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RECOMMENDATION FOR SEASONAL INFLUENZA VACCINE COMPOSITION FOR NEW ZEALAND FOR 2019

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DISCLAIMER

CONTENTS

List of tables iii
List of figures iv
Recommendations 1
Influenza epidemiology 3
World-wide influenza activity, February to September 2018 3
Influenza activity in Australia, February to September 2018 4
Influenza activity in South Africa, February to September 2018 6
Influenza activity in New Zealand in 2018 7
Community-based surveillance 7
Hospital-based surveillance 16
Ministry of Health data on publicly funded hospital discharges 23
New Zealand strain characterisations 26
Circulating strains in 2018 26
Predominant strains during 1997–2018 28
Influenza A(H1N1)pdm09 30
Seasonal influenza A(H3N2) 30
Influenza B 34
Oseltamivir resistance 34
Influenza vaccine effectiveness 36
Recent strain characterisation for southern hemisphere viruses and likely vaccine candidates 38
Influenza A(H1N1)pdm09 38
Seasonal influenza A(H3N2) 39
Influenza B 40
Summary of vaccine composition recommendation 42
Explanation of “like” strains suitable for inclusion in vaccine 42
Appendix 1 - Composition of the Australian Influenza Vaccine Committee 2018 43
Appendix 2 – Isolates received for analysis at the Australian WHO Collaborating Centre 44
Appendix 3 – Influenza A(H1N1)pdm09 45
Appendix 4 - Influenza A (H3N2) 49
Appendix 5 - Influenza B 52
Appendix 6 - WHO Recommendation for influenza vaccines 57

LIST OF TABLES

Table 1. Influenza vaccine recommendations for New Zealand, 1991–2018 2
Table 2. Demographic characteristics of ILI and influenza cases, since 30 April 2018 11
Table 3. Weekly consultation rate for influenza-like illness by District Health Board, 2018 12
Table 4. Influenza and non-influenza respiratory viruses among ILI cases, 30 April–30 September 2018 13
Table 5. Demographic characteristics of SARI cases and related influenza cases, since 30 April 2018 20
Table 6. Influenza and non-influenza respiratory viruses among SARI cases, 30 April to 30 September 2018 21
Table 7. Influenza virus identifications by type and sub-type and lineage-typed, 2018 26
Table 8. Antiviral susceptibility to oseltamivir for influenza viruses, 2014–2018^ 35
Table 9. Antiviral susceptibility to zanamivir for influenza viruses, 2014–2018^ 35
Table 10. Estimated influenza vaccine effectiveness, by participant age group and by influenza virus type and subtype in New Zealand, 2018 influenza season 37
Table 11. Influenza Viruses Analysed at the Melbourne WHO CC 44
Table 12. (H1N1)pdm09 viruses (1) 46
Table 13. Summary – HI Characterization of Influenza A(H3N2) Isolates 49
Table 14. A(H3) Focus Reduction Assay (3) 50
Table 15. B viruses (B/Victoria lineage) 54
Table 16. B viruses (B/Yamagata lineage) 55

LIST OF FIGURES

Figure 1. Weekly consultation rates for influenza-like illness in New Zealand, 2018.....8
Figure 2. Weekly ILI consultation rates in 2018 compared to 2013–2017.....9
Figure 3. Weekly ILI-associated influenza rates in 2018 compared to 2013–2017 9
Figure 4. Weekly Consultation Rates for Influenza-like Illness in New Zealand, 1992–2018 10
Figure 5. Temporal distribution of the number and proportion of influenza viruses from ILI specimens, by type and week.....14
Figure 6. Temporal distribution of the number and proportion of non-influenza viruses from ILI specimens, by type and week[1] 14
Figure 7. Weekly number of ILI-related calls to Healthline, 2010–2018.....15
Figure 8. Weekly resident SARI and SARI-associated influenza incidence, 2018 17
Figure 9. Weekly hospitalisation rates for SARI in 2018 compared to 2012–2017.....17
Figure 10. Weekly hospitalisation rates for SARI-associated influenza in 2018 compared to 2012–2017 18
Figure 11. Seriousness of disease indicator in 2018 compared to 2012–2017 19
Figure 12. Temporal distribution of the number and proportion of influenza viruses from SARI specimens, by type and week[1] 22
Figure 13. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1] 22
Figure 14. Influenza hospital discharges, 2000–2018* 23
Figure 15. Influenza hospital discharges by week, 2018* 24
Figure 16. Influenza hospital discharge rates by age group, 2018* 24
Figure 17. Hospital discharge rates by prioritised ethnic group, 2018* 25
Figure 18. Total influenza viruses by type and week specimen taken, 2018.....27
Figure 19. Total influenza A and B viruses by week specimen taken, 2018.....27
Figure 20. Influenza viruses by type, 1997–2018 28
Figure 21. Influenza A viruses by subtypes 1997–2018 29
Figure 22. Influenza B viruses by lineages, 1990–2018 30
Figure 23..Phylogenetic relationships among influenza A(H1N) haemagglutinin genes 31
Figure 24..Phylogenetic relationships among influenza A(H3N2) haemagglutinin genes.....32
Figure 25. Phylogenetic relationships among influenza B (Yamagata) haemagglutinin genes ..33
Figure 26. Antigenic cartographic representation of A(H1N1)pdm09 viruses.....45
Figure 27. Phylogenetic relationships among influenza A(H1N1)pdm09 HA genes.....48
Figure 28. Phylogenetic relationships among influenza A (H3) N2 genes 51
Figure 29. Antigenic cartographic representation of B Victoria viruses.....52
Figure 30. Antigenic cartographic representation of B Yamagata viruses.....52
Figure 31. B viruses (B/Victoria lineage) 53
Figure 32. Phylogenetic relationships among influenza B neuraminidase genes B/Yamagata Lineage 56

RECOMMENDATIONS

The Australian Influenza Vaccine Committee (AIVC) met with a New Zealand representative (Appendix 1) in Canberra on 10 October 2018 to consult on the influenza vaccine composition for 2019 for New Zealand, Australia and South Africa (Table 1). The recommended composition for quadrivalent vaccines was:

- A(H1N1) an A/Michigan/45/2015 (H1N1)pdm09-like virus
- A(H3N2) an A/Switzerland/8060/2017 (H3N2)-like virus
- B a B/Phuket/3073/2013-like virus (belonging to B/Yamagata lineage)
- B a B/Colorado/06/2017-like virus (belonging to B/Victoria lineage)

