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ANNUAL SUMMARY OF OUTBREAKS IN NEW ZEALAND 2016

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ABBREVIATIONS

Abbreviation	Description
DHB	District health board
ESR	Institute of Environmental Science & Research Ltd.
FBVE	Foodborne Viruses in Europe
NRL	Norovirus Reference Laboratory
PHU	Public Health Unit
RSV	Respiratory syncytial virus
VTEC/STEC	Verocytotoxin- or 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 2016.

Key findings were:

Outbreaks and associated case rates increased slightly in 2016

There was a non-significant increase in reported outbreaks (▲8.5%, 610 outbreaks) and a significant increase in the number of cases associated with outbreaks (▲22.8%, 11,030 cases) compared with 2015 (559 outbreaks involving 8514 cases). A total of 194 (2.6%) outbreak-associated cases were hospitalised (161 in 2015, 3.3%) and 10 cases died (19 cases in 2015).

The number of outbreaks per 100,000 population increased to 13.0 outbreaks per 100,000 population from 12.1 in 2015, but was the second lowest rate reported since 2008 (10.5 outbreaks). Otago and Wellington reported the highest number of outbreaks per 100,000 population (22.2 and 20.2 respectively), more than one and a half times the national rate.

The national outbreak-associated cases rate was higher in 2016 (235.1 per 100,000 population) than 2015 (185.3) but remained lower than the rate reported in 2009 (250.4), 2012 (237.4) 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 of outbreaks, accounting for 91.8% of outbreaks, with the most common causes reported as norovirus (30.3%), *Giardia* (7.4%) and *Cryptosporidium* (5.4%). Over half of the cases associated with outbreaks were caused by norovirus (50.3%), whereas the proportions caused by the next two most common enteric pathogens identified were much lower, *Campylobacter* spp. (9.1%) and sapovirus (6.1%).

The most commonly reported non-enteric agents were influenza and influenza-like illness which accounted for 3.3% of outbreaks, 10.1% of associated cases and three deaths, followed by *Bordetella pertussis* which accounted for 2.8% of outbreaks

Hospitalisations and deaths

In 2016 there were 53 outbreaks where cases were hospitalised. A total of 194 hospitalisations were reported among 1870 cases. The largest number of hospitalisations was due to *Campylobacter* spp (41 hospitalisations, 4.2% of cases). The pathogens or conditions with the highest proportion of hospitalised cases were ciguatera fish poisoning (100.0%, 4/4 cases) and *Neisseria meningitidis* serogroup B (100.0%, 2/2 cases), followed by dengue fever (50.0%, 6/12 cases).

Ten deaths were associated with eight different outbreaks in 2016. The deaths were associated with *Campylobacter* spp. (3), norovirus (2), VTEC/STEC infection (1), influenza A (1) and parainfluenza (1)[*]. A pathogen was not identified in three deaths (gastroenteritis (2), acute respiratory infection (1)).

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[*] Both norovirus and influenza A were identified in one outbreak involving one death

Largest outbreak of campylobacteriosis recorded in EpiSurv

In 2016, a nationally significant localised outbreak of *Campylobacter* was reported. A large multi-agency investigation led by Hawke's Bay DHB was conducted to investigate a waterborne outbreak of *Campylobacter* involving 964 notified cases and three deaths. It is estimated that 5500 of Havelock North's 14,000 residents became ill with campylobacteriosis after consuming contaminated drinking water from the town supply. This was the largest outbreak recorded in EpiSurv since recording began in 1997.

Long-term care facilities the most common outbreak setting

Long-term care facilities (33.3%), childcare centres (18.0%) and private homes (16.4%) continued to be the most common settings for outbreaks. The highest number of cases associated with outbreaks were reported from long-term care facilities (39.8%), childcare centres (19.0%) and schools (12.4%).

Person-to-person the most common mode of transmission

In 2016, 82.3% of outbreaks recorded person-to-person as a mode of transmission, the majority of these as the primary mode, followed by foodborne (15.6%) and environmental (11.1%) transmission. Multiple modes of transmission were implicated in 16.1% of outbreaks.

Norovirus and salmonella the most implicated pathogens in foodborne outbreaks

Norovirus (18.9%), *Salmonella* (12.6%) and *Campylobacter* (8.4%) were the pathogens most commonly associated with foodborne outbreaks in 2016. Since 2008, norovirus and *Campylobacter* have been the most implicated pathogens in foodborne outbreaks.

Trends remain the same as previous years

The 2016 outbreaks showed continuing trends:

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

The proportion of outbreaks set in childcare centres and schools increased in 2016 compared with 2007–2015. Almost two-thirds of outbreaks (65.1%) in 2016 were in institutions, an increase from previous years. Since 2007, institutional outbreaks have accounted for around half of the outbreaks reported each year. Commercial food operators and private homes were the most commonly reported settings prior to 2007.

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

Over the 2007–2016 period an increase in outbreaks involving person-to-person transmission has been reported. This increases 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 2016.

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 each outbreak 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: http://www.surv.esr.cri.nz/episurv/index.php and in the appendix of this report.

DATA ANALYSIS

This report contains an analysis of outbreak data reported between 1 January and 31 December 2016, and recorded on the EpiSurv database as at 7 April 2017. Any amendments made to outbreak data after 7 April 2017 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 2016 [3].

Rates were calculated using national and PHU population figures based on Statistics New Zealand mid-year population estimates for 2016. Tests for statistical significance were calculated using the two-tailed test for difference in proportions (Fisher's exact).

DATA LIMITATIONS

The available outbreak 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. Many reported outbreaks remain 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 (4 outbreaks) reported into EpiSurv in 2016. 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 610 reported outbreaks (13.0 outbreaks per 100,000 population) in 2016, an increase from the 563 (12.3 outbreaks per 100,000 population) reported in 2015. All but one of the outbreaks were recorded as final reports. A total of 11,030 cases were associated with outbreaks; 33.5% (3696/11,030) of the cases were either clinically or laboratory confirmed and 66.5% (7334/11,030) were classified as probable cases. In 2016, the national rate was 235.1 outbreak-associated cases per 100,000 population, higher than the rate in 2015 (185.5 cases per 100,000 population).

DISTRIBUTION OF OUTBREAKS BY PUBLIC HEALTH UNIT

In 2016, Auckland PHU (29.0%, 162/610) had the highest proportion of outbreaks reported followed by Wellington PHU (17.9%, 100/610). Wellington PHU also reported the highest proportion of outbreak-associated cases (21.7%, 1843/11,030) followed by Canterbury (19.2%, 1638/11,030) (Table 1). Otago PHU reported the highest outbreak rate (22.2 per 100,000 population) and West Coast reported the highest outbreak-associated case rate (2329.2 per 100,000 population) (Table 1, Figure 1).

Table 1. Number and rate of outbreaks and associated cases by PHU Office, 2016

PHU Office	Outbreaks			Cases		
	Total	% of outbreaks (n=610)	Outbreak rate[1]	Total	% of cases (n=11,030)	Case rate[1]
Northland	13	2.3	7.6	274	3.2	159.9
Auckland[2]	162	29.0	9.9	1626	19.1	99.6
Waikato	52	9.3	13.0	937	11.0	234.5
Bay of Plenty	26	4.7	11.5	292	3.4	128.8
Rotorua	19	3.4	17.8	220	2.6	206.4
Taranaki	15	2.7	12.8	224	2.6	191.8
Hawke's Bay	28	5.0	17.3	1443	17.0	894.1
Gisborne	6	1.1	12.6	135	1.6	282.4
Whanganui	6	1.1	9.5	102	1.2	161.9
Manawatu	21	3.8	12.1	321	3.8	184.3
Wellington[3]	100	17.9	20.2	1843	21.7	371.5
Nelson Marlborough[4]	18	3.2	12.3	483	5.7	329.9
West Coast	6	1.1	18.5	757	8.9	2329.2
Canterbury	70	12.5	13.0	1638	19.2	303.6
South Canterbury	6	1.1	10.1	64	0.8	108.1
Otago	49	8.8	22.2	565	6.6	255.7
Southland	13	2.3	13.3	106	1.2	108.1
Total	**610**	**100**	**13.0**	**11,030**	**100**	**235.1**

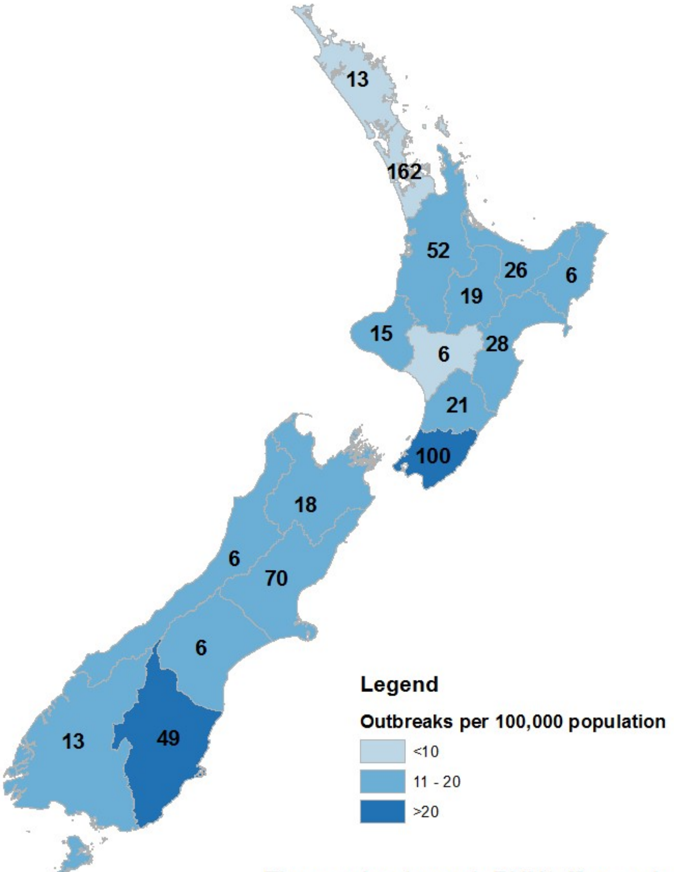
[1] Crude rate of outbreaks per 100,000 population is calculated using Statistics New Zealand population estimates for 2016.

