/11,963) of the outbreak-associated cases in 2017 (Table 2). The most frequently reported non-enteric pathogens and conditions were influenza and influenza-like-illness (5.3% of outbreaks, 34/644) followed by *Bordetella pertussis* (3.1% of outbreaks, 20/644). Outbreaks due to influenza and influenza-like illnesses also had the highest median number of cases associated with an outbreak (20 cases). Outbreaks due to the mumps virus had the highest proportion of associated cases (9.9%, 1190/11,963).

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* Includes outbreaks of acute respiratory infection and influenza-like-illness where no specific pathogens were identified.

Table 2. Outbreaks and associated cases by pathogen, 2017

Pathogen or condition	Outbreaks[1]			Cases[1]	
	Total	% of outbreaks (n=644)	Median cases per outbreak	Total	% of cases (n=11,963)
Enteric	**567**	**88.0**	**12**	**9,816**	**82.1**
Norovirus	261	40.5	20	6517	54.5
Cryptosporidium spp.	27	4.2	4	184	1.5
Giardia spp.	24	3.7	3.5	170	1.4
Sapovirus	15	2.3	11	233	1.9
Salmonella spp.[2]	13	2.0	2	40	0.3
STEC infection[3]	11	1.7	3	197	1.6
Shigella spp.	8	1.2	4	32	0.3
Campylobacter spp.	7	1.1	5	31	0.3
Hepatitis A	5	0.8	3	20	0.2
Rotavirus	4	0.6	20.5	96	0.8
Adenovirus	2	0.3	27	54	0.5
Ciguatera fish poisoning	2	0.3	15.5	31	0.3
Histamine (scombroid) fish poisoning	2	0.3	3.5	7	0.1
Paratyphoid fever	2	0.3	7	14	0.1
Staphylococcus aureus	2	0.3	6	12	0.1
Typhoid fever	2	0.3	13	26	0.2
Astrovirus	1	0.2	7	7	0.1
Clostridium difficile	1	0.2	13	13	0.1
Neurotoxin	1	0.2	3	3	0.0
Vibrio fluvialis	1	0.2	27	27	0.2
Yersinia spp.	1	0.2	5	5	0.0
Pathogen not identified[4]	191	29.7	10	2438	20.4
Non-enteric	**77**	**12.0**	**9**	**2147**	**17.9**
Influenza and influenza-like illness[5]	34	5.3	20	765	6.4
Bordetella pertussis	20	3.1	5	160	1.3
Mumps virus	14	2.2	5	1190	9.9
Mycobacterium tuberculosis	3	0.5	2	10	0.1
Measles virus	3	0.5	2	11	0.1
Invasive pneumococcal disease	1	0.2	5	5	0.0
Varicella zoster virus	1	0.2	3	3	0.0
Leptospira spp.	1	0.2	3	3	0.0

[1] More than one agent was reported in 16 outbreaks, therefore the numbers don't add up to the group totals.

[2] Includes non-typhoidal *Salmonella* species only. Outbreaks of *S*. Typhi and *S*. Paratyphi are reported separately.

[3] One outbreak involving 157 cases originally reported as STEC infection was later determined to be caused by an atypical enteropathogenic *E. coli* (EPEC).

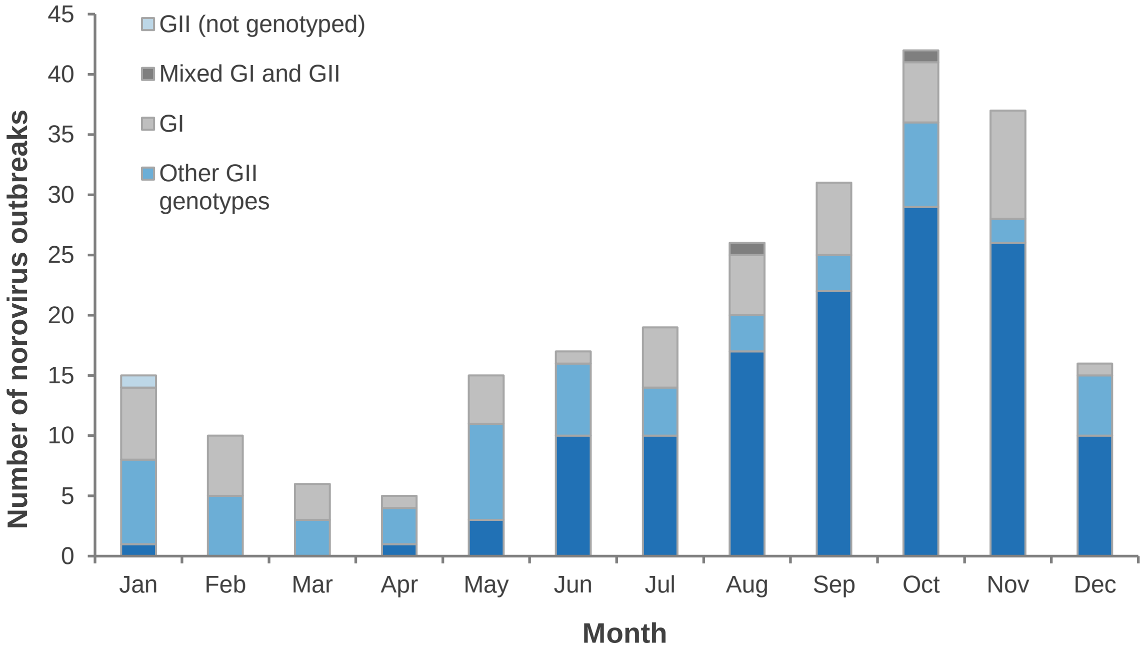
[4] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

[5] Includes outbreaks of influenza A (16 outbreaks with 383 cases), influenza B (6 outbreaks, 67 cases), influenza-like illness (6 outbreaks, 163 cases), acute respiratory infection (4 outbreaks, 98 cases), influenza not otherwise specified (1 outbreak, 24 cases), influenza A and RSV (1 outbreak, 30 cases).

NOROVIRUS OUTBREAKS – GENOTYPES AND OUTBREAK SETTING

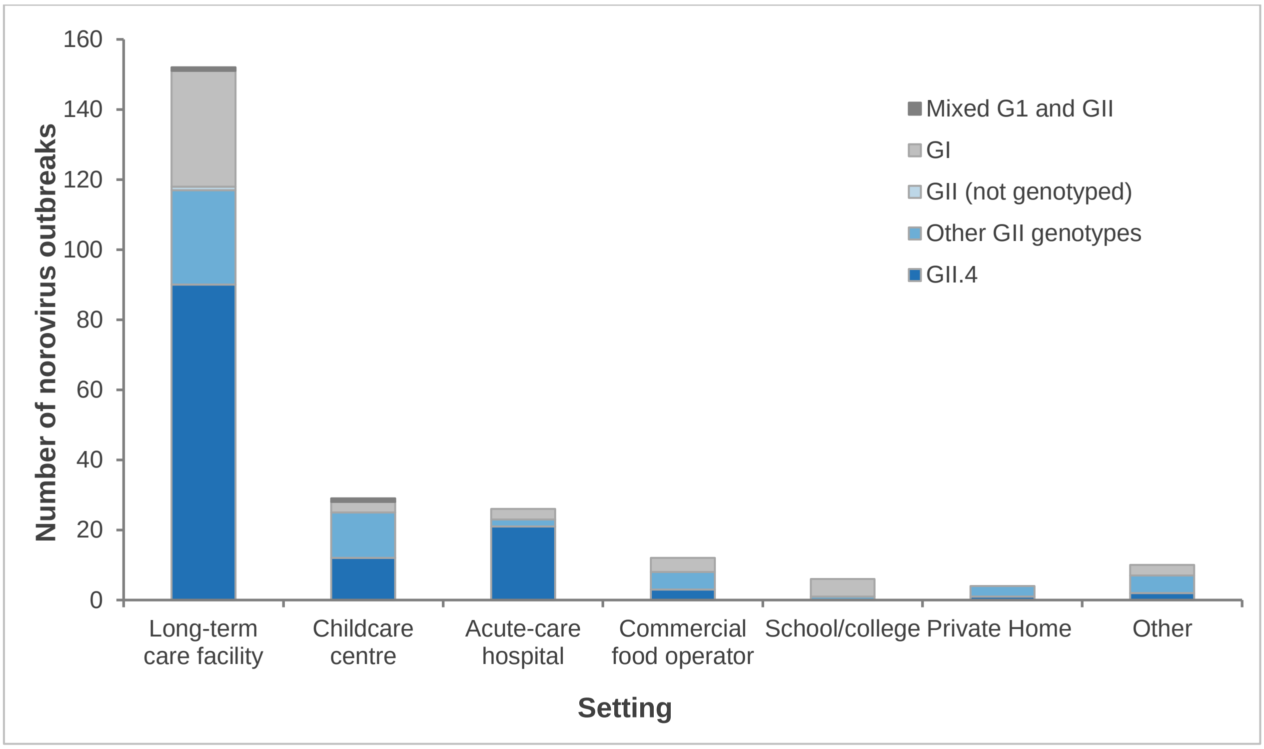
In 2017, there were 239 norovirus outbreaks confirmed by the NRL. This is an increase from 2015 and 2016 (184 and 188 outbreaks respectively). The highest number of outbreaks occurred in October (42 outbreaks) and the lowest numbers occurred in March and April (6 and 5 outbreaks respectively) (Figure 2).

