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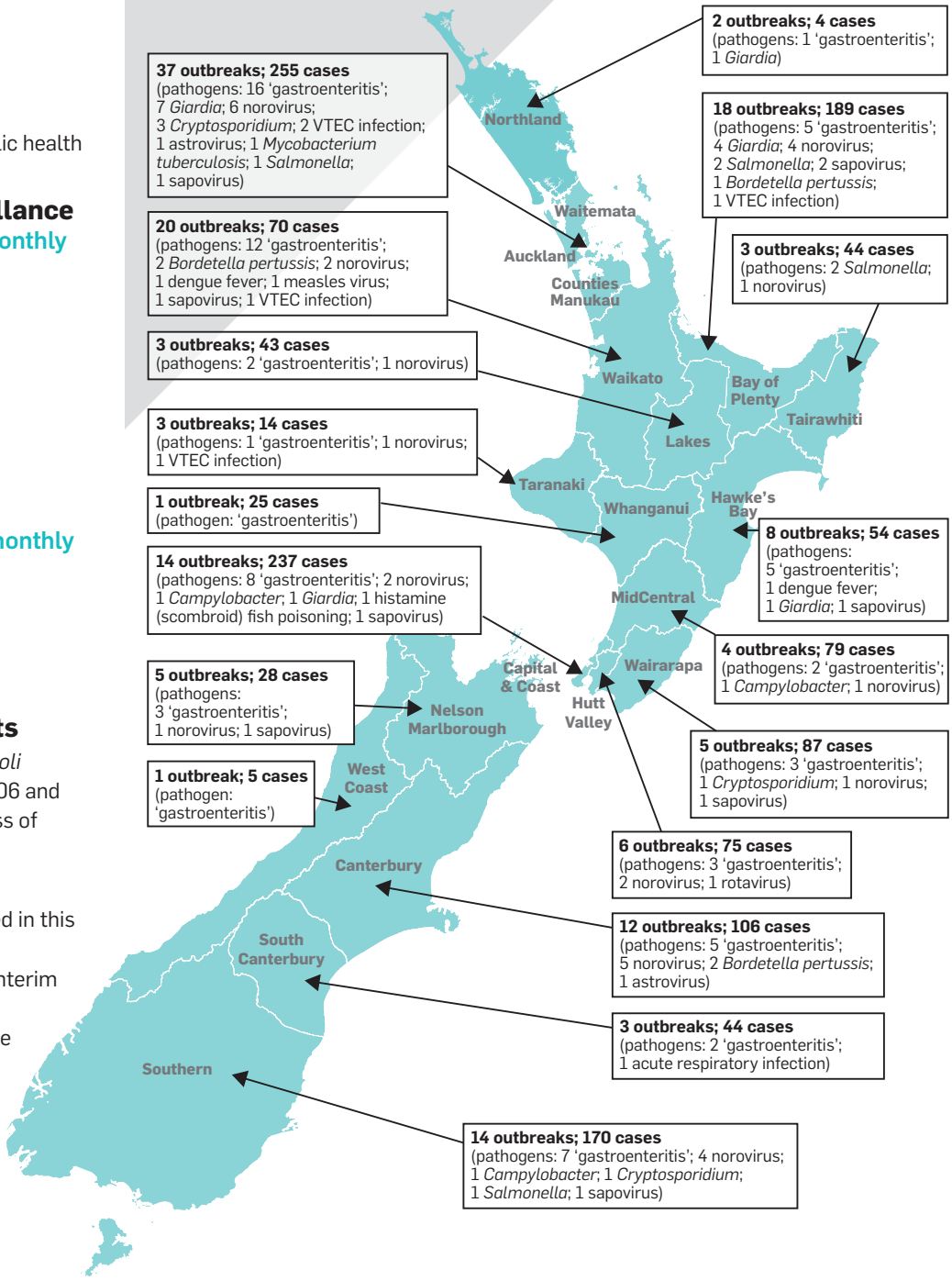
NEW ZEALAND

Public Health Surveillance Report

September 2016: Covering April to June 2016

CONTENTS AND HIGHLIGHTS



This quarter's outbreaks

Notification and outbreak data in this issue are drawn from the April to June quarter of 2016. The outbreak map on this page consists of all outbreak information, final and interim. The total number of outbreaks and cases by region and outbreaks by pathogen are reported, as notified up to 4 July 2016. Outbreaks reporting exposures in more than one geographic location are assigned to the district health board with the most cases. Five outbreaks involved more than one pathogen therefore individual pathogen outbreak numbers may not sum to group totals.

The latest reports from Sexually Transmitted Infections Surveillance, Antimicrobial Resistance, Virology and Enteric Reference Laboratories are available at www.surv.esr.cri.nz

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1. EDITORIAL

Whole genome sequencing in public health microbiology

In recent years we have seen significant advances in available sequencing technology. Microbial whole genome sequencing (WGS) using high-throughput sequencing (HTPS) technology has the potential to greatly improve our knowledge and understanding of infectious diseases. It has the capacity to replace some traditional testing methods and provide valuable information to public health services and clinicians.