The recommended composition for trivalent vaccines was:

- A(H1N1) an A/Michigan/45/2015 (H1N1)pdm09-like virus
- A(H3N2) an A/Switzerland/8060/2017 (H3N2)-like virus
- B a B/Phuket/3073/2013-like virus (belonging to B/Yamagata lineage)

Table 1. Influenza vaccine recommendations for New Zealand, 1991–2018

Decision		Use year	A H3N2	A H1N1	B (Trivalent)	B (Quadrivalent)
NZ & WHO*	2018	2019	A/Switzerland/8060/2017	A/Michigan/45/2015	B/Phuket/3073/2013	B/Colorado/06/2017
NZ & WHO*	2017	2018	A/Singapore/INFIMH-16-0019/2016	A/Michigan/45/2015	B/Phuket/3073/2013	B/Brisbane/60/2008
NZ & WHO*	2016	2017	A/Hong Kong/4801 /2014	A/Michigan/45/2015	B/Brisbane/60/2008	B/Phuket/3073/2013
NZ & WHO*	2015	2016	A/Hong Kong/4801 /2014	A/California/7/2009	B/Brisbane/60/2008	B/Phuket/3073/2013
NZ & WHO*	2014	2015	A/Switzerland/9715293/2013	A/California/7/2009	B/Phuket/3073/2013	B/Brisbane/60/2008
NZ & WHO*	2013	2014	A/Texas/50/2012	A/California/7/2009	B/Massachusetts/2/2012	B/Brisbane/60/2008
NZ & WHO*	2012	2013	A/Victoria/361/2011	A/California/7/2009	B/Wisconsin/1/2010	
NZ & WHO*	2011	2012	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2010	2011	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2009	2010	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2008	2009	A/Brisbane/10/2007	A/Brisbane/59/2007	B/Florida/4/2006	
NZ & WHO*	2007	2008	A/Brisbane/10/2007	A/Solomon Islands/3/2006	B/Florida/4/2006	
NZ & WHO*	2006	2007	A/Wisconsin/67/2005	A/New Caledonia/20/99	B/Malaysia/2506/2004	
NZ & WHO*	2005	2006	A/California/7/2004	A/New Caledonia/20/99	B/Malaysia/2506/2004	
NZ & WHO*	2004	2005	A/Wellington/1/2004	A/New Caledonia/20/99	B/Shanghai/361/2002	
NZ & WHO*	2003	2004	A/Fujian/411/2002	A/New Caledonia/20/99	B/Hong Kong/330/2001	
NZ & WHO*	2002	2003	A/Moscow/10/99	A/New Caledonia/20/99	B/Hong Kong/330/2001	
NZ & WHO*	2001	2002	A/Moscow/10/99	A/New Caledonia/20/99	B/Sichuan/379/99	
NZ	2000	2001	A/Sydney/5/97	A/New Caledonia/20/99	B/Beijing/184/93	
WHO*	2000	2001	A/Moscow/10/99	A/New Caledonia/20/99	B/Beijing/184/93	
NZ & WHO*	1999	2000	A/Sydney/5/97	A/Beijing/262/95	B/Beijing/184/93	
NZ	1998	1999	A/Sydney/5/97	A/Bayern/7/95	B/Beijing/184/93	
WHO**	1997–98		A/Wuhan/359/95	A/Bayern/7/95	B/Beijing/184/93	
NZ	1997	1998	A/Wuhan/359/95	A/Texas/36/91	B/Beijing/184/93	
WHO**	1996–97		A/Wuhan/359/95	A/Singapore/6/86***	B/Beijing/184/93	
NZ	1996	1997	A/Johannesburg/33/94	A/Texas/36/91	B/Beijing/184/93	
WHO**	1995-96		A/Johannesburg/33/94	A/Singapore/6/86	B/Beijing/184/93	
NZ	1995	1996	A/Guangdong/25/93	A/Texas/36/91	B/Panama/45/90	
WHO**	1994–95		A/Shangdong/9/93	A/Singapore/6/86	B/Beijing/184/93	
NZ	1994	1995	A/Beijing/32/92	A/Texas/36/91	B/Panama/45/90	
WHO**	1993–94		A/Beijing/32/92	A/Singapore/6/86	B/Panama/45/90	
NZ	1993	1994	A/Shanghai/24/90	A/Texas/36/91	B/Panama/45/90	
WHO**	1992–93		A/Beijing/353/89	A/Singapore/6/86	B/Yamagata/16/88 or B/Panama/45/90	
NZ	1992	1993	A/Beijing/353/89	A/Victoria/36/88	B/Yamagata/16/88 or B/Panama/45/90	
WHO**	1991–92		A/Beijing/353/89	A/Singapore/6/86	B/Yamagata/16/88 or B/Panama/45/90	

* WHO recommendations are for the Southern Hemisphere winter

* * WHO recommendations are for the Northern Hemisphere winter

INFLUENZA EPIDEMIOLOGY

WORLD-WIDE INFLUENZA ACTIVITY, FEBRUARY TO SEPTEMBER 2018

Between February and September 2018, influenza activity was reported globally, with influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses co-circulating.

NORTHERN HEMISPHERE TEMPERATE REGION

In the northern hemisphere, influenza activity declined from February to April and remained at inter-seasonal levels in most countries. Influenza A(H1N1)pdm09 was the predominant type A in most countries in Europe, northern and western Africa and Asian. Influenza A(H3N2) was the predominant type A in northern Europe, North America and some countries in Asia. Influenza B viruses circulated in higher proportions than influenza A viruses in many countries in Europe.

Influenza activity in northern Africa was high in several countries in February and March with widespread A(H1N1)pdm09 outbreaks in Algeria and A(H3N2) in Morocco.

SOUTHERN HEMISPHERE TEMPERATE REGION

In the southern hemisphere, influenza activity increased from March to June. In the southern cone of South America there was co-circulation of influenza A and B viruses, and in South Africa A(H1N1)pdm09 virus predominated with regional activity of influenza B virus reported later in the winter season. Influenza activity was low in Australia and New Zealand throughout this period.

TROPICAL AND SUBTROPICAL REGIONS

Influenza activity in the tropical and subtropical region of Asia was high with regional widespread outbreaks reported in South-East Asia. Influenza activity in tropical regions of South America was generally high with A(H1N1)pdm09, A(H3N2) and B outbreaks reported.