Figure 2. NRL-confirmed norovirus outbreaks by month and genotype, 2017



The majority (63.6%, 152/239) of norovirus outbreaks confirmed by the NRL occurred in long-term care facilities. Outbreaks were also associated with childcare centres (12.1%, 29/239), acute-care hospitals (10.9%, 26/239), commercial food operators (5.0%, 12/239), schools (2.5%, 6/239) and private homes (1.7%, 4/239). Other settings were reported in 10 outbreaks (Figure 3).

Figure 3. NRL-confirmed norovirus outbreaks by setting and genotype, 2017



Norovirus genogroup II (GII) was identified in 77.8% (186/239) of outbreaks, and norovirus genogroup I (GI) was identified in 21.3% (51/239) of outbreaks. Both GI and GII were identified in 0.8% (2/239) of outbreaks.

The norovirus genotype was determined for 99.6% (238/239) of NRL-confirmed outbreaks. One norovirus GII was unable to be genotyped. GII.4 was the most common genotype identified and was associated with 55.0% (131/238) of genotyped outbreaks (including two mixed GI and GII outbreaks). In 2017, three GII.4 variants were identified. The variant in one GII.4 outbreak was not determined. The most common GII.4 variant identified was GII.P16/GII.4 (103 outbreaks). This was an increase from 2016 when 19 GII.P16/GII.4 outbreaks associated were identified. The other GII.4 variants identified were New Orleans_2009/Sydney 2012 (14 outbreaks) and the Sydney 2012 variant (13 outbreaks). In total, seven GI genotypes and ten GII genotypes (as defined by typing of the viral capsid) were identified. The second most common genotype identified in 2017 was GI.3 (12.2%, 29/238), followed by GII.P16/GII.2 (7.6%, 18/238), GI.6 (6.3%, 15/238) and GII.6 (5.9%, 14/238). Less commonly identified genotypes included GII.P17/GII.17 (2.1%, 5/238), GII.P7/GII.14 (1.7%, 4/238) and GII.P16/GII.13 (1.3%, 3/238).

Each norovirus outbreak setting was associated with a variety of norovirus genotypes (Figure 3). However, the majority of norovirus outbreaks in acute-care hospitals and long-term care facilities were due to GII.4 (80.8%, 21/26 and 60.3%, 91/151 respectively), compared with a lower proportion (31.1%, 19/61) for other settings.

HOSPITALISATIONS AND DEATHS

Hospitalisation information was recorded for 58.4% (376/644) of outbreaks involving 51.5% (6164/11,963) of associated cases. Of these outbreak-associated cases, 3.2% (195/6164) were hospitalised (Table 3). A higher percentage of cases associated with enteric outbreaks were hospitalised (19.7%, 160/811 cases) compared with non-enteric outbreaks (12.1%, 35/289 cases). The enteric pathogen or condition with the highest proportion of hospitalised cases was neurotoxin (100.0%, 3/3 cases), followed by typhoid fever (76.9%, 20/26) and paratyphoid fever (72.7%, 8/11 cases). Of the non-enteric pathogens and conditions, *Mycobacterium tuberculosis* (87.5%, 7/8 cases) represented the highest proportion of hospitalised cases, followed by *Leptospira* spp. (66.7%, 2/3 cases).

Twenty-one deaths were associated with 10 different outbreaks in 2017. The deaths were associated with norovirus (10), influenza A (8) and typhoid fever (1). A pathogen was not identified in two deaths where an influenza-like illness was reported.

Table 3. Hospitalised outbreak cases and total outbreak cases by pathogen or condition, 2017

Pathogen or condition	Outbreaks[1]	Cases[1]		
	Total	Total	No. of cases hospitalised[2]	% of cases hospitalised
Enteric	**52**	**811**	**160**	**19.7**
Norovirus	21	534	91	17.0
Typhoid fever	2	26	20	76.9
Paratyphoid fever	1	11	8	72.7
Shigella spp.	3	14	7	50.0
Salmonella spp.[3]	4	19	6	31.6
Cryptosporidium spp.	3	10	3	30.0
Giardia spp.	3	46	3	6.5
Hepatitis A	2	13	3	23.1
Histamine (scombroid) fish poisoning	2	7	3	42.9
Neurotoxin	1	3	3	100.0
STEC infection	3	22	3	13.6
Rotavirus	2	56	2	3.6
Adenovirus	1	32	1	3.1
Campylobacter spp,	1	3	1	33.3
Pathogen not identified[4]	7	111	10	9.0
Non-enteric	**17**	**289**	**35**	**12.1**
Influenza and influenza-like-illness[5]	8	218	18	8.3
Mycobacterium tuberculosis	3	8	7	87.5
Bordetella pertussis	3	16	4	25.0
Leptospira spp.	1	3	2	66.7
Measles virus	1	7	1	14.3
Chickenpox	1	3	1	33.3
Total	**69**	**1100**	**195**	**17.7**

[1] More than one enteric agent was reported in four outbreaks, therefore the numbers don't add up to the group totals.

[2] Hospitalisation information was recorded for 58.4% (376/644) of outbreaks, relating to 51.5% (6164/11,963) of cases. Only outbreaks where one or more hospitalisations were recorded were included in the table (69 outbreaks involving 1100 cases).

[3] Includes non-typhoidal *Salmonella* species only. Outbreaks of *S*. Typhi and *S*. Paratyphi are reported separately.

[4] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

[5] Includes outbreaks of influenza A (6 outbreaks with 191 cases), influenza B (2 outbreaks, 27 cases) and influenza-like illness (1 outbreak, 34 cases).

OUTBREAK SETTINGS

The most common outbreak settings recorded were long-term care facilities (40.5%, 261/644) followed by childcare centres (18.3%, 118/644) and private homes (10.7%, 69/644). Outbreaks in long-term care facilities had the highest number of associated cases (5882) (Table 4). Overall, 75.6% (487/644) of all outbreaks and 80.2% (9589/11,963) of cases reported in 2017 were set in institutions. The setting was unknown in 2.6% (17/644) of outbreaks.

Table 4. Outbreaks and associated cases by setting of exposure/transmission, 2017

Outbreak setting	Outbreaks[1]		Cases[1]	
	Total	% of outbreaks (n=644)	Total	% of cases (n=11,963)
Institutions	**487**	**75.6**	**9589**	**80.2**
Long-term care facility	261	40.5	5882	49.2
Childcare centre	118	18.3	1934	16.2
Hospital (acute-care)	40	6.2	548	4.6
School	28	4.3	644	5.4
Hostel/boarding house	8	1.2	133	1.1
Hotel/motel	6	0.9	86	0.7
Camp	4	0.6	99	0.8
Marae	4	0.6	45	0.4
Prison	1	0.2	5	0.0
Other institution	19	3.0	239	2.0
Commercial food operators	**41**	**6.4**	**304**	**2.5**
Restaurant/café/bakery	25	3.9	194	1.6
Fast food restaurant	4	0.6	12	0.1
Takeaway	4	0.6	8	0.1
Caterer	3	0.5	69	0.6
Supermarket/delicatessen	3	0.5	15	0.1
Temporary or mobile service	1	0.2	3	0.0
Other food outlet	3	0.5	14	0.1
Workplace	**16**	**2.5**	**1143**	**9.6**
Workplace	14	2.2	1216	10.2
Farm	6	0.9	19	0.2
Other	**88**	**13.7**	**845**	**7.1**
Private home	69	10.7	246	2.1
Aeroplane / cruise ship	5	0.8	458	3.8
Community/church or sports gathering	3	0.5	35	0.3
Petting zoo	1	0.2	2	0.0
Other setting	17	2.6	161	1.3
Unknown setting	**17**	**2.6**	**190**	**1.6**

[1] More than one setting was recorded in 20 outbreaks, therefore the numbers don’t add up to the group totals.

MODES OF TRANSMISSION

In 2017, the most commonly reported mode of transmission was person-to-person (85.2%, 549/644 outbreaks), followed by foodborne (9.5% 61/644) and environmental (9.2%, 59/644) (Table 5). Person-to-person transmission also accounted for the highest percentage of associated cases (92.0%, 11,000/11,963), followed by environmental transmission (11.3%, 1352/11,963). The mode of transmission was unknown for 3.9% (28 outbreaks).

Table 5. Outbreaks and associated cases by mode of transmission, 2017

Mode of transmission	Outbreaks				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=644)[1]	Total	% of cases (n=11,963)[1]
Person-to-person	478	71	549	85.2	11,000	92.0
Foodborne	54	7	61	9.5	719	6.0
Environmental	7	52	59	9.2	1352	11.3
Zoonotic	11	2	13	2.0	46	0.4
Waterborne	9	2	11	1.7	32	0.3
Sexual contact	1	0	1	0.2	4	0.0
Other	4	1	5	0.8	99	0.8
Unknown	28	-	28	3.9	226	1.9

[1] More than one mode of transmission was recorded for 78 outbreaks therefore the totals add up to more than 100%.

Note: No outbreaks with vectorborne or parenteral transmission were reported in 2017.

FOODBORNE OUTBREAKS

Causal agent

Of the 61 foodborne outbreaks reported in 2017 (with 719 associated cases), 68.9% (42/61 outbreaks) were linked to a pathogen or condition (Table 6). Pathogens most commonly associated with foodborne outbreaks were norovirus (27.9%, 17/61 outbreaks), *Campylobacter* spp. and *Salmonella* spp. (6.6%, 4/61 outbreaks each). Enteric viruses (norovirus and hepatitis A) were implicated in 31.1% (19/61) of the foodborne outbreaks while enteric bacteria (*Campylobacter* spp., *Salmonella* spp., *Shigella* spp., STEC infection, *S. aureus* and *V. fluvialis*) were implicated in 24.6% (15/61) of the foodborne outbreaks.