New HTPS technology produces thousands or millions of sequences concurrently. This allows the sequencing of whole bacterial and viral genomes within a much shorter timeframe. Further, new bench-top technology, rapidly falling costs and improved turnaround time to results have led several leading public health laboratories overseas to start using the technology.

In keeping with overseas trends, ESR and the Ministry of Health have undertaken a genomics transition project. The project aims to establish how and where to introduce WGS so as to improve the service currently provided and to replace ageing testing methods.

WGS has important applications for epidemiological surveillance, outbreak investigation and hospital infection control. WGS has been used mostly to characterise pathogens (in particular to characterise bacterial pathogens) and to identify, type and detect antimicrobial resistance and virulence genes. WGS has the potential to supersede traditional typing techniques by providing a far greater resolution between bacterial isolates. This provides more detailed information for epidemiological purposes. These purposes include outbreaks of foodborne disease caused by pathogens such as *Salmonella, Listeria* or verotoxin-producing *Escherichia coli* (VTEC); and outbreaks of healthcare-associated infections such as methicillin-resistant *Staphylococcus aureus* or *Clostridium difficile.*

Potential applications for WGS include identifying organisms more accurately, detecting resistance more accurately, profiling virulence, describing the evolution and epidemiology of important pathogens, and tracking mobile antimicrobial resistance elements.

WGS is unlikely to surpass novel identification methods such as mass spectrometry for routine use in a diagnostic laboratory. In the near future WGS is also unlikely to be applied directly to clinical specimens because of limiting factors such as the low copy number of pathogen DNA and other sources of DNA present in the specimen. WGS may play an important role in identifying organisms not identified using routine methods. Examples include organisms requiring 16S rRNA sequencing for identification; and fastidious pathogens that are hard to culture.

WGS has potential applications in detecting genetic determinants of antibiotic resistance. However, questions remain about how accurate WGS is in predicting resistance given that a resistance genotype is not always congruent with the phenotype. Sensitivity and robustness of phenotypic antimicrobial susceptibility testing (AST) is currently hard to match with genoptype. This is partly due to a lack of high-quality data linking the two. However, WGS can be useful where complete or near-complete congruence exists between phenotype and genotype and where traditional phenotypic AST testing is slow or challenging. One example is slow-growing bacteria (such as *Mycobacterium tuberculosis* and the non-tuberculous Mycobacteria).

WGS can be used to detect genetic markers of virulence in bacterial pathogens, for example Panton-Valentine Leucocidin (PVL) in *S. aureus*, and VTEC. Again, applying WGS remains investigational due to uncertainties around some target gene expression and the phenotypic significance of gene presence.

WGS has been used to describe the evolution and epidemiology of important pathogens and to track mobile antimicrobial resistance elements. So it could be applied to help inform hospital infection control responses where they suspect transmission within the healthcare setting. WGS also has important applications in the future of:

- culture-independent diagnostics and metagenomics—sequencing of DNA content in a clinical or environmental specimen
- subsequent filtering out of extraneous DNA (human or non-pathogen)
- using bioinformatic analysis to identify the potential pathogen—very important for discovering novel pathogens.

The cost of adopting WGS has implications for resource and infrastructure requirements. For example, any new technology and methods must be able to replace the existing technology to provide more benefits than existing methods (such as for identifying pathogens).

A skilled team of bioinformatics experts is essential for post-sequencing analysis, and adequate computational power is required to process, analyse and report sequence data within a timeframe that is clinically acceptable. Adequate information technology resources are also needed for data storage and backup. With falling costs and ongoing development of systems that are easier to use, WGS is likely to replace traditional methods such as pulse-field gel electrophoresis, multilocus sequence typing, DNA microarray and 16S rRNA sequencing.

The cost to introduce WGS is just one obstacle being tackled. WGS faces a number of other obstacles before it is widely adopted. Five limitations are noted below.

1. The data generated does not necessarily translate directly into knowledge of gene expression and transcription.
2. Studies comparing WGS to traditional methods lack robust validation and comparisons about their respective usefulness.
3. Automated analysis processes need to be developed and evaluated further to produce high-quality data and reports.

4. Standardisation of testing (in terms of selection of reference genomes, availability and quality of reference databases and methodologies) is a problem. Two issues this problem raises are how identical two isolates from a suspected outbreak are and how similar the two isolates are when defining an outbreak. A high degree of accuracy is essential.
5. Standardisation of data reporting is also a problem. WGS produces detailed and complex genomic information that few clinicians, epidemiologists and public health practitioners can fully understand. One reason is that some results do not suit straightforward 'yes/no' reporting.

Resolving these obstacles will take significant work. Solutions will require epidemiologists, public health practitioners and clinicians to cooperate closely and coordinate their activities.

Reported by Chris Hewison, Clinical Microbiologist, Health Group, ESR.