(Abridged from the Weekly Epidemiological Record, 2018 93(42):553-576).

INFLUENZA LABORATORY SURVEILLANCE FROM WHO COLLABORATING CENTRE AT MELBOURNE

The WHO Collaborating Centre for Reference and Research on Influenza in Melbourne, Australia (Melbourne WHOCC) analysed influenza isolates received from across Oceania during 1 February to 19 September 2018. Influenza A(H1N1)pdm09 virus was the predominant strain which accounted for 49% (662/1341) of isolates, while 21% (283/1341) were A(H3N2), 17% (231/1341) were B/Yamagata lineage and 7% (93/1341) were B/Victoria lineage (Table 11 in Appendix 2).

INFLUENZA ACTIVITY IN AUSTRALIA, FEBRUARY TO SEPTEMBER 2018

Influenza activity in Australia in 2018 in general was at a low level with some regional variations. Clinical severity for the season was moderate as measured through the proportion of patients admitted directly to ICU, and deaths attributed to influenza. The impact of influenza was low on society as measured through the burden on hospitals and the proportion of people with ILI taking time off work. A(H1N1)pdm09 was the dominant influenza A subtype.

There are 6 influenza surveillance systems in Australia, which can be divided into three categories.

INFLUENZA-LIKE-ILLNESS SURVEILLANCE

- **Australian Sentinel Practice Research Network (ASPREN).** This system has general practitioners (GPs) who report influenza-like illness (ILI) presentation rates in New South Wales, South Australia, Victoria, Queensland, Tasmania, Western Australia and the Northern Territory. As jurisdictions joined ASPREN at different times and the number of GPs reporting has changed over time, the representativeness of ASPREN data in 2018 may be different from that of previous years. The national case definition for ILI is presentation with fever, cough and fatigue. Overall, the rate of ILI consultations peaked during the week 37 ending 16 September. The peak ILI rate was lower than the previous 5 years (2013–2017).

- **FluTracking.** FluTracking is an online health surveillance system to detect influenza epidemics. It involves participants from around Australia completing a simple online weekly survey, which collects data on the rate of ILI symptoms in communities. Overall, the rates of fever and cough among participants in 2018 peaked in week 33 ending 15 August, lower than the previous 5 years.

LABORATORY SURVEILLANCE

- **National Notifiable Disease Surveillance System (NNDSS).** In Australia, laboratory-confirmed cases of influenza became notifiable to state and territory health departments from 1 January 2001. From 1 January to 21 October 2018, there have been 44,694 laboratory-confirmed notifications of influenza diagnosed and reported to NNDSS. Of these, 77% were influenza A (67% influenza A(unsubtyped), 7% influenza A(H1N1)pdm09 and 3% influenza A(H3N2)), 23% were influenza B, and less than 1% were influenza C, influenza A&B co-infections or untyped. Where subtyping information was available, all jurisdictions have reported a greater proportion of influenza A(H1N1)pdm09 than influenza A(H3N2).
- **WHOCC Laboratory Surveillance.** This is conducted by the Melbourne WHO Collaborating Centre (WHOCC). As of 22 October 2018, a total of 972 influenza viruses from Australia were received for analysis at the Melbourne. Of these, 82% were influenza A (58% influenza A(H1N1)pdm09 and 24% influenza A(H3N2)), 18% were influenza B (17% influenza B Yamagata lineage and 1% influenza B Victoria lineage), and less than 1% were influenza A(H1N1) and influenza A(H3N2) co-infections. None of the 687 influenza viruses tested for neuraminidase inhibitor resistance, demonstrated reduced inhibition to the antiviral drugs Zanamivir or Oseltamivir by enzyme inhibition assays.

SEVERITY SURVEILLANCE

- **Influenza hospitalisations.** The Influenza Complications Network (FluCAN) collects detailed clinical information on all hospitalised cases of influenza and pneumonia from a sample of four sentinel hospitals across Australia. Since 3 April 2018, a total of 725 people have been admitted with confirmed influenza. Of these, 34.8% of people admitted with confirmed influenza were children aged 15 years and younger, 38.9% were adults aged between 16 and 64 years, and 26.3% were adults aged 65 years and older. Of the children admitted with confirmed influenza to date, 7.1% were admitted to ICU. This is slightly less than the percentage of adults aged between 16 and 64 years (9.2%) and adults aged 65 years and older (7.8%) that were admitted to ICU.

- **Death associated with influenza and pneumonia.** Nationally reported influenza deaths are notified by jurisdictions to the NNDSS. As of 21 October, 55 influenza associated deaths have been notified to the NNDSS. The majority of deaths were due to influenza A (75%, n=41). The median age of deaths notified was 80 years (range 1 to 100 years). The number of influenza associated deaths reported to the NNDSS is reliant on the follow up of cases to determine the outcome of their infection and most likely does not represent the true mortality impact associated with this disease.

(Abridged from the Australian Influenza Surveillance Report 2018, No.11, Department of Health and Ageing, Australia and a report by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).

INFLUENZA ACTIVITY IN SOUTH AFRICA, FEBRUARY TO SEPTEMBER 2018

Influenza surveillance in South Africa in 2018 consisted of 4 main surveillance programmes:

- **Viral watch programme.** This program was established in 1984. It focuses on patients with ILI consultations seen mainly by general practitioners (90%) as well as a few paediatricians and primary health care clinics across the country. This program includes doctors and primary health care nurses from eight of nine South African provinces.

- **ILI surveillance in public health clinics.** This programme was established in 2012. It systematically enrols patients meeting a clinical case definition of ILI. Patients are enrolled at two government funded primary health care clinics in two provinces of South Africa. Detailed epidemiologic data are collected on all patients.

- **National syndromic surveillance for pneumonia.** The SARI (pneumonia) surveillance programme was established in 2009 and it monitors SARI cases in hospitalised patients. Detailed epidemiologic data are collected on all patients. This programme currently includes six hospitals as five sentinel sites covering five provinces.

- **Private hospital consultation surveillance.** This programme was established in 2002. It is based on hospital discharge data (ICD-codes J10-J18) for those private hospitals. No specimens for pathogens testing were collected for surveillance purpose.