Table 6. Foodborne outbreaks and associated cases by pathogen or condition, 2017

Pathogen or condition	Outbreaks		Cases	
	Total	% of outbreaks (n=61)[1]	Total	% of cases (n=719)[1]
Norovirus	17	27.9	308	42.8
Campylobacter spp.	4	6.6	19	2.6
Salmonella spp.	4	6.6	15	2.1
Shigella spp.	3	4.9	17	2.4
Ciguatera fish poisoning	2	3.3	31	4.3
Typhoid fever	2	3.3	26	3.6
Staphylococcus aureus	2	3.3	12	1.7
Hepatitis A	2	3.3	8	1.1
Histamine (scombroid) fish poisoning	2	3.3	7	1.0
STEC infection	1	1.6	157	21.8
Vibrio fluvialis	1	1.6	27	3.8
Paratyphoid fever	1	1.6	11	1.5
Giardia spp.	1	1.6	3	0.4
Neurotoxin	1	1.6	3	0.4
Pathogen not identified[2]	19	31.1	102	14.2

[1] More than one agent was reported in two foodborne outbreaks, therefore the totals add up to more than 100%.

[2] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

Setting where contaminated foods/beverages were prepared

The setting where foods and beverages were prepared was recorded in 85.2% (52/61) of foodborne outbreaks and 94.3% (678/719) of associated cases in 2017. The preparation settings most commonly associated with foodborne outbreaks included commercial food operators (50.8%, 31/61) and private homes (13.1%, 8/61) (Table 7). Foodborne outbreaks where the food was prepared on a cruise ship had the highest number of cases (21.8%, 157/719) followed by restaurants, cafés, or bakeries (20.9%, 150/719).

Table 7. Foodborne outbreaks and associated cases by setting of food preparation, 2017

Preparation setting	Outbreaks		Cases[1]	
	Total	% of outbreaks (n=61)	Total	% of cases (n=719)
Commercial food operators	**31**	**50.8**	**241**	**33.5**
Restaurant/café/bakery	19	31.1	150	20.9
Takeaway	3	4.9	8	1.1
Caterers	2	3.3	35	4.9
Supermarket/delicatessen	2	3.3	9	1.3
Fast food restaurant	2	3.3	5	0.7
Other food outlet	3	4.9	34	4.7
Institutions	**10**	**16.4**	**246**	**34.2**
School	2	3.3	104	14.5
Long-term care facility	2	3.3	77	10.7
Marae	2	3.3	16	2.2
Hotel/motel	1	1.6	23	3.2
Childcare centre	1	1.6	7	1.0
Acute care hospital	1	1.6	5	0.7
Other institutions	1	1.6	14	1.9
Other	**13**	**21.3**	**249**	**34.6**
Private home	8	13.1	55	7.6
Overseas manufacturer	2	3.3	31	4.3
Cruise ship	1	1.6	157	21.8
Community/church gathering	1	1.6	5	0.7
Other setting*	1	1.6	1	0.1
Unknown preparation setting	**9**	**14.8**	**41**	**5.7**

[1] Two preparation settings were recorded in two foodborne outbreaks, therefore the numbers don't add up to the group totals.

[2] Case was linked to an international outbreak set at a Rainbow festival in Italy. See: https://ecdc.europa.eu/en/news-events/typhoid-fever-outbreak-linked-rainbow-gathering-northern-italy

Additional information on foodborne outbreaks can be found in the Foodborne disease in New Zealand 2017 report [5].

PERSON-TO-PERSON OUTBREAKS

Causal agents

In 2017, there were 549 person-to-person outbreaks (primary and secondary mode of transmission) with 11,000 associated cases. A causal agent was identified in 73.8% (405/549) of these outbreaks. As in 2016, the most common causal agent was norovirus, which was recorded in 44.1% (242/549) of person-to-person outbreaks and involved 56.5% (6219/11,000) of outbreak-associated cases (Table 8). Other common pathogens and conditions included *Giardia* spp. (3.8%, 21/549) and *B. pertussis* (3.6%, 20/549). Influenza or influenza-like illness accounted for 34 (6.2%) outbreaks and 765 (7.0%) associated cases. There was also a high number of cases associated with mumps (10.8%, 1190/11,000) in 2017.

Table 8. Person-to-person outbreaks and associated cases by pathogen or condition, 2017

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=549)[2]	Total	% of cases (n=11,000)[2]
Norovirus	211	31	242	44.1	6219	56.5
Influenza and influenza-like-illness[3]	31	3	34	6.2	765	7.0
Giardia spp.	17	4	21	3.8	160	1.5
Bordetella pertussis	20	0	20	3.6	160	1.5
Cryptosporidium spp.	13	5	18	3.3	115	1.0
Sapovirus	9	6	15	2.7	233	2.1
Mumps virus	14	0	14	2.6	1190	10.8
Salmonella spp.[4]	4	5	9	1.6	31	0.3
STEC infection	7	1	8	1.5	35	0.3
Rotavirus	4	0	4	0.7	96	0.9
Hepatitis A	2	1	3	0.5	12	0.1
Shigella spp.	1	2	3	0.5	11	0.1
Measles virus	3	0	3	0.5	11	0.1
Mycobacterium tuberculosis	3	0	3	0.5	10	0.1
Adenovirus	2	0	2	0.4	54	0.5
Campylobacter spp.	1	1	2	0.4	12	0.1
Clostridium difficile	1	0	1	0.2	13	0.1
Astrovirus	0	1	1	0.2	7	0.1
Staphylococcus aureus	0	1	1	0.2	7	0.1
Invasive pneumococcal disease	1	0	1	0.2	5	0.0
Yersinia spp.	1	0	1	0.2	5	0.0
Chicken Pox	1	0	1	0.2	3	0.0
Pathogen not identified[5]	144	13	157	28.6	2160	19.6

[1] Includes outbreaks where person-to-person transmission was either the primary or secondary mode of transmission reported.

[2] Multiple agents were reported in 15 person-to-person outbreaks, therefore the totals add up to more than 100%.

[3] Includes outbreaks of influenza A (16 outbreaks with 383 cases), influenza B (6 outbreaks, 67 cases), influenza-like illness (5 outbreaks, 129 cases), acute respiratory infection (4 outbreaks, 98 cases), influenza not otherwise specified (1 outbreak, 24 cases), influenza A and RSV (1 outbreak, 30 cases).

[4] Includes non-typhoidal *Salmonella* species only.

[5] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

WATERBORNE OUTBREAKS

Causal agents

There were 11 waterborne outbreaks with 32 associated cases in 2017. A causal agent was identified in most (90.9%, 10/11) of the outbreaks (Table 9). The most commonly reported waterborne pathogens and conditions were *Giardia* spp. (27.3%, 3/11 outbreaks), *Cryptosporidium* spp., *Salmonella* spp. and *Shigella* spp. (18.2%, 2/11 outbreaks each).

Table 9. Waterborne outbreaks and associated cases by pathogen, 2017

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=11)	Total	% of cases (n=32)
Giardia spp.	2	1	3	27.3	9	28.1
Cryptosporidium spp.	2	0	2	18.2	6	18.8
Salmonella spp.[2]	2	0	2	18.2	4	12.5
Shigella spp.	1	1	2	18.2	6	18.8
STEC infection	1	0	1	9.1	3	9.4
Pathogen not identified[2]	1	0	1	9.1	4	12.5

[1] Includes outbreaks where waterborne transmission was either the primary or secondary mode of transmission reported.

[2] Includes non-typhoidal *Salmonella* species only.

[3] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

ENVIRONMENTAL OUTBREAKS

Causal agents

There were 59 environmental outbreaks with 1352 associated cases reported in 2017. Of these outbreaks, 79.7% (47/59) were linked to a specific causal agent (Table 10). The most common causal agent identified in environmental outbreaks was norovirus (47.5%, 28/59), followed by *Cryptosporidium* spp. (10.2%, 6/59). Environmental transmission was the secondary mode reported in all of the norovirus outbreaks. Norovirus also accounted for the highest proportion of associated cases (69.7%, 942/1352) followed by influenza A (7.5%, 101/1352).

Table 10. Environmental outbreaks and associated cases by pathogen or condition, 2017

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=59)[2]	Total	% of cases (n=1352)[2]
Norovirus	0	28	28	47.5	942	69.7
Cryptosporidium spp.	2	4	6	10.2	79	5.8
Giardia spp.	3	1	4	6.8	40	3
Influenza A	0	3	3	5.1	101	7.5
Sapovirus	0	2	2	3.4	35	2.6
Campylobacter spp.	0	2	2	3.4	9	0.7
Hepatitis A	1	1	2	3.4	9	0.7
Shigella spp.	0	1	1	1.7	2	0.1
Salmonella spp.	0	1	1	1.7	2	0.1
Pathogen not identified[3]	1	11	12	20.3	193	14.3

[1] Includes outbreaks where environmental transmission was either the primary or secondary mode of transmission reported.

[2] Three pathogens were reported in one environmental outbreak, therefore the totals add up to more than 100%.

[3] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

ZOONOTIC OUTBREAKS

Causal agents

There were 13 zoonotic outbreaks, with 46 associated cases in 2017. All were linked to a specific pathogen (Table 11). *Cryptosporidium* spp. was the most commonly identified pathogen and was linked to 53.8% (7/13) of zoonotic outbreaks and 60.9% (28/46) of the associated cases.