[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 of outbreaks per 100,000 population by PHU, 2016



The number in each PHU/office region
is the count of outbreaks for that region.

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 will conduct epidemiological and microbiological investigations in conjunction with affected PHUs. The Ministry of Health will also be involved in the investigation and response and, if the outbreak is likely to be foodborne, the Ministry for Primary Industries will also be involved.

In 2016, there were no multi-regional gastrointestinal outbreaks investigated at the national level. However, a large localised outbreak of *Campylobacter* associated with a town water supply in Havelock North was investigated by Hawke’s Bay District Health Board (DHB) in collaboration with Hawke’s Bay District Council, Hawke’s Bay Regional Council, ESR, Massey University and the Ministry of Health. A total of 964 cases were officially reported, including 941 from Hawkes Bay DHB and 23 cases from other DHBs. It is estimated that 5500 of Havelock North’s 14,000 residents became ill with campylobacteriosis after consuming contaminated drinking water supplied by two bores on the outskirts of Havelock North [4].

CAUSAL AGENTS

A causal agent was identified in 63.6% (388/610) of outbreaks, involving 76.5% (8436/11,030) of all outbreak-associated cases. In 25 of these outbreaks, two or more causal agents were identified. No specific pathogen or condition was identified in the remaining 222 outbreaks, the vast majority of which were recorded as gastroenteritis (96.8%, 215/222). Acute respiratory infection and influenza-like-illness accounted for the remaining seven outbreaks where no specific pathogen was identified.

As with previous years, enteric agents were implicated in the majority of outbreaks (91.8%, 561/610) and their associated cases (87.6%, 10,378/11,030) (Table 2). Norovirus (30.3%, 185/610) was the most common causal agent implicated in outbreaks in 2016. Norovirus also had the highest proportion of associated cases (50.3%, 5548/11,030) and the highest median number of cases associated with each outbreak (22 cases).

Non-enteric agents accounted for 8.5% (52/610) of outbreaks and 12.8% (1412/11,030) of the outbreak-associated cases in 2016 (Table 2). The most frequently reported non-enteric pathogens and conditions were influenza and influenza-like-illness (3.3% of outbreaks, 20/610). Outbreaks due to influenza and influenza-like-illness also had the highest proportion of associated cases (10.1%, 1119/11,030) and the highest median number of cases associated in each outbreak (20 cases).

Table 2. Outbreaks and associated cases by pathogen, 2016

Pathogen or condition	Outbreaks[1]			Cases[1]	
	Total	% of outbreaks (n=610)	Median cases per outbreak	Total	% of cases (n=11,030)
Enteric	**561**	**91.8**	**10**	**10,378**	**87.6**
Norovirus	185	30.3	22	5548	50.3
Giardia spp.	45	7.4	4	238	2.2
Cryptosporidium spp.	33	5.4	4	188	1.7
Sapovirus	24	3.9	23	668	6.1
Salmonella spp.[2]	24	3.9	3	130	1.2
VTEC/STEC infection	16	2.6	2.5	52	0.5
Campylobacter spp.	15	2.5	3	1008	9.1
Rotavirus	9	1.5	22	223	2.0
Astrovirus	6	1.0	18.5	135	1.2
Yersinia spp.	3	0.5	24	88	0.8
Shigella spp.	2	0.3	6.5	13	0.1
Histamine (scombroid) fish	2	0.3	2.5	5	0.0
Aeromonas spp.	1	0.2	14	14	0.1
Staphylococcus aureus	1	0.2	14	14	0.1
Clostridium difficile	1	0.2	11	11	0.1
Bacillus cereus	1	0.2	7	7	0.1
Ciguatera fish poisoning	1	0.2	4	4	0.0
Clostridium perfringens	1	0.2	2	2	0.0
Pathogen not identified[3]	215	35.2	8	2473	22.4
Non-enteric	**52**	**8.5**	**9.5**	**1412**	**12.8**
Influenza and influenza-like illness[4]	20	3.3	20	1119	10.1
Bordetella pertussis	17	2.8	3	108	1.0
Mycobacterium tuberculosis	5	0.8	6	48	0.4
Measles virus	3	0.5	5	98	0.9
Varicella zoster virus	2	0.3	9	18	0.2
Dengue fever	2	0.3	6	12	0.1
Neisseria meningitidis serogroup B	2	0.3	2	4	0.0
Mumps virus	1	0.2	5	5	0.0

[1] More than one agent was reported in 25 outbreaks, therefore the numbers don't add up to the group totals.

[2] Includes non-typhoidal *Salmonella* species only. No outbreaks of *Salmonella* Typhi or *S.* Paratyphi were reported in 2016.

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

[4] Includes outbreaks of influenza A (8 outbreaks with 850 cases), influenza B (3 outbreaks, 100 cases), parainfluenza (2 outbreaks, 48 cases), acute respiratory infection (5 outbreaks, 94 cases) and influenza-like illness (2 outbreaks, 27 cases).

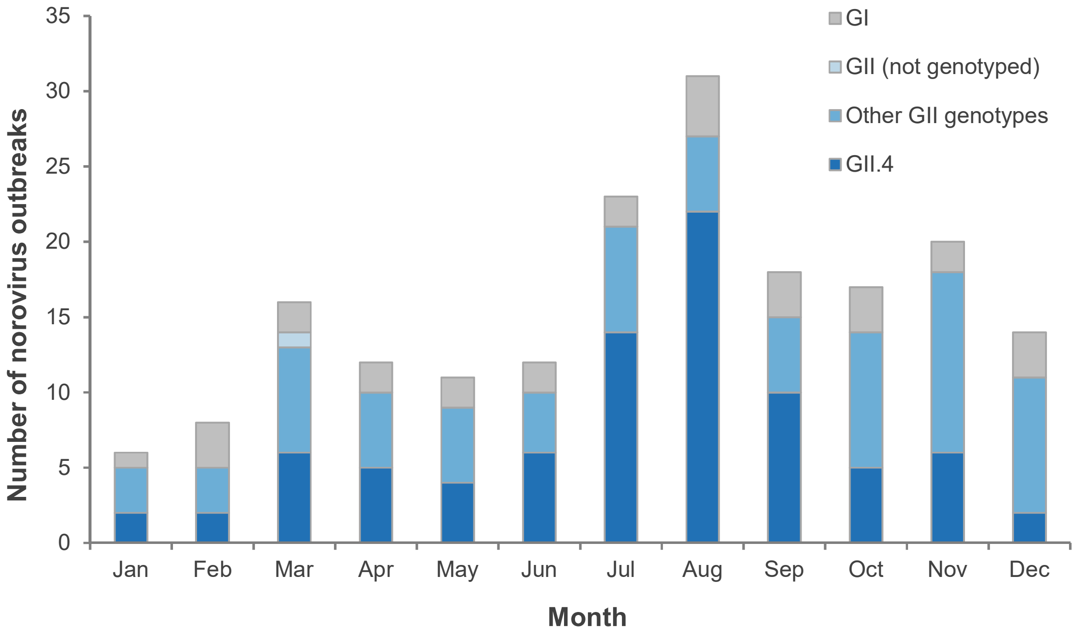
NOROVIRUS OUTBREAKS – GENOTYPES AND OUTBREAK SETTING

Norovirus genotyping is carried out in the Norovirus Reference Laboratory (NRL) at ESR. Phylogenetic analysis is used for genotyping. The Norovirus Typing Tool is used to compare sequences with those in the GenBank database and in the FBVE (Foodborne Viruses in Europe) database [5].

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 samples 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 in EpiSurv.

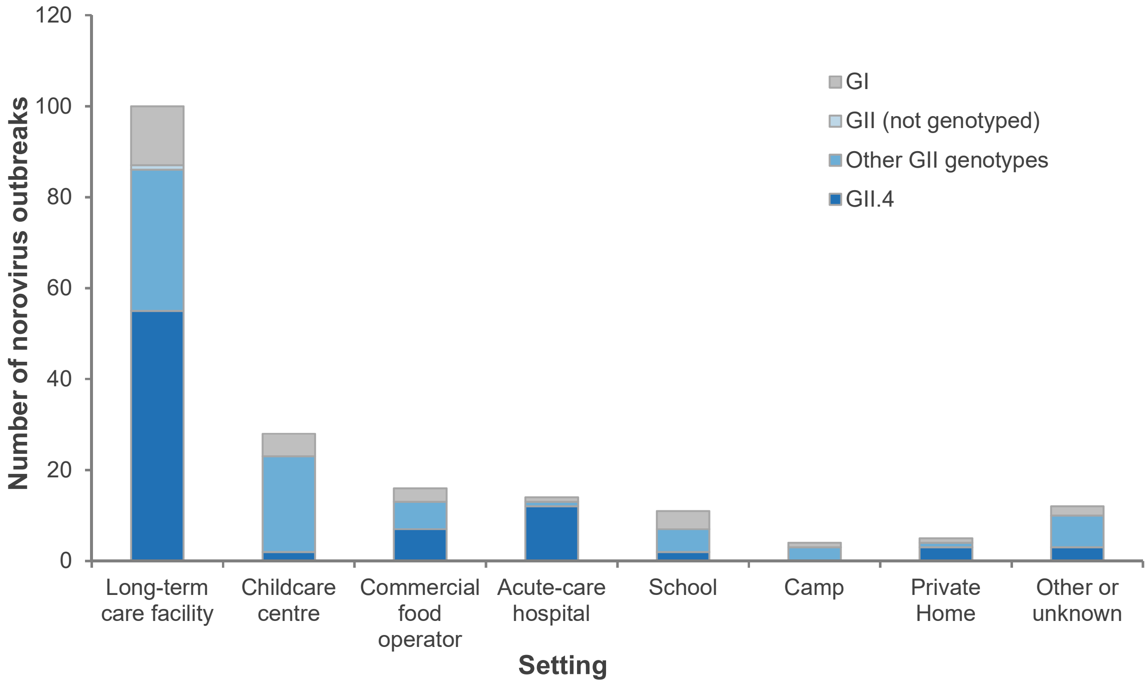
In 2016 there were 188 norovirus outbreaks confirmed by the NRL. This is similar to the number of NRL-confirmed outbreaks in 2015 (184 outbreaks) but a decrease from 2014 (312 outbreaks). The highest number of outbreaks occurred in August (31 outbreaks) and the lowest numbers occurred in January and February (6 and 8 outbreaks respectively) (Figure 2).