In 2018, a total of 5300 suspected influenza specimens were processed up to week 34. Of which, 811 influenza viruses were detected. This gave an overall detection rate of 15%. Among all detected influenza viruses, influenza A(H1N1)pdm09 was the predominant strain accounting for 75% (610/811) influenza viruses with influenza B detected in 22% (181/811) and influenza A(H3N2) in 2% (14/811). Six influenza A positive specimens were not subtyped. Both influenza B/Victoria and B/Yamagata lineage viruses circulated and were detected at frequencies of 51% (92/181) and 39% (70/181) respectively.

A total of 28 influenza A(H1N1)pdm09 viruses were sequenced and all of them were clustered genetically in subgroup 6B.1.

A total of two seasonal influenza A(H3N2) viruses were sequenced and they were clustered genetically in 3C.2a1 subgroup.

A total of two influenza B/Yamagata lineage viruses were subjected to sequencing (in progress).

No genetic mutations associated with reduced susceptibility to oseltamivir were observed in the neuraminidases of influenza A (27) and B (2) viruses.

(Abridged from a report by Dr Florette Treurnicht, National Institute for Communicable Diseases, South Africa).

INFLUENZA ACTIVITY IN NEW ZEALAND IN 2018

The national influenza surveillance system in New Zealand is an essential public health tool for assessing and implementing strategies to control influenza. The surveillance system includes community-based surveillance (National sentinel general practice surveillance, Healthline - telephone health advice service) and hospital-based surveillance (SARI surveillance, Ministry of Health data on publicly funded hospital discharges, laboratory-based surveillance for outpatients and hospital in-patients).

COMMUNITY-BASED SURVEILLANCE

NATIONAL SENTINEL GENERAL PRACTICE SURVEILLANCE

New Zealand's longitudinal sentinel GP-based surveillance system was established in 1989 as part of the World Health Organization's (WHO) Global Influenza Surveillance and Response System. It is operated nationally by the ESR and locally by influenza surveillance co-ordinators in the public health services (PHS). Previously (1989–2015), every week during the influenza season from May to September (weeks 18–39), GPs are required to record the number of consultations for influenza-like illness (ILI) each week and the age group of the patient (<1, 1–4, 5–19, 20–34, 35–49, 50–64, 65+), for each case patient who meets the case definition for ILI, on a standardised form.

While the sentinel GP-based surveillance system has been operating successfully for a number of years, the manual method of data collection is outdated and time-consuming. The process adds extra time to the sentinel practices during the busy winter season and only provides the surveillance system with very limited consultation data.

In 2016, a modernised electronic data collection was introduced, enhanced influenza-like illness surveillance (e-ILI). It used an interactive advance form designed by HealthLink to record a consultation-seeking patient with ILI. Symptoms and onset dates including demography (age, sex, and ethnicity), clinical information, medication, vaccination status, and specimen collection were collected electronically and data was sent directly to ESR.

The ILI case definition was also modified to "an acute respiratory illness with a history of fever or measured fever of ≥38°C, AND cough, AND onset within the past 10 days".

The syndromic eILI surveillance was all-year-round. The virological specimen collection and testing for those ILI patients was only during the influenza season, May-September inclusive.

Each participating practice from the Auckland and Wellington regions collected respiratory samples (ie, a nasopharyngeal or throat swab) from all ILI patients seen. For the remaining areas, three respiratory samples, one each from the first ILI patient examined on Monday, Tuesday and Wednesday were collected weekly.

All practices forwarded these samples to the WHO National Influenza Centre at ESR apart for those in the Canterbury, South Canterbury and West Coast DHBs who forwarded their samples to Canterbury Health Laboratories for virus characterisation. Laboratory identification included molecular detection using the polymerase chain reaction (PCR), isolation of the virus or direct detection of viral antigens. Influenza viruses were typed as A or B. Influenza A viruses were further

sub-typed as A(H3N2) or A(H1N1)pdm09. Influenza B viruses were further lineage-typed as B/Yamagata or B/Victoria lineage. Eight non-influenza respiratory viruses were also tested: respiratory syncytial virus, parainfluenza virus types 1, 2 and 3, rhinovirus, adenovirus, human metapneumovirus and enterovirus.

Canterbury Health Laboratory reported to ESR weekly on the total number of swabs received from each DHB and the influenza viruses identified, and updated details on influenza types and sub-types from previous weeks. ESR reports national information on epidemiological and virological surveillance of influenza weekly and yearly to relevant national and international organisations, including the WHO, with reports published on the ESR website: https://surv.esr.cri.nz/virology.php.

Consultation rates were calculated using the registered patient populations of the participating practices as a denominator.

The values for the different intensity levels were based on the framework from Pandemic Influenza Severity Assessment (PISA) – a WHO guide to assess the severity of influenza in seasonal epidemics and pandemics (http://apps.who.int/iris/bitstream/handle/10665/259392/WHO-WHE-IHM-GIP-2017.2-eng.pdf;jsessionid=0D8C59A6D4E84A8C5AB9329CADAE374D?sequence=1)

In 2018, 80 sentinel practices were recruited from all 20 DHBs under ESR's sentinel GP-based surveillance with a total patient roll of 440,650. Virus transmissibility which reflects the ease of movements of the influenza virus between individuals and communities was low in 2018. Influenza like illness (ILI) and ILI-associated influenza consultation rates in 2018 were low and the activity was later than previous years of 2013–2017 (Figure 1 to 4). From week 18 (commencing 30 April) through week 39 (ending 30 September), consultation activity remained below the seasonal threshold. The ILI consultation rate peaked in week 35 with the ILI consultation rate of 30.0 per 100,000.

