SURVEILLANCE REPORT

SUMMARY OF OUTBREAKS IN NEW ZEALAND 2015

E/S/R

THE SCIENCE BEHIND THE TRUTH

Prepared as part of a Ministry of Health contract for scientific services by the Health Intelligence Team, Institute of Environmental Science and Research Limited

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SUMMARY

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SUMMARY

This report summarises data on outbreaks that were reported to the Institute of Environmental Science and Research Limited (ESR) during 2015.

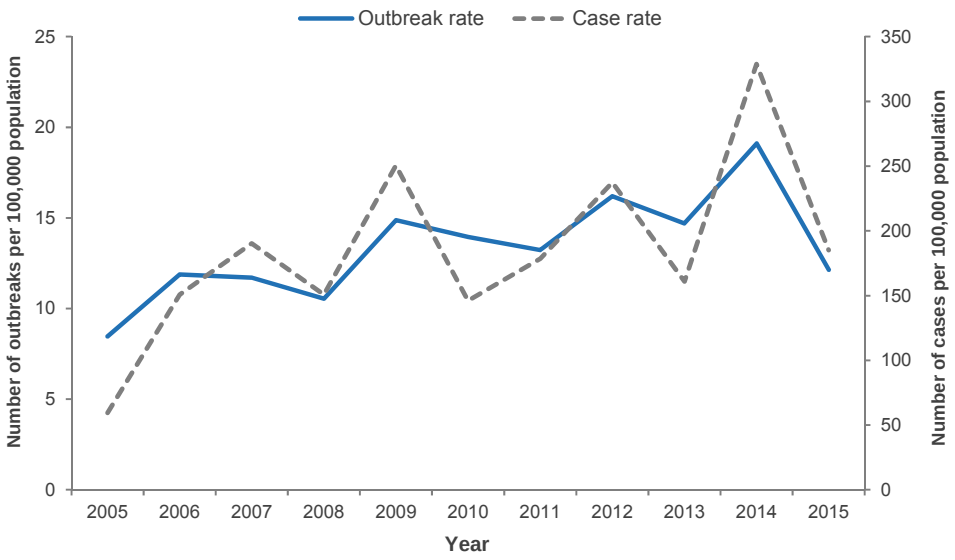
Key findings were:

OUTBREAK AND ASSOCIATED-CASE RATE LOW IN 2015

There was a significant decrease in reported outbreaks (▼35.3%, 558 outbreaks) and cases associated with outbreaks (▼42.6%, 8510 cases) compared with 2014 (862 outbreaks involving 14,825 cases). A total of 161 (3.3%) outbreak associated cases were hospitalised (3.5% in 2014) and 19 cases died (28 cases in 2014).

The outbreak rate of 12.1 outbreaks per 100,000 population was the lowest rate reported since 2008. Manawatu and Southland reported the highest rate of outbreaks, just over double the national rate.

Outbreak rates and associated cases by year, 2005–2015



MOST COMMON CAUSES OF OUTBREAKS IN 2015

The cause was identified in 73.8% of outbreaks involving 80.3% of all outbreak-associated cases. Enteric agents were implicated as the cause of 90% of outbreaks with the most common causes reported as norovirus (35.1%) *Giardia* (8.1%) and *Cryptosporidium* (3.8%). Over half of the cases associated with outbreaks were caused by norovirus (57.5%), whereas the proportions caused by the next two most common enteric pathogens identified were much lower, *Giardia* (2.4%) and sapovirus (1.9%). Four deaths were associated with norovirus outbreaks in 2015.

The most commonly reported non-enteric agents were influenza and influenza-like illness which accounted for 4.5% of outbreaks, 9.2% of associated cases and 12 deaths, followed by *Bordetella pertussis* which was identified in 3.6% of outbreaks. An outbreak of respiratory syncytial virus (RSV) was reported for the first time in 2015.

MAJOR DECREASE IN ROTAVIRUS ASSOCIATED OUTBREAKS AND CASES

There was a statistically significant reduction in the number of outbreaks (▼93.6%, 3 outbreaks) and associated cases (▼93.3%, 57 cases) reported with rotavirus as the cause compared with 2014 (47 outbreaks, 854 cases). This decrease is most likely associated with the introduction of the infant rotavirus vaccination programme in July 2014.

LONG-TERM CARE FACILITIES THE MOST COMMON OUTBREAK SETTING

The most common settings for outbreaks continued to be long-term care facilities (31.4%), private homes (21.5%) and childcare centres (14.9%). The most cases associated with outbreaks were reported from long-term care facilities (49.3%), childcare centres (16.8%) and schools (10.3%).

PERSON-TO-PERSON TRANSMISSION CONTINUES TO BE THE MOST COMMON MODE OF TRANSMISSION

In 2015, 84.4% of outbreaks recorded person-to-person transmission as a mode of transmission, the majority of these as the primary mode, followed by environmental (17.9%) and foodborne (14.0%). Multiple modes of transmission were implicated in almost a third of outbreaks. This is similar to findings from the previous two years.

FOODBORNE OUTBREAKS DUE TO NOROVIRUS AND CAMPYLOBACTER REMAIN THE MOST IMPLICATED PATHOGENS IN FOODBORNE OUTBREAKS

In 2015, there were 78 foodborne outbreaks (with 509 associated cases) reported. Of these outbreaks, 67.9% were linked to a pathogen or condition. The pathogens most commonly associated with foodborne outbreaks included norovirus (23.1%), *Campylobacter* (14.1%) and *Clostridium perfringens* (6.4%). Norovirus and *Campylobacter* have been the first and second most implicated pathogens in foodborne outbreaks since 2008.

THE SOURCE OF FOODBORNE OUTBREAKS WAS IDENTIFIED IN 23% OF OUTBREAKS

A source or vehicle was recorded in 23% of the foodborne outbreaks in 2015. It should be noted that in very few outbreaks was a source confirmed by epidemiological or microbiological methods. Of these, poultry was implicated in almost one third and dairy and oils/sugars each implicated in another 22.2% of foodborne outbreaks. However the highest number of outbreak-associated cases were linked to eating pork (40.4% of cases) and dairy (18.3%). *Campylobacter* was the most commonly identified causal agent in poultry and dairy-related outbreaks (2 outbreaks respectively) but *C. perfringens* was the causal agent most commonly associated with meat dishes (4 outbreaks).

Time and temperature abuses were reported as contributing to almost half of all foodborne outbreaks (49%), closely followed by contamination of food (44%). Unsafe sources accounted for 17% of the outbreaks, including 5% associated with drinking raw milk.

In 2015, one multi-regional foodborne outbreak was investigated at the national level. This outbreak involved seven cases of hepatitis A reported from five district health boards (DHBs). The cases were epidemiologically linked to the consumption of imported frozen berries. A product recall was initiated by the Ministry for Primary industries.

MOST OUTBREAKS WERE DETECTED BY AN INCREASE IN CASES

Most outbreaks were recognised by increases in disease incidence (60.0%), person-to-person contact with other cases (18.3%) or attendance at a common event (8.8%).

For the 536 outbreaks where dates were available, just over half (53.7%) of all outbreaks were reported to the PHU within a week of the onset of illness in the first case. The overall median reporting delay for outbreaks was six days (▲ from 5.0 days in 2014).

CONTROL MEASURES WERE TAKEN FOR AT LEAST 93% OF OUTBREAKS

Control measures were reported for 92.5% of outbreaks in 2015. The most common measures undertaken were health education and advice regarding the source (76.0%) and cleaning and disinfection (63.8%).

TRENDS

As noted over the past 10 years (2006 to 2015), the 2015 data showed three continuing trends:

1. ▲ in outbreaks in institutional settings
2. ▲ in outbreaks associated with person to person transmission
3. ▼ in outbreaks linked to commercial food operators

In 2015, the most common outbreak settings were long-term care facilities, private homes and childcare centres, which is similar to observations from 2006 to 2014. Since 2006, outbreaks in institutions have constituted about half, and those in private homes about a quarter to a third, of all outbreaks reported each year. Over the same time period an increase in outbreaks involving person-to person transmission has also been documented. These increases could be partly explained by:

1. Increases in long-term care facilities due to the ageing population, and in early childhood education facilities and Te Kōhanga Reo due to the funded 20 hours of early childcare introduced in 2007.
2. The introduction of national guidelines for the “Management of Norovirus Outbreaks in Hospitals and Elderly Care Institutions” in early 2009 may have led to increased reporting of outbreaks.

Prior to 2006, commercial food operators and private homes were the most commonly reported settings and foodborne transmission was the most commonly reported transmission mode.

INTRODUCTION

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1. INTRODUCTION

This report summarises data on outbreaks that were reported to the Institute of Environmental Science and Research Limited (ESR) during 2015.

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 surveillance system.

Investigating outbreaks provides information to [1]:

- 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

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2. METHODS

OUTBREAK DEFINITION

The Guidelines for the Investigation and Control of Disease Outbreaks [1] states 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 early as an interim report that can be finalised when further data becomes available. Data is entered into EpiSurv at each PHU via a secure web-based portal. The real-time data is collated and analysed by ESR on behalf of the Ministry of Health. The national database is supplemented by data from ESR's Enteric Reference Laboratory, and virology and public health laboratories. If an outbreak is first identified by these laboratory sources, 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 2015, and recorded on the EpiSurv database as at 25 February 2016. Any amendments made to outbreak data on EpiSurv after 25 February 2016 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 2015*.

This report does not include details about outbreaks of lead absorption (4 outbreaks) reported into EpiSurv in 2015. 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.

Rates were calculated using national and PHU population figures based on Statistics New Zealand mid-year population estimates for 2015.

The categories and subcategories used in this report were based on the fields in the outbreak report form with two exceptions: implicated food sources were grouped into one or more food categories, and reporting delay was calculated as the difference between the date of onset of illness for the first case and the outbreak report date.

DATA LIMITATIONS

The available outbreak data was restricted to the outbreaks recorded in EpiSurv by PHUs. 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 data contained in this report.

Data quality issues including timeliness contribute to the limitations. Timeliness of reporting is discussed briefly in this report. An annual report on data quality in EpiSurv is published separately.

Reports prior to 2005 used different methods of data analysis for the *Annual Summary of Outbreaks in New Zealand*. In 2003 and 2004, interim outbreak reports were excluded from analysis. In 2002, causal agents were categorised as laboratory-confirmed or suspected. As a result of these different analytical methods, comparisons with outbreak trends in past reports should be restricted to reports from 2005 onwards.

RESULTS

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3. RESULTS

CHARACTERISTICS OF OUTBREAKS

There were 558 reported outbreaks (12.1 outbreaks per 100,000 population) in 2015, a decrease from the 863 (19.1 outbreaks per 100,000 population) reported in 2014. All but one outbreak were recorded as final reports. A total of 8510 cases were associated with outbreaks, 31.4% (2672/8510) of the cases were either clinically or laboratory confirmed and 68.6% (5838/8510) were probable cases. In 2015, the national rate was 185.2 outbreak cases per 100,000 population, around half the rate in 2014 (328.8 cases per 100,000 population).