Figure 2. NRL-confirmed norovirus outbreaks by month and genotype, 2016



The majority (53.2%, 100/188) of norovirus outbreaks confirmed by the NRL occurred in long-term care facilities (including one where an acute-care hospital was identified as a second setting). Outbreaks were also associated with childcare centres (14.9%, 28/188), commercial food operators (8.5%, 16/188), acute-care hospitals (7.4%, 14/188), schools (5.9%, 11/188, including one where a camp was identified as a second setting), and private homes (2.7%, 5/188). Other settings were reported in 12 outbreaks (Figure 3). The setting was unknown in three outbreaks.

Figure 3. NRL-confirmed norovirus outbreaks by setting and genotype, 2016



Norovirus genogroup II (GII) was identified in 84.6% (159/188) of outbreaks, and norovirus genogroup I (GI) was identified in 15.4% (29/188) of outbreaks.

The norovirus genotype was determined for 98.9% (186/188) of NRL -confirmed outbreaks. One norovirus GII and one GI were unable to be genotyped. GII.4 was the most common genotype identified and was associated with 45.2% (84/186) of genotyped outbreaks. In 2016, three GII.4 variants were identified. The variant in one GII.4 outbreak was not determined. The GII.4 variants identified were New Orleans_2009/Sydney_2012 (34 outbreaks), Sydney_2012 variant (30 outbreaks) and GII.P16/GII.4 (19 outbreaks). This contrasts to 2014 and 2015 when Sydney_2012 variant was the only GII.4 identified. In total, five GI genotypes and seven GII genotypes (as defined by typing of the viral capsid) were identified. The second most common genotype identified in 2016 was GII.P16/GII.2 (14.5%, 27/186), followed by GII.P12/GII.3 and GII.P17/GII.17 (10.2%, 19/186 each) and GI.3 (8.1%, 15/186). Less commonly identified genotypes included GI.6 (3.2%, 6/186), and GII.7 (6%, 6/186).

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 (85.7%, 12/14 and 55.0%, 55/100 respectively), compared with a lower proportion (23.0%,17/74) for other settings.

HOSPITALISATIONS AND DEATHS

Hospitalisation information was recorded for 60.2% (367/610) of outbreaks involving 67.9% (7489/11,030) of associated cases. Of these outbreak-associated cases, 3.3% (194/7489) were hospitalised (Table 3). A higher percentage of cases associated with non-enteric outbreaks were hospitalised (23.8%, 67/282 cases) compared with enteric outbreaks (8.0%, 121/1588 cases). The non-enteric pathogen or condition with the highest proportion of hospitalised cases was *Neisseria meningitidis* serogroup B (100.0%, 2/2 cases), followed by dengue fever (50.0%, 6/12 cases). Of the enteric pathogens and conditions ciguatera fish poisoning (100.0%, 4/4 cases) represented the highest proportion of hospitalised cases, followed by *Salmonella* spp. (83.3%, 15/18 cases).

Ten deaths were associated with eight different outbreaks in 2016. The deaths were associated with *Campylobacter* spp. (3 deaths), norovirus (2), VTEC/STEC infection (1), influenza A (1) and parainfluenza (1). A pathogen was not identified in three deaths (gastroenteritis (2), acute respiratory infection (1)). Note both norovirus and influenza A were identified in one outbreak involving one death.

Table 3. Hospitalised outbreak cases and total outbreak cases by pathogen or condition, 2016

Pathogen or condition	Outbreaks[1]	Cases[1]		
	Total	Total	No. of cases hospitalised[2]	% of cases hospitalised
Enteric	**35**	**1588**	**127**	**8.0**
Campylobacter spp.	2	971	41	4.2
Norovirus	13	409	29	7.1
Sapovirus	2	40	22	55.0
Salmonella spp.[3]	4	18	15	83.3
VTEC/STEC infection	3	9	6	66.7
Ciguatera fish poisoning	1	4	4	100.0
Rotavirus	2	56	2	3.6
Giardia spp.	2	11	2	18.2
Yersinia enterocolitica	1	24	1	4.2
Astrovirus	1	14	1	7.1
Cryptosporidium spp.	1	2	1	50.0
Pathogen not identified[4]	4	37	4	10.8
Non-enteric	**18**	**282**	**67**	**23.8**
Measles virus	2	94	27	28.7
Influenza and influenza-like-illness[5]	5	119	20	16.8
Mycobacterium tuberculosis	4	44	8	18.2
Dengue fever	2	12	6	50.0
Bordetella pertussis	4	11	4	36.4
Neisseria meningitidis serogroup B	1	2	2	100.0
Total	**53**	**1870**	**194**	**10.4**

[1] More than one enteric agent was reported in 25 outbreaks, therefore the numbers don't add up to the group totals.

[2] Hospitalisation information was recorded for 60.2% (367/610) of outbreaks, relating to 67.9% (7489/11,030) of cases. Only outbreaks where one or more hospitalisations were recorded were included in the table (53 outbreaks involving 1870 cases).

[3] Includes non-typhoidal *Salmonella* species only. No outbreaks of *Salmonella* Typhi or *Salmonella* Paratyphi were reported in 2016.

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

[5] Includes outbreaks of influenza A (6 outbreaks with 813 cases), influenza B (2 outbreaks, 70 cases), acute respiratory infection (2 outbreaks, 57 cases) and influenza-like illness (1 outbreak, 14 cases).

OUTBREAK SETTINGS

The most common outbreak setting recorded was long-term care facilities (33.3%, 203/610) followed by childcare centres (18.0%, 110/610) and private homes (16.4%, 100/610). Outbreaks in long-term care facilities had the highest number of associated cases (39.8%, 4393/11,030) (Table 4). Overall, 65.1% (397/610) of all outbreaks and 78.3% (8636/11,030) of cases reported in 2016 were set in institutions. The setting was unknown in 3.1% (19/610) of outbreaks.

Table 4. Outbreaks and associated cases by setting of exposure/transmission, 2016

Outbreak setting	Outbreaks[1]		Cases[1]	
	Total	% of outbreaks (n=610)	Total	% of cases (n=11,030)
Institutions	**397**	**65.1**	**8636**	**78.3**
Long-term care facility	203	33.3	4393	39.8
Childcare centre	110	18.0	2095	19.0
School	29	4.8	1363	12.4
Hospital (acute-care)	29	4.8	370	3.4
Camp	8	1.3	188	1.7
Hotel/motel	4	0.7	77	0.7
Hostel/boarding house	3	0.5	30	0.3
Other institution	15	2.5	199	1.8
Commercial food operators	**70**	**11.5**	**474**	**4.3**
Restaurant/café/bakery	46	7.5	317	2.9
Takeaway	11	1.8	48	0.4
Supermarket/delicatessen	3	0.5	7	0.1
Caterer	1	0.2	10	0.1
Fast food restaurant	1	0.2	7	0.1
Other food outlet	9	1.5	88	0.8
Workplace	**9**	**1.5**	**35**	**0.3**
Farm	5	0.8	15	0.1
Workplace	4	0.7	20	0.2
Other	**128**	**21.0**	**1728**	**15.7**
Private home	100	16.4	411	3.7
Other setting	22	3.6	228	2.1
Community/church or sports gathering	8	1.3	1102	10.0
Aeroplane	1	0.2	5	0.0
Unknown setting	**19**	**3.1**	**267**	**2.4**

[1] More than one setting was recorded in 21 outbreaks, therefore the numbers don't add up to the group totals.

MODES OF TRANSMISSION

In 2016, the most commonly reported mode of transmission was person-to-person (82.3%, 502/610 outbreaks), followed by foodborne (15.6% 95/610) and environmental (11.1%, 68/610) (Table 5). Person-to-person transmission also accounted for the highest percentage of associated cases (85.0%, 9376/11,030), followed by environmental transmission (16.7%, 1842/11,030). The mode of transmission was unknown for 4.1% (25 outbreaks).

Table 5. Outbreaks and associated cases by mode of transmission, 2016

Mode of transmission	Outbreaks				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=610)[1]	Total	% of cases (n=11,030)[1]
Person-to-person	414	88	502	82.3	9376	85.0
Foodborne	78	17	95	15.6	1139	10.3
Environmental	13	55	68	11.1	1842	16.7
Waterborne	10	4	14	2.3	1007	9.0
Zoonotic	8	5	13	2.1	47	0.4
Vectorborne	2	0	2	0.3	12	0.1
Other	2	0	2	0.3	5	0.0
Unknown	-	-	25	4.1	111	1.0

[1] More than one mode of transmission was recorded for 98 outbreaks therefore the totals add up to more than 100%.

Note: No outbreaks with sexual contact or parenteral transmission were reported in 2016.