2. NOTIFIABLE DISEASE SURVEILLANCE

The following is a summary of disease notifications for the April to June quarter of 2016 and cumulative notifications and rates calculated for a 12-month period (July 2015 to June 2016). For comparative purposes notification numbers and rates are presented in brackets for the same periods in the previous year. A robust method of constructing 95% confidence intervals is used to determine 'statistically significant differences' throughout this report unless otherwise stated [see Newcombe RG and Altman DG 2000. Proportions and their differences. In: Statistics with Confidence. BMJ Books, Bristol.]. Information in this section is based on data recorded in EpiSurv by public health service staff up to 4 July 2016. As the data may be updated over time, this information should be regarded as provisional.

National surveillance data tables are available at www.surv.esr.cri.nz

Vaccine preventable disease

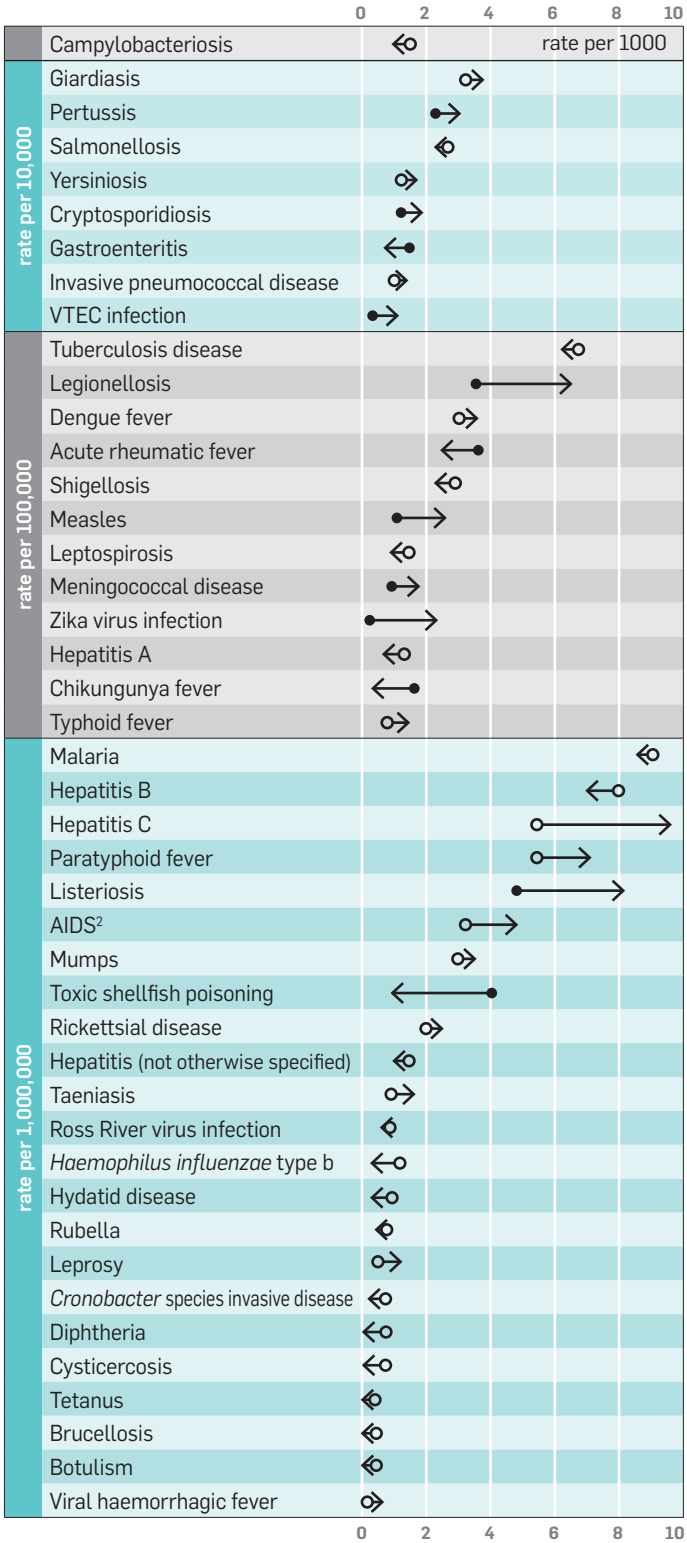
Invasive pneumococcal disease

- ***Notifications:*** 121 notifications in the quarter (2015, 102); 469 notifications over the last 12 months (2015, 459), giving a rate of 10.2 cases per 100,000 population (2015, 10.2), not a statistically significant change.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (61 cases). Cases were aged between 3 months and 92 years, with 9 cases aged <2 years.