DISTRIBUTION OF OUTBREAKS BY PUBLIC HEALTH UNIT

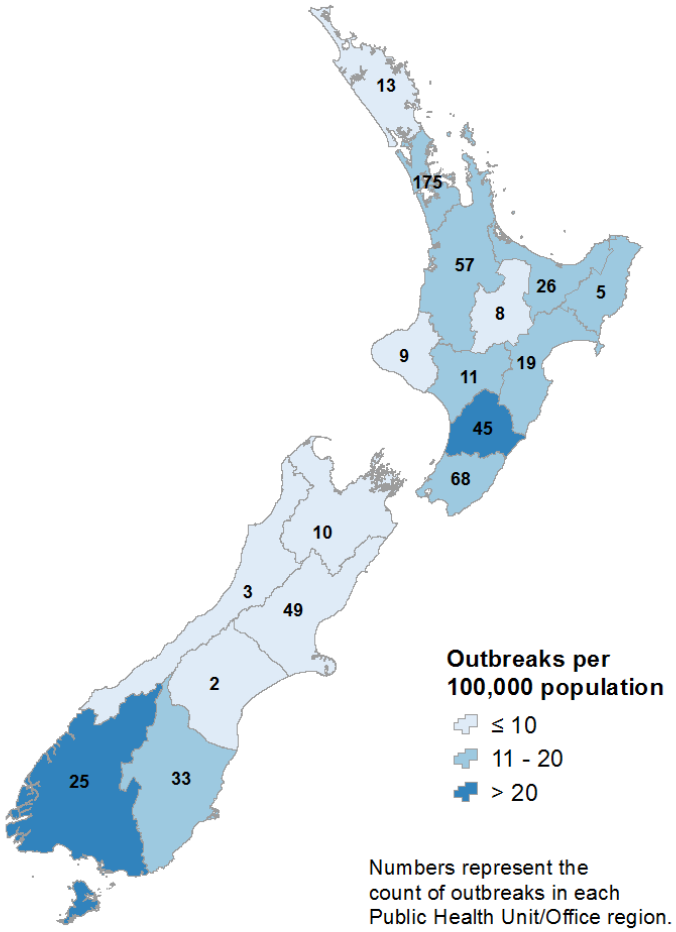
In 2015, Auckland PHU reported the highest number of outbreaks and associated cases, which represented 31.4% (175/558) of outbreaks and 21.5% (1827/8510) of associated cases (Table 1). Wellington PHU reported the second highest number of outbreaks (12.2%, 68/558 outbreaks), followed by Waikato (10.2%, 57/558 outbreaks), and Canterbury (8.8%, 49/558 outbreaks) PHUs. Manawatu PHU reported the highest outbreak rate (26.1 per 100,000 population) and the Southland office (Public Health South) the highest case rate (477.1 per 100,000 population) (Figure 1), while Nelson Marlborough PHU reported the lowest outbreak rate for a PHU where at least five outbreaks were reported (6.9 per 100,000 population).

Table 1. Number and rate of outbreaks and associated cases by PHU Office, 2015

PHU Office	Outbreaks			Cases		
	Total	% of outbreaks (n=558)	Outbreak rate[1]	Total	% of cases (n=8510)	Case rate[1]
Northland	13	2.3	7.7	153	1.8	90.9
Auckland[2]	175	31.4	11.0	1827	21.5	115.1
Waikato	57	10.2	14.6	611	7.2	156.4
Bay of Plenty	26	4.7	11.7	355	4.2	160.3
Rotorua	8	1.4	7.6	69	0.8	65.8
Taranaki	9	1.6	7.8	218	2.6	188.1
Hawke's Bay	19	3.4	11.8	335	3.9	208.7
Gisborne	5	0.9	10.5	107	1.3	225.7
Whanganui	11	2.0	17.6	296	3.5	472.8
Manawatu	45	8.1	26.1	590	6.9	342.8
Wellington[3]	68	12.2	13.9	1420	16.7	290.8
Nelson Marlborough[4]	10	1.8	6.9	163	1.9	112.6
West Coast[5]	3	0.5	9.2	44	0.5	134.6
Canterbury	49	8.8	9.3	1154	13.6	219.3
South Canterbury[5]	2	0.4	3.4	78	0.9	133.1
Otago	33	5.9	15.2	626	7.4	288.9
Southland	25	4.5	25.7	464	5.5	477.1
Total	**558**	**100.0**	**12.1**	**8510**	**100**	**185.2**

[1] Crude rate of outbreaks per 100,000 population is calculated using Statistics New Zealand population estimates for 2015.
[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.
[5] Rates calculated where fewer than five outbreaks were recorded should be interpreted with caution.

Figure 1. Number of outbreaks per 100,000 population by PHU, 2015



MULTI-REGIONAL GASTROINTESTINAL OUTBREAKS

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 then the Ministry for Primary Industries will also be involved.

In 2015, one multi-regional gastrointestinal outbreak was investigated at the national level (the same number as in 2014 and 2013). An increase in locally acquired hepatitis A cases reported during October and November 2015 triggered an investigation. PHU staff administered a hypothesis-generating questionnaire, the results of which showed that cases had eaten imported frozen berries. Genotyping and sequencing of the hepatitis A virus showed that all cases that had consumed the frozen berries had the same genotype (1A) and sequence type. A product recall was initiated by the Ministry of Primary Industries on 03 December 2015. A total of seven cases across five District Health Boards (DHBs) were reported between October and December 2015.

CAUSAL AGENTS

A causal agent was identified in 73.8% (412/558) of outbreaks involving 80.3% (6834/8510) of all outbreak associated cases. In 10 of these outbreaks, two or more causal agents were identified. No specific pathogen or condition was identified in the remaining 26.2% (146/558) of outbreaks, all of which were recorded as gastroenteritis outbreaks.

Enteric agents were implicated in the majority of outbreaks (89.8%, 501/558) and their associated cases (87.3%, 7433/8510) (Table 2). The most common single causal agent implicated in outbreaks in 2015 was norovirus, at 35.1% (196/558) of reported outbreaks. Outbreaks due to norovirus also had the highest proportion of associated cases (57.5%, 4893/8510). The next most common enteric causal agents were *Giardia* spp. (8.1% of outbreaks, 45/558) and *Cryptosporidium* spp. (3.8%, 21/558). The enteric agents with the highest median number of associated cases in each outbreak were norovirus (20 cases, 196 outbreaks), sapovirus (18 cases, 9 outbreaks) and rotavirus (18 cases, 3 outbreaks).

Non-enteric agents accounted for 10.4% (58/558) of outbreaks and 13.1% (1115/8510) of the outbreak associated cases in 2015 (Table 2). The most frequently reported non-enteric pathogens and conditions reported were influenza and influenza-like-illness (4.5% of outbreaks, 25/558) and *B. pertussis* (3.6% of outbreaks, 20/558). The median number of cases associated with non-enteric outbreaks in 2015 was highest for respiratory syncytial virus (RSV) outbreaks (1 outbreak involving 33 cases) followed by influenza and influenza-like-illness (25 outbreaks with a median of 28 cases) and varicella zoster virus (1 outbreak, 22 cases). Other important non-enteric outbreaks in 2015 included *Legionella* spp. (4 outbreaks with a median of 7.5 cases), *M. tuberculosis* (2 outbreaks with a median of 3.5 cases) and measles virus (2 outbreaks with a median of 3.0 cases).

Table 2. Outbreaks and associated cases by pathogen, 2015

Pathogen or condition	Outbreaks[1]			Cases[1]	
	Total	% of outbreaks (n=558)	Median cases per outbreak	Total	% of cases (n=8510)
Enteric	**501**	**89.8**	**8**	**7433**	**87.3**
Norovirus	196	35.1	20	4893	57.5
Giardia spp.	45	8.1	3	207	2.4
Cryptosporidium spp.	21	3.8	4	94	1.1
Campylobacter spp.	19	3.4	4	88	1.0
Salmonella spp.[2]	18	3.2	2	101	1.2
VTEC/STEC infection	17	3.0	3	94	1.1
Shigella spp.	12	2.2	2	56	0.7
Sapovirus	9	1.6	18	164	1.9
Clostridium perfringens	5	0.9	11	67	0.8
Rotavirus	3	0.5	18	57	0.7
Aeromonas spp.	3	0.5	5	40	0.5
Salmonella Typhi	3	0.5	2	7	0.1
Astrovirus	2	0.4	6	12	0.1
Hepatitis A	2	0.4	4.5	9	0.1
Staphylococcus aureus	2	0.4	3.5	7	0.1
Yersinia spp.	2	0.4	2.5	5	0.1
Bacillus cereus	1	0.2	5	5	0.1
Clostridium difficile	1	0.2	3	3	0.0
Dientamoeba Fragilis	1	0.2	3	3	0.0
Pathogen not identified[3]	146	26.2	8.5	1676	19.7
Non-enteric	**58**	**10.4**	**9.5**	**1115**	**13.1**
Influenza and influenza-like illness[4]	25	4.5	28	787	9.2
Bordetella pertussis	20	3.6	4	223	2.6
Legionella spp.	4	0.1	7.5	30	0.4
Mycobacterium tuberculosis	2	0.4	3.5	7	0.1
Measles virus	2	0.4	3	6	0.1
Respiratory syncytial virus (RSV)	1	0.1	33	33	0.4
Varicella zoster virus	1	0.2	22	22	0.3
Leptospira spp.	1	0.2	3	3	0.0
Diphtheria	1	0.2	2	2	0.0
Haemophilus influenzae b	1	0.1	2	2	0.0

[1] More than one enteric agent was reported in 10 outbreaks with 308 cases including one outbreak involving 38 cases where both an enteric and a non-enteric agent were identified. This means that the numbers don't add up to the group totals.

[2] Includes nontyphoidal *Salmonella* species only. *Salmonella* Typhi and *Salmonella* Paratyphi are reported separately.

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

[4] Includes outbreaks of influenza A (13 outbreaks with 416 cases), influenza B (5 outbreaks, 260 cases), rhinovirus (1 outbreak, 23 cases) and influenza-like illness (7 outbreaks, 165 cases).

NOROVIRUS OUTBREAKS—GENOTYPES AND OUTBREAK SETTING

Norovirus genotyping is carried out in the ESR Norovirus Reference Laboratory (NRL). 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 [2].

A separate dataset generated from the NRL is used to analyse norovirus outbreak strains. The number of outbreaks reported to the NRL differs from the number recorded in EpiSurv, because not all samples from the norovirus outbreaks reported in EpiSurv are sent to ESR for analysis. For this reason, the numbers of norovirus-associated, sapovirus-associated and astrovirus-associated outbreaks reported in this section differ from the number reported elsewhere in this report.