In 2016, a higher proportion of cases (9.0%) were associated with waterborne outbreaks than in previous years (2015: 1.0%, 2014: 0.9%, 2013: 3.2%). This was primarily due to a large *Campylobacter* outbreak (involving 964 cases) linked to drinking water in Havelock North.

FOODBORNE OUTBREAKS

Causal agent

Of the 95 foodborne outbreaks reported in 2016 (with 1139 associated cases), 54.7% (52/95 outbreaks) were linked to a pathogen or condition (Table 6). Pathogens most commonly associated with foodborne outbreaks were norovirus (18.9%, 18/95 outbreaks) and *Salmonella* spp. (12.6%, 12/95 outbreaks). Enteric bacteria (*Campylobacter* spp., *Salmonella* spp., *Yersinia* spp., *Shigella* spp., VTEC/STEC, *S. aureus, B. cereus* and *C. perfringens*) were implicated in 28.4% (27/95) of the foodborne outbreaks. Enteric viruses (norovirus and sapovirus) were implicated in 20.0% (19/95) of the foodborne outbreaks.

Table 6. Foodborne outbreaks and associated cases by pathogen or condition, 2016

Pathogen or condition	Outbreaks		Cases	
	Total	% of outbreaks (n=95)[1]	Total	% of cases (n=1139)[1]
Norovirus	18	18.9	542	47.6
Salmonella spp.	12	12.6	78	6.8
Campylobacter spp.	8	8.4	28	2.5
Giardia spp.	4	4.2	18	1.6
Yersinia spp.	2	2.1	75	6.6
Histamine (scombroid) fish poisoning	2	2.1	5	0.4
Sapovirus	1	1.1	65	5.7
Staphylococcus aureus	1	1.1	14	1.2
VTEC/STEC infection	1	1.1	11	1.0
Shigella spp.	1	1.1	8	0.7
Bacillus cereus	1	1.1	7	0.6
Ciguatera fish poisoning	1	1.1	4	0.4
Clostridium perfringens	1	1.1	2	0.2
Cryptosporidium spp.	1	1.1	2	0.2
Pathogen not identified[2]	43	45.3	292	25.6

[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 83.2% (79/95) of foodborne outbreaks and 70.1% (799/1139) of associated cases in 2016. The preparation settings most commonly associated with foodborne outbreaks included commercial food operators (60.0%, 57/95) and private homes (9.5%, 9/95) (Table 7). Foodborne outbreaks where the food was prepared in restaurants, cafés, or bakeries had the highest number of associated cases (20.4%, 232/1139).

Table 7. Foodborne outbreaks and associated cases by setting of food preparation, 2016

Preparation setting	Outbreaks		Cases[1]	
	Total	% of outbreaks (n=95)	Total	% of cases (n=1139)
Commercial food operators	**57**	**60.0**	**329**	**28.9**
Restaurant/café/bakery	35	36.8	232	20.4
Takeaway	12	12.6	52	4.6
Supermarket/delicatessen	3	3.2	7	0.6
Fast food restaurant	1	1.1	7	0.6
Other food outlet	7	7.4	34	3.0
Institutions	**8**	**8.4**	**260**	**22.8**
Long-term care facility	2	2.1	38	3.3
Hotel/motel	2	2.1	67	5.9
School	1	1.1	68	6.0
Childcare centre	1	1.1	54	4.7
Camp	1	1.1	24	2.1
Hostel/boarding house	1	1.1	9	0.8
Other	**16**	**16.8**	**214**	**18.8**
Private home	9	9.5	45	4.0
Community/church gathering	2	2.1	62	5.4
Workplace	1	1.1	5	0.4
Farm	1	1.1	2	0.2
Overseas manufacturer	1	1.1	2	0.2
Other setting	2	2.1	98	8.6
Unknown preparation setting	**16**	**16.8**	**340**	**29.9**

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

Additional information on foodborne outbreaks can be found in the Foodborne disease in New Zealand 2016 report [6].

PERSON-TO-PERSON OUTBREAKS

Causal agents

In 2016, there were 502 person-to-person outbreaks (primary and secondary mode of transmission) with 9376 associated cases. A causal agent was identified in 66.7% (335/502) of these outbreaks. The most common causal agent was norovirus, which was recorded in 34.9% (175/502) of person-to-person outbreaks and involved 57.7% (5412/9376) of outbreak-associated cases (Table 8). Other common pathogens and conditions included *Giardia* spp. (6.6%, 33/502) and sapovirus (4.8%, 24/502). Influenza or influenza-like illness accounted for 20 (4.0%) outbreaks and had a high number of associated cases (11.9%, 1119/9376).

Table 8. Person-to-person outbreaks and associated cases by pathogen or condition, 2016

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=502)[2]	Total	% of cases (n=9376)[2]
Norovirus	145	30	175	34.9	5412	57.7
Giardia spp.	28	5	33	6.6	178	1.9
Sapovirus	21	3	24	4.8	668	7.1
Cryptosporidium spp.	17	4	21	4.2	132	1.4
Influenza and influenza-like-illness[3]	19	1	20	4.0	1119	11.9
Bordetella pertussis	16	1	17	3.4	108	1.2
Salmonella spp.[4]	10	5	15	3.0	91	1.0
VTEC/STEC infection	9	5	14	2.8	37	0.4
Rotavirus	7	2	9	1.8	223	2.4
Astrovirus	5	1	6	1.2	135	1.4
Mycobacterium tuberculosis	5	0	5	1.0	48	0.5
Campylobacter spp.	3	2	5	1.0	14	0.1
Measles virus	3	0	3	0.6	98	1.0
Varicella zoster virus	2	0	2	0.4	18	0.2
Neisseria meningitidis serogroup B	1	1	2	0.4	4	<0.1
Aeromonas spp.	0	1	1	0.2	14	0.1
Yersinia spp.	1	0	1	0.2	13	0.1
Clostridium difficile	1	0	1	0.2	11	0.1
Shigella spp.	1	0	1	0.2	5	0.1
Mumps virus	1	0	1	0.2	5	0.1
Pathogen not identified[5]	138	29	167	33.3	2206	23.5

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

[2] Multiple agents were reported in 20 person-to-person outbreaks, therefore the totals add up to more than 100%.

[3] Includes non-typhoidal *Salmonella* species only. No outbreaks of *Salmonella* Typhi or *S.* Paratyphi were reported in 2016.

[4] Includes outbreaks of influenza A (8 outbreaks with 850 cases), influenza B (3 outbreaks, 100 cases), parainfluenza (2 outbreaks, 48 cases), acute respiratory infection (5 outbreaks, 94 cases) and influenza-like illness (2 outbreaks, 27 cases).

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

WATERBORNE OUTBREAKS

Causal agents

There were 14 waterborne outbreaks with 1007 associated cases in 2016. A causal agent was identified in most (92.9%, 13/14) of the outbreaks (Table 9). The most commonly reported waterborne pathogens and conditions were *Giardia* spp. (35.7%, 5/14 outbreaks), *Cryptosporidium* spp. and VTEC/STEC infection (21.4%, 3/14 outbreaks each). In 2016 the largest proportion of cases linked to waterborne outbreaks was due to *Campylobacter* spp. This was due to a large outbreak involving 964 notified cases associated with a contaminated drinking water supply in Havelock North during August 2016. This was the largest waterborne outbreak recorded in New Zealand since recording began in EpiSurv in 1997.

Table 9. Waterborne outbreaks and associated cases by pathogen, 2016

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=14)	Total	% of cases (n=1007)
Giardia spp.	4	1	5	35.7	16	1.6
Cryptosporidium spp.	3	-	3	21.4	9	0.9
VTEC/STEC infection	2	1	3	21.4	9	0.9
Campylobacter spp.	1	1	2	14.3	967	96.0
Pathogen not identified[2]	-	1	1	7.1	6	0.6

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

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

ENVIRONMENTAL OUTBREAKS

Causal agents

There were 68 environmental outbreaks with 1842 associated cases reported in 2016. Of these outbreaks, 73.5% (50/68) were linked to a specific causal agent (Table 10). The most common causal agent identified in environmental outbreaks was norovirus (38.2%, 26/68), followed by *Giardia* spp. (14.7%, 10/68). Environmental transmission was the secondary mode reported in all of the norovirus outbreaks. Norovirus also accounted for the highest proportion of associated cases (70.0%, 1350/1842) followed by influenza A (38.2%, 737/1842).

Table 10. Environmental outbreaks and associated cases by pathogen or condition, 2016

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=68)[2]	Total	% of cases (n=1842)[2]
Norovirus	0	26	26	38.2	1350	70.0
Giardia spp.	6	4	10	14.7	56	2.9
Cryptosporidium spp.	5	0	5	7.4	41	2.1
VTEC/STEC infection	0	3	3	4.4	9	0.5
Campylobacter spp.	0	3	3	4.4	9	0.5
Influenza A	0	2	2	2.9	737	38.2
Sapovirus	0	2	2	2.9	48	2.5
Rotavirus	0	2	2	2.9	29	1.5
Salmonella spp.	2	0	2	2.9	5	0.3
Astrovirus	0	1	1	1.5	14	0.7
Pathogen not identified[3]	2	16	18	26.5	315	16.3

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

[2] Two pathogens were reported in six environmental outbreaks, 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 47 associated cases in 2016. All were linked to a specific pathogen (Table 11). *Cryptosporidium* spp. was the most commonly identified pathogen and was linked to 30.8% (4/13) of zoonotic outbreaks and 44.7% (21/47) of the associated cases.