Measles

- ***Notifications:*** 95 notifications in the quarter (2015, 7); 102 notifications over the last 12 months (2015, 59), giving a rate of 2.2 cases per 100,000 population (2015, 1.3), a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (6 cases) and from the same quarter last year (7 cases). 15 cases were aged <15 months. 86 cases were confirmed and

National surveillance data 12-monthly notification rate changes[1]



Notifications per 1000 or 10,000 or 100,000 or 1,000,000 population.
Rate change symbol key:
- Rate increase from the previous 12-month period
- Rate decrease from the previous 12-month period
- Statistically significant rate change
- Statistically non-significant rate change

[1] Rates are calculated for the 12-month period July 2015 to June 2016 and compared to previous 12-month rates.
[2] Data provided by the AIDS Epidemiology Group, University of Otago. Note: changes in the 12-month notification rate should be interpreted with caution as this often reflects late notifications.

9 notifications were still under investigation, some of which will be classified 'not a case'. All except one of the confirmed cases were epidemiologically and/or genotypically linked to a single outbreak.

Pertussis

- ***Notifications:*** 238 notifications in the quarter (2015, 228); 1261 notifications over the last 12 months (2015, 939), giving a rate of 27.4 cases per 100,000 population (2015, 20.8), a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (290 cases).

Enteric infections

Campylobacteriosis

- ***Notifications:*** 1089 notifications in the quarter (2015, 1078); 6273 notifications over the last 12 months (2015, 6408), giving a rate of 136.5 cases per 100,000 population (2015, 142.1), not a statistically significant decrease.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (1592 cases).

Gastroenteritis (acute)

- ***Notifications:*** 123 notifications in the quarter (2015, 114); 521 notifications over the last 12 months (2015, 691), giving a rate of 11.3 cases per 100,000 population (2015, 15.3), a statistically significant decrease.
- ***Note:*** this is not a notifiable disease per se except in persons with a suspected common source or with a high risk occupation. The term 'gastroenteritis' provides a catch-all category for enteric diseases that are not notifiable unless they meet the criteria above and for syndromic reports that come through public health units, including direct reports from the public where the causative pathogen may never be known.

Listeriosis

- ***Notifications:*** 12 notifications in the quarter (2015, 7); 37 notifications over the last 12 months (2015, 21), giving a rate of 0.8 cases per 100,000 population (2015, 0.5), a statistically significant increase.
- ***Comments:*** 2 perinatal cases were reported. 1 case was a still birth at 36 weeks gestation and 1 case was a live birth at 34 weeks gestation.

Salmonellosis

- ***Notifications:*** 257 notifications in the quarter (2015, 237); 1067 notifications over the last 12 months (2015, 1049), giving a rate of 23.2 cases per 100,000 population (2015, 23.3), not a statistically significant decrease.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (347 cases).

VTEC infection

- ***Notifications:*** 112 notifications in the quarter (2015, 61); 469 notifications over the last 12 months (2015, 226), giving a rate of 10.2 cases per 100,000 population (2015, 5.0), a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (169 cases) and a statistically significant increase from the same quarter last year (61 cases). The increase may be due to a recent change in laboratory methods in the Auckland region, all faecal specimens are now screened for VTEC using PCR.

Yersiniosis

- ***Notifications:*** 202 notifications in the quarter (2015, 100); 753 notifications over the last 12 months (2015, 711), giving a rate of 16.4 cases per 100,000 population (2015, 15.8), not a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (149 cases) and from the same quarter last year (100 cases).

Infectious respiratory diseases

Acute rheumatic fever

- ***Notifications:*** 53 notifications in the quarter (2015, 39); 129 notifications over the last 12 months (2015, 165), giving a rate of 2.8 cases per 100,000 population (2015, 3.7), a statistically significant decrease.
- ***Comments:*** there has been a statistically significant increase from the previous quarter (28 cases). Cases were distributed by age as follows: 10 (5–9 years), 19 (10–14 years), and 24 (≥15 years). 49 cases were an initial attack and 4 cases were a recurrent attack of acute rheumatic fever.
- ***Note:*** this information is based on report date and may not reflect the actual onset of acute rheumatic fever. This information should not be used to assess trends in the disease rates over time.

Meningococcal disease

- ***Notifications:*** 14 notifications in the quarter (2015, 11); 70 notifications over the last 12 months (2015, 43), giving a rate of 1.5 cases per 100,000 population (2015, 1.0), a statistically significant increase.
- ***Comments:*** Cases were distributed by age as follows: 2 (<1 year), 3 (1–4 years), and 9 (≥15 years). All cases were laboratory confirmed and had the strain group identified: group B (10 cases, including NZB:P1.7-2,4 (6 cases)), group C (2 cases) and group Y (2 cases). Strain type B:P1.7-2.4 was previously known as the 'NZ epidemic strain'.

Environmental exposures & infections

Cryptosporidiosis

- ***Notifications:*** 190 notifications in the quarter (2015, 81); 862 notifications over the last 12 months (2015, 590), giving a rate of 18.8 cases per 100,000 population (2015, 13.1), a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (134 cases) and from the same quarter last year (81 cases). The increase in notifications may be partly due to a change in laboratory practice in the Northern region, where since late June 2015, all faecal specimens are screened for *Cryptosporidium* and *Giardia* regardless of whether parasite screening requested.