Figure 1. Weekly consultation rates for influenza-like illness in New Zealand, 2018

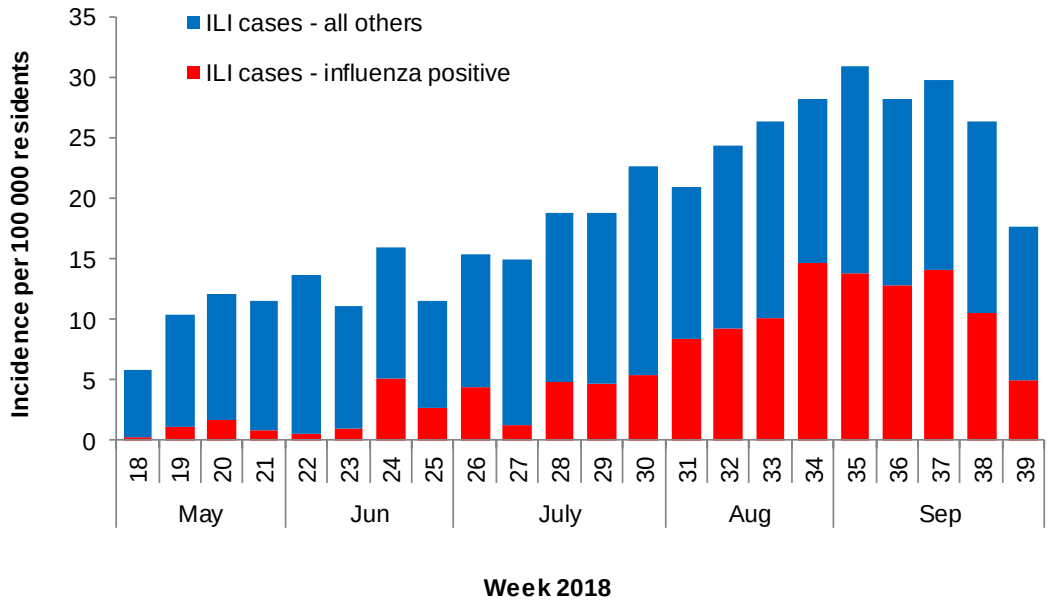


Figure 2. Weekly ILI consultation rates in 2018 compared to 2013–2017

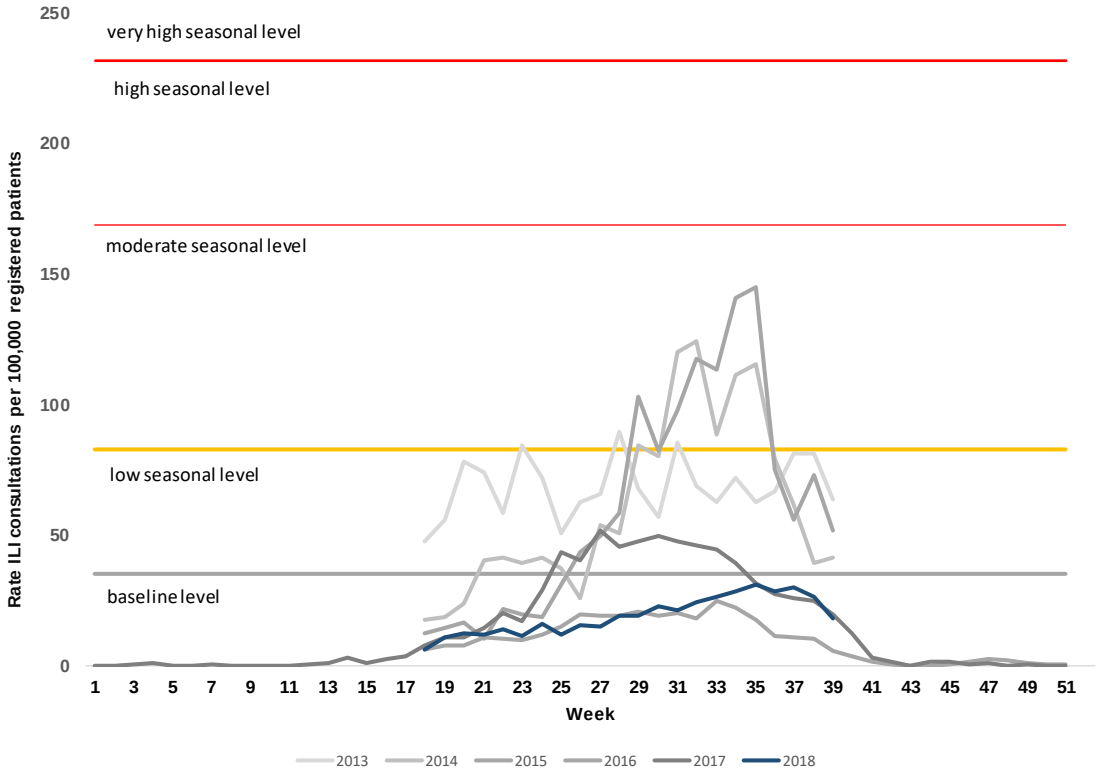


Figure 3. Weekly ILI-associated influenza rates in 2018 compared to 2013–2017

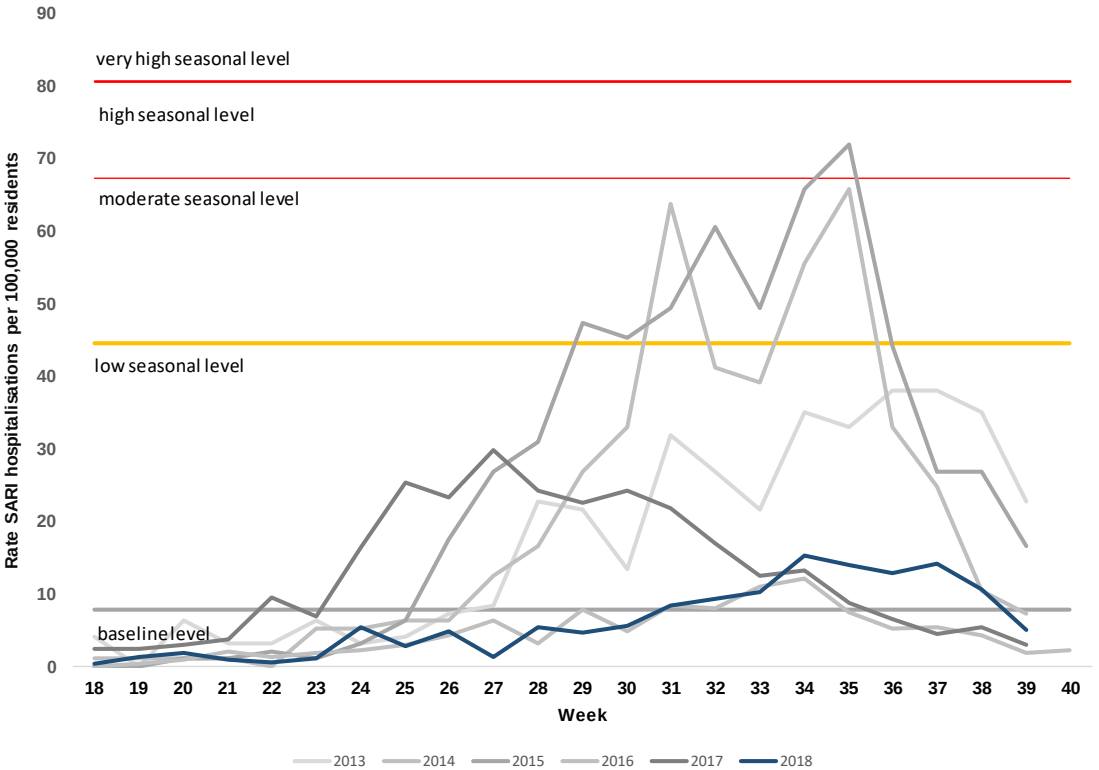
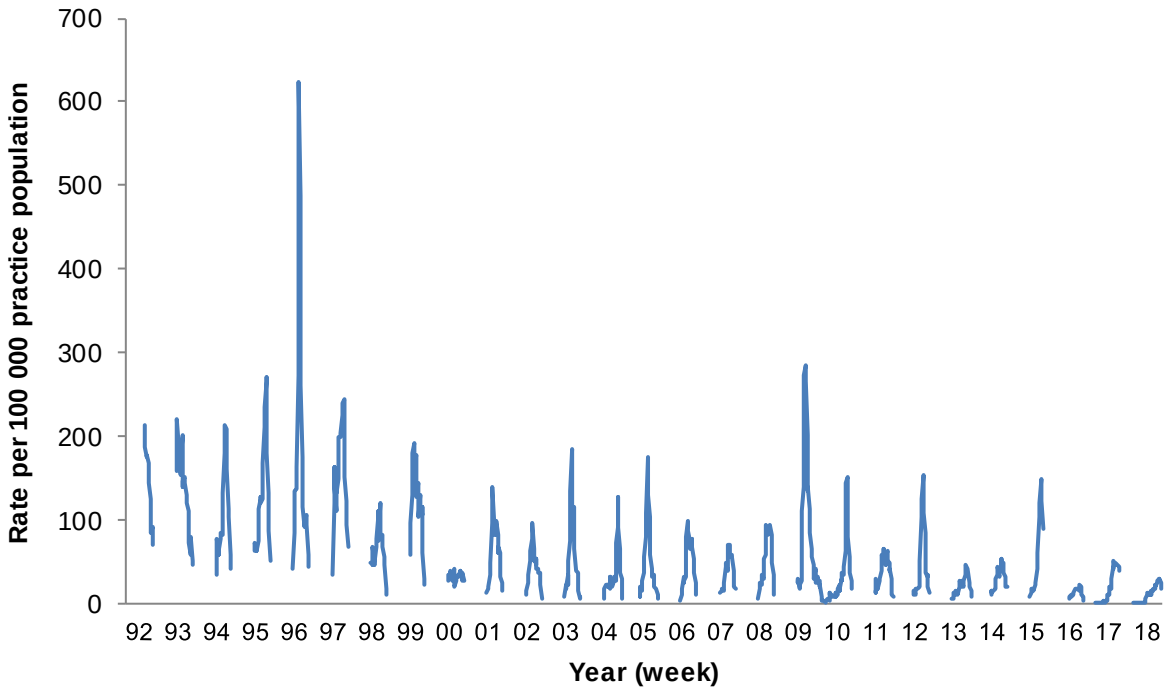


Figure 4. Weekly Consultation Rates for Influenza-like Illness in New Zealand, 1992–2018



From week 18 (commencing 30 April 2018) through week 39 (ending 30 September 2018), a total of 1830 consultations for ILI were reported from the 20 DHBs. The cumulative incidence of ILI consultation during this period was 415.3 per 100,000 population. The average weekly ILI consultation rate between weeks 18 and 39 was 18.3 per 100,000 population. Among the patients that met the ILI case definition, 1466 (80.1%) had a specimen tested for influenza. Of these, 462 (31.5%) cases had influenza viruses detected (Table 2).

Table 2. Demographic characteristics of ILI and influenza cases, since 30 April 2018

Characteristics	ILI & influenza cases among sentinel practices				