In 2015 there were 184 norovirus outbreaks confirmed by the NRL. This is a decrease in NRL laboratory-confirmed outbreaks from 2014 (312 outbreaks) but an increase from 2013 (157 outbreaks). The highest number of outbreaks occurred in March (24 outbreaks) and the lowest number occurred in May and August (8 outbreaks each) (Figure 2).

The majority (58.2%, 107/184) of norovirus outbreaks confirmed by the NRL occurred in long-term care facilities. Outbreaks were also associated with childcare centres (15.2%, 28/184), commercial food operators (9.2%, 17/184), acute-care hospitals (6.5%, 12/184), school/college (3.3%, 6/184), private homes (2.2%, 3/184) and hostel/boarding houses (1.1%, 2/184). Other settings were reported in seven outbreaks including one associated with recreational shellfish gathering (Figure 3). The setting was unknown in two outbreaks.

Norovirus genogroup II (GII) was identified in 90.8% (167/184) of outbreaks, norovirus genogroup I (GI) was identified in 7.1% (13/184) of outbreaks, and both norovirus GI and GII were detected in four (2.2%) outbreaks.

The norovirus genotype was determined for 97.3% (179/184) of NRL laboratory-confirmed outbreaks. Five GII viruses were unable to be typed. GII.4 was the most common genotype identified and was associated with 51.4% (92/179) of genotyped outbreaks. As in 2014, the Sydney_2012 variant (that emerged in late 2012) was the only GII.4 variant identified in 2015. In total, four GI genotypes and nine GII genotypes (as defined by typing of the viral capsid) were identified. As in 2014 but representing a higher proportion, the second most common genotype identified in 2015 was GII.6 (10.6%, 19/179). Less commonly identified genotypes included GII.P12/GII.3 (10.1%, 18/179), GII.2 (7.8%, 14/179), GII.P21/GII.3 (4.5%, 8/179), and GII.17 (4.5%, 8/179 that included two mixed GI and GII outbreaks).

Each norovirus outbreak setting was associated with a variety of norovirus genotypes (Figure 3). However a higher proportion of genotyped outbreaks were associated with GII.4 for the acute-care hospital setting (83.3%, 10/12) and to a lesser extent, with long-term care facilities (60.4%, 64/106) compared to other settings (26.3%, 16/61).

Gastroenteritis outbreaks caused by other enteric viruses confirmed by the NRL*

During 2015, the ESR NRL further analysed specimens from 102 gastroenteritis outbreaks (for which a pathogen had not been identified at the time of analysis) for other enteric viral pathogens. Sapovirus was identified in five outbreaks in the following settings: commercial food operators (2 outbreaks), childcare

* Note: The NRL does not test for rotavirus. However, outbreaks of rotavirus confirmed in diagnostic laboratories and notified to EpiSurv are reported in Table 1.

centres (2 outbreaks, one of which also was associated with norovirus) and long-term care facilities (1 outbreak). Astrovirus was identified in two outbreaks both of which were in a childcare centre.

Figure 2. Norovirus Reference Laboratory-confirmed norovirus outbreak typing by month, 2015

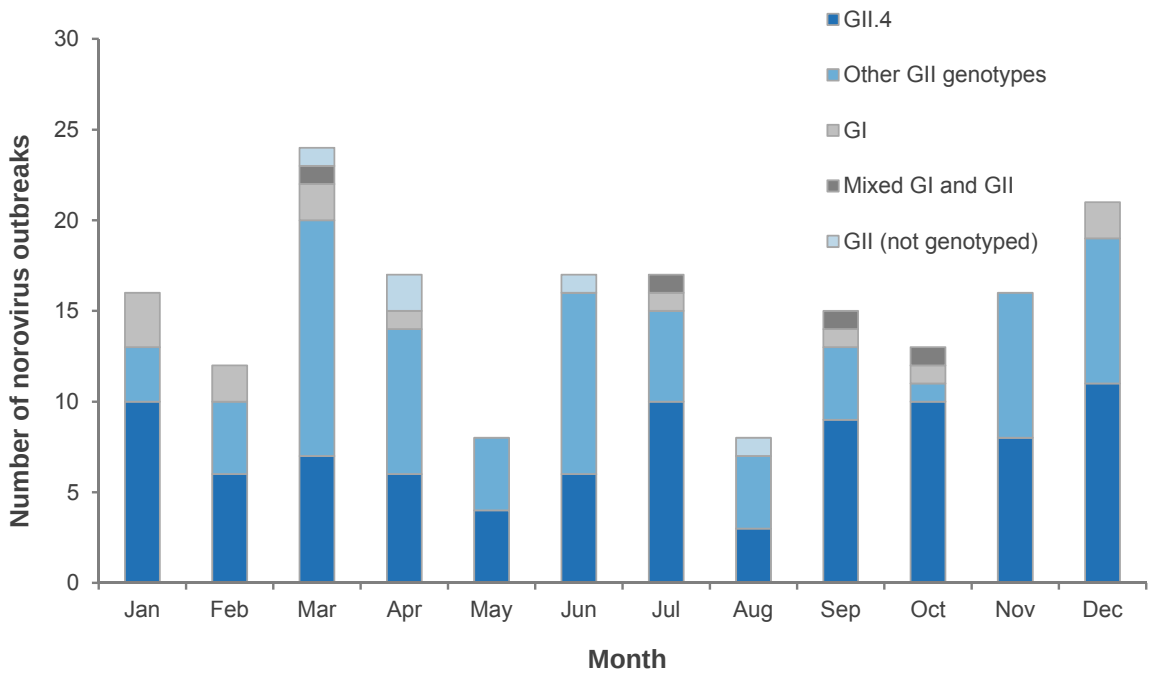
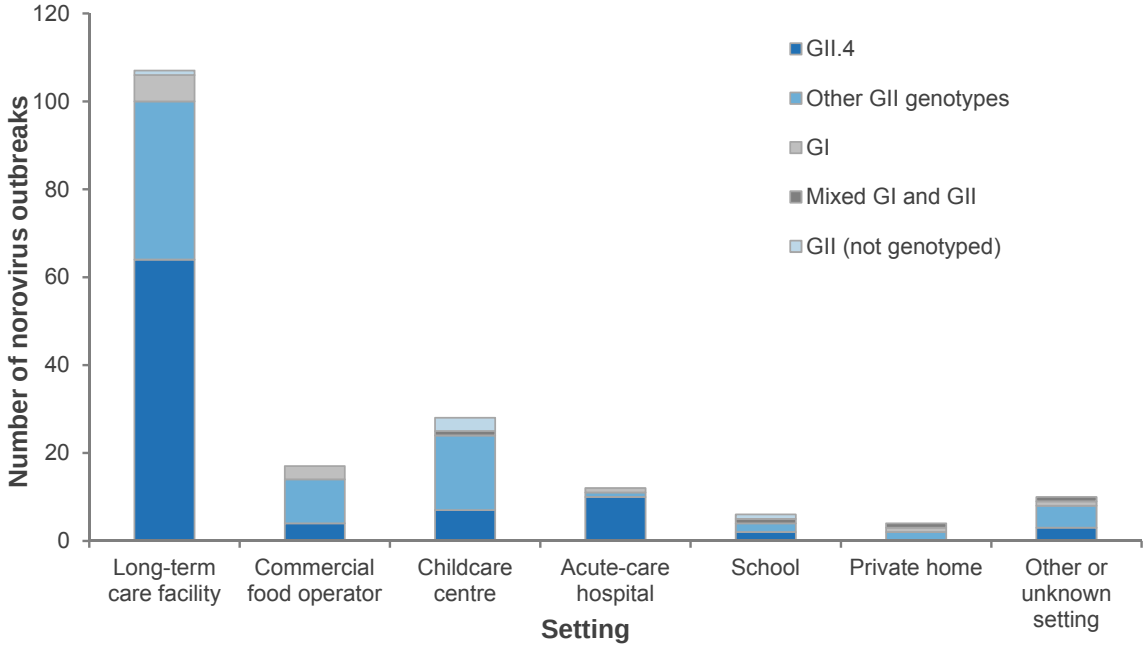


Figure 3. Norovirus Reference Laboratory-confirmed norovirus outbreak strains by setting, 2015



HOSPITALISATIONS AND DEATHS ASSOCIATED WITH OUTBREAKS

Hospitalisation information was recorded for 62.2% (347/558) of outbreaks involving 57.4% (4882/8510) of associated cases. Overall, 3.3% (161/4882) of outbreak-associated cases with hospitalisation information recorded were hospitalised. The number of cases hospitalised for outbreaks due to enteric pathogens (113 cases) was substantially higher than the number of cases hospitalised due to non-enteric pathogens (48 cases) (Table 3). However, a higher percentage of cases associated with non-enteric outbreaks were hospitalised (18.2%) compared with enteric outbreaks (13.6%). The non-enteric pathogen or condition with the highest proportion of hospitalised cases was *Haemophilus influenza*e b (100.0%, 2/2 cases), followed by *Leptospira* spp. (66.7%, 2/3 cases) and *Legionella* spp. (63.3%, 19/30 cases). Of the enteric pathogens *Clostridium difficile* (100.0%, 3/3 cases) represented the highest proportion of hospitalised cases.

Nineteen deaths were associated with 12 different outbreaks in 2015. The deaths were associated with influenza A (7), norovirus (4) Influenza-like illness (3), rhinovirus and *Legionella* spp. (2 each) and gastroenteritis (1) infections.

Table 3. Hospitalised outbreak cases and total outbreak cases by pathogen or condition, 2015

Pathogen or condition	Outbreaks[1]	Cases[1]		
	Total	Total	No. of cases hospitalised[2]	% of cases hospitalised
Enteric	**48**	**830**	**113**	**13.6**
Norovirus	20	565	60	10.6
Salmonella spp.[3]	5	70	6	8.6
Shigella spp.	4	11	5	45.5
Hepatitis A	1	7	5	71.4
Campylobacter spp.	2	6	3	50.0
Clostridium difficile	1	3	3	100.0
Salmonella Typhi	2	5	3	60.0
Cryptosporidium spp.	2	12	2	16.7
VTEC/STEC infection	2	8	2	25.0
Rotavirus	1	18	1	5.6
Clostridium perfringens	1	33	1	3.0
Aeromonas spp.	1	33	1	3.0
Pathogen not identified[4]	8	110	23	20.9
Non-enteric	**18**	**264**	**48**	**18.2**
Legionella spp.	4	30	19	63.3
Influenza and influenza-like-illness[5]	6	176	16	9.1
Mycobacterium tuberculosis	2	7	3	42.9
Bordetella pertussis	2	9	3	33.3
Respiratory syncytial virus (RSV)	1	33	2	6.1
Haemophilus influenzae b	1	2	2	100.0
Leptospira spp.	1	3	2	66.7
Measles virus	1	4	1	25.0
Total	**66**	**1094**	**161**	**14.7**

[1] More than one enteric agent was reported in 10 outbreaks with 308 cases including one outbreak involving 38 cases where both an enteric and a non-enteric agent were identified. This means that the numbers may not add up to the group totals.