Giardiasis

- ***Notifications:*** 394 notifications in the quarter (2015, 363); 1631 notifications over the last 12 months (2015, 1537), giving a rate of 35.5 cases per 100,000 population (2015, 34.1), not a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (496 cases).

Legionellosis

- ***Notifications:*** 57 notifications in the quarter (2015, 61); 298 notifications over the last 12 months (2015, 168), giving a rate of 6.5 cases per 100,000 population (2015, 3.7), a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (85 cases). 7 notifications were still under investigation. The increase in notifications may be partly due to the LegiNZ study, which began in May 2015. This one year study was based in 20 hospitals, representing 17 DHBs. During the study all lower respiratory samples from hospitalised patients with suspected pneumonia were tested for *Legionella* spp. by PCR. An increase in case detection in these regions was expected.

Leptospirosis

- ***Notifications:*** 28 notifications in the quarter (2015, 14); 68 notifications over the last 12 months (2015, 73), giving a rate of 1.5 cases per 100,000 population (2015, 1.6), not a statistically significant decrease.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (14 cases) and from the same quarter last year (14 cases). There were 22 male cases and 6 female cases. 15 cases were recorded as engaged in occupations identified as high risk for exposure. The most commonly recorded occupations for these cases was farmer or farm worker (12 cases). 10 cases were still under investigation.

Toxic shellfish poisoning

- ***Notifications:*** 1 notification in the quarter (2015, 0); 5 notifications over the last 12 months (2015, 17), giving a rate of 0.1 cases per 100,000 (2015, 0.4), a statistically significant decrease.

New, exotic & imported infections

Chikungunya fever

- ***Notifications:*** 12 notifications in the quarter (2015, 9); 19 notifications over the last 12 months (2015, 77), giving a rate of 0.4 cases per 100,000 population (2015, 1.7), a statistically significant decrease.
- ***Comments:*** there has been a statistically significant quarterly increase from the previous quarter (3 cases). All 12 cases were laboratory confirmed and had travelled overseas during the incubation period of the disease. Countries visited were Fiji (10 cases), Brazil (1 case), India and United States of America (1 case).

Dengue fever

- ***Notifications:*** 48 notifications in the quarter (2015, 14); 163 notifications over the last 12 months (2015, 150), giving a rate of 3.5 cases per 100,000 population (2015, 3.3), not a statistically significant increase.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (77 cases) and a statistically significant increase from the same quarter last year (14 cases). 38 cases were laboratory confirmed and 8 notifications were still under investigation. Overseas travel information was recorded for 43 (89.6%) cases. The most commonly visited countries were Indonesia (24 cases) and Papua New Guinea (6 cases).

Zika virus infection

- ***Notifications:*** 13 notifications in the quarter (2015, 1); 103 notifications over the last 12 months (2015, 3), giving a rate of 2.2 per 100,000 population.
- ***Comments:*** there has been a statistically significant quarterly decrease from the previous quarter (83 cases) and a statistically significant increase from the same quarter last year (1 case). 12 cases were laboratory confirmed and 1 notification was still under investigation. All 13 cases had travelled overseas during the incubation period for the disease. Countries visited were Fiji (10 cases), Indonesia (1 case), Nicaragua and United States of America (1 case) and Venezuela (1 case).

3. OTHER SURVEILLANCE REPORTS

Verotoxin-producing *Escherichia coli* infections in Taranaki between 2006 and 2015: a serious farm-related illness of increasing incidence in children

Verotoxin-producing *Escherichia coli* (VTEC) infections cause a severe bloody diarrhoeal illness with a proportion of cases developing life-threatening complications.[1] New Zealand reported its first case in 1993.[2] The purpose of this report is to describe the epidemiology of VTEC infections in the Taranaki District Health Board (DHB) area between 2006 and 2015.

We analysed all VTEC cases notified to the Taranaki Medical Officer of Health between 1 January 2006 and 31 December 2015. We defined a case as a person with a clinically compatible illness, confirmed in the laboratory.[2] We did not include asymptomatic people with positive laboratory results in our analysis. The figures used to calculate rates were an average of the 2006 and 2013 Census statistics for the population usually living in the Taranaki DHB.[3] We used EpiInfo™ to estimate relative risks (RR), with 95% confidence intervals (CI) and p-values.[4]