Table 11. Zoonotic outbreaks and associated cases by pathogen or condition, 2016

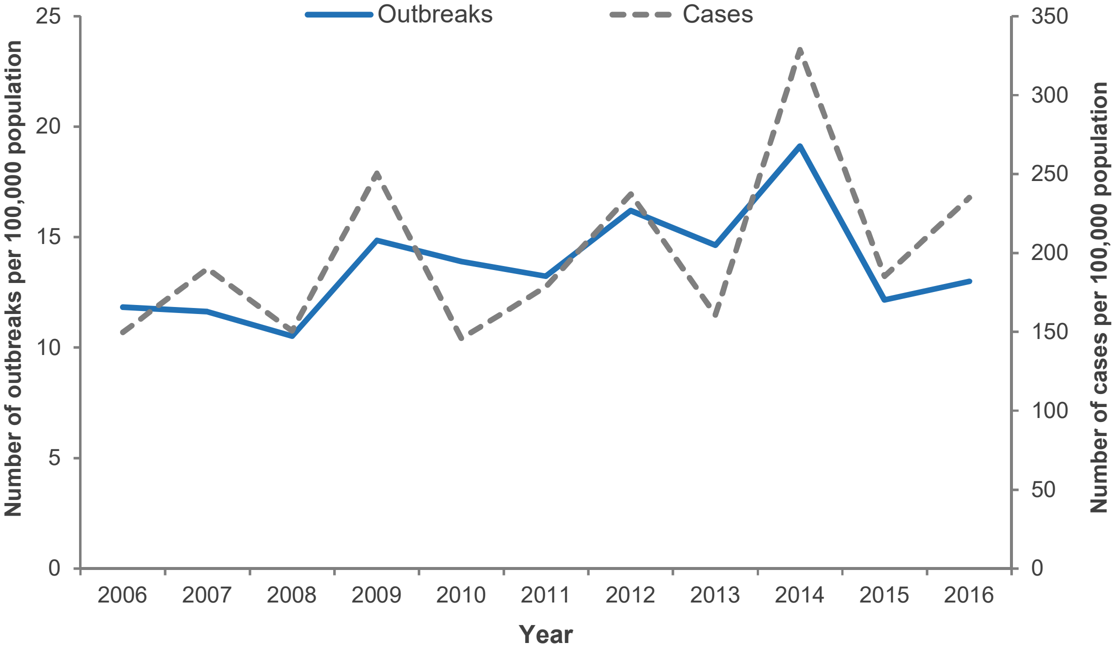
Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=13)	Total	% of cases (n=47)
Cryptosporidium spp.	3	1	4	30.8	21	44.7
Giardia spp.	1	2	3	23.1	11	23.4
Campylobacter spp.	2	1	3	23.1	8	17.0
VTEC/STEC infection	2	1	3	23.1	7	14.9

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

TIME TRENDS 2006–2016

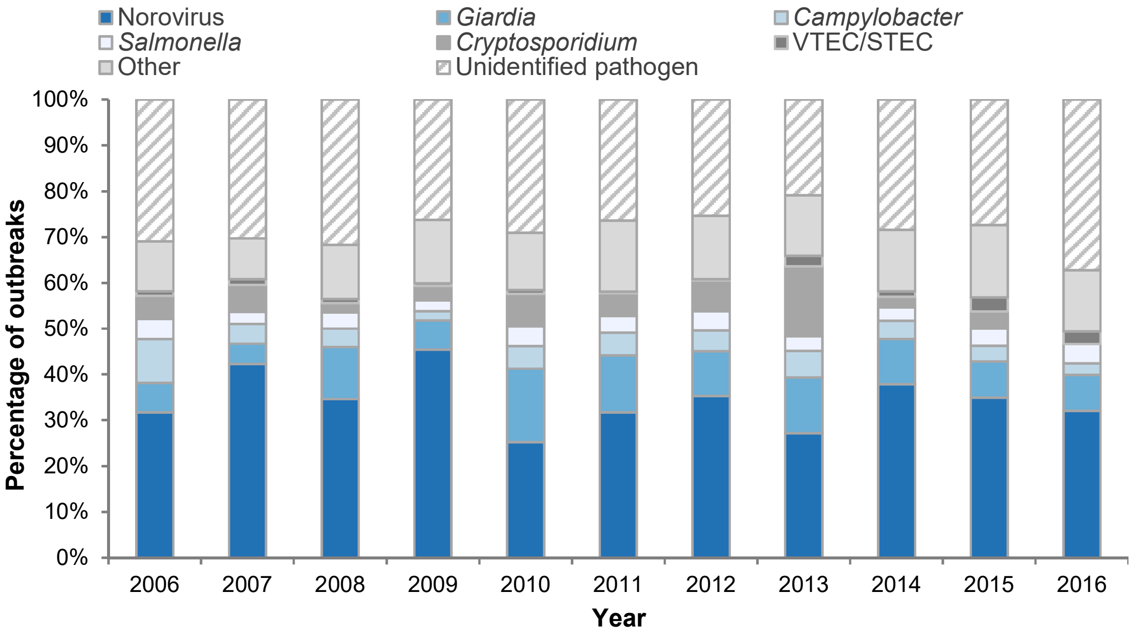
Between 2006 and 2014, both the number of outbreaks per 100,000 population and the number of cases per 100,000 increased overall, although there was a lot of variability during that time period. The outbreak rate peaked in 2014 (19.1 outbreaks per 100,000 population) and then decreased significantly ($p<0.05$) in 2015 to 12.2 outbreaks per 100,000. The rate in 2016 (13.0 outbreaks per 100,000) was similar to that reported in 2015 (Figure 4). Similarly, the number of cases per 100,000 peaked in 2014 with 328.7 of cases per 100,000 and then decreased to 185.3 per 100,000 in 2015. However, the rate increased significantly in 2016 to 235.1 per 100,000 population, which is largely due to the Havelock North campylobacteriosis outbreak (involving 964 cases) reported in August 2016.

Figure 4. Outbreaks and associated cases per 100,000 by year, 2006–2016



From 2006 to 2015, the proportion of outbreaks linked to an identified causal agent was around 75% (range 68.7–79.3%). In 2016, this proportion was lower at 64.8% (395/610). The causal agent associated with the highest number of outbreaks and outbreak cases during 2006–2015 was norovirus, although the number and percentage varied considerably from year to year. In 2016, 185 norovirus outbreaks were reported with 5548 associated cases. This figure is much lower than the number of norovirus outbreaks reported in 2014 (326 outbreaks and 9390 cases), when the highest number of norovirus outbreaks and cases were recorded since reporting began in EpiSurv in 1997. Since 2006, norovirus outbreaks have accounted for around a third of outbreaks reported each year, with the exception of 2009 when the proportion was 45.4% (290/639 outbreaks) (Figure 5).

Figure 5. Percentage of outbreaks by pathogen or condition and year, 2006–2016



The number of reported rotavirus outbreaks has progressively increased, from six in 2006 (78 cases) to 47 in 2014 (854 cases). In 2015, there was a significant decrease in the number of rotavirus outbreaks (three outbreaks including two where norovirus was also identified) and associated cases (57 cases) reported. This decrease is most likely associated with the introduction of rotavirus vaccine to the infant immunisation schedule in July 2014 [7]. In 2016, there were nine rotavirus outbreaks (with 223 associated cases) including two outbreaks where influenza A was also identified and one outbreak where norovirus was also identified. Five outbreaks were in childcare centres in the Wellington region, and the remaining four outbreaks were in long-term care facilities.

There was a decrease in the number of outbreaks due to VTEC/STEC infection in 2016 (16 outbreaks, 52 cases) compared to 2015 (17 outbreaks, 94 cases). 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 common mode of transmission (primary and secondary) reported for VTEC/STEC outbreaks in 2016 was person-to-person (14 outbreaks, 37 cases). The introduction of more sensitive testing methods in diagnostic laboratories since mid-2015 may have contributed to the increased detection of outbreaks of some enteric diseases.

The number of outbreaks and cases due to *Cryptosporidium* spp. increased in 2016 (33 outbreaks, 188 cases) compared with 2015 (21 outbreaks, 94 cases). However, the number of outbreaks and cases were significantly lower than reported in 2013 (99 outbreaks, 550 cases) when outbreaks of *Cryptosporidium* spp. peaked. The most common mode of transmission (primary and secondary) reported for *Cryptosporidium* spp. outbreaks in 2016 was person-to-person (21 outbreaks, 132 cases).

The number of outbreaks due to *Giardia* spp. increased from 2007 (22 outbreaks, 117 cases) and peaked in 2010 (97 outbreaks, 378 cases). In 2016, there were 45 outbreaks with 238 associated cases, similar to 2015 (45 outbreaks, 207 cases) and significantly lower than the number of outbreaks reported between 2010 and 2014 (range 70–97). The most common mode of transmission (primary and secondary) reported for *Giardia* spp. outbreaks in 2016 was person-to-person (33 outbreaks, 178 cases).

There was a large reduction in the number of outbreaks and associated cases 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 [8]. 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 (15 outbreaks) was the lowest since 2009, while the number of associated cases was the largest since recording began (1008 cases). The Havelock North waterborne outbreak in August 2016 accounted for 964 notified cases. There were 44 cases associated with the remaining 14 outbreaks reported in 2016. More than half (57.1%, 8/14) were due to foodborne transmission; raw milk was implicated in three of the outbreaks involving 16 cases and chicken liver pate was implicated in three outbreaks involving seven cases. A source was not identified in the other two foodborne outbreaks.

Outbreaks of other pathogens and conditions that have emerged in recent years include varicella zoster virus (chicken pox) (2014: 2 outbreaks, 45 cases; 2015: 1 outbreak, 22 cases, 2016: 2 outbreaks, 18 cases) and respiratory syncytial virus (RSV) (2015: 1 outbreak, 33 cases). In 2016 there were two outbreaks of dengue fever involving 12 cases. Both outbreaks involved travel groups to Bali, Indonesia, where the infection was acquired. Prior to these, the last dengue fever outbreaks were reported in 2010 (2 outbreaks, 4 cases).