[2] Hospitalisation information was recorded for 62.2% (347/558) of outbreaks, relating to 57.4% (4882/8510) of cases.

[3] Includes nontyphoidal *Salmonella* species only. *Salmonella* Typhi and *Salmonella* Paratyphi are reported separately.

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

[5] Includes outbreaks of influenza A (4 outbreaks with 133 cases), influenza B (1 outbreak, 53 cases), and influenza-like illness (2 outbreak, 43 cases).

OUTBREAK SETTINGS

The most common outbreak settings recorded were long-term care facilities (31.4%, 175/558) followed by private homes (21.5%, 120/558), childcare centres (14.9%, 83/558) and restaurants/cafés/bakeries (7.7%, 43/558). Outbreaks in long-term care facilities had the highest number of associated cases (49.3%, 4198/8510) (Table 4). Overall, 58.1% (324/558) of all outbreaks and 84.1% (7155/8510) of cases reported in 2015 were set in institutions. The setting was unknown in 4.5% (25/558) of outbreaks.

Table 4. Outbreaks and associated cases by setting of exposure/transmission, 2015

Outbreak setting	Outbreaks[1]		Cases[1]	
	Total	% of outbreaks (n=558)	Total	% of cases (n=8510)
Institutions	**324**	**58.1**	**7155**	**84.1**
Long-term care facility	175	31.4	4198	49.3
Childcare centre	83	14.9	1431	16.8
Hospital (acute-care)	26	4.7	455	5.3
School	21	3.8	877	10.3
Camp	2	0.4	8	0.1
Hostel/boarding house	3	0.5	63	0.7
Hotel/motel	1	0.2	10	0.1
Prison	1	0.2	22	0.3
Marae	1	0.2	4	0.0
Other institution	13	2.3	105	1.2
Commercial food operators	**64**	**11.5**	**341**	**4.0**
Restaurant/café/bakery	43	7.7	233	2.7
Takeaway	9	1.6	23	0.3
Caterer	2	0.4	32	0.4
Supermarket/delicatessen	2	0.4	9	0.1
Temporary or mobile food premises	2	0.4	6	0.1
Fast food restaurant	0	-	0	-
Other food outlet	6	1.1	38	0.4
Workplace	**18**	**3.2**	**188**	**2.2**
Farm	10	1.8	47	0.6
Workplace	9	1.6	146	1.7
Other	**142**	**25.4**	**921**	**10.8**
Private home	120	21.5	713	8.4
Other setting	16	2.9	112	1.3
Mode of travel[2]	4	0.7	86	1.0
Community/church or sports gathering	4	0.7	34	0.4
Petting zoo	0	-	0	-
Unknown setting	**25**	**4.5**	**141**	**1.7**

[1] More than one setting was recorded in 21 outbreaks with a total of 287 associated cases. This means the numbers might not add up to the group totals.

[2] Includes outbreaks where the exposure setting was recorded as a cruise ship (3) and an aircraft (1).

MODES OF TRANSMISSION

In 2015, the most commonly reported mode of transmission was person-to-person (84.4%, 471/558 outbreaks), followed by environmental (17.9% 100/558) and foodborne (14.0%, 78/558) modes (Table 5). Outbreaks where person-to-person transmission was reported accounted for the highest percentage of cases (94.0%, 8000/8510), followed by environmental transmission (22.7%, 1929/8510). The mode of transmission was unknown for 4.3% (24 outbreaks).

Table 5. Outbreaks and associated cases by mode of transmission, 2015

Mode of transmission	Outbreaks				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=558)[1]	Total	% of cases (n=8510)[1]
Person-to-person	396	75	471	84.4	8000	94.0
Environmental	14	86	100	17.9	1929	22.7
Foodborne	61	17	78	14.0	509	6.0
Zoonotic	14	10	24	4.3	98	1.2
Waterborne	9	10	19	3.4	89	1.0
Other	3	5	8	1.4	84	1.0
Unknown	-	-	24	4.3	143	1.7

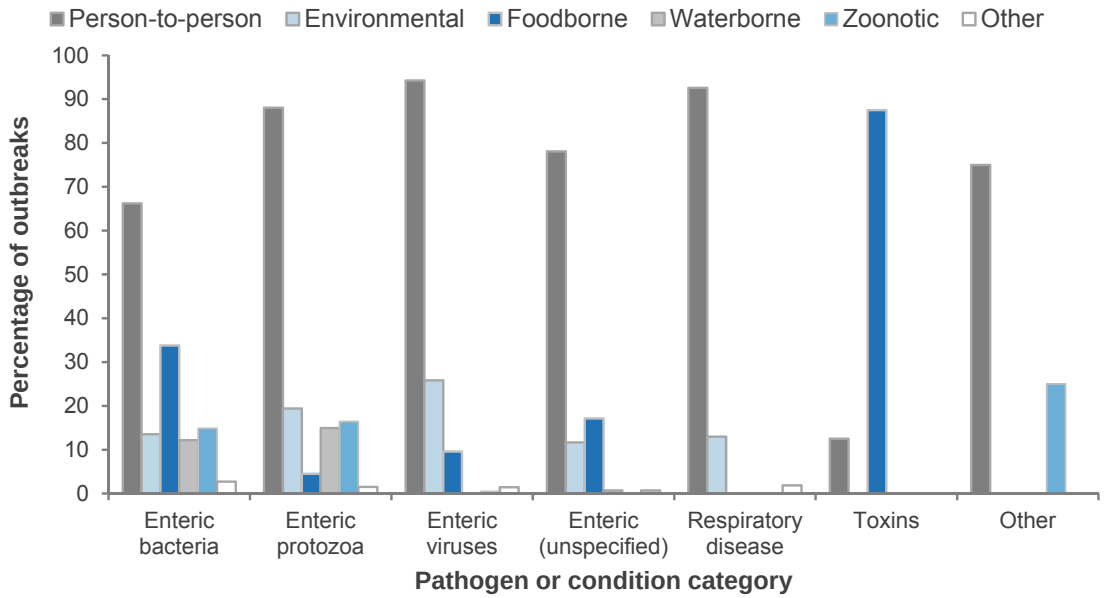
[1] More than one mode of transmission was recorded for 174 outbreaks involving 2342 associated cases. This means the totals may add up to more than 100%.

Note: No outbreaks with vectorborne, sexual contact or parenteral as mode(s) of transmission were reported in 2015.

Person-to-person was the most common mode of transmission for enteric viruses (94.3%, 197/209), followed by respiratory disease (92.6%, 50/54), enteric protozoa (87.9%, 58/66), unspecified enteric pathogens (78.2%, 115/147), and enteric bacteria (66.2%, 49/74) (Figure 4). Almost a third (30.0%, 141/471) of the person-to-person outbreaks also had another mode of transmission reported.

Foodborne transmission was the most common mode reported in outbreaks due to toxins (87.5%, 7/8) followed by enteric bacteria (33.8%, 25/74) and unspecified enteric pathogens (17.1%, 25/146) (Figure 4). Environmental transmission was reported in outbreaks of enteric viruses (25.8%, 54/209) and enteric protozoa (19.4%, 13/67) while waterborne transmission was mostly associated with outbreaks of enteric protozoa (16.4%, 11/67) and enteric bacteria (12.2%, 9/74). Zoonotic transmission was reported in 25.0% (1/4) of “other” pathogen outbreaks followed by 16.4% (11/67) enteric protozoa outbreaks and 14.9% (11/74) of outbreaks due to enteric bacteria.

Figure 4. Percentage of outbreaks by pathogen category and mode of transmission, 2015



Note: More than one mode of transmission was recorded for 174 outbreaks. This means the totals may add up to more than 100%.

FOODBORNE OUTBREAKS

Causal agent

Of the 78 foodborne outbreaks reported in 2015 (with 509 associated cases), 67.9% (53/78 outbreaks) were linked to a pathogen or condition (Table 6). Pathogens most commonly associated with foodborne outbreaks included norovirus (23.1%, 18/78 outbreaks) and *Campylobacter* spp. (14.1%, 11/78 outbreaks). Enteric bacteria (*Campylobacter* spp., *Salmonella* spp., *Shigella* spp., *Yersinia* spp., *Aeromonas* spp., *C. perfringens* and *S.* Typhi) were implicated in 32.1% (25/78) of the foodborne outbreaks, and enteric viruses (hepatitis A, norovirus and rotavirus) were implicated in 25.6% (20/78) of the foodborne outbreaks.

Table 6. Foodborne outbreaks and associated cases by pathogen or condition, 2015

Pathogen or condition	Outbreaks		Cases	
	Total	% of outbreaks (n=78)[1]	Total	% of cases (n=509)[1]
Norovirus	18	23.1	212	41.7
Campylobacter spp.	11	14.1	46	9.0
Clostridium perfringens	5	6.4	67	13.2
Shigella spp.	5	6.4	39	7.7
Aeromonas spp.	3	3.8	40	7.9
Salmonella spp.	3	3.8	30	5.9
Giardia spp.	2	2.6	30	5.9
Staphylococcus aureus	2	2.6	7	1.4
Yersinia spp.	2	2.6	5	1.0
Hepatitis A	1	1.3	7	1.4
Bacillus cereus	1	1.3	5	1.0
Sapovirus	1	1.3	3	0.6
Salmonella Typhi	1	1.3	2	0.4
Pathogen not identified[2]	25	32.1	69	13.6

[1] More than one agent was reported in three foodborne outbreaks with 64 associated cases. This means totals may add up to more than 100%.

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

Vehicle/source implicated

Of the 78 foodborne outbreaks reported in 2015, 18 (23.1%) had a food source or vehicle of infection specified. The main foods implicated in these outbreaks were poultry (27.8%, 5 outbreaks), dairy and oils/sugars (22.2%, 4 outbreaks each), followed by grains/beans (16.7%, 3 outbreaks) (Table 7). The outbreaks with the highest number of associated cases were those linked to pork (40.4%, 44 cases) and dairy (18.3%, 20 cases).

It should be noted that very few outbreaks have a suspected source confirmed by epidemiological or microbiological methods. It is also important to appreciate that implicated foods are mostly associations. These could be spurious as they have not taken into account the prevalence of commonly consumed foods in the general population. Approximately a quarter of foodborne outbreaks have a source identified. Investigators will generally only report a source based on compelling evidence or other supporting data or previous experience suggesting the food vehicle is the likely source.