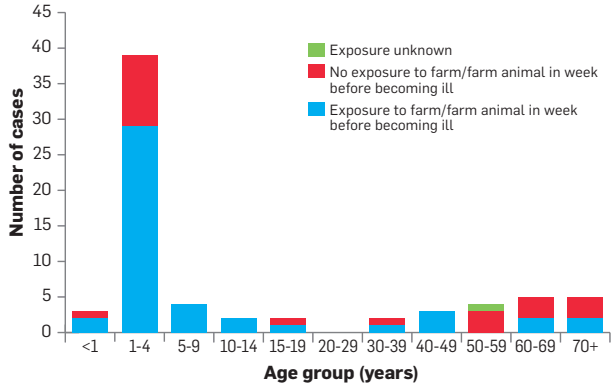
Taranaki saw 67 clinically compatible laboratory-confirmed cases of VTEC between 2006 and 2015. The confirmed cause was the *E. coli* O157:H7 strain. The number of VTEC notifications has been increasing in Taranaki since 2005. Most health districts throughout New Zealand have seen an increase in confirmed cases but this trend has been more pronounced in the upper North Island.[5] In Taranaki

cases, people of New Zealand/European ethnicity had the highest notification rate, with an average of 7.5 per 100,000 population a year over the 10 years, followed by Māori, with an average of 4.7 per 100,000. Thirty-nine cases (58.2%) were children aged 1–4 years. A child in that age range was almost 21 times (RR 21.3, 95% CI 13.2–34.6, p<0.0001) as likely to be infected with VTEC as a person of any other age. Thirty-two (47.8%) infected people required hospital treatment, and 10 (14.9%) developed haemolytic uraemic syndrome. Of these, 5 (7.5%) were children who subsequently had tertiary-level treatment at Starship Hospital in Auckland.

There was a marked seasonal difference between infected people living in rural areas and those living in urban areas. In urban areas, notifications were highest in autumn and lowest in winter; while in rural areas, notifications were lowest in autumn and very high in spring. The two most common reported risk factors were coming into contact with animals (including pets and farm animals), and coming into contact with manure. A person exposed to a farm setting was twice as likely (RR 2.3, 95% CI 1.4–3.9, p<0.0007) to become infected than someone not living on or visiting a farm.

The most striking feature of the epidemiology of VTEC infection in Taranaki was the high number of cases in children aged 1–4 years exposed to a farm setting or to farm animals (Figure 1). Ruminants, particularly cattle, and to a lesser extent, sheep and possibly goats, are the most important reservoir hosts for *E. coli* O157:H7.6 The proportion of ruminants carrying *E. coli* O157:H7 varies from 8.7% to 35.2% in cattle.[7] Carriage in animals is asymptomatic and often transient. Young animals are at higher risk of being a carrier.[7] The Taranaki region has a high number of cattle, with 493,361 milking cows[8] compared to a human population of 109,608.[3] A national prospective case control study carried out between July 2011 and July 2012 concluded that environmental contact and animal contact with cattle (rather than food exposures) were important pathways for sporadic cases of VTEC in New Zealand.[9]

FIGURE 1. Number of VTEC infection cases in Taranaki by exposure to farm/farm animals in the week before becoming ill, 2006–2015



In Taranaki, the number of VTEC notifications is greater than for leptospirosis (another farming-related infectious disease) and is increasing. Many people working in the farming industry in Taranaki appear not to know the risks of VTEC infection for their preschool children.

The Taranaki DHB aims to turn the curve on VTEC disease using an "advocacy, communication, social mobilisation" approach originally developed for tuberculosis control.[10] A combination of interventions will include:

- increasing the awareness of VTEC infection and the importance of hand hygiene in farming families;
- working with general practitioners to improve early diagnosis and appropriate treatment of VTEC infection; and
- raising the issue of reducing VTEC carriage in animals and VTEC contamination of the environment with the farming sector.

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Reported by Claire Richardson, Medical Student, University of Otago, Jonathan Jarman, Medical Officer of Health and Greg Simmons, Medical Officer of Health, Taranaki District Health Board.

4. OUTBREAK SURVEILLANCE

The following is a summary of the outbreak trends for the April to June quarter 2016. Comparisons are made to the previous quarter (January to March 2016), and to the same quarter in the previous year (April to June 2015). Information in this section is based on data recorded in EpiSurv by public health service staff up to 4 July 2016. As the data may be updated over time, this information should be regarded as provisional.

General

- 159 outbreaks notified in this quarter (1529 cases).
- 99 are final reports (1204 cases); 60 are interim reports (325 cases) that have yet to be finalised and closed.

All data that follow relate to final reports only.

- 12.2 cases on average per outbreak, compared with 13.4 cases per outbreak in the previous quarter

(15.0 cases per outbreak in the same quarter of last year).
- 12 hospitalisations: dengue fever (4), VTEC infection (4), *Bordetella pertussis* (1), *Giardia* (1), *Salmonella* (1), and sapovirus (1).
- 1 death: 'gastroenteritis'.
- Four outbreaks involved more than one pathogen therefore individual pathogen outbreak numbers may not sum to group totals.

Pathogens

- 40 'gastroenteritis' outbreaks (483 cases).
- 21 norovirus outbreaks (474 cases).
- 13 *Giardia* outbreaks (43 cases).
- 7 sapovirus outbreaks (143 cases).
- 5 *Cryptosporidium* outbreaks (58 cases).
- 5 VTEC infection outbreaks (12 cases).
- 4 *Salmonella* outbreaks (9 cases).
- 2 *B. pertussis* outbreaks (4 cases).
- 2 *Campylobacter* outbreaks (4 cases).
- 1 acute respiratory infection outbreak (21 cases).
- 1 astrovirus outbreak (22 cases).
- 1 dengue fever outbreak (4 cases).
- 1 histamine (scombroid) fish poisoning outbreak (3 cases).