Table 11. Zoonotic outbreaks and associated cases by pathogen or condition, 2017

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=13)	Total	% of cases (n=46)
Cryptosporidium spp.	7	0	7	53.8	28	60.9
Campylobacter spp.	1	1	2	15.4	9	19.6
STEC infection	1	1	2	15.4	4	8.7
Leptospira spp.	1	0	1	7.7	3	6.5
Salmonella spp.	1	0	1	7.7	2	4.3

[1] Includes outbreaks where zoonotic transmission was either the primary or secondary mode of transmission reported.

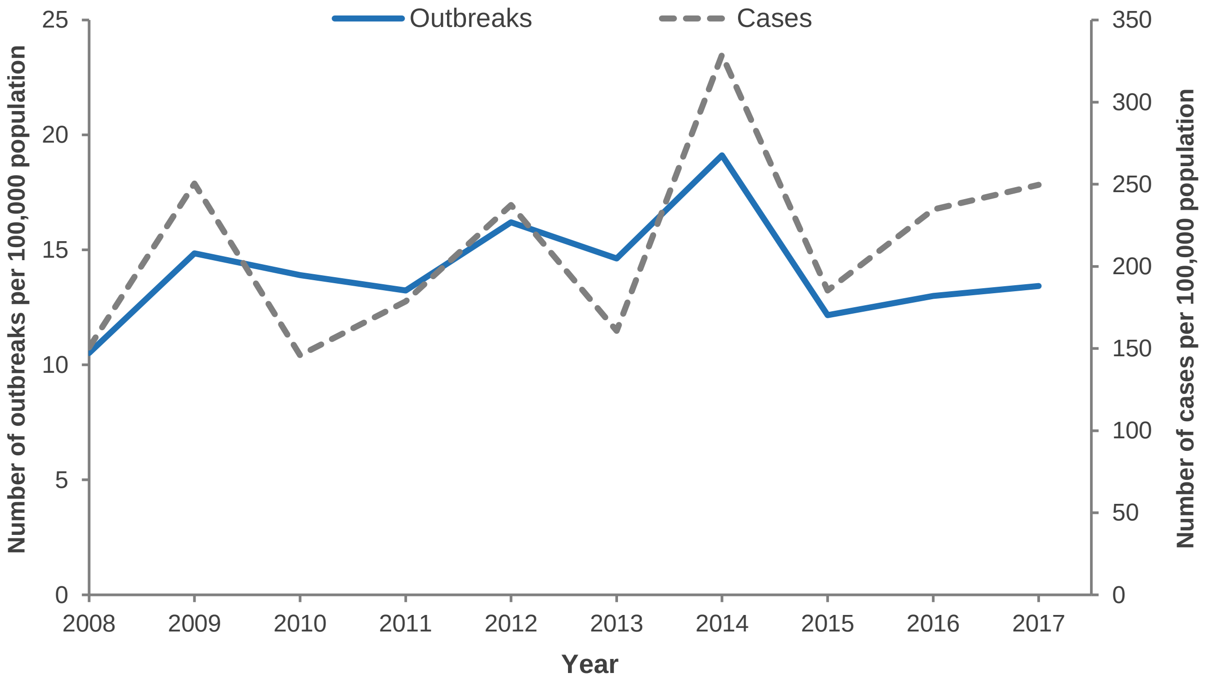
SEXUAL CONTACT OUTBREAKS

There was one sexual contact outbreak involving four cases in 2017. The outbreak of shigellosis involved contact between men who have sex with men (MSM).

TIME TRENDS 2008–2017

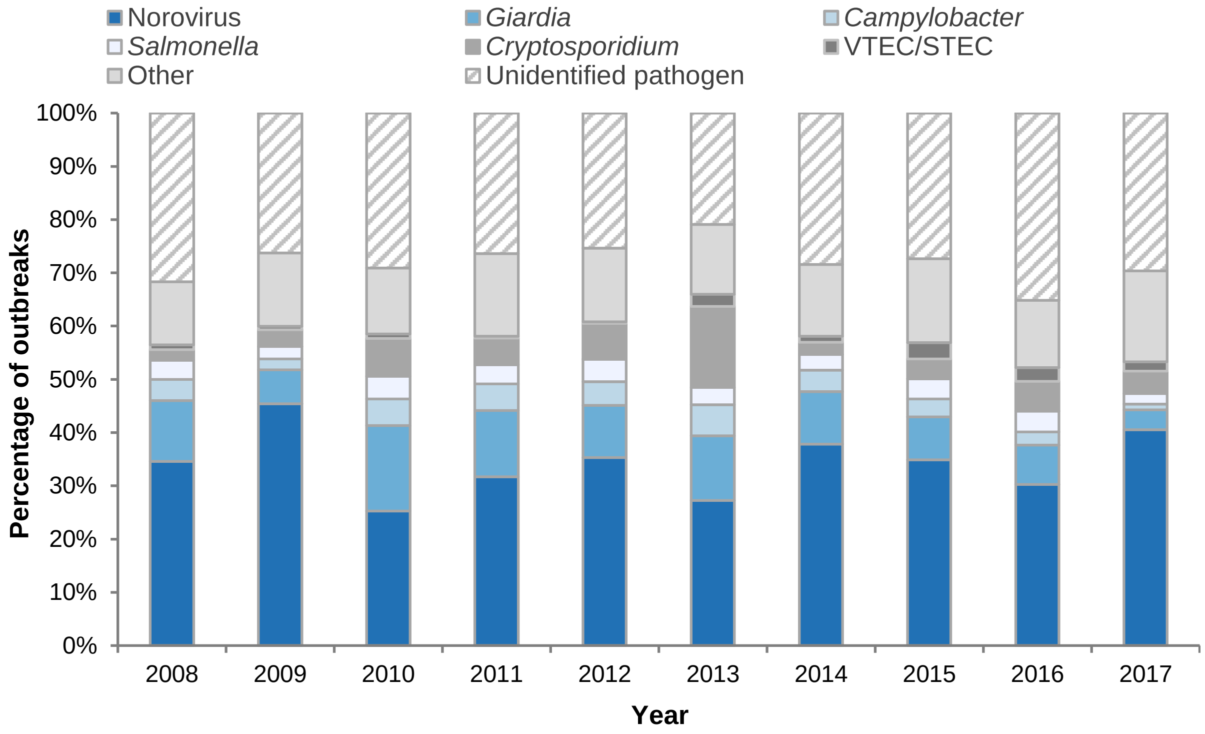
Between 2008 and 2014, both the number of outbreaks per 100,000 population and the number of cases per 100,000 increased overall, although there was variability during that time period. The annual outbreak rate peaked in 2014 (19.1 outbreaks per 100,000 population) and then decreased significantly ($p<0.05$) in 2015 to 12.2 outbreaks per 100,000. The rate in 2016 (13.0 outbreaks per 100,000) and 2017 (13.4 outbreaks per 100,000) has remained similar to that reported in 2015 (Figure 4). Similarly, the number of outbreak-associated cases per 100,000 peaked in 2014 with 328.8 cases per 100,000 and then decreased to 185.3 per 100,000 in 2015. However, the rate increased significantly in 2016 to 234.6 cases per 100,000 population, which was largely due to the Havelock North campylobacteriosis outbreak (involving 964 cases) reported in August 2016. The case rate in 2017 (249.6 per 100,000) was slightly higher than reported in 2016. A large mumps outbreak involving 1076 cases in Auckland contributed to the elevated rate in 2017.

Figure 4. Outbreaks and associated cases per 100,000 by year, 2008–2017



In 2017, a causal agent was identified in 70.3% of outbreaks which is similar to the previous 10 years (range: 64.8–79.1% per year 2007 to 2016). The causal agent associated with the highest number of outbreaks and associated cases during 2008–2016 was norovirus. In 2017, 261 norovirus outbreaks were reported with 6517 associated cases. The highest number of norovirus outbreaks recorded since reporting began in 1997 occurred in 2014 (326 outbreaks and 9390 cases). Since 2008, norovirus outbreaks have accounted for around a third of outbreaks reported each year, with the exception of 2009 when the proportion was almost half (45.4%, 290/639 outbreaks) (Figure 5).

Figure 5. Percentage of outbreaks by pathogen or condition and year, 2008–2017



The number of rotavirus outbreaks reported each year has significantly decreased since a peak in 2014 (47 outbreaks, 854 cases). In 2017 there were four outbreaks involving 96 cases all set in childcare centres. The decrease follows the introduction of a rotavirus vaccine to the national immunisation schedule in July 2014 [6].

There was a decrease in the number of outbreaks due to STEC infection in 2017 compared to recent years (2017: 11, 2016:16, 2015: 17, 2014:10, 2013: 16 outbreaks). However, the number of outbreaks and associated cases reported annually since 2012 has increased significantly. Between 2006 and 2012 there was an average of four outbreaks and 16 associated cases reported each year. The most commonly reported mode of transmission for STEC outbreaks in 2017 was person-to-person (8 outbreaks, 35 cases).

The number of outbreaks and associated cases due to *Cryptosporidium* spp. was lower in 2017 (27 outbreaks, 184 cases) than in 2016 (34 outbreaks, 191 cases) and was significantly lower than reported in 2013 (99 outbreaks, 550 cases) when outbreaks of *Cryptosporidium* spp. peaked. As with previous years the most commonly reported mode of transmission for *Cryptosporidium* spp. outbreaks in 2017 was person-to-person (18 outbreaks, 115 cases).