In 2016, there were three outbreaks of measles involving 98 cases reported. This was higher than reported in 2015 (2 outbreaks, 6 cases) and also the fourth highest number of outbreak cases for measles since recording began in EpiSurv in 1997. The years with the largest number of measles outbreak cases were 2011 (6 outbreaks, 582 cases), 2014 (19 outbreaks, 243 cases) and 2009 (3 outbreaks, 205 cases). Waikato DHB reported the largest outbreak in 2016 involving 89 cases across five DHBs.

The most common outbreak settings in 2016 were long-term care facilities, childcare centres and private homes. Approximately one fifth (18.0%, 100 outbreaks) of outbreaks were set in childcare centres, which is the highest proportion since recording began (range 2.4–15.5%). Since 2006, outbreaks in institutions have accounted for 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.

Outbreaks involving person-to-person transmission have been the most frequently reported mode of transmission since 2006. This was a change from foodborne transmission, which was the most frequent mode between 1998 and 2006 (range 28.3–52.9%). Between 2007 and 2016, the proportion of foodborne outbreaks reported each year ranged from 13.2 to 23.3% (2016: 15.6%, 95 outbreaks). In 2016, the number of outbreaks with person-to-person transmission (82.3%, 502/610) was more than four times higher than any other mode of transmission, similar to the previous five years. Foodborne transmission (15.6%, 95/610) was the second most common mode of transmission in 2016. In outbreaks reported from 2013 to 2015 environmental transmission was the second most common mode of transmission reported.

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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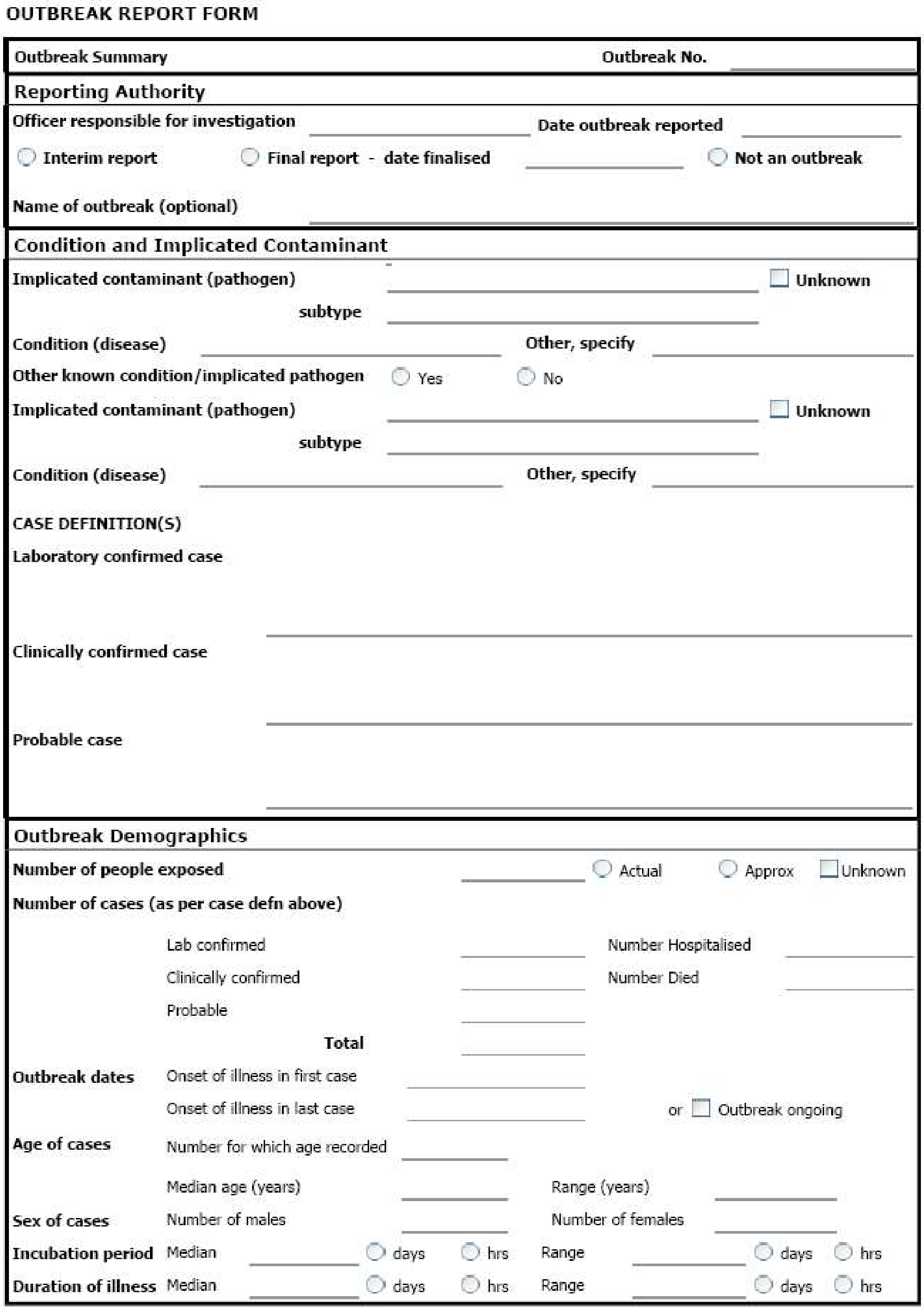
APPENDIX

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

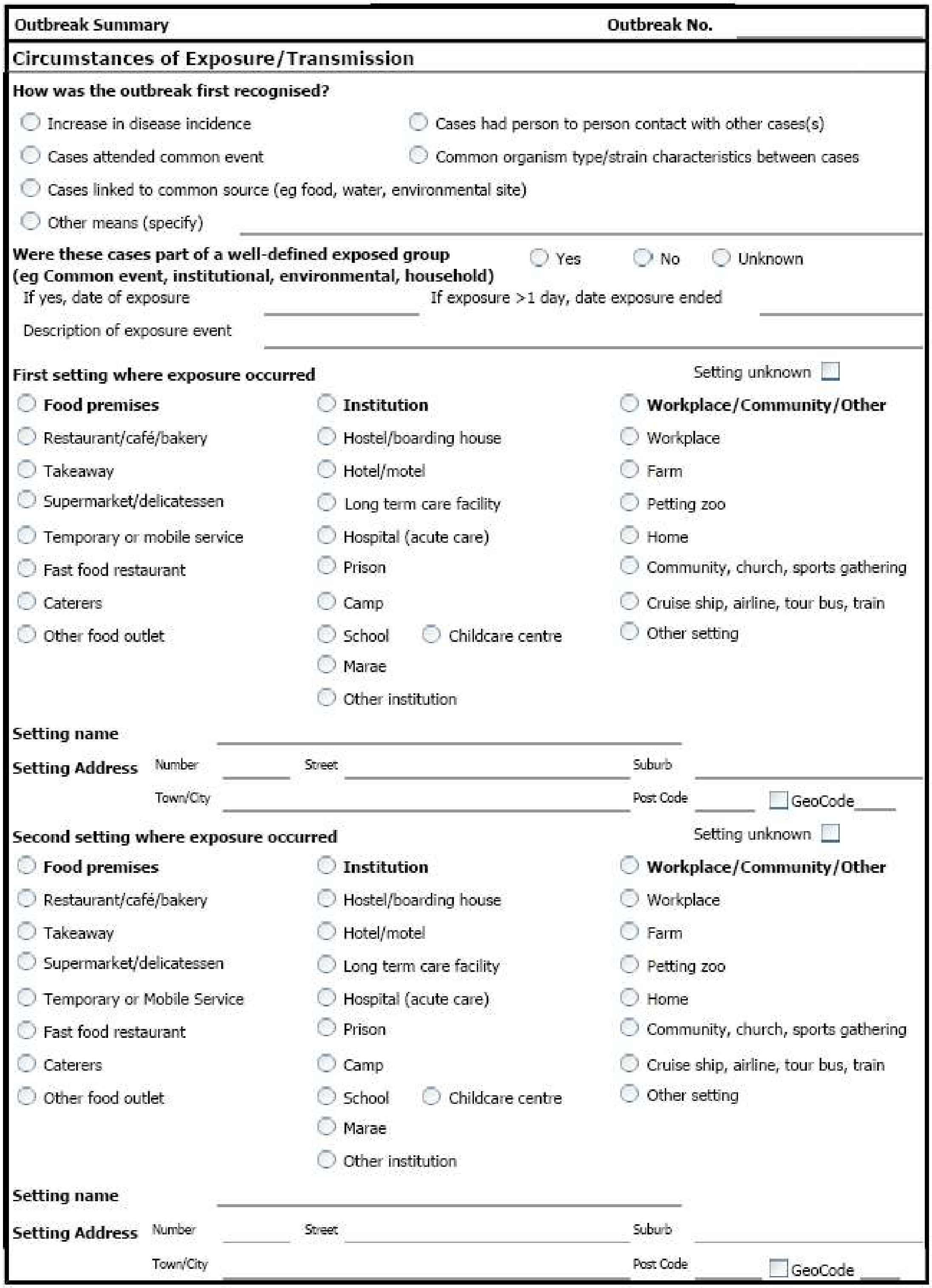
Age of cases Number for which age recorded ____________