Modes of Transmission

Note that reporting allows for multiple modes of transmission to be selected. In some instances no modes of transmission are selected for outbreaks notified to ESR.

- 81 person-to-person, from (non-sexual) contact with an infected person (including droplets): 30 'gastroenteritis' (405 cases), 20 norovirus (466 cases), 12 *Giardia* (39 cases), 7 sapovirus (143 cases), 5 VTEC infection (12 cases), 4 *Cryptosporidium* (55 cases), 2 *B. pertussis* (4 cases), 2 *Salmonella* (4 cases), 1 acute respiratory infection (21 cases), and 1 astrovirus (22 cases).
- 12 foodborne, from consumption of contaminated food or drink (excluding water): 7 'gastroenteritis' (94 cases), 2 norovirus (96 cases), 1 *Campylobacter* (2 cases), 1 histamine (scombroid) fish poisoning (3 cases), and 1 *Salmonella* (2 cases).
- 8 environmental, from contact with an environmental source (eg, swimming): 3 norovirus (87 cases), 2 'gastroenteritis' (18 cases), 1 *Giardia* (2 cases), 1 *Salmonella* (2 cases), and 1 VTEC infection (2 cases).
- 2 waterborne, from consumption of contaminated drinking water: 1 *Giardia* (2 cases) and 1 VTEC infection (3 cases).
- 2 zoonotic: 2 VTEC infection (5 cases).
- 1 vectorborne: dengue fever (4 cases).
- 9 mode of transmission unknown: 4 'gastroenteritis' (19 cases), 2 *Salmonella* (5 cases), 1 *Campylobacter* (2 cases), 1 *Cryptosporidium* (3 cases), 1 *Giardia* (4 cases), and 1 norovirus (8 cases).

Circumstances of Exposure

Common 'settings' where the exposures occurred are identified below.

- 32 long term care facility: 14 'gastroenteritis' (157 cases), 14 norovirus (298 cases), 4 sapovirus (48 cases), 1 acute respiratory infection (21 cases), and 1 astrovirus (22 cases).
- 22 private home: 10 *Giardia* (33 cases), 4 VTEC infection (10 cases), 3 *Cryptosporidium* (11 cases), 1 *B. pertussis* (2 cases), 1 *Campylobacter* (2 cases), 1 'gastroenteritis' (8 cases), 1 norovirus (2 cases), and 1 *Salmonella* (2 cases).
- 18 childcare centre: 13 'gastroenteritis' (197 cases), 2 norovirus (32 cases), 2 sapovirus (76 cases), 1 *Cryptosporidium* (44 cases), and 1 *Giardia* (2 cases).
- 5 restaurant/café/bakery: 3 'gastroenteritis' (13 cases), 1 *Campylobacter* (2 cases), and 1 norovirus (6 cases).
- 4 other institution: 3 'gastroenteritis' (24 cases) and 1 sapovirus (19 cases).
- 2 community/church/sports gathering: 1 'gastroenteritis' (34 cases) and 1 norovirus (28 cases).
- 2 hostel/boarding house: 2 'gastroenteritis' (23 cases).
- 2 other food outlet: 1 'gastroenteritis' (2 cases) and 1 histamine (scombroid) fish poisoning (3 cases).
- 1 camp: norovirus (40 cases).
- 1 farm: VTEC infection (2 cases).
- 1 hotel/motel: *Salmonella* (2 cases).
- 1 hospital acute care: 'gastroenteritis' (23 cases).
- 1 school: norovirus (68 cases).
- 1 supermarket/delicatessen: 'gastroenteritis' (2 cases).
- 1 takeaways: 'gastroenteritis' (4 cases).
- 1 workplace: *B. pertussis* (2 cases).
- 1 other setting: *Salmonella* (2 cases).
- 2 outbreaks had two or more exposure settings recorded.
- 5 outbreaks had no exposure settings recorded.

Common 'settings' where food was prepared in foodborne outbreaks are identified below.

- 3 restaurant/café/bakery: 2 'gastroenteritis' (10 cases) and 1 *Campylobacter* (2 cases).
- 2 community/church/sports gathering: 'gastroenteritis' (34 cases) and 1 norovirus (28 cases).
- 1 private home: histamine (scombroid) fish poisoning (3 cases).
- 1 hotel/motel: *Salmonella* (2 cases).
- 1 hostel/boarding house: 'gastroenteritis' (9 cases).
- 1 other food outlet: 'gastroenteritis' (2 cases).
- 1 school: norovirus (68 cases).
- 1 takeaways: 'gastroenteritis' (4 cases).