	ILI cases	Influenza cases	Prop Influenza positive[1] (%)	ILI incidence (per 100,000)	Influenza incidence[2] (per 100,000)
Overall	**1830**	**462**	**31.5 (100.0)**	**415.3**	**130.9**
Age group (years)					
<1	17	1	9.1 (0.2)	374.4	34.0
1–4	185	42	32.6 (9.1)	766.8	249.6
5–19	422	120	36.5 (26.0)	477.7	174.3
20–34	381	94	29.9 (20.3)	422.5	126.5
35–49	383	111	34.3 (24.0)	454.8	155.8
50–64	286	65	28.3 (14.1)	346.7	98.0
65–79	124	25	24.8 (5.4)	239.2	59.2
>80	32	4	14.3 (0.9)	214.3	30.6
Unknown	0	0	0.0		
Ethnicity					
Māori	200	43	30.7 (9.3)	333.5	102.4
Pacific peoples	69	15	27.3 (3.2)	251.9	68.7
Asian	183	51	33.6 (11.0)	477.1	160.1
European and Other	1377	353	31.5 (76.4)	437.2	137.9
Unknown	0	0	0.0		
Sex					
Female	1050	258	30.5 (55.8)	454.1	138.3
Male	780	204	33.0 (44.2)	372.5	122.8
Unknown	0	0	0.0		

[1]Proportion of cases tested which were positive for influenza viruses

[2]Adjusted to positivity of tested cases

As in previous years, 2018 consultation rates for ILI varied greatly among DHBs (Table 3). From week 18 (commencing 30 April) through week 39 (ending 30 September), Waitemata DHB had the highest average consultation rate (76.1 per 100,000), followed by Auckland (62.2 per 100,000), and South Canterbury (44.5 per 100,000).