The number of outbreaks and associated cases due to *Giardia* spp. was also lower in 2017 (24 outbreaks, 170 cases) than in 2016 (45 outbreaks, 238 cases). The number of outbreaks and associated cases steadily increased between 2007 (21 outbreaks, 111 cases) and 2010 (97 outbreaks, 378 cases) when outbreaks of *Giardia* spp. peaked. The number of outbreaks reported each year from 2015 to 2017 (range: 24–46) is significantly lower than the number of outbreaks reported between 2010 and 2014 (range: 71–97). Similar to *Cryptosporidium* spp. the most commonly reported mode of transmission for *Giardia* spp. outbreaks in 2017 was person-to-person (21 outbreaks, 160 cases).

There were seven outbreaks of *Campylobacter* spp. reported in 2017, the lowest recorded since a peak in 2006 (47 outbreaks). There was a large reduction in the number of outbreaks of *Campylobacter* spp. reported in 2007, when numbers reduced by more than half from 2006 (47 outbreaks, 221 cases) to 2007 (21 outbreaks, 60 cases). This decrease was most likely due to interventions put in place in New Zealand in 2006 to reduce the incidence of poultry-associated foodborne campylobacteriosis [7]. The number of outbreaks and associated cases of *Campylobacter* spp. increased steadily between 2009 (13 outbreaks, 69 cases) and 2014 (35 outbreaks, 241 cases). In 2016, the number of outbreaks reported (16 outbreaks) was the lowest since 2009, while the number of associated cases was the largest since recording began (1014 cases). The Havelock North waterborne outbreak in August 2016 accounted for 967 notified cases. In 2017, more than half (57.1%, 4/7) of the reported *Campylobacter* spp. outbreaks were due to foodborne transmission.

The introduction of more sensitive testing methods in diagnostic laboratories since mid-2015 may have contributed to the increased detection of outbreaks for some enteric diseases. Concurrently, some laboratories have reduced or stopped culturing for some organisms, meaning that outbreak detection through monitoring trends in pathogen subtypes is affected at local and national levels. This means there is greater potential to miss outbreaks or detect them later than would have occurred if all notifiable organisms were available for subtyping.

Outbreaks of other pathogens and conditions that have been reported in recent years include varicella zoster virus (chicken pox) (2014: 2 outbreaks, 45 cases; 2015: 1 outbreak, 22 cases, 2016: 2 outbreaks, 18 cases, 2017: 1 outbreak, 3 cases) and adenovirus (2017: 2 outbreaks; 54 cases). Both outbreaks involving adenovirus also had another enteric pathogen identified (norovirus and *Giardia* spp.), and were set in institutions.

In 2017, there were three outbreaks of measles reported involving 11 cases, compared to three outbreaks involving 98 cases in 2016. The number of measles outbreaks and associated cases has significantly decreased since 2014 (19 outbreaks, 243 cases) when the largest number of outbreaks was reported. The highest number of cases linked to outbreaks was reported in 2011 when 582 cases were linked to six outbreaks.

The most common outbreak settings in 2017 were long-term care facilities, childcare centres and private homes, similar to 2016. Approximately one fifth (18.3%, 118 outbreaks) of outbreaks were set in childcare centres, which is the highest proportion since recording began (range: 2.4–18.0%). Since 2006, outbreaks in institutions have accounted for around one-half to two-thirds of all outbreaks reported annually, and those in private homes for around one-fifth to one-third. Before 2006, commercial food operators and private homes were the most commonly reported settings.

Since 2006, the most frequently reported mode of transmission for outbreaks has been person-to-person transmission. Prior to this, foodborne transmission was the most frequently reported mode (range: 1998 to 2006 28.3–52.9% of outbreaks per year). Between 2007 and 2016, the proportion of foodborne outbreaks reported each year ranged from 13.3 to 23.1%. In 2017, 9.5% (61 outbreaks) of outbreaks were reported to have foodborne transmission, the lowest proportion since recording began. In 2017, the number of outbreaks with person-to-person transmission (85.2%, 549/644) was more than eight times higher than any other mode of transmission. Foodborne transmission was the second most common mode of transmission in 2017 (9.5%, 61 outbreaks) and 2016 (15.6%, 95/610) surpassing environmental transmission which was the second most common mode of transmission reported from 2013 to 2015.

GLOSSARY

Common event outbreak

An outbreak due to the exposure of a group of persons to a noxious influence that is common to the individuals in the group, where the exposure is brief and essentially simultaneous and all resultant cases develop within one incubation period of the disease. Cases therefore have exposures that are grouped in place and time (synonymous with point source outbreak).

Common site outbreak

An outbreak due to the exposure of a group of persons to a noxious influence that is common to the individuals in the group, where exposures have occurred at the same place (or site) but over a longer time period than those of common event outbreaks (ie, grouped in place but not in time).

Common source outbreak

An outbreak due to the exposure of a group of persons in the community to a noxious influence that is common to the individuals in the group. These outbreaks are subcategorised into common event (where exposures are grouped in time and place), dispersed common source (grouped in time but not in place) and common site (grouped in place but not in time).

Community-wide outbreak

An outbreak among individuals in a community where transmission is predominantly by direct exposure of susceptible people to infectious people (synonymous with person-to-person outbreak).

Contamination

The presence of a disease-causing agent on a body surface, in clothes, bedding, toys or other inanimate articles, or substances such as water and food.

Dispersed common source outbreak

Outbreak due to the exposure of a group of persons in the community to a noxious influence that is common to the individuals in the group, where the exposures are not grouped in place (and may or may not be grouped in time). These outbreaks are often due to a distributed vehicle of infection transmission, such as a commercially prepared food item or a water supply.

Environment

All factors that are external to the individual human host.

EpiSurv

The national notifiable disease surveillance system that ESR manages to record data about notifiable diseases and outbreaks reported by public health units.

Exposure

Proximity and/or contact with a potential source of a disease agent in such a manner that effective transmission of the agent and harmful or protective effects of the agent may occur.

Household outbreak

An outbreak confined to members of a single household.

Institutional outbreak

An outbreak confined to the population of a specific residential or other institutional setting, such as a hospital, long-term care facility, prison, childcare centre or school.

Outbreak

Two or more cases of a specific disease or health-related condition linked to a common source, in particular, where the common source is exposure at a common event, or food or water dispersed in a community, an environmental source or a source in an institutional setting; OR a community-wide or person-to-person outbreak; OR any other situation where the outbreak investigation or control measures are being used or considered.

Source (of illness)

The person, animal, object or substance from which a disease agent passes to a host.

Transmission of illness

Any mechanism by which a disease agent is spread through the environment or to another person. Mechanisms are defined as either direct or indirect.

Vehicle

An inanimate intermediate in the indirect transmission of a pathogen from a reservoir or infected host to a susceptible host; vehicles include foods, clothing and instruments.

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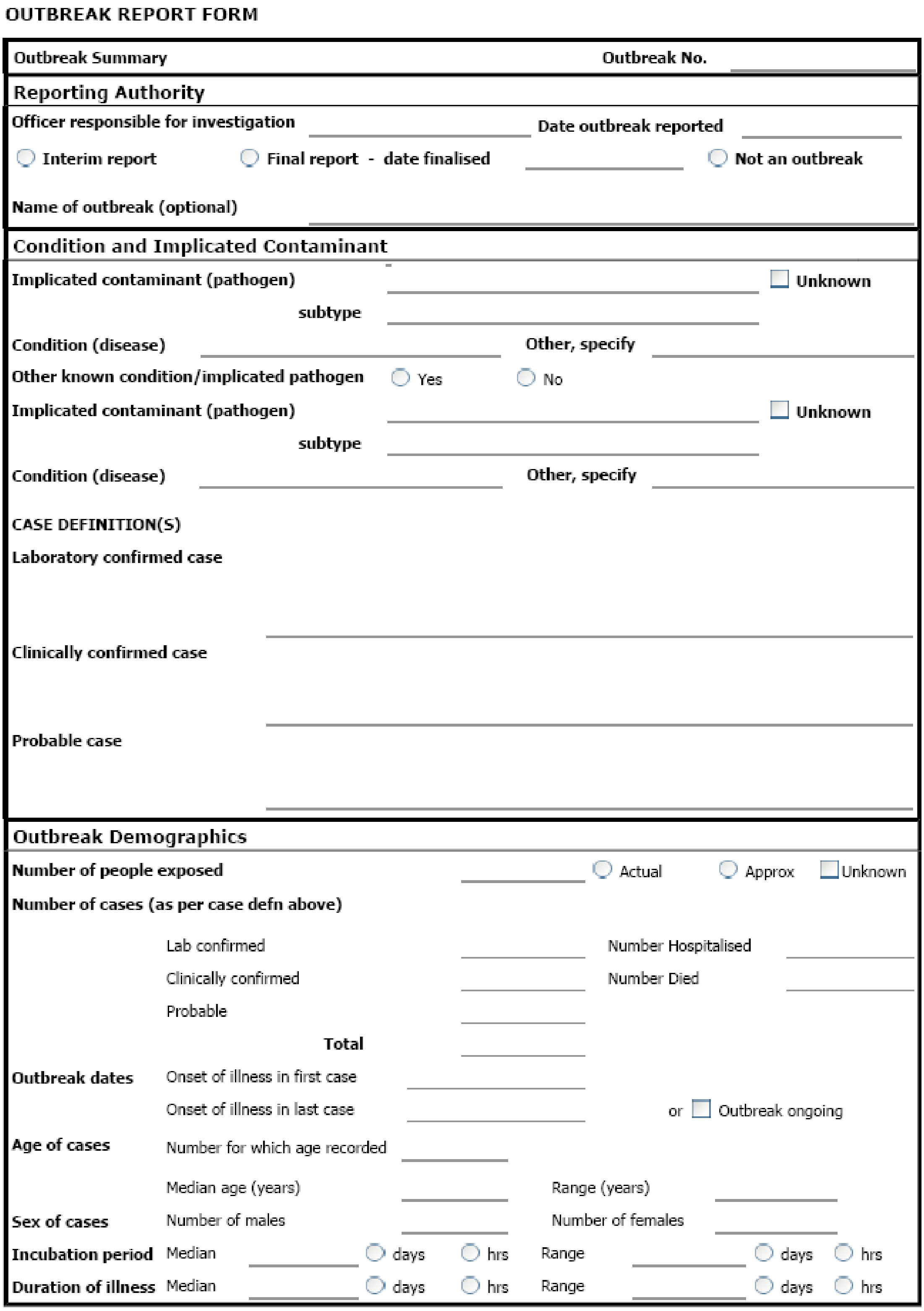
APPENDIX