Table 7: Foodborne outbreaks and associated cases by implicated vehicle/source, 2015

Implicated vehicle/source	Outbreaks		Cases	
	Total	% of outbreaks (n=18)[1]	Total	% of cases (n=109)[1]
Poultry	5	27.8	15	13.8
Dairy	4	22.2	20	18.3
Oils/sugar	4	22.2	13	11.9
Grains/beans	3	16.7	8	7.3
Meat (pork)	2	11.1	44	40.4
Fruit/nut	2	11.1	15	13.8
Vegetables (leafy)	2	11.1	8	7.3
Vegetables (stalk)	2	11.1	5	4.6
Shellfish (molluscs)	2	11.1	4	3.7
Rice	1	5.6	5	4.6
Fish	1	5.6	3	2.8
Meat (beef)	1	5.6	2	1.8
Meat (lamb)	1	5.6	2	1.8

[1] More than one vehicle/source was implicated in five foodborne outbreaks with 16 associated cases. This means the numbers may not add up to the group totals.

Note: Mixed foods were assigned to multiple categories based on the groupings published by Painter et al 2009 [4]. Only explicit ingredients were assigned to a category. All foods within a mixed item were given equal priority.

Foodborne outbreaks associated with poultry (27.8%, 5 outbreaks) and dairy (22.2%, 4 outbreaks) as possible vehicles or sources were most commonly due to *Campylobacter* spp. (2 outbreaks each) (Table 8). Outbreaks of *C. perfringens* were most commonly associated with meat dishes (pork (2 outbreaks), poultry and lamb (1 outbreak each)). One outbreak of hepatitis A was linked to consumption of imported frozen berries.

Whanganui DHB reported the largest foodborne outbreak within a single DHB where a food source was identified. The outbreak involved 33 cases (6.5%). *C. perfringens* and *Aeromonas hydrophila* were identified as the causative agents in the outbreak which was attributed to eating roast pork in gravy served at a wedding anniversary celebration lunch. An epidemiological study carried out by Whanganui public health service identified that individuals who had consumed the roast pork in gravy were almost 14 times as likely to develop illness than those who did not (risk ratio 13.9, $p<0.05$).

Table 8. Foodborne outbreaks by causal agent and implicated vehicle/source, 2015

Implicated vehicle/source[1]	Pathogen or condition										
	Campylobacter spp.	*Clostridium perfringens*	*Aeromonas* spp.	*Bacillus cereus*	*Cryptosporidium* spp.	Hepatitis A	Norovirus	*Staphylococcus aureus*	*Yersinia* spp.	Pathogen not identified[2]	Total outbreaks
Poultry	2	1		1				1		1	**5**
Dairy	2				1					1	**4**
Oils/sugar				1				1	1	2	**4**
Grains/beans		1								2	**3**
Fruit/nut						1				1	**2**
Meat (pork)		2	1								**2**
Shellfish (molluscs)			1				1				**2**
Vegetables (stalk)		1								1	**2**
Rice				1				1			**1**
Fish									1		**1**
Meat (beef)										1	**1**
Vegetables (leafy)	1									1	**1**
Meat (lamb)		1									**1**
Total	**5**	**4**	**2**	**1**	**1**	**1**	**1**	**1**	**1**	**3**	**18**

[1] More than one vehicle/source was implicated in five foodborne outbreaks with 16 associated cases. This means the numbers may not add up to the group totals.

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

Setting where contaminated foods/beverages were prepared

The settings where foods and beverages were prepared were recorded in 93.6% (73/78) of foodborne outbreaks and 93.1% (474/509) of associated cases in 2015. The preparation settings most commonly associated with foodborne outbreaks included commercial food operators (56.4%, 44/221) and private homes (20.5%, 16/78) (Table 9). Foodborne outbreaks where the food was prepared in restaurants, cafés, or bakeries had the highest number of associated cases (28.7%, 146/509), followed by food prepared in long-term care facilities (19.1%, 97/509).

Table 9. Foodborne outbreaks and associated cases by setting of food preparation, 2015

Preparation setting	Outbreaks		Cases[1]	
	Total	% of outbreaks (n=78)	Total	% of cases (n=509)
Commercial food operators	**44**	**56.4**	**221**	**43.4**
Restaurant/café/bakery	27	34.6	146	28.7
Takeaway	8	10.3	19	3.7
Caterers	2	2.6	26	5.1
Temporary or mobile service	2	2.6	6	1.2
Other food outlet	5	6.4	24	4.7
Institutions	**10**	**12.8**	**188**	**36.9**
Long-term care facility	5	6.4	97	19.1
School	2	2.6	52	10.2
Marae	2	2.6	15	2.9
Childcare centre	1	1.3	24	4.7
Other	**21**	**26.9**	**72**	**14.1**
Private home	16	20.5	46	9.0
Overseas manufacturer	2	2.6	12	2.4
Farm	1	1.3	11	2.2
Community/church gathering	1	1.3	3	0.6
Other setting	2	2.6	7	1.4
Unknown preparation setting	**5**	**6.4**	**35**	**6.9**

[1] Two preparation settings were recorded in two foodborne outbreaks with seven associated cases, therefore numbers may not sum to group totals.

Contributing factors

The factors contributing to foodborne outbreaks most commonly involved time and temperature abuses (48.7%, 38/78) or contamination of food (43.6%, 34/78). The most common time and temperature abuses were undercooking (24.4%, 19/78), improper storage prior to preparation (20.5%, 16/78), and inadequate reheating of previously cooked food (15.4%, 12/78) (Table 10). Contamination of food occurred via cross-contamination with other food (30.8%, 24/78) or by an infected food handler (23.1%, 18/78). Unsafe sources accounted for 16.7% (13/78) of the outbreaks, including 9.0% (7/78) that were associated with use of ingredients from unsafe sources. The majority of contributing factors reported were suspected only.

Table 10. Foodborne outbreaks by contributing factor, 2015

Contributing factor	Outbreaks[1]				Cases[1]	
	Confirmed	Suspected	Total	% of foodborne outbreaks (n=78)	Total	% of foodborne cases (n=509)
Time/temperature abuse	**1**	**37**	**38**	**48.7**	**196**	**38.5**
Undercooking	0	19	19	24.4	127	25.0
Improper storage prior to preparation	0	16	16	20.5	104	20.4
Inadequate reheating of previously cooked food	1	11	12	15.4	96	18.9
Preparation too far in advance	1	8	9	11.5	110	21.6
Inadequate cooling or refrigeration	0	9	9	11.5	81	15.9
Improper hot holding	1	6	7	9.0	44	8.6
Inadequate thawing	0	3	3	3.8	42	8.3
Contamination of food	**1**	**33**	**34**	**43.6**	**224**	**44.0**
Cross contamination	0	24	24	30.8	122	24.0
Contamination from an infected food handler	1	17	18	23.1	150	29.5
Unsafe sources	**1**	**12**	**13**	**16.7**	**86**	**16.9**
Use of ingredients from unsafe sources	1	6	7	9.0	48	9.4
Consumption of raw food	0	4	4	5.1	40	7.9
Consumption of unpasteurised milk	0	4	4	5.1	29	5.7
Use of untreated water in food preparation	0	3	3	3.8	41	8.1
Other factors	**1**	**0**	**1**	**1.3**	**5**	**1.0**

[1] More than one contributing factor was recorded in 36 foodborne outbreaks with 251 associated cases. This means the numbers may not add up to the group totals.

PERSON-TO-PERSON OUTBREAKS

Causal agents

In 2015, there were 471 person-to-person outbreaks (primary and secondary mode of transmission) with 8000 associated cases. A causal agent was linked in 75.8% (357/471) of these outbreaks (Table 11). The most common causal agent was norovirus, which was recorded in 39.9% (188/471) of person-to-person outbreaks and involved 60.5% (4841/8000) of outbreak-associated cases. Other common pathogens and conditions included *Giardia* spp. (9.1%, 43/471) and influenza and influenza-like illness (5.3%, 25/471). Enteric viruses (astrovirus, norovirus, rotavirus, and sapovirus) were implicated in 41.8% (197/471) of person-to-person outbreaks and enteric protozoa (*Giardia* spp., *Cryptosporidium* spp. and *Dientamoeba fragilis*) were implicated in 12.5% (59/471) of outbreaks.

The most commonly identified pathogen in person-to-person outbreaks with 20 or more associated cases was norovirus, accounting for 66.2% (98/148) of these outbreaks. The two largest person-to-person outbreaks reported in 2015 were also attributed to norovirus. The largest outbreak involved 165 cases and was spread by person-to-person transmission throughout a long-term care facility in Christchurch. The second largest outbreak, reported from a student boarding house in Auckland involved 136 cases and was also spread through person-to-person contact.

Table 11. Person-to-person outbreaks and associated cases by pathogen or condition, 2015

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=471)[2]	Total	% of cases (n=8000)[2]
Norovirus	168	20	188	39.9	4841	60.5
Giardia spp.	28	15	43	9.1	179	2.2
Influenza and influenza-like-illness[3]	24	1	25	5.3	787	9.8
Bordetella pertussis	20	0	20	4.2	223	2.8
VTEC/STEC infection	13	3	16	3.4	92	1.2
Cryptosporidium spp.	7	8	15	3.2	62	0.8
Salmonella spp.[4]	11	3	14	3.0	35	0.4
Shigella spp.	5	4	9	1.9	23	0.3
Sapovirus	7	0	7	1.5	153	1.9
Campylobacter spp.	1	5	6	1.3	30	0.4
Rotavirus	3	0	3	0.6	57	0.7
Astrovirus	2	0	2	0.4	12	0.2
Mycobacterium tuberculosis	2	0	2	0.4	7	0.1
Measles virus	2	0	2	0.4	6	0.1
Salmonella Typhi	2	0	2	0.4	5	0.1
Respiratory syncytial virus (RSV)	1	0	1	0.2	33	0.4
Varicella zoster virus	1	0	1	0.2	22	0.3
Aeromonas spp.	0	1	1	0.2	5	0.1
Clostridium difficile	1	0	1	0.2	3	<0.1
Dientamoeba Fragalis	0	1	1	0.2	3	<0.1
Yersinia spp.	1	0	1	0.2	2	<0.1
Haemophilus influenzae b	1	0	1	0.2	2	<0.1
Diphtheria	1	0	1	0.2	2	<0.1
Pathogen not identified[5]	100	14	114	24.2	1545	19.3

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

[2] Two agents were reported in seven person-to-person outbreaks with 244 cases. This means totals may add up to more than 100%.

[3] Includes outbreaks of influenza A (13 outbreaks with 416 cases), influenza B (5 outbreaks, 270 cases), and influenza-like illness (8 outbreaks, 203 cases) and rhinovirus (1 outbreak, 23 cases).