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

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 ☐

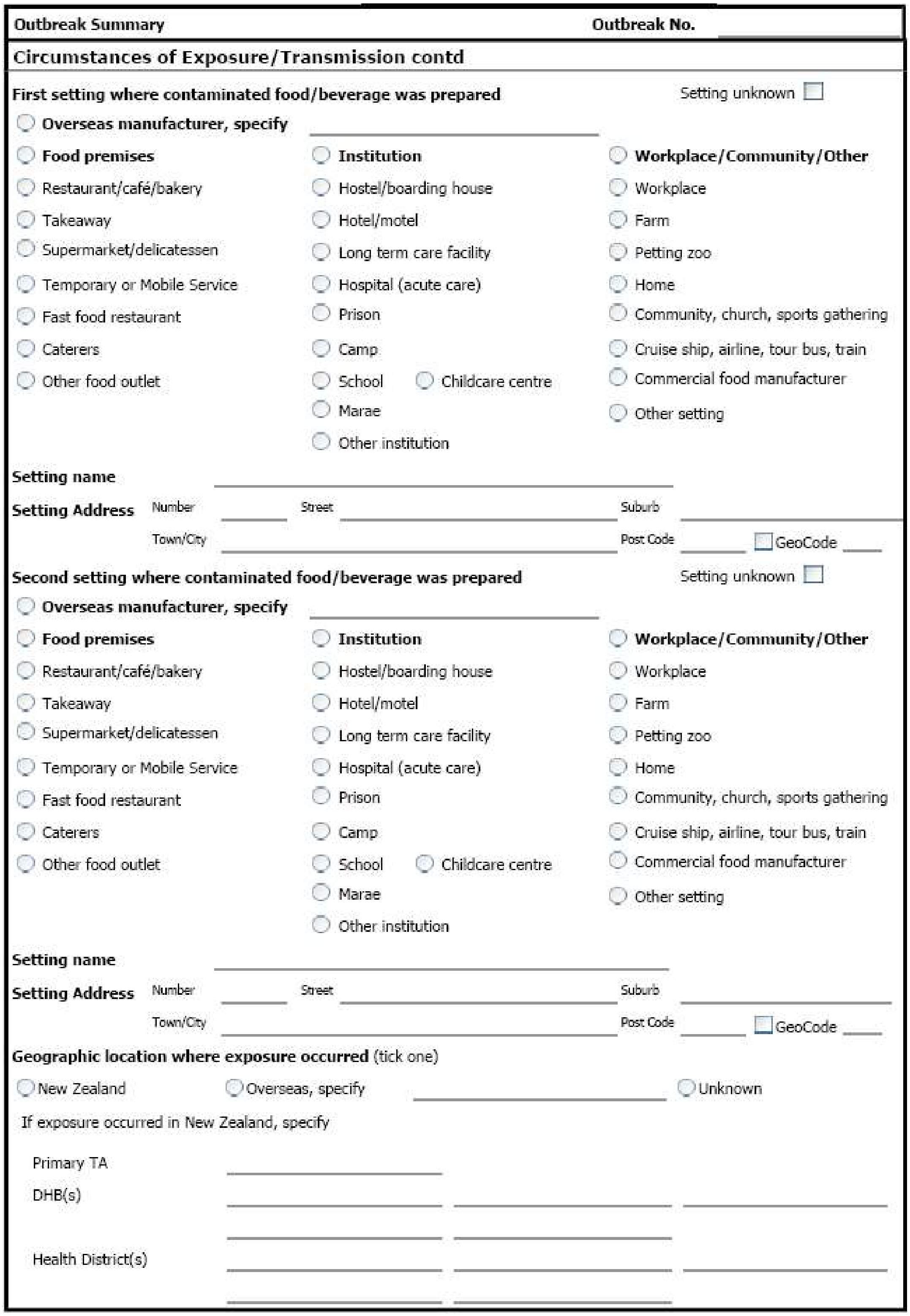
○ **Food premises**
○ Restaurant/café/bakery
○ Takeaway
○ Supermarket/delicatessen
○ Temporary or Mobile Service
○ Fast food restaurant
○ Caterers
○ Other food outlet

○ **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 ________

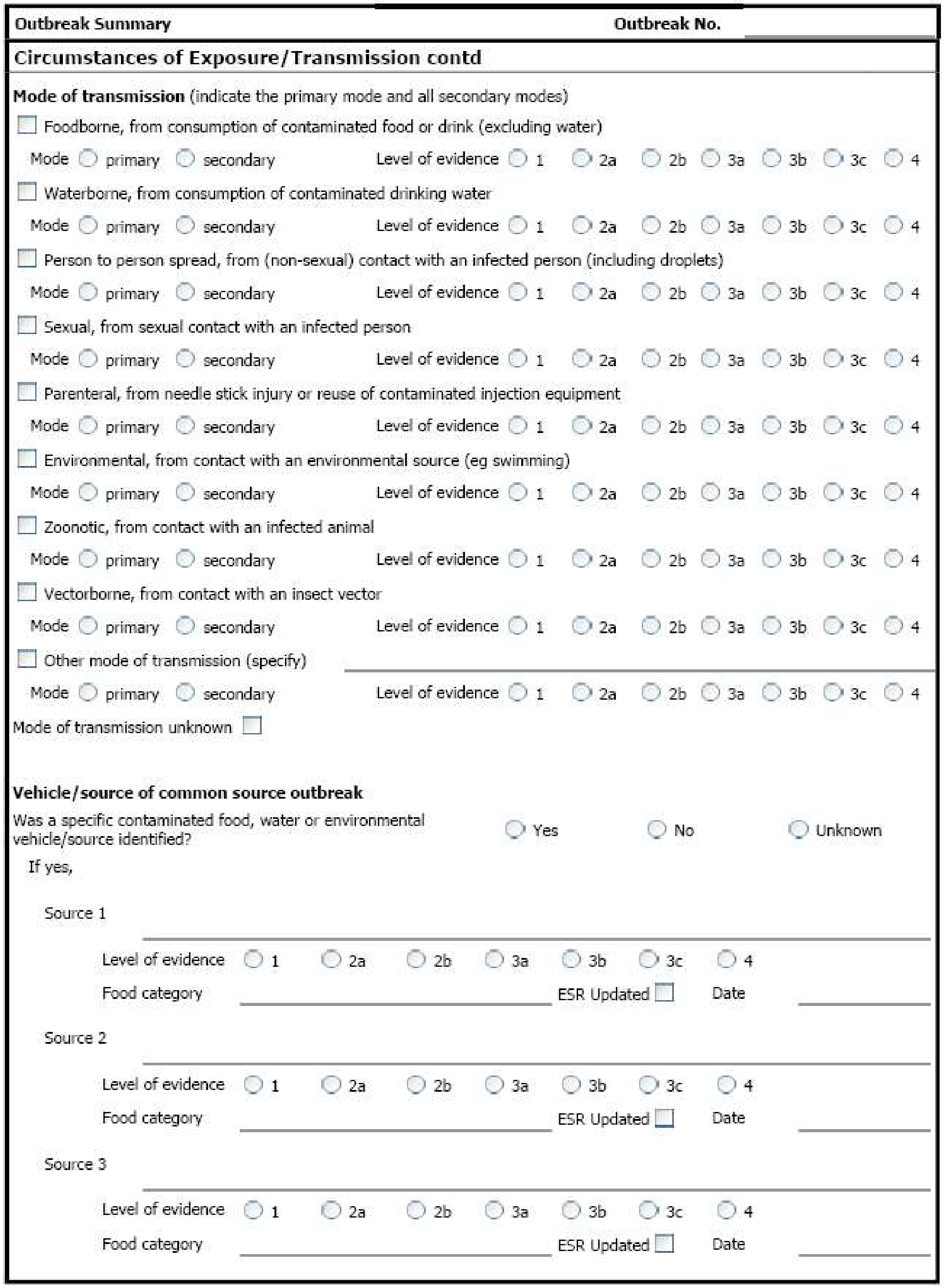
Setting Address Number ____ Street ________ Suburb ________
Town/City ________ Post Code ____ ☐ GeoCode ____

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

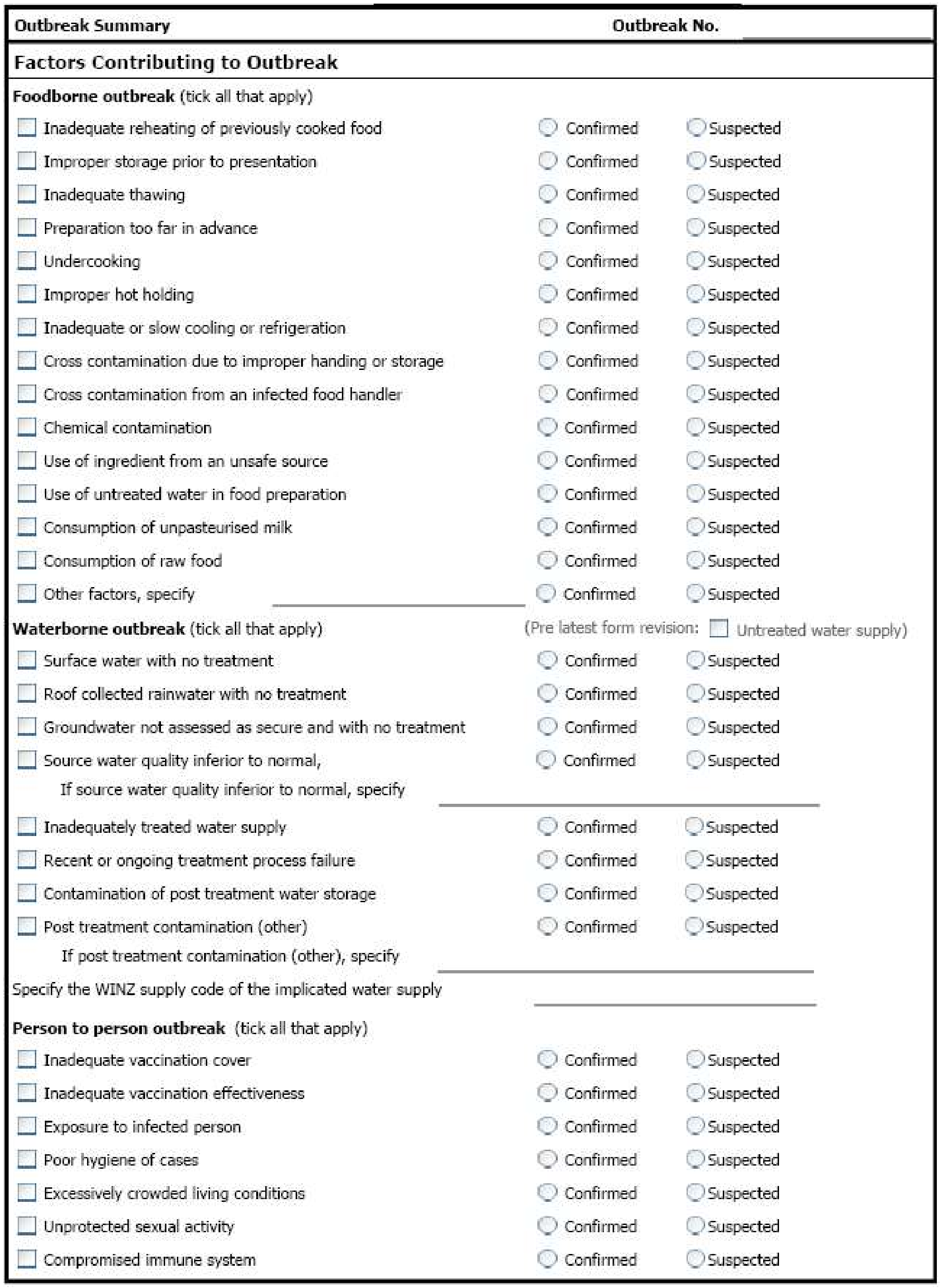
Was a specific contaminated food, water or environmental vehicle/source identified? ○ Yes ○ No ○ Unknown