OUTBREAK REPORT FORM



OUTBREAK REPORT FORM

Outbreak Summary **Outbreak No.**

Reporting Authority

Officer responsible for investigation **Date outbreak reported**

○ **Interim report** ○ **Final report - date finalised** ○ **Not an outbreak**

Name of outbreak (optional)

Condition and Implicated Contaminant

Implicated contaminant (pathogen) ☐ **Unknown**

subtype

Condition (disease) **Other, specify**

Other known condition/implicated pathogen ○ Yes ○ No

Implicated contaminant (pathogen) ☐ **Unknown**

subtype

Condition (disease) **Other, specify**

CASE DEFINITION(S)

Laboratory confirmed case

Clinically confirmed case

Probable case

Outbreak Demographics

Number of people exposed ○ Actual ○ Approx ☐ Unknown

Number of cases (as per case defn above)

Lab confirmed		Number Hospitalised	
Clinically confirmed		Number Died	
Probable			
Total			

Outbreak dates Onset of illness in first case

Onset of illness in last case or ☐ Outbreak ongoing

Age of cases Number for which age recorded

Median age (years) Range (years)

Sex of cases Number of males Number of females

Incubation period Median ○ days ○ hrs Range ○ days ○ hrs

Duration of illness Median ○ days ○ hrs Range ○ days ○ hrs

Outbreak Summary **Outbreak No.**

Circumstances of Exposure/Transmission

How was the outbreak first recognised?

○ Increase in disease incidence
○ Cases attended common event
○ Cases linked to common source (eg food, water, environmental site)
○ Other means (specify)
○ Cases had person to person contact with other cases(s)
○ Common organism type/strain characteristics between cases

Were these cases part of a well-defined exposed group (eg Common event, institutional, environmental, household) ○ Yes ○ No ○ Unknown

If yes, date of exposure
If exposure >1 day, date exposure ended

Description of exposure event

First setting where exposure occurred Setting unknown ☐

○ **Food premises**
○ Restaurant/café/bakery
○ Takeaway
○ Supermarket/delicatessen
○ Temporary or mobile service
○ Fast food restaurant
○ Caterers
○ Other food outlet

○ **Institution**
○ Hostel/boarding house
○ Hotel/motel
○ Long term care facility
○ Hospital (acute care)
○ Prison
○ Camp
○ School ○ Childcare centre
○ Marae
○ Other institution

○ **Workplace/Community/Other**
○ Workplace
○ Farm
○ Petting zoo
○ Home
○ Community, church, sports gathering
○ Cruise ship, airline, tour bus, train
○ Other setting

Setting name

Setting Address Number Street Suburb
Town/City Post Code ☐ GeoCode

Second setting where exposure occurred Setting unknown ☐

○ **Food premises**
○ Restaurant/café/bakery
○ Takeaway
○ Supermarket/delicatessen
○ Temporary or Mobile Service
○ Fast food restaurant
○ Caterers
○ Other food outlet

○ **Institution**
○ Hostel/boarding house
○ Hotel/motel
○ Long term care facility
○ Hospital (acute care)
○ Prison
○ Camp
○ School ○ Childcare centre
○ Marae
○ Other institution

○ **Workplace/Community/Other**
○ Workplace
○ Farm
○ Petting zoo
○ Home
○ Community, church, sports gathering
○ Cruise ship, airline, tour bus, train
○ Other setting

Setting name

Setting Address Number Street Suburb
Town/City Post Code ☐ GeoCode

Outbreak Summary **Outbreak No.** ____

Circumstances of Exposure/Transmission contd

First setting where contaminated food/beverage was prepared Setting unknown ☐

○ **Overseas manufacturer, specify** ____

○ **Food premises**
○ Restaurant/café/bakery
○ Takeaway
○ Supermarket/delicatessen
○ Temporary or Mobile Service
○ Fast food restaurant
○ Caterers
○ Other food outlet

○ **Institution**
○ Hostel/boarding house
○ Hotel/motel
○ Long term care facility
○ Hospital (acute care)
○ Prison
○ Camp
○ School ○ Childcare centre
○ Marae
○ Other institution

○ **Workplace/Community/Other**
○ Workplace
○ Farm
○ Petting zoo
○ Home
○ Community, church, sports gathering
○ Cruise ship, airline, tour bus, train
○ Commercial food manufacturer
○ Other setting

Setting name ____

Setting Address Number ____ Street ____ Suburb ____
Town/City ____ Post Code ____ ☐ GeoCode ____

Second setting where contaminated food/beverage was prepared Setting unknown ☐

○ **Overseas manufacturer, specify** ____

○ **Food premises**
○ Restaurant/café/bakery
○ Takeaway
○ Supermarket/delicatessen
○ Temporary or Mobile Service
○ Fast food restaurant
○ Caterers
○ Other food outlet

○ **Institution**
○ Hostel/boarding house
○ Hotel/motel
○ Long term care facility
○ Hospital (acute care)
○ Prison
○ Camp
○ School ○ Childcare centre
○ Marae
○ Other institution

○ **Workplace/Community/Other**
○ Workplace
○ Farm
○ Petting zoo
○ Home
○ Community, church, sports gathering
○ Cruise ship, airline, tour bus, train
○ Commercial food manufacturer
○ Other setting

Setting name ____

Setting Address Number ____ Street ____ Suburb ____
Town/City ____ Post Code ____ ☐ GeoCode ____

Geographic location where exposure occurred (tick one)

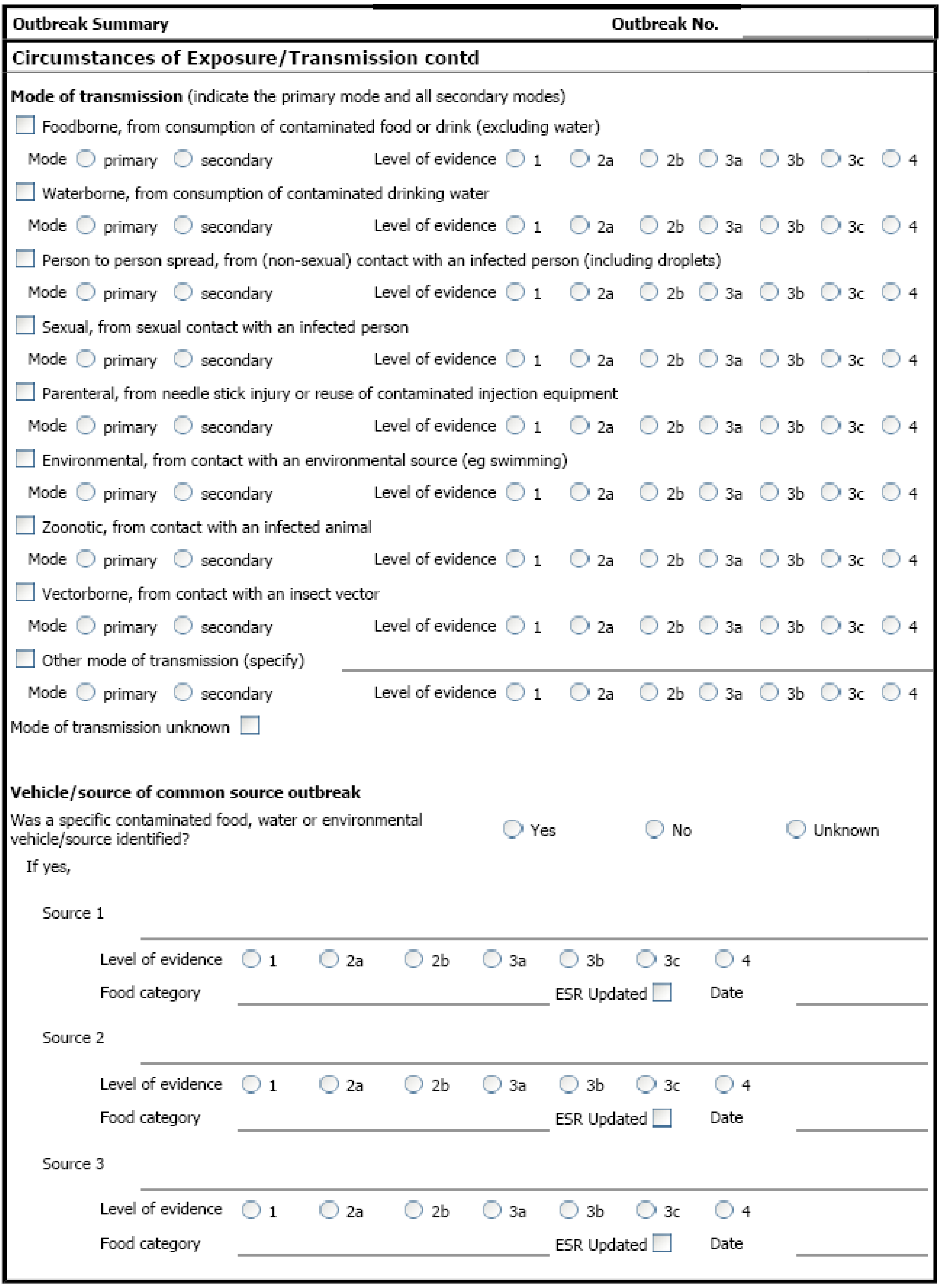
○ New Zealand ○ Overseas, specify ____ ○ Unknown