[4] Includes nontyphoidal *Salmonella* species only. *Salmonella* Typhi and *Salmonella* Paratyphi are reported separately.

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

Contributing factors

Exposure to infected people was the primary contributing factor for 97.9% (461/471 outbreaks) of person-to-person outbreaks reported in 2015. Other contributing factors reported were poor hygiene (29.1%, 137/471), a compromised immune system (11.9%, 56/471), inadequate vaccination cover (7.6%, 36/471), excessively crowded living conditions (2.3%, 11/471), inadequate vaccination effectiveness (3.8%, 18/471) and unprotected sexual activity (0.2%, 1/471).

WATERBORNE OUTBREAKS

Causal agents

There were 19 waterborne outbreaks with 89 associated cases in 2015, all of which were linked to a specific pathogen (Table 12). The most commonly reported waterborne pathogens were *Giardia* spp. (42.1%, 8/19 outbreaks) and *Campylobacter* spp. (21.1%, 4/19 outbreaks). Enteric protozoa (*Giardia* spp., *Cryptosporidium* spp. and *Dientamoeba fragalis*) were implicated in 57.9%, (11/19) of waterborne outbreaks and enteric bacteria (*Campylobacter* spp., *Salmonella* spp., *Shigella* spp., VTEC/STEC infection and *Yersinia* spp.) were implicated in 47.4% (9/19) of waterborne outbreaks. Two pathogens (*Giardia* spp. and *Shigella* spp.) were implicated in one outbreak involving 26 cases. The infections in this outbreak were acquired while students on a school trip were travelling in Nepal.

Table 12. Waterborne outbreaks and associated cases by pathogen, 2015

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=19)[2]	Total	% of cases (n=89)[2]
Giardia spp.	3	5	8	42.1	50	56.2
Campylobacter spp.	2	2	4	21.1	23	25.8
Shigella spp.	0	2	2	10.5	28	31.5
Cryptosporidium spp.	2	0	2	10.5	5	5.6
Dientamoeba fragalis	1	0	1	5.3	3	3.4
Salmonella spp.	1	0	1	5.3	2	2.2
VTEC/STEC infection	0	1	1	5.3	2	2.2
Yersinia spp.	0	1	1	5.3	2	2.2

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

[2] Two pathogens were reported in one waterborne outbreak involving 26 cases. This means the totals may add up to more than 100%.

Contributing factors

The most common contributing factor linked to waterborne outbreaks was untreated water (73.7%, 14/19 outbreaks) followed by an inadequately treated water supply (26.3%, 5/19) (Table 13). All of the contributing factors associated with waterborne outbreaks were reported as suspected only.

Table 13. Waterborne outbreaks by contributing factor, 2015

Contributing factor	Outbreaks				Cases	
	Confirmed	Suspected	Total	% of outbreaks (n=19)[1]	Total	% of cases (n=89)[1]
Untreated drinking-water supply[2]	0	14	14	73.7	72	80.9
Inadequately treated water supply	0	5	5	26.3	37	41.6
Source water quality inferior to normal	0	2	2	10.5	32	36.0
Contamination of post treatment water storage	0	1	1	5.3	3	3.4

[1] Two outbreaks involving 29 cases had two or more contributing factors. This means the totals may add up to more than 100%.

[2] Includes surface water with no treatment, roof-collected rainwater with no treatment, groundwater not assessed as secure and no treatment.

Note: No outbreaks with recent or ongoing treatment process failure or other sources of post-treatment contamination were reported in 2015.

ENVIRONMENTAL OUTBREAKS

Causal agents

There were 100 environmental outbreaks with 1929 associated cases reported in 2015. Of these outbreaks, 83.0% (83/100) were linked to a specific causal agent (Table 14). The most common causal agent identified in environmental outbreaks was norovirus (53.0%, 53/100), followed by *Giardia* spp. (8.0%, 8/100). Even so, environmental transmission was the secondary mode reported in the majority (96.2%, 51/53) of the norovirus outbreaks. Norovirus also accounted for the highest proportion of associated cases (71.0%, 1369/1929). *Shigella* spp. (100.0%, 2/2) and *Legionella* spp. (75.0%, 3/4) were responsible for the highest proportion of outbreaks where environmental transmission was the primary mode reported. Enteric viruses (norovirus and sapovirus) were implicated in 54.0% (54/100) of the environmental outbreaks, while enteric protozoa (*Giardia* spp. and *Cryptosporidium* spp.) were implicated in 13.0% (13/100) of the environmental outbreaks.

Table 14. Environmental outbreaks and associated cases by pathogen or condition, 2015

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=100)[2]	Total	% of cases (n=1929)[2]
Norovirus	2	51	53	53.0	1369	71.0
Giardia spp.	4	4	8	8.0	53	2.7
Cryptosporidium spp.	2	3	5	5.0	29	1.5
Legionella spp.	3	1	4	4.0	30	1.6
VTEC/STEC infection	1	2	3	3.0	35	1.8
Campylobacter spp.	0	3	3	3.0	19	1.0
Shigella spp.	2	0	2	2.0	28	1.5
Influenza and influenza-like-illness[3]	0	2	2	2.0	26	1.3
Salmonella spp.	0	2	2	2.0	6	0.3
Sapovirus	0	1	1	1.0	22	1.1
Bordetella pertussis	0	1	1	1.0	3	0.2
Pathogen not identified[4]	1	16	17	17.0	335	17.4

[1] Includes outbreaks where environmental transmission was either the primary or secondary mode of transmission reported.
[2] Two pathogens were reported in one environmental outbreak involving 26 cases. This means totals may add up to more than 100%.
[3] Includes outbreaks of influenza A (1 outbreak with 18 cases) and influenza-like illness (1 outbreak, 8 cases)
[4] All enteric outbreaks with no identified pathogen were recorded as gastroenteritis.

Contributing factors

The major contributing factors to environmental outbreaks were exposure to contaminated environment(s)[†] (89.0%, 89/100), exposure to other recreational waters (9.0%, 9/100), exposure to infected animals (6.0%, 6/100), and exposure to contaminated swimming/spa pools (6.0%, 6/100). At least one suspected or confirmed contributing factor was recorded for each outbreak.

[†] Includes exposure to contaminated land, air (including ventilation) and built environments (including dwellings).

ZOONOTIC OUTBREAKS

Causal agents

There were 24 zoonotic outbreaks, with 98 associated cases in 2015. All were linked to a specific pathogen (Table 15). *Campylobacter* spp. was the most commonly identified pathogen and was linked to 29.2% (7/24) of zoonotic outbreaks and 35.7% (35/98) of the associated cases. Enteric protozoa (*Cryptosporidium* spp. and *Giardia* spp.) and enteric bacteria (*Campylobacter* spp., *Salmonella* spp. and VTEC/STEC infection) were equally represented in the zoonotic outbreaks (45.8%, 11/24 each).

Table 15. Zoonotic outbreaks and associated cases by pathogen or condition, 2015

Pathogen or condition	Outbreaks[1]				Cases	
	Primary mode	Secondary mode	Total	% of outbreaks (n=24)	Total	% of cases (n=98)
Campylobacter spp.	3	4	7	29.2	35	35.7
Cryptosporidium spp.	6	0	6	25.0	27	27.6
Giardia spp.	1	4	5	20.8	19	19.4
VTEC/STEC infection	1	2	3	12.5	8	8.2
Leptospira spp.	1	0	1	4.2	3	3.1
Salmonella spp.	1	0	1	4.2	3	3.1
Sapovirus	1	0	1	4.2	3	3.1

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

Contributing factors

Almost all (95.8%, 23/24) zoonotic outbreaks recorded direct exposure to infected animals as a contributing factor. Multiple settings were identified in two outbreaks. The most common setting for a zoonotic outbreak was a private home (58.3%, 14/24 outbreaks) followed by farms (29.2%, 7/24).

OUTBREAKS WITH OVERSEAS TRANSMISSION

In 2015, 14 outbreaks with overseas transmission were reported involving 74 cases. Travel to Fiji and Indonesia was associated with the most outbreaks (14.3%, 2 outbreaks each). All other overseas exposure locations listed in Table 16 were associated with a single outbreak each. The majority of cases associated with overseas transmission were infected with *Shigella* spp. (47.3%, 35/74 cases), followed by *Giardia* spp. (45.9%, 34/74 cases).

Table 16. Outbreaks with overseas transmission by exposure location and pathogen, 2015

Destination	Pathogen or condition[1]								
	Shigella spp.	*Giardia* spp.	*Salmonella* spp.	*Aeromonas* spp.	*Cryptosporidium* spp.	Diphtheria	Norovirus	VTEC/STEC infection	Total
Afghanistan		1							1
Australia		1							1
Bahamas							1		1
Fiji				1				1	2
Indonesia	1		1						2
Nepal	1	1							1
Oman		1							1
Pakistan						1			1
Rarotonga	1								1
Taiwan			1						1
United States of America					1				1
Vanuatu	1								1
Total outbreaks	**4**	**4**	**2**	**1**	**1**	**1**	**1**	**1**	**14**
Total cases	**35**	**34**	**4**	**5**	**2**	**2**	**1**[2]	**17**	**74**

[1] Two pathogens were reported in one outbreak with 26 cases. This means the numbers might not add up to the totals.

[2] One outbreak of norovirus occurred on a cruise ship. While one case was laboratory-confirmed in New Zealand, the number of probable cases was not able to be obtained from the ship.

OUTBREAK RECOGNITION, INVESTIGATION AND CONTROL

Timeliness of reporting

For the 96.1% (536/558) of outbreaks where the timeliness of reporting data was available, just over half (53.7%, 288/536) were reported to a PHU within a week of the onset of illness in the first case. A further 36.0% (193/536) of outbreaks were reported from 7 to 30 days (inclusive) after the onset of illness in the first case.

Reporting delay (the time between the date of onset of illness in the first case and the date of reporting) varied among the different modes of transmission (Table 17). The shortest median reporting delay (4.0 days) was associated with foodborne outbreaks, followed by person-to-person (6.0 days), environmental outbreaks (7.0 days) and zoonotic and waterborne outbreaks (18.0 days).

Table 17. Median reporting delay by outbreak type, 2015

Outbreak type	No. of outbreaks[1,2]	Median reporting delay (days)
Person-to-person	450	6.0
Environmental	94	7.0
Foodborne	77	4.0
Zoonotic	24	17.5
Waterborne	18	18.0
Other mode	7	9.0
Total	**536**	**6.0**

[1] More than one mode of transmission was recorded for 174 outbreaks. This means the numbers do not add up to the group total.

[2] Outbreaks were excluded if the date of onset of illness in the first case was missing.

Recognition of outbreaks

In 2015, 60.0% (335/558) of outbreaks were identified through an increase in disease incidence and 18.3% (102/558) by cases reporting person-to-person contact with other cases (Table 18). Other means of outbreak recognition reported included cases attending a common event (8.8%, 49/558) or being linked to a common source (6.5%, 36/558).