Table 3. Weekly consultation rate for influenza-like illness by District Health Board, 2018

DHB	Rate per 100,000																						
	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	Average rate
Auckland	27.4	27.4	29.9	29.9	32.4	37.4	47.4	29.9	42.4	44.9	87.3	49.9	49.9	87.3	107.2	97.3	109.7	102.2	97.3	84.8	87.3	59.8	62.2
Bay of Plenty	0.0	4.9	0.0	0.0	4.9	0.0	9.7	19.4	14.6	14.6	19.4	14.6	4.9	0.0	4.9	9.7	4.9	9.7	9.7	0.0	0.0	4.9	6.9
Canterbury	2.0	6.0	10.0	8.0	6.0	10.0	6.0	6.0	10.0	6.0	10.0	6.0	16.0	10.0	12.0	20.1	20.1	26.1	38.1	42.1	26.1	16.0	14.2
Capital & Coast	7.9	2.6	5.2	23.6	10.5	13.1	10.5	5.2	10.5	18.4	5.2	15.7	13.1	10.5	18.4	44.6	57.7	65.6	34.1	76.1	36.7	31.5	23.5
Counties Manukau	0.0	0.0	6.3	3.1	9.4	0.0	3.1	0.0	0.0	3.1	0.0	0.0	18.9	12.6	3.1	3.1	3.1	0.0	0.0	3.1	9.4	3.1	3.7
Hawke's Bay	0.0	21.4	21.4	14.3	7.1	7.1	14.3	7.1	28.6	14.3	14.3	7.1	28.6	35.7	21.4	14.3	14.3	28.6	42.9	50.0	64.3	14.3	21.4
Hutt Valley	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.3	0.1
Lakes	0.0	16.5	0.0	16.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5
MidCentral	3.3	9.9	9.9	0.0	13.2	0.0	3.3	0.0	3.3	0.0	3.3	6.6	3.3	3.3	6.6	9.9	9.9	16.5	19.8	6.6	3.3	0.0	6.0
Nelson Marlborough	10.0	10.0	0.0	10.0	20.1	10.0	10.0	0.0	20.1	20.1	10.0	40.1	0.0	10.0	10.0	0.0	20.1	0.0	0.0	20.1	0.0	40.1	11.8
Northland	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.6	78.6	39.3	15.7	47.2	23.6	7.9	23.6	15.7	15.7	23.6	7.9	14.7
South Canterbury	9.4	9.4	9.4	0.0	47.1	0.0	18.8	37.7	9.4	28.3	37.7	28.3	56.5	37.7	47.1	56.5	94.2	150.7	94.2	65.9	103.6	37.7	44.5
Southern	0.0	9.2	3.1	6.1	3.1	0.0	15.3	3.1	0.0	0.0	0.0	6.1	21.5	15.3	18.4	9.2	6.1	9.2	3.1	15.3	9.2	30.7	8.4
Tairawhiti	29.7	29.7	29.7	0.0	0.0	29.7	0.0	0.0	0.0	44.5	0.0	0.0	0.0	14.8	0.0	0.0	0.0	29.7	14.8	0.0	14.8	14.8	11.5
Taranaki	0.0	13.3	4.4	17.7	4.4	0.0	0.0	0.0	0.0	4.4	0.0	0.0	4.4	4.4	0.0	4.4	0.0	4.4	8.8	0.0	0.0	0.0	3.2
Waikato	9.4	16.9	22.6	13.2	20.7	3.8	16.9	16.9	13.2	9.4	16.9	16.9	24.4	20.7	22.6	22.6	16.9	15.0	11.3	15.0	15.0	7.5	15.8
Wairarapa	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	40.1	0.0	40.1	0.0	40.1	0.0	0.0	0.0	0.0	40.1	0.0	0.0	0.0	0.0	7.3
Waitemata	0.0	23.8	53.6	41.7	59.6	107.3	125.2	89.4	119.2	95.4	89.4	119.2	125.2	71.5	65.6	101.3	89.4	47.7	95.4	65.6	71.5	17.9	76.1
West Coast	4.8	0.0	0.0	4.8	0.0	0.0	0.0	0.0	14.3	4.8	4.8	0.0	0.0	4.8	4.8	0.0	0.0	0.0	0.0	4.8	4.8	4.8	2.6
Whanganui	0.0	0.0	0.0	0.0	30.7	0.0	0.0	0.0	0.0	30.7	0.0	0.0	30.7	0.0	61.4	0.0	61.4	122.8	30.7	30.7	61.4	30.7	22.3
New Zealand	**5.7**	**10.1**	**11.7**	**11.2**	**13.2**	**10.8**	**15.4**	**11.2**	**15.0**	**14.6**	**18.3**	**18.3**	**22.1**	**20.3**	**23.6**	**25.6**	**27.4**	**30.0**	**27.4**	**28.9**	**25.6**	**17.2**	**18.3**

Between 30 April to 30 September 2018, a total of 1473 ILI specimens were tested for influenza viruses (Table 4) and 466 (31.6%) were positive, with more influenza A (426) than influenza B (39) viruses. Additionally, a total of 1432 ILI specimens were tested for non-influenza viruses and 438 (30.6%) were positive with non-influenza viruses.

Table 4. Influenza and non-influenza respiratory viruses among ILI cases, 30 April–30 September 2018

Influenza viruses	**ILI**
	Cases (%)
No. of specimens tested	1473
No. of positive specimens (%)[1]	466 (31.6)
Influenza A	426
A (not subtyped)	30
A(H1N1)pdm09	335
A(H1N1)pdm09 by PCR	289
A/Michigan/45/2015 (H1N1)pdm09 - like	46
A(H3N2)	61
A(H3N2) by PCR	58
A/Hong Kong/4801/2014 (H3N2) - like	2
A/Singapore/INFIMH-16-0019/2016 (H3N2) - like	1
Influenza B	39
B (lineage not determined)	3
B/Yamagata lineage	33
B/Yamagata lineage by PCR	17
B/Phuket/3073/2013 - like	16
B/Victoria lineage	3
B/Victoria lineage by PCR	3
B/Brisbane/60/2008 - like	0
Influenza and non-influenza co-detection (% +ve)	18 (3.9)
Non-influenza respiratory viruses	**ILI**
	Cases (%)
No. of specimens tested	1432
No. of positive specimens (%)[1]	438 (30.6)
Respiratory syncytial virus (RSV)	74
Parainfluenza 1 (PIV1)	40
Parainfluenza 2 (PIV2)	3
Parainfluenza 3 (PIV3)	29
Rhinovirus (RV)	175
Adenovirus (AdV)	62
Human metapneumovirus (hMPV)	62
Enterovirus	18
Single virus detection (% of positives)	416 (95.0)
Multiple virus detection (% of positives)	22 (5.0)

[1]Number of specimens positive for at least one of the listed viruses; note a specimen may be positive for more than one virus.