5. OUTBREAK CASE REPORTS

Bordetella pertussis outbreak in the Southern District, 2015

Pertussis (whooping cough) infection is a highly infectious, vaccine-preventable disease caused by the bacterium *Bordetella pertussis*.[1] The incubation period is usually 7–10 days, but it can be up to 21 days.[1]

In the initial catarrhal stage (1–2 weeks), symptoms include a runny nose followed by a slight cough. The paroxysmal stage then starts, as spasms of coughing develop. These may be severe, ending in vomiting or apnoea or breathlessness. Young

babies may have episodes of apnoea or cyanosis before the cough. Clinical presentations can vary with age and the individual's underlying immunity.[1]

Epidemic cycles of pertussis occur every 3–5 years in New Zealand.[2] Immunity in older children and adults can wane over time. This provides a reservoir of susceptible individuals for future epidemics.[1] On 28 July 2015 Public Health South (PHS) staff identified an outbreak of pertussis after five children aged up to 11 were notified with confirmed or suspected pertussis infection within two days. All lived in the Wanaka region of the Southern District Health Board (DHB). Two children were in the same class at a primary school, and three were from one family. All five were reported as unvaccinated.

PHS established an outbreak investigation and management team within its Invercargill and Dunedin offices. The team's roles had a CIMS-like structure, including communications, case management, data collection and analysis. Data was analysed with EpiInfo™ 7 and/or Microsoft Excel 2013.

The PHS outbreak team had three objectives.

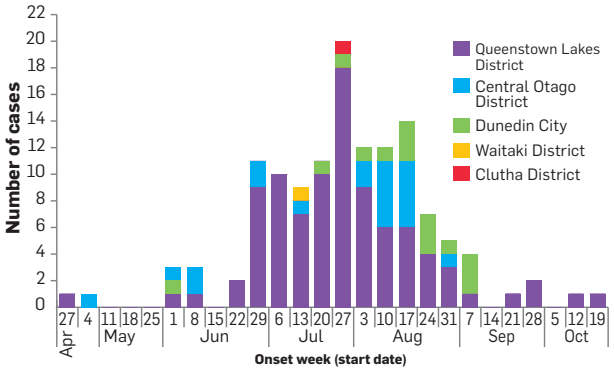
1. Quickly determine the extent of the pertussis infection within the Wanaka/Hawea region and the Southern DHB.
2. Implement effective public health measures to manage the outbreak and protect those populations more vulnerable to the disease and its complications.
3. Prevent pertussis-related mortality and morbidity across the DHB.

The team received 318 pertussis notifications within four months (27 July to 27 November 2015). Of these, 43 were confirmed cases, 74 probable cases and 12 suspected cases. The remaining 189 (59.4%) were classified as not a case. No hospitalisations or deaths were reported. Ages ranged up to 80 years, with a median of 13 years, and a mean of 22 years. Only 3 cases were under the age of 12 months. Sex distribution was about equal, with 48.8% female and 51.2% male. Ethnicity, in general terms, reflected the background population. Figure 2 shows an epidemic curve of cases including background cases with an onset date before the outbreak started.

Although the outbreak was initially recognised in unvaccinated children, retrospective analysis indicated infection in vaccinated and unvaccinated people. The National Immunisation Register was used to confirm vaccination status.

The majority of cases lived in the Queenstown Lakes District Council area, specifically the Wanaka region. The Southern DHB currently has a high Early Childhood Schedule vaccination rate of 94–95% and the immunisation team were already aware of the pool of unvaccinated children in this area.

FIGURE 2. Number of pertussis cases notified in Southern DHB by onset week and territorial local authority, 27 April to 27 October 2015



The 2015 pertussis outbreak in the Southern DHB is an example of a community-wide outbreak where 'transmission predominantly occurs by direct exposure of susceptible people to infectious people'.[3] The epidemic curve is typical of person-to-person spread within the community, showing a 'relatively slow, progressive rise'.[3]

Effective communication with the cases, caregivers contacts and stakeholders was critical in reducing morbidity and mortality rates. The media took an active interest in the outbreak, allowing PHS to communicate regularly with the public.

A number of factors contributed to nobody being hospitalised or dying during this outbreak. These factors included:

- the high vaccination rates in the Southern DHB;
- the quick public health response that led to more people getting vaccinated during the outbreak;
- people following advice about how to control infection.

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1. Ministry of Health 2014. Immunisation Handbook 2014. Ministry of Health: Wellington. Available at: http://www.health.govt.nz/publication/immunisation-handbook-2014 [accessed 3 March 2016].
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3. Institute of Environmental Science and Research Limited 2012. Guidelines for the Investigation and Control of Disease Outbreaks. Institute of Environmental Science and Research Limited: Porirua.

Reported by Katherine Graham, Public Health Registrar and Heather Clark, Health Protection Officer, Public Health South.

6. LABORATORY SURVEILLANCE

Read Laboratory-based legionellosis surveillance, 2015 at https://surv.esr.cri.nz/surveillance/NZPHSR.php or use the code reader

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