Table 18. Outbreaks by means of recognition, 2015

Means of recognition	No. of outbreaks	% of total outbreaks (n=558)
Increase in disease incidence	335	6409
Cases had person to person contact with other case(s)	102	1111
Cases attended common event	49	332
Cases linked to common source (e.g. food, water, environmental site)	36	372
Common organism type/strain characteristics between cases	15	107
Other means	21	179

Control measures

In 2015, the outbreak control measures undertaken were reported in 92.5% (516/558) of outbreaks. The most common measures were health education and advice regarding the source (76.0%, 392/516) and cleaning and disinfection (63.8%, 329/516) (Table 19). No control measures were taken in 6.6% (37/558) of outbreaks.

Table 19. Outbreaks by control measures undertaken, 2015

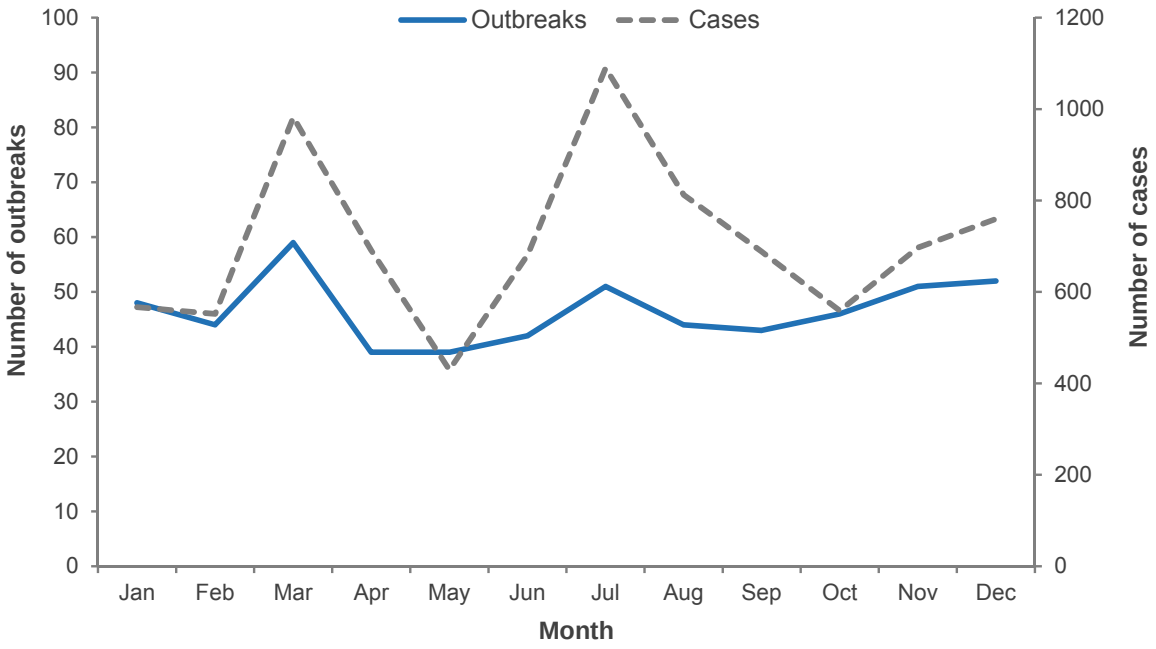
Outbreak control measure	No. of outbreaks[1]	% of total outbreaks (n=516)
Source	**484**	**93.8**
Health education and advice	392	76.0
Cleaning, disinfection	329	63.8
Exclusion	318	61.6
Isolation	256	49.6
Modification of procedures	186	36.0
Health warning	119	23.1
Closure	94	18.2
Treatment	55	10.7
Removal	22	4.3
Contacts and potential contacts	**150**	**29.1**
Health education and advice	150	29.1
Chemoprophylaxis	16	3.1
Vaccination	10	1.9
Vehicle and vector	**5**	**1.0**
Treatment	4	0.8
Removal	1	0.2
Other control measures	**71**	**13.8**
No control measures	**37**	**6.6**

[1] More than one control measure was recorded for some outbreaks. This means the numbers may not add up to the group totals.

SUMMARY OF TRENDS

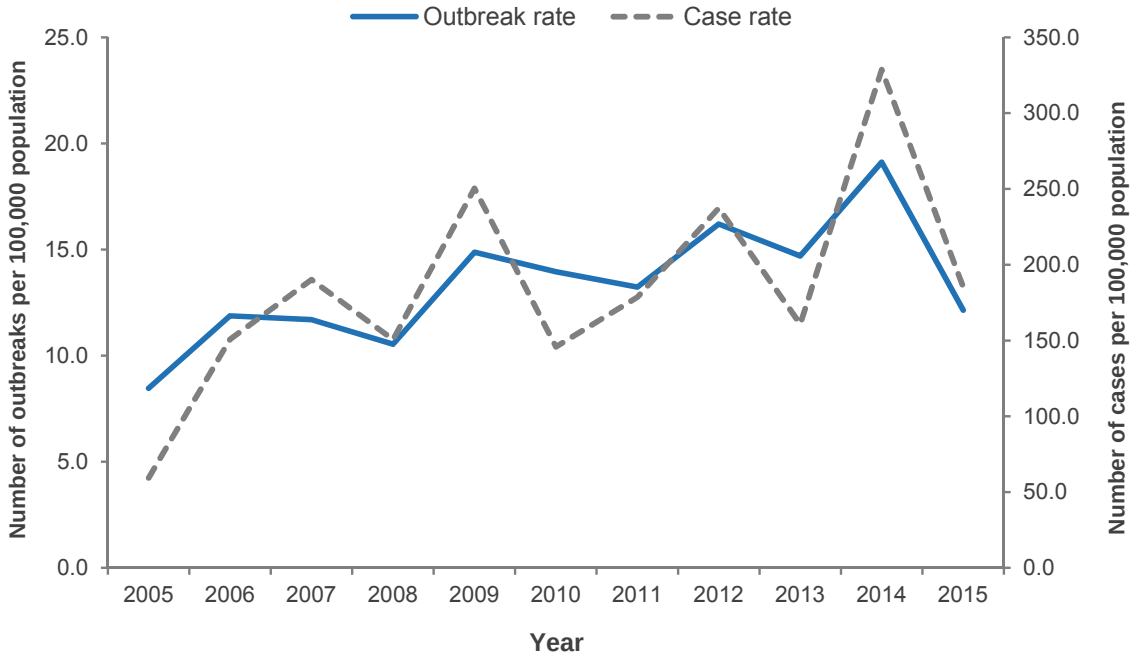
In 2015, the highest number of outbreaks was reported in March (59 outbreaks) followed by December (52 outbreaks) (Figure 5). The March peak was largely driven by an increase in norovirus outbreaks (23 outbreaks, 600 cases), which accounted for over a third of all outbreaks reported that month. The highest number of outbreak-related cases occurred in July (1090 cases) followed by March (982 cases). Norovirus was responsible for around half the cases in each of the peak months (July: 49.7%, 542/1090 cases and March: 61.1%, 600/982 cases). In 2014, the highest number of outbreaks and associated cases (125 outbreaks, 2406 cases) was also reported in March. This high number was also driven by an increase in norovirus outbreaks (63 outbreaks, 1650 cases).

Figure 5. Number of outbreaks and associated cases by month, 2015



Between 2005 and 2014, both the outbreak rate and the case rate have tracked upwards. The national annual outbreak rate for 2015 (12.1 outbreaks per 100,000 population) has decreased significantly ($p<0.05$) from the rate in 2014 (19.1 outbreaks per 100,000) (Figure 6), and is the lowest annual rate reported since 2008 (10.5 outbreaks per 100,000). The 2015 outbreak case rate (185.2 per 100,000 population) is also significantly lower than what was recorded in 2014.

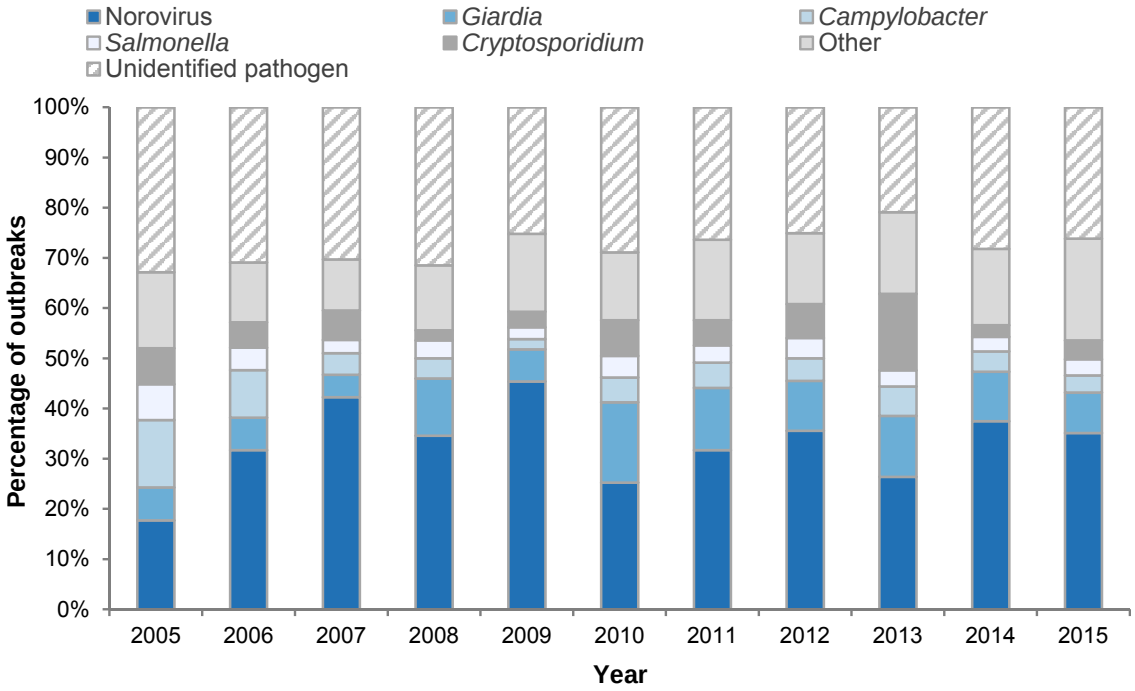
Figure 6. Outbreak rates and associated cases by year, 2005–2015



Since 2001, the number of outbreaks linked to an identified causal agent has remained close to 70% (range 65.4–79.1%). In 2015, 73.8% (412/558) of outbreaks were linked to an identified pathogen or condition. Since 2002, the causal agent associated with the greatest number of outbreaks and outbreak cases has been norovirus, although the number and percentage of norovirus outbreaks and cases has varied considerably from year to year. In 2015, 196 norovirus outbreaks were reported with 4893 associated cases. This figure is much lower than the number of outbreaks observed in 2014 (323 outbreaks and 9390 cases) (Figure 7), when the highest number of outbreaks and cases recorded since reporting began in 1998 occurred. Since 2006, norovirus outbreaks have accounted for around a third of the number outbreaks reported each year, with the exception of 2009 when the proportion was closer to half (45.4%, 290/639 outbreaks).