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

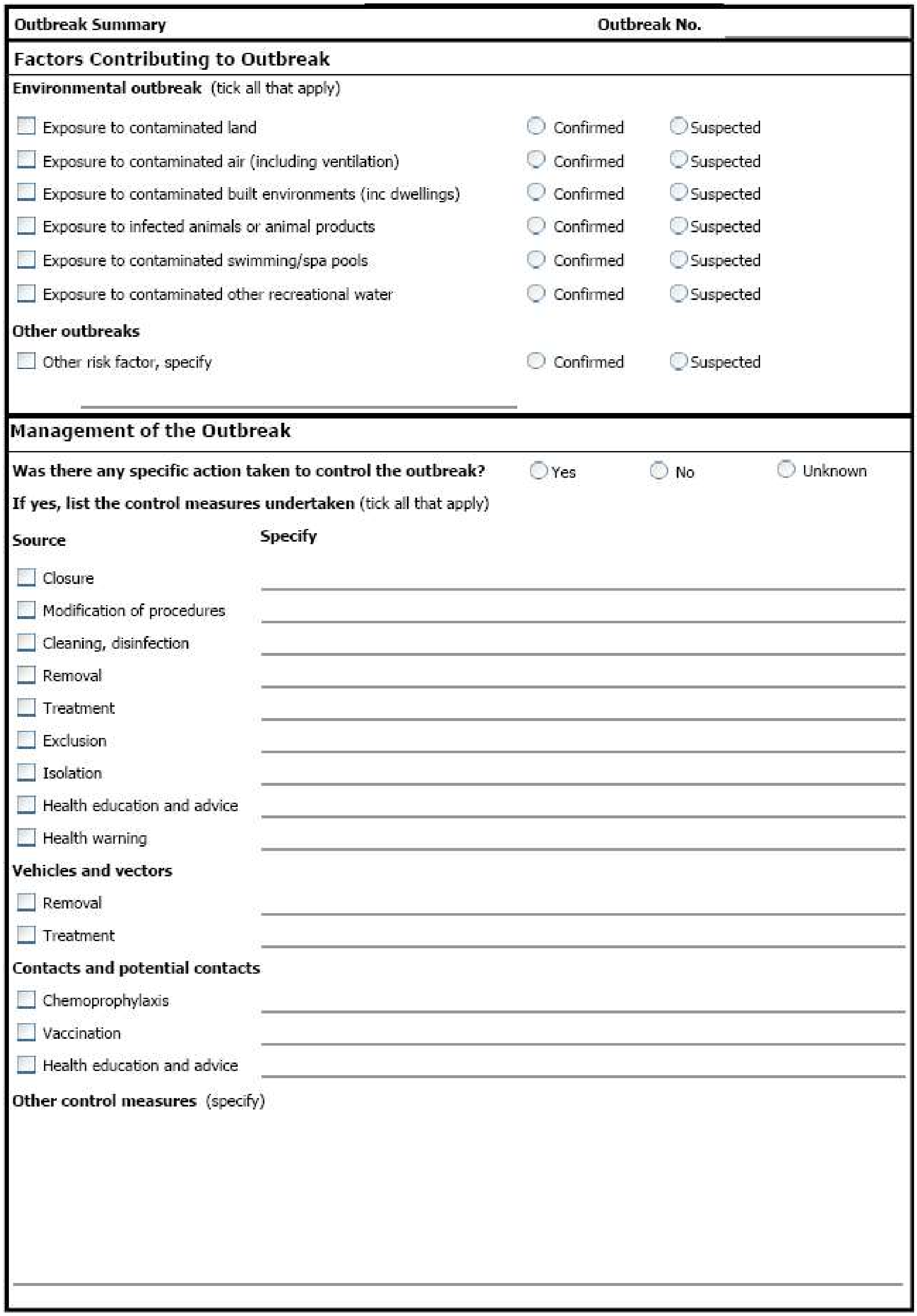
Waterborne outbreak (tick all that apply) (Pre latest form revision: ☐ Untreated water supply)

☐ 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

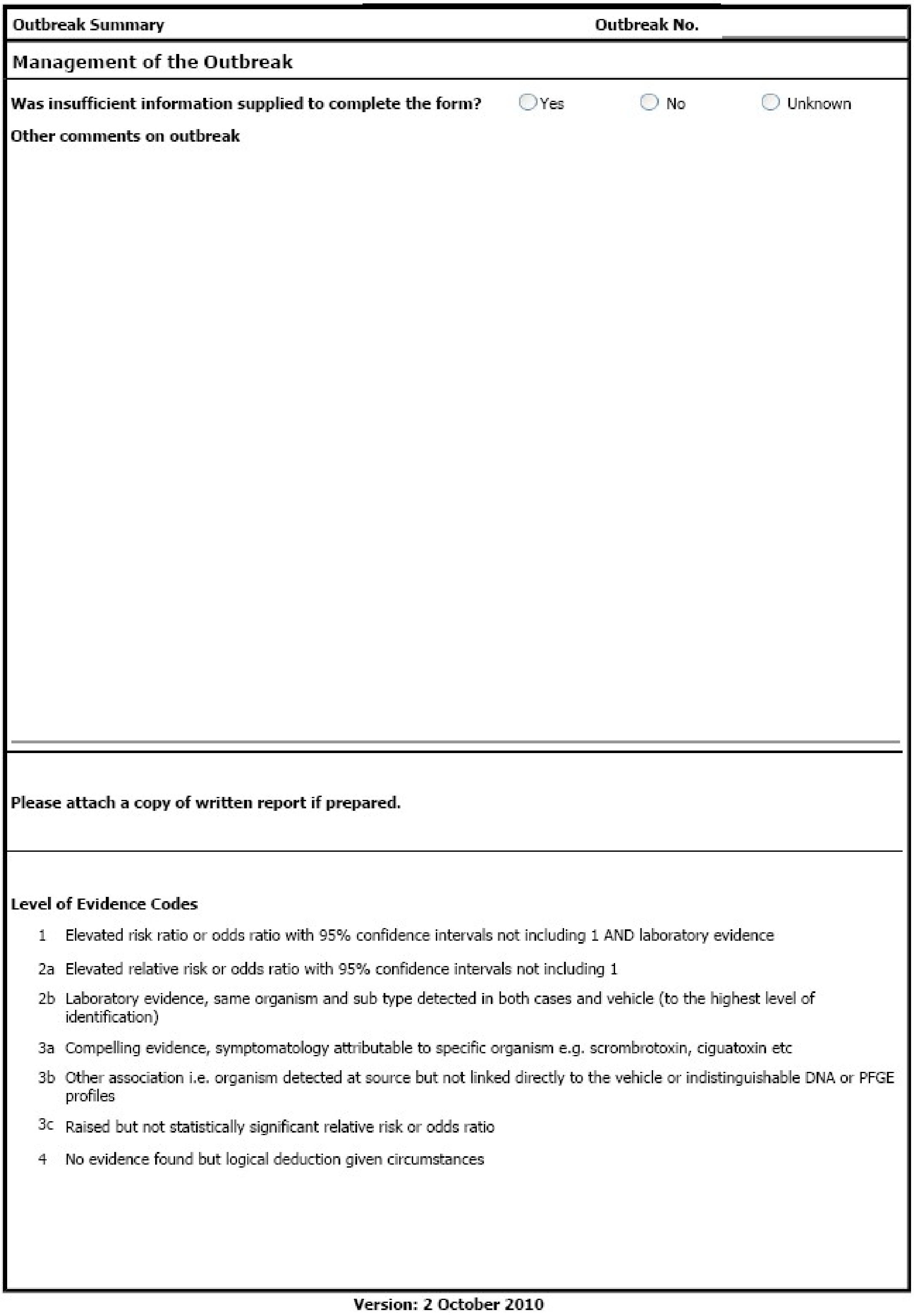
Was there any specific action taken to control the outbreak? ○ Yes ○ No ○ Unknown

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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