NOTIFIABLE DISEASES COMMENTARY

This commentary is based on the *Annual Notifiable Disease Report* (2016) and discusses changes in disease notifications compared to previous years, factors that may influence the changes, and possible implications for the future.

At a glance

A total of 16,305 notifiable disease cases were reported through EpiSurv, New Zealand's notifiable disease database, in 2016 compared with 14,306 in 2015.

- **Increased:** AIDS, campylobacteriosis, cryptosporidiosis, dengue fever, measles, shigellosis, VTEC/STEC infection, yersiniosis and Zika virus infection.
- **Decreased:** Chikungunya fever, leprosy and pertussis.

On the increase

Campylobacter increased

Campylobacteriosis remained the most commonly notified disease in New Zealand, with 7456 cases notified in 2016, compared with 6218 cases in 2015.

The DHB with the highest notification rate was Hawke's Bay (825.9 per 100,000), where, in August 2016, there was a large campylobacteriosis outbreak due to contamination of the drinking water supply for Havelock North. This outbreak involved 964 notified cases, however, it is estimated 5,500 of the town's 14,000 residents became ill with campylobacteriosis and 45 were hospitalised.(1)

Cryptosporidiosis increased

There were 1062 cases (22.6 per 100,000) of cryptosporidiosis notified in 2016—an approximately 50% increase from 2015 (696 cases, 15.1 per 100,000). The recent increase in notifications may be partially explained by changes in laboratory methods and screening criteria (refer to *Changes in laboratory testing methods* section on page 8).

The DHB with the largest increase in notifications was Northland, with 106 cases in 2016 compared with 27 cases in 2015. Waitemata, Auckland, Taranaki, Capital & Coast and Canterbury DHBs also had significant rate increases from 2015 to 2016.

Cryptosporidiosis has been associated with agricultural land use and climate variability in New Zealand.(2) Warmer temperatures were recorded throughout New Zealand in 2016 (0.5-1.2°C above the annual average; the warmest year on record) and may explain some of the increase in notifications.(3)

Dengue fever increased

Notifications of dengue fever significantly increased in 2016, with 191 cases (4.1 per 100,000) notified in 2016, compared with 125 cases (2.7 per 100,000) in 2015. All cases had travelled overseas during the incubation period, with Indonesia (62 cases) and Samoa (61 cases) the most commonly visited countries.

The WHO reported large dengue outbreaks globally in 2016, including over 2.38 million cases in the Americas (Brazil reporting approximately 1.5 million cases), and more than 375,000 suspected cases in the Western Pacific (particularly the Philippines). Although international dengue surveillance has improved in recent years, dengue is thought to remain largely underreported and misclassified.(4) Dengue is expected to spread to other areas due to climate change, increasing urbanisation and international travel. Outbreaks of all four dengue serotypes were detected in the Pacific in 2016.(5)

Protection against mosquito bites remains the mainstay of dengue prevention. However, a vaccine against all four serotypes of dengue (Dengvaxia (CYD-TDV) Sanofi Pasteur) has recently been licensed overseas.(6) It has been recommended by the WHO for those aged 9 years and older in countries with high dengue incidence only, due to lower efficacy and higher risk of adverse effects among people not previously exposed to the virus.(6)

Measles increased

In 2016, 103 confirmed cases of measles were notified, of which 76 were laboratory-confirmed and 27 were epidemiologically linked to a confirmed case. This compares with 10 cases in 2015.

The highest rate was in the <1 year age group (23.6 per 100,000, 14 cases) followed by the 15–19 years age group (8.2 per 100,000, 26 cases). The <1 year age group are not eligible for MMR vaccination, and the 15–19 year age group were estimated to have a low proportion of population immunity in a recent New Zealand study.(7)

The source of the virus was recorded for all cases, of these 6 (5.8%) cases were imported from Indonesia (4 cases) and India (2 cases). The remaining 97 (94.2%) cases were import-related (ie, locally-acquired infections spread from an imported case).

Three measles outbreaks were reported in 2016, commencing in January, April and July, and involving 98 cases. India and Indonesia were identified as the source country for two outbreaks. The source country of the other outbreak was not identified but the index and related cases shared the same genotype, which was different from that of the other outbreaks. There were two sporadic cases of measles reported in 2016: genotyping and rash onset dates suggested they were unrelated to identified outbreaks, and due to undetected importations.