The number of reported rotavirus outbreaks progressively increased each year from 6 in 2005 (53 cases) to 47 in 2014 (854 cases). In 2015, there was a significant decrease in the number of outbreaks (3 outbreaks including 2 that also had norovirus identified) and associated cases (57 cases) reported. This decrease is most likely associated with the introduction of the infant rotavirus vaccination programme in July 2014.‡

Figure 7. Percentage of outbreaks by pathogen or condition and year, 2005–2015



The number of outbreaks due to *Cryptosporidium* spp. (21 outbreaks, 94 cases) was similar to what was recorded in 2014 (20 outbreaks, 60 cases). Outbreaks due to *Cryptosporidium* spp. increased progressively from 2008 (9 outbreaks, 53 cases) through to 2013 (99 outbreaks, 550 cases) when the number of outbreaks peaked. The most common modes of transmission (primary and secondary) reported for *Cryptosporidium* spp. outbreaks in 2015 were person-to-person (15 outbreaks, 62 cases) and zoonotic transmission (6 outbreaks, 27 cases).

‡ http://www.health.govt.nz/our-work/preventative-health-wellness/immunisation/new-zealand-immunisation-schedule/2014-immunisation-schedule-change

The number of outbreaks due to *Giardia* spp. increased between 2007 (22 outbreaks, 117 cases) and 2010 (97 outbreaks, 378 cases). In 2015, there were 45 outbreaks with 207 associated cases, the lowest number recorded since 2009 (41 outbreaks, 131 cases).

The number of outbreaks and associated cases linked to *Campylobacter* spp. increased steadily between 2009 (13 outbreaks, 69 cases) and 2014 (35 outbreaks, 241 cases). In 2015 the number of outbreaks reported reduced by half (19 outbreaks) while the number of associated cases reduced by more than half (88 cases), when compared to 2014. A large reduction in the number of outbreaks and associated cases reported annually was previously observed in 2007 when numbers reduced by more than half from 2005 (47 outbreaks, 252 cases) to 2007 (21 outbreaks, 60 cases). This decrease was most likely due to interventions put in place in New Zealand to reduce the incidence of poultry associated foodborne campylobacteriosis in 2006 [5]. Before these interventions, the highest number of outbreaks and cases associated with campylobacteriosis was reported in 1998 (61 outbreaks, 321 cases).

Campylobacter spp. has consistently remained one of the five most commonly reported causal agents for outbreaks since 1998. In 2015, the most common modes of primary and secondary transmission reported for *campylobacter* spp. outbreaks were foodborne (11 outbreaks, 46 cases) and zoonotic (7 outbreaks, 35 cases). Five of the foodborne outbreaks had a food source implicated, with the most common vehicles reported as raw or unpasteurised milk (2 outbreaks, 7 cases), undercooked chicken or chicken livers (2 outbreaks, 4 cases) and green salad (1 outbreak, 6 cases).

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) and respiratory syncytial virus (RSV) (2015: 1 outbreak, 33 cases). All of these outbreaks were reported to Regional Public Health in Wellington.

In 2015, the most common outbreak settings were long-term care facilities and private homes, which is similar to observations from 2006 to 2014. Since 2006, outbreaks in institutions have constituted about half of all outbreaks reported annually and those in private homes about a quarter to a third. Before 2006, commercial food operators and private homes were the most commonly reported settings.

In the last 10 years, outbreaks involving person-to-person transmission have become the most frequently reported mode of transmission. This is a change from foodborne transmission, which was often the most frequent mode between 1998 and 2006 (ranging from: 28.3–52.9%). Between 2007 and 2015 the proportion of foodborne outbreaks reported each year ranged from 13.2 to 23.3% (2015: 14.0%, 78 outbreaks). The proportion of outbreaks with person-to-person transmission reported has increased considerably from the 2001–2003 period (20.2–33.9%) to the 2009–2015 period (73.6–87.6%). In 2015, the number of outbreaks with person-to-person transmission (84.4%, 471 outbreaks) was more than four times higher than any other mode of transmission. Similar to what was seen in the previous four years. Outbreaks attributed to environmental transmission (17.9%, 100/558) remained the second most common mode of transmission in 2015. In outbreaks reported from 2010 to 2012 foodborne transmission was the second most common mode of transmission reported.

Since 1998, poultry has been one of the most commonly implicated food sources reported in foodborne outbreaks. The proportion of foodborne outbreaks attributed to poultry increased from 15.2% in 2011 to 46.7% in 2014. In 2015, the proportion reduced to 27.8% although poultry was still the most commonly implicated source in foodborne outbreaks where a source was implicated. Outbreaks implicating dairy

represented the largest proportion of foodborne outbreaks where a source was reported in 2013 (40.6%) and 2012 (26.7%). It is important to note that very few outbreaks have a suspected source confirmed by epidemiological or laboratory methods. In 2015, only 23.1% (18/78) of the foodborne outbreaks recorded an identified food source. In some outbreaks multiple sources are implicated.

In 2015, 14 outbreaks involving 74 cases had identified overseas transmission. This is lower than the annual number of outbreaks with overseas transmission reported since 2011 (ranging from 17–24 outbreaks with 104–443 associated cases). Fiji and Indonesia (2 outbreaks each) were the most commonly reported countries visited. In 2013 and 2014, travel in Fiji (4 outbreaks respectively) was the most commonly reported country of exposure. Between 2006 and 2010, the annual number of outbreaks with overseas transmission reported ranged from 5–14, with the total number of outbreak-associated cases ranging from 21–286. India and Samoa were the only countries associated with more than two outbreaks annually during this period.

The median delay between the date of onset of illness in the first case and the outbreak report date in 2015 was 6.0 days. This delay is slightly longer than the delay that was reported for 2014 (5.0 days), but shorter than what was reported in 2013 (9.0 days). The reporting delay between 2008 and 2012 ranged from 4.0 to 7.5 days. The median delay for zoonotic and waterborne outbreaks decreased in 2015 (18.0 days) when compared to previous years (ranging from 21.0 to 25.0 days between 2013 and 2014).

Health education and advice related to the outbreak source has been the most common control measure used since 2001 and was provided in 76.0% (392/516) of the outbreaks with a control measure reported in 2015. Between 2007 and 2015, cleaning and disinfection was the second most common control measure reported, a change from modification of procedures pertaining to the source, which was the second most common control measure between 2001 and 2006. The proportion of outbreaks reporting no control measures decreased from 27.8% (108/389) of outbreaks in 2001 to 6.6% (37/558) of outbreaks in 2015.

GLOSSARY

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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.

ESR

Institute of Environmental Science and Research Limited.

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.

REFERENCES

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REFERENCES

1. ESR, 2012. *Guidelines for the investigation and control of disease outbreaks.* Wellington. Institute of Environmental Science and Research Ltd.
2. Kroneman A, Vennema H, Deforche K, et al., 2011. An automated genotyping tool for enteroviruses and noroviruses. *Journal of Clinical Virology*. 51(2): pp. 121-5.
3. Eden JS, Hewitt J, Lim KL, et al., 2014. The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. *Virology*. 450-451: pp. 106-13.
4. Painter JA, Ayers T, Woodruf R, et al., 2009. Recipes for foodborne outbreaks: a scheme for categorizing and grouping implicated foods. *Foodborne Pathogen and Disease*. 6(10): pp. 1259-64.
5. Sears A, Baker MG, Wilson N, et al., 2011. Marked campylobacteriosis decline after interventions aimed at poultry, New Zealand. *Emerging Infectious Diseases*. 17(6): pp. 1007-15.

APPENDIX

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APPENDIX

OUTBREAK REPORT FORM (VERSION: 2 OCTOBER 2010)

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	**Institution**	**Workplace/Community/Other**
○ Restaurant/café/bakery	○ Hostel/boarding house	○ Workplace
○ Takeaway	○ Hotel/motel	○ Farm
○ Supermarket/delicatessen	○ Long term care facility	○ Petting zoo
○ Temporary or mobile service	○ Hospital (acute care)	○ Home
○ Fast food restaurant	○ Prison	○ Community, church, sports gathering
○ Caterers	○ Camp	○ Cruise ship, airline, tour bus, train
○ Other food outlet	○ School ○ Childcare centre	○ Other setting
	○ Marae	
	○ Other institution	

Setting name _____

Setting Address Number _____ Street _____ Suburb _____

Town/City _____ Post Code _____ ☐ GeoCode ____

Second setting where exposure occurred Setting unknown ☐

Food premises	**Institution**	**Workplace/Community/Other**
○ Restaurant/café/bakery	○ Hostel/boarding house	○ Workplace
○ Takeaway	○ Hotel/motel	○ Farm
○ Supermarket/delicatessen	○ Long term care facility	○ Petting zoo
○ Temporary or Mobile Service	○ Hospital (acute care)	○ Home
○ Fast food restaurant	○ Prison	○ Community, church, sports gathering
○ Caterers	○ Camp	○ Cruise ship, airline, tour bus, train
○ Other food outlet	○ School ○ Childcare centre	○ Other setting
	○ Marae	
	○ Other institution	

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	**Institution**	**Workplace/Community/Other**
○ Restaurant/café/bakery	○ Hostel/boarding house	○ Workplace
○ Takeaway	○ Hotel/motel	○ Farm
○ Supermarket/delicatessen	○ Long term care facility	○ Petting zoo
○ Temporary or Mobile Service	○ Hospital (acute care)	○ Home
○ Fast food restaurant	○ Prison	○ Community, church, sports gathering
○ Caterers	○ Camp	○ Cruise ship, airline, tour bus, train
○ Other food outlet	○ School ○ Childcare centre	○ Commercial food manufacturer
	○ Marae	○ Other setting
	○ Other institution	

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	**Institution**	**Workplace/Community/Other**
○ Restaurant/café/bakery	○ Hostel/boarding house	○ Workplace
○ Takeaway	○ Hotel/motel	○ Farm
○ Supermarket/delicatessen	○ Long term care facility	○ Petting zoo
○ Temporary or Mobile Service	○ Hospital (acute care)	○ Home
○ Fast food restaurant	○ Prison	○ Community, church, sports gathering
○ Caterers	○ Camp	○ Cruise ship, airline, tour bus, train
○ Other food outlet	○ School ○ Childcare centre	○ Commercial food manufacturer
	○ Marae	○ Other setting
	○ Other institution	

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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