The temporal distribution of the number and proportion of the influenza viruses and non-influenza respiratory viruses, from 30 April to 30 September 2018, is shown in Figure 5 and Figure 6. Influenza A(H1N1)pdm09 was the predominant strain during this period.

Figure 5. Temporal distribution of the number and proportion of influenza viruses from ILI specimens, by type and week

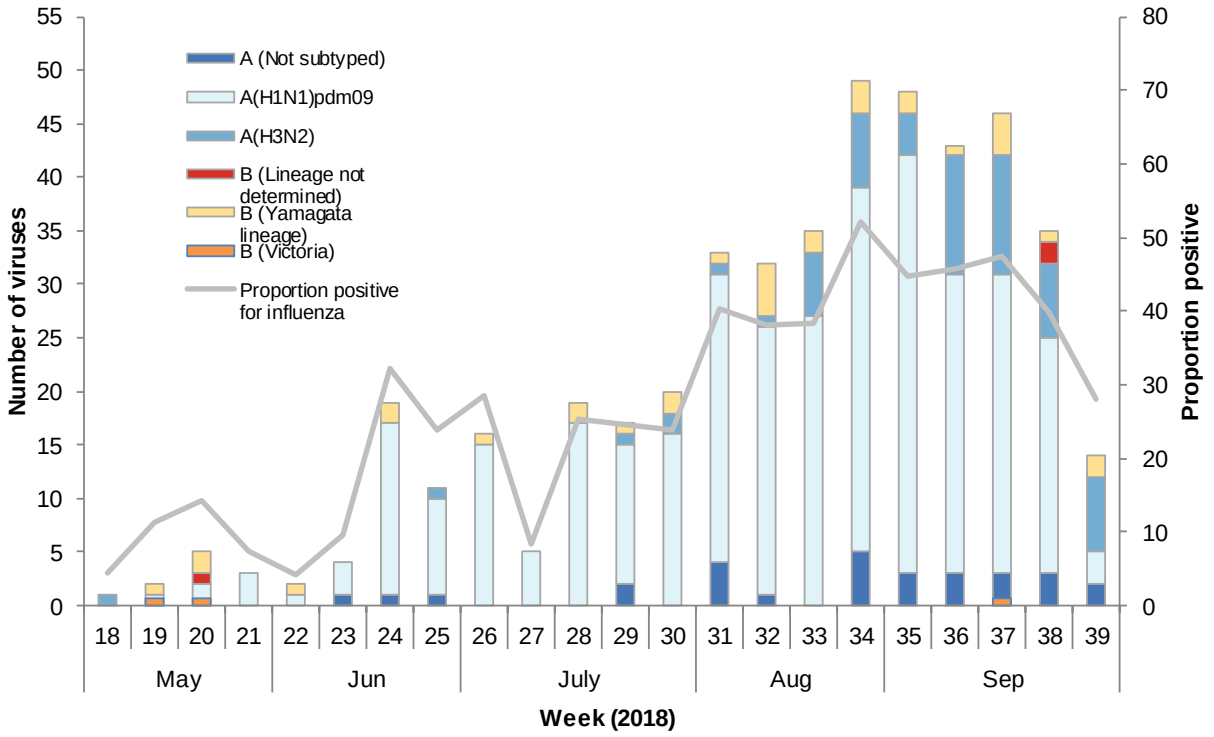
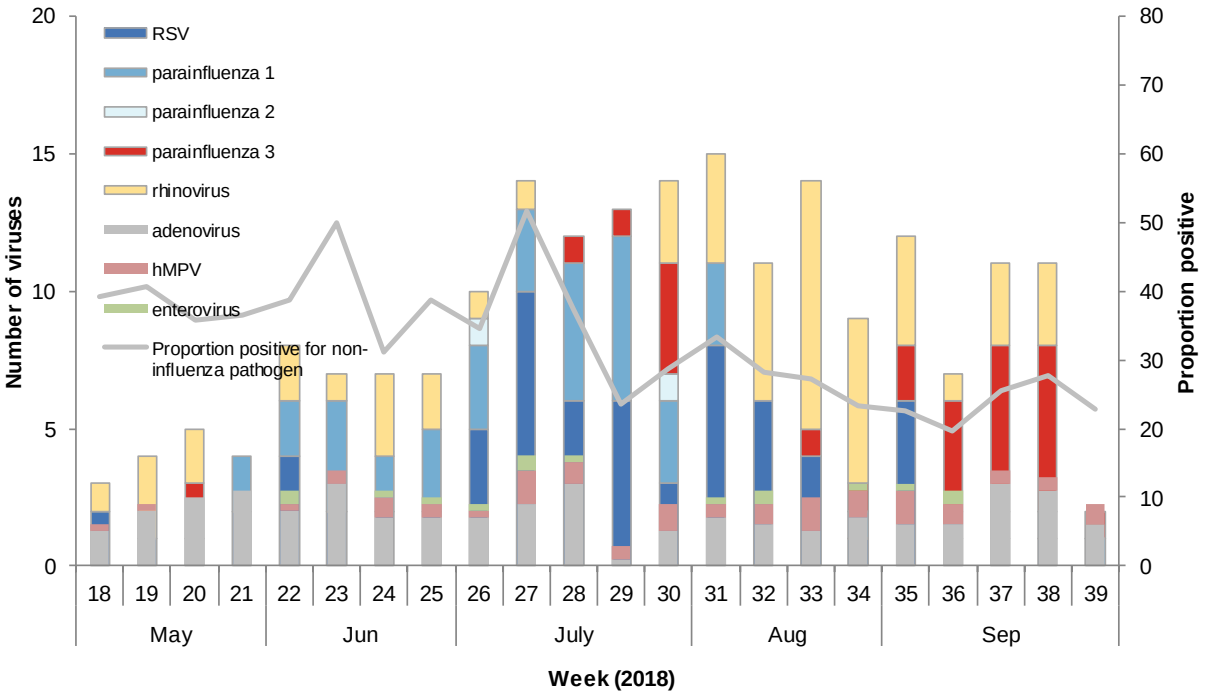


Figure 6. Temporal distribution of the number and proportion of non-influenza viruses from ILI specimens, by type and week[1]



HEALTHLINE