If exposure occurred in New Zealand, specify

Primary TA ____

DHB(s) ____ ____ ____
____ ____

Health District(s) ____ ____ ____
____ ____



Outbreak Summary **Outbreak No.**

Circumstances of Exposure/Transmission contd

Mode of transmission (indicate the primary mode and all secondary modes)

☐ Foodborne, from consumption of contaminated food or drink (excluding water)

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Waterborne, from consumption of contaminated drinking water

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Person to person spread, from (non-sexual) contact with an infected person (including droplets)

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Sexual, from sexual contact with an infected person

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Parenteral, from needle stick injury or reuse of contaminated injection equipment

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Environmental, from contact with an environmental source (eg swimming)

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Zoonotic, from contact with an infected animal

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Vectorborne, from contact with an insect vector

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

☐ Other mode of transmission (specify) ____________________

Mode ○ primary ○ secondary Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

Mode of transmission unknown ☐

Vehicle/source of common source outbreak

Was a specific contaminated food, water or environmental vehicle/source identified? ○ Yes ○ No ○ Unknown

If yes,

Source 1 ____________________

Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

Food category ____________________ ESR Updated ☐ Date ____________

Source 2 ____________________

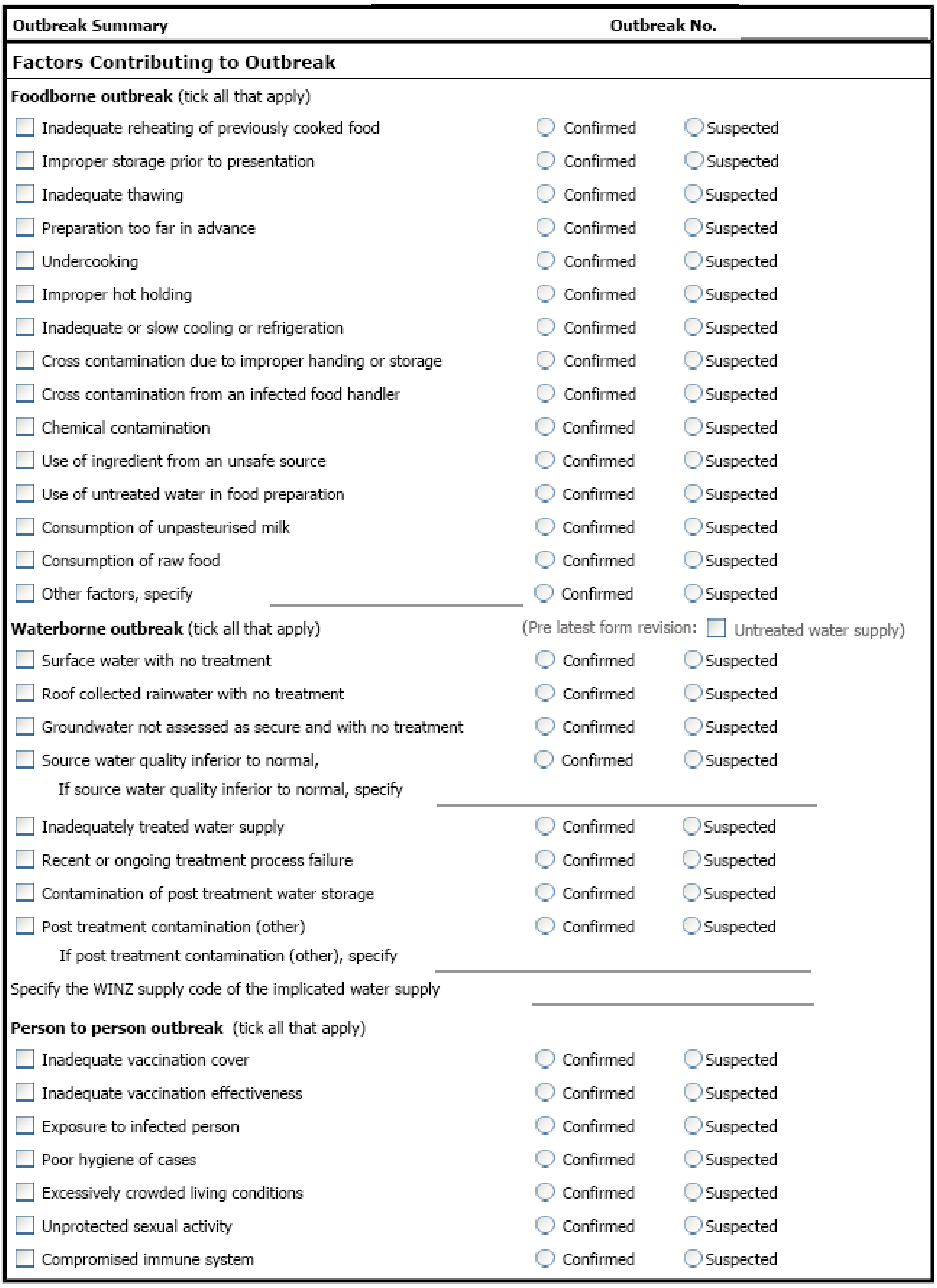
Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

Food category ____________________ ESR Updated ☐ Date ____________

Source 3 ____________________

Level of evidence ○ 1 ○ 2a ○ 2b ○ 3a ○ 3b ○ 3c ○ 4

Food category ____________________ ESR Updated ☐ Date ____________



Outbreak Summary **Outbreak No.** ____________

Factors Contributing to Outbreak

Foodborne outbreak (tick all that apply)

☐ Inadequate reheating of previously cooked food	○ Confirmed	○ Suspected
☐ Improper storage prior to presentation	○ Confirmed	○ Suspected
☐ Inadequate thawing	○ Confirmed	○ Suspected
☐ Preparation too far in advance	○ Confirmed	○ Suspected
☐ Undercooking	○ Confirmed	○ Suspected
☐ Improper hot holding	○ Confirmed	○ Suspected
☐ Inadequate or slow cooling or refrigeration	○ Confirmed	○ Suspected
☐ Cross contamination due to improper handing or storage	○ Confirmed	○ Suspected
☐ Cross contamination from an infected food handler	○ Confirmed	○ Suspected
☐ Chemical contamination	○ Confirmed	○ Suspected
☐ Use of ingredient from an unsafe source	○ Confirmed	○ Suspected
☐ Use of untreated water in food preparation	○ Confirmed	○ Suspected
☐ Consumption of unpasteurised milk	○ Confirmed	○ Suspected
☐ Consumption of raw food	○ Confirmed	○ Suspected
☐ Other factors, specify ____________	○ Confirmed	○ Suspected