New Zealand remains susceptible to outbreaks of measles from returning travellers and overseas visitors. Estimates of the risk of importation of measles from different countries concluded the risk of imported measles was highest from Australia and the United Kingdom

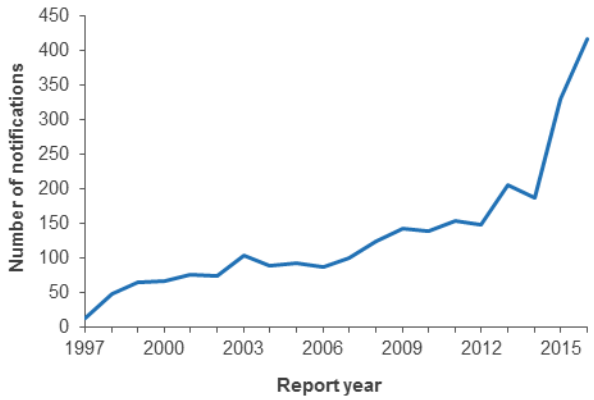
as a result of the volume of travellers, and Thailand and China as a result of the disease incidence.(7)

VTEC/STEC increased

In 2016, 418 cases of verocytotoxin- or Shiga toxin-producing *Escherichia coli* (VTEC/STEC) infection were notified compared with 330 notifications in 2015. There has been a significant yearly increase in cases since 2014 when 187 cases were reported.

The number of notifications of VTEC/STEC infection has been increasing since 1997 (Figure 1). This increase is partly due to changes in laboratory testing practices, with increasingly sensitive assays used for the detection of VTEC/STEC. Screening of all faecal specimens using PCR was introduced in Auckland in July 2015 and resulted in increased VTEC/STEC detection.

Figure 1. VTEC/STEC notifications by year, 1997–2016



Of the 491 isolates of VTEC/STEC confirmed at ESR in 2016, 42% were identified as *E. coli* O157:H7, 37% as *E. coli* non-O157 serotypes, and 21% as undetermined serotypes. Identification of non-O157 types has increased; E. coli non-O157 accounted for 29% of cases in 2015 and 10% of cases in 2014. The most common non-O157 serotype in 2016 was O26:H2 (9.4%), followed by O128:H2 (5.1%).

The VTEC serotype distribution identified in New Zealand has similarities to that seen in the United States and Europe, with around half of cases caused by O157 and O26 being the next most common serotype.(8, 9) Non-O157 serotypes are an increasing proportion of VTEC cases.

Paediatric haemolytic uraemic syndrome (HUS) surveillance shows a stable number of cases over time (10) and is similar to HUS cases recorded in notification data. A total of 56 cases of HUS were reported in EpiSurv between 2012 and 2016, 39 of which were O157 and 8 were non-O157.

The relative disease severity of infection by different serotypes is not clearly known.(11) An analysis of VTEC cases in Germany between 2004 and 2011 showed cases of O104 were

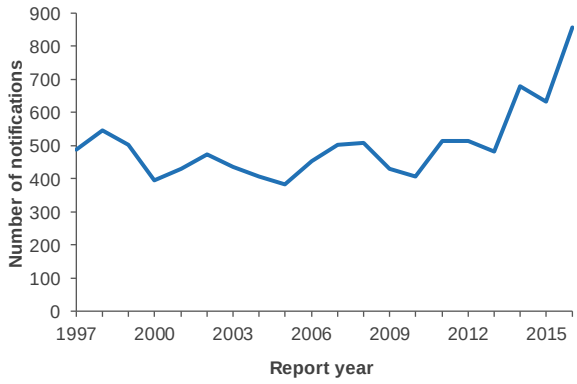
33% more likely to be hospitalised than O157, and all other non-O157 cases combined were 59% less likely to be hospitalised.(11) For the years 2012–2016 in New Zealand, 35% of O157 cases and 25% of non-O157 cases notified were reported to have been hospitalised.

The increasing detection of VTEC has implications for public health response since all cases are currently routinely investigated. Identification of VTEC serotypes combined with an understanding of their pathogenicity would be useful to inform the prioritisation of public health investigations.