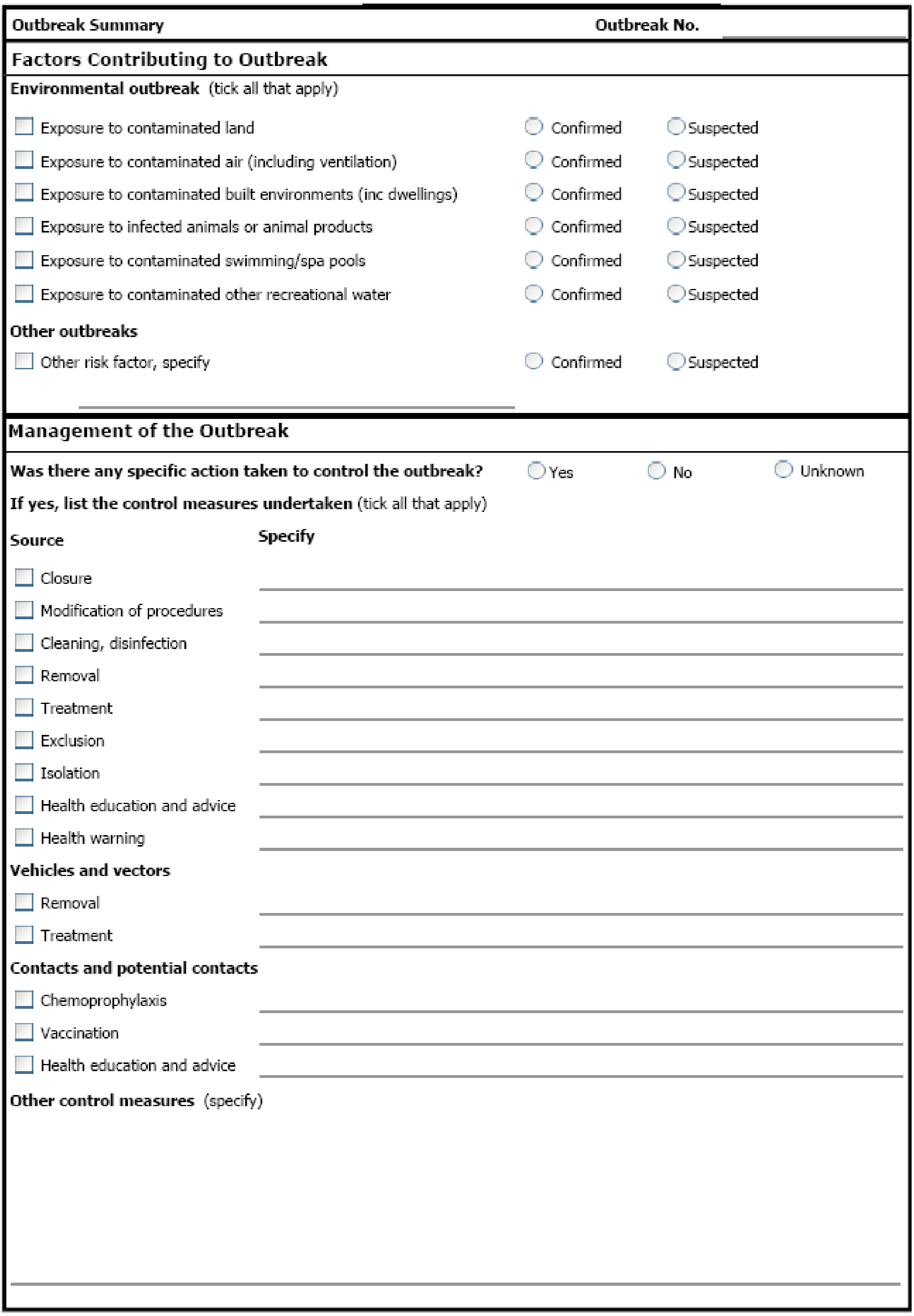
Waterborne outbreak (tick all that apply) (Pre latest form revision: ☐ Untreated water supply)

☐ Surface water with no treatment	○ Confirmed	○ Suspected
☐ Roof collected rainwater with no treatment	○ Confirmed	○ Suspected
☐ Groundwater not assessed as secure and with no treatment	○ Confirmed	○ Suspected
☐ Source water quality inferior to normal,	○ Confirmed	○ Suspected
If source water quality inferior to normal, specify ____________		
☐ Inadequately treated water supply	○ Confirmed	○ Suspected
☐ Recent or ongoing treatment process failure	○ Confirmed	○ Suspected
☐ Contamination of post treatment water storage	○ Confirmed	○ Suspected
☐ Post treatment contamination (other)	○ Confirmed	○ Suspected
If post treatment contamination (other), specify ____________		

Specify the WINZ supply code of the implicated water supply ____________

Person to person outbreak (tick all that apply)

☐ Inadequate vaccination cover	○ Confirmed	○ Suspected
☐ Inadequate vaccination effectiveness	○ Confirmed	○ Suspected
☐ Exposure to infected person	○ Confirmed	○ Suspected
☐ Poor hygiene of cases	○ Confirmed	○ Suspected
☐ Excessively crowded living conditions	○ Confirmed	○ Suspected
☐ Unprotected sexual activity	○ Confirmed	○ Suspected
☐ Compromised immune system	○ Confirmed	○ Suspected



Outbreak Summary **Outbreak No.** ____________

Factors Contributing to Outbreak

Environmental outbreak (tick all that apply)

☐ Exposure to contaminated land	○ Confirmed	○ Suspected
☐ Exposure to contaminated air (including ventilation)	○ Confirmed	○ Suspected
☐ Exposure to contaminated built environments (inc dwellings)	○ Confirmed	○ Suspected
☐ Exposure to infected animals or animal products	○ Confirmed	○ Suspected
☐ Exposure to contaminated swimming/spa pools	○ Confirmed	○ Suspected
☐ Exposure to contaminated other recreational water	○ Confirmed	○ Suspected

Other outbreaks

☐ Other risk factor, specify ____________	○ Confirmed	○ Suspected

Management of the Outbreak

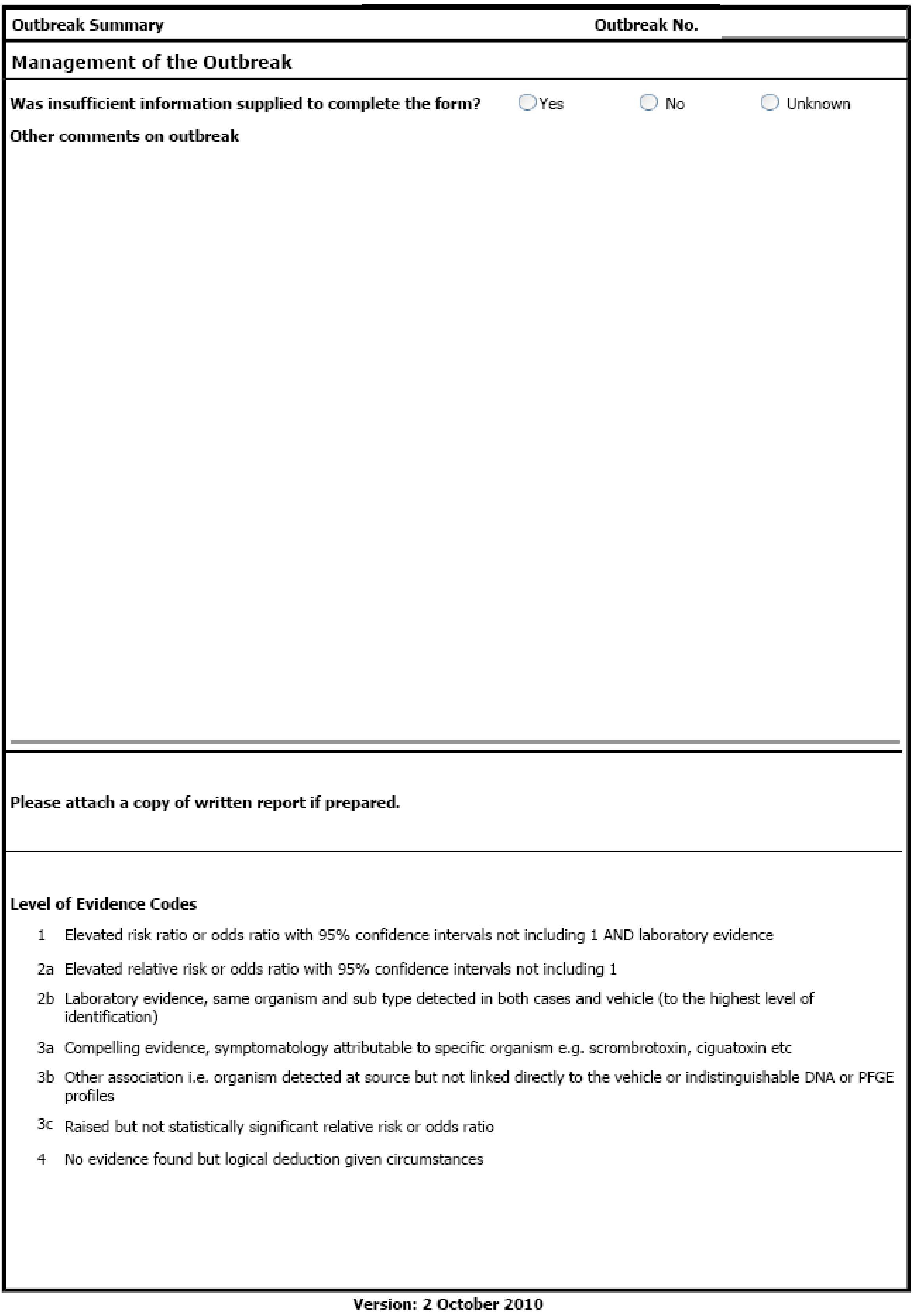
Was there any specific action taken to control the outbreak? ○ Yes ○ No ○ Unknown

If yes, list the control measures undertaken (tick all that apply)

Source	**Specify**
☐ Closure	____________
☐ Modification of procedures	____________
☐ Cleaning, disinfection	____________
☐ Removal	____________
☐ Treatment	____________
☐ Exclusion	____________
☐ Isolation	____________
☐ Health education and advice	____________
☐ Health warning	____________
Vehicles and vectors	
☐ Removal	____________
☐ Treatment	____________
Contacts and potential contacts	
☐ Chemoprophylaxis	____________
☐ Vaccination	____________
☐ Health education and advice	____________

Other control measures (specify)

____



Outbreak Summary **Outbreak No.**

Management of the Outbreak

Was insufficient information supplied to complete the form? ○ Yes ○ No ○ Unknown

Other comments on outbreak

Please attach a copy of written report if prepared.

Level of Evidence Codes

1	Elevated risk ratio or odds ratio with 95% confidence intervals not including 1 AND laboratory evidence
2a	Elevated relative risk or odds ratio with 95% confidence intervals not including 1
2b	Laboratory evidence, same organism and sub type detected in both cases and vehicle (to the highest level of identification)
3a	Compelling evidence, symptomatology attributable to specific organism e.g. scrombrotoxin, ciguatoxin etc
3b	Other association i.e. organism detected at source but not linked directly to the vehicle or indistinguishable DNA or PFGE profiles
3c	Raised but not statistically significant relative risk or odds ratio
4	No evidence found but logical deduction given circumstances

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Science for Communities

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