Yersiniosis increased

In 2016, 857 cases of yersiniosis were notified compared with 634 in 2015. Since 2005 there has been an increasing trend in number of notified yersiniosis cases by year (Figure 2). For yersiniosis cases where hospitalisation status was recorded, 11% were hospitalised which is a similar proportion for the years 2012–2015.

Figure 2. Yersiniosis notifications by year, 1997–2016



ESR confirmed 748 isolates as *Yersinia enterocolitica* and 32 isolates as *Y. pseudotuberculosis* during 2016. The most common *Y. enterocolitica* biotypes identified were biotype 2 (55%), biotype 1A (21%), biotype 4 (13%) and biotype 3 (11%).

There were no clear epidemiological links for the majority of yersiniosis cases in 2016. Multiple Locus Variable-number tandem repeat analysis (MLVA) was performed on a selection of *Y. enterocolitica* biotype 2 isolates from cases reported between August 2015 and August 2016. Of the 74 isolates tested, 34 different MLVA profiles were identified, although some of these profiles were very closely related. The variation in profiles suggests multiple sources. Whole genome sequencing is planned to further investigate possible linkages between cases.

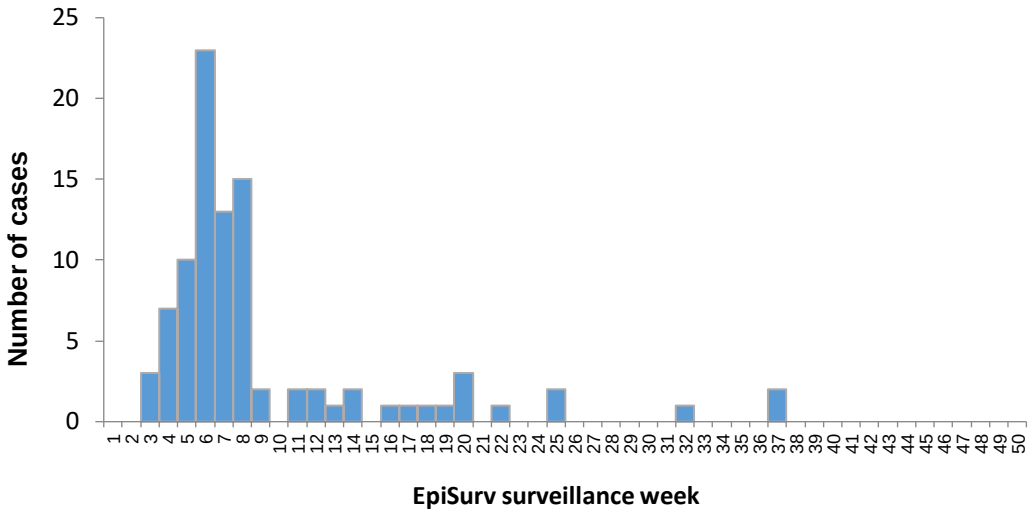
Investigation of cases reported in the Auckland region found an association with consumption of bean sprouts. The MLVA profiles for nine cases of *Y. enterocolitica* biotype 2 reported between May and August 2016 that were known to have eaten bean sprouts were different, although some were very closely related.

Zika virus infection increased

In 2016, there were 100 cases of Zika virus infection notified compared with nine cases in 2015. This increase was associated with Zika virus outbreaks in the Pacific.(5) New Zealand's ability to detect imported Zika virus infection supports surveillance in the Pacific by providing laboratory confirmation of suspected outbreaks. Collecting data on exposure locations supports control activities in the Pacific. Of the 100 cases of Zika virus infection in 2016, 99 had travelled overseas, with Tonga (58 cases), Samoa (23 cases) and Fiji (9 cases) the most commonly visited countries. One case, with no recent travel history, was the first case in New Zealand to be associated with sexual transmission.(12)

The highest number of Zika virus infection cases were notified in the summer (Figure 3), during which time Zika outbreaks were detected in American Samoa, the Marshall Islands, Samoa, New Caledonia, Tonga and Fiji.(5) This time of year corresponds with high temperatures and increased rainfall in the Pacific (which help mosquitoes to propagate).

Figure 3. Zika virus infection cases notified in New Zealand by surveillance week, 2016



New Zealand implemented enhanced surveillance of Zika virus infection following the WHO's declaration of possible Zika virus complications as a Public Health Emergency in 2016.(13) This, along with heightened awareness due to public health messaging and media coverage, may have contributed to increased detection in 2016.

On the decrease

Chikungunya decreased

In contrast to Zika and dengue, there was a significant decrease in Chikungunya fever notifications with 28 cases in 2016 compared with 48 cases in 2015. All cases had travelled overseas, with the most commonly visited countries being Fiji (14 cases), India (9 cases) and Brazil (3 cases). Chikungunya is anticipated to continue to spread internationally, including in the Pacific where the virus can spread rapidly due to the presence of mosquito species that can carry it.(14)

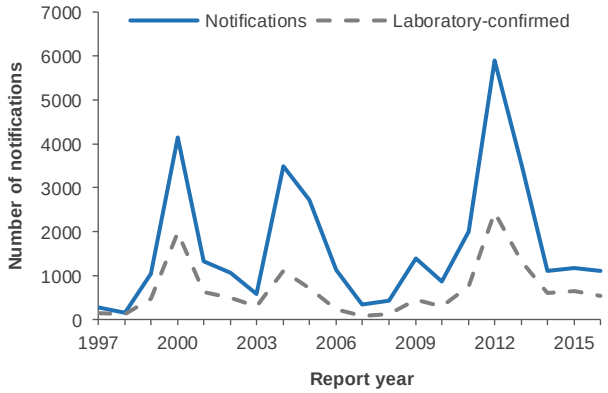
Pertussis decreased in 2016 but a national outbreak in 2017 is possible

There was a significant decrease in pertussis notifications in 2016, with 1096 cases reported, compared with 1168 cases in 2015. In 2016, the age group with the highest notification rate was <1 year olds (114.8 per 100,000, a non-significant decrease from 2015). Approximately 56% of infants with pertussis were hospitalised in 2016, compared with 62% in 2015.

In 2016, approximately 49% of cases were laboratory-confirmed (13% by isolation, 72% by PCR, and 15% by isolation and PCR). This represents a significant change in diagnostic practice from 2015, where the proportion of laboratory-confirmed cases by isolation and PCR were similar.

A national epidemic is expected in 2017 or 2018 according to the 3-5 yearly epidemic cycle (Figure 4). However, it is possible that the introduction of funded pertussis vaccination in pregnancy in 2013, and improved vaccination timeliness and coverage in infancy, may reduce the incidence of severe disease in infants.(15) Changes in laboratory diagnostic practices, with increasing use of sensitive PCR testing since 2011, may have increased our ability to detect pertussis, elevating the baseline rate of this disease.

Figure 4. Pertussis notifications and laboratory-confirmed cases by year, 1997–2016

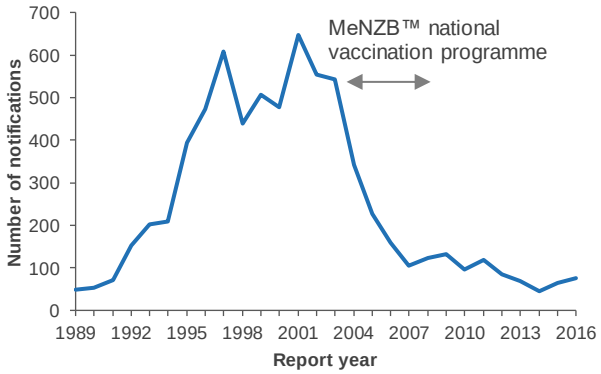


Emerging issues

Meningococcal disease

In 2016, 75 cases of meningococcal disease were notified which was slightly higher than the 64 cases in 2015 and continues an increasing trend since the low of 45 cases reported in 2014 (Figure 5). However, the number of cases in 2016 remains significantly lower than the 647 cases in 2001 during the meningococcal disease epidemic (driven by the B:P1.7-2,4 strain).

Figure 5. Meningococcal disease notifications by year, 1989–2016



The age group with the highest rate in 2016 was <1 year olds (18.6 per 100,000), followed by 1–4 years (6.9 per 100,000). The ethnic group with the highest notification rate was Pacific peoples (4.3 per 100,000), followed by Māori (2.6 per 100,000).

Group B strains continue to be the most prevalent, infecting 67% of laboratory-confirmed cases in 2016 that were able to be typed. Although this was similar to the proportion seen in 2015 (70% group B), the pattern of strain types identified within the B group cases was different (Table 1). As in 2014, half of group B cases in 2016 were typed as the epidemic strain, whereas in 2015 only a quarter were the epidemic strain and three quarters were other strains.

Table 1. Meningococcal disease strain group distribution by year, 2012–2016

Group / strain	Year				
	2012	2013	2014	2015	2016
Group B	**43**	**30**	**26**	**41**	**47**
B:P1.7-2,4	15	11	13	10	23
Other Group B	28	19	13	31	24
Group C	**23**	**17**	**6**	**6**	**8**
C:P1.5-1,10-8	18	15	5	3	4
Other Group C	5	2	1	3	4
Other	**2**	**10**	**4**	**12**	**12**
Group W135	0	5	0	6	5
Group Y	2	4	3	6	7
Group E	0	0	1	0	0
Non-groupable	0	1	0	0	0
Total	**68**	**57**	**36**	**59**	**67**

*Includes total number of laboratory-confirmed cases where strain group was determined.

Although the number of cases of group W is low, it is of concern that group W disease became predominant in Australia in 2016 (109/253 cases, 43%). Group B was predominant there from 2002 to 2015. While most group W cases in Australia have been reported in adults, there has been an increase in cases in children aged <5 years. Many of the group W cases belong to a hypervirulent sequence type (ST 11 in clonal complex 11), associated with a higher risk of invasive disease and a higher case fatality rate.(16) A similar increase in group W cases has also been reported in the United Kingdom (210 cases in 2015/16).(17) This increase started in 2009/10 and led to the introduction of the meningococcal ACYW conjugate vaccine to the national immunisation programme in 2015, replacing meningococcal C in the adolescent school-based programme.(17, 18)

Of the five DHBs that had rates above the national average in 2016, the highest rate was for Southern DHB. The predominant strain reported amongst Southern cases was the epidemic strain (B:1.7-2,4). However further analysis showed that, although there were increased cases seen in the 15–24 years age group in Dunedin City and Queenstown-Lakes District, they did not meet the threshold to be reported as a community outbreak.

Of the 26 cases reported in children <5 years of age, all were able to be typed and 65% were group B strains, compared with 82% in 2015. This is less than the 80–86% reported in children aged <5 years in England 2014/15.(18) The rates of confirmed meningococcal disease in children aged <5 years in England prior to introduction of their infant meningococcal B vaccination programme in 2015, was comparable with New Zealand at 19 per 100,000 for <1 year and 6 per 100,000 for 1–4 year olds.(17) Two vaccines for meningococcal group B (Bexsero and Trumenba), both covering a broad range of group B types, have been approved for use in other countries including Australia, Europe and the United States.(19)

In New Zealand, meningococcal group C and quadrivalent (A,C,Y,W135) conjugate vaccines are recommended for some high-risk groups and available free for some high-risk individuals, but a meningococcal group B vaccine is not currently licensed.(19)

Changes in laboratory testing methods

Notifications may be affected by changes in laboratory methodology, particularly with the recent introduction of culture independent diagnostic testing (CIDT). These new testing methods include multiplex PCR, which tests for several diseases at the same time. This means more diseases are likely to be detected and in a more timely manner. As CIDT becomes more widely adopted, it is likely that notifications will increase. This will need to be considered when interpreting future trends in notification data.

Labtests (the community laboratory serving Northland, Waitemata, Auckland and Counties Manukau DHBs) introduced PCR for enteric diseases in July 2015 and notification based on PCR alone occurred soon after. This change in testing from culture alone resulted in about 17% more campylobacteriosis cases (personal communication, Dr Gary McAuliffe, Labtests, Auckland).

PCR screening for cryptosporidiosis was extended to include all community faecal specimens from June 2015 in Auckland and Northland, rather than just for specimens where parasite testing was requested. This resulted in 27% of cryptosporidiosis cases being diagnosed from non-requested screening at the time the test was implemented (personal communication, Dr Arlo Upton, Labtests, Auckland).

Additionally, the move to CIDT could result in an overall reduction in bacterial culture which could limit the further characterisation of organisms such as *Campylobacter* species and may affect the identification of outbreaks and common sources of infection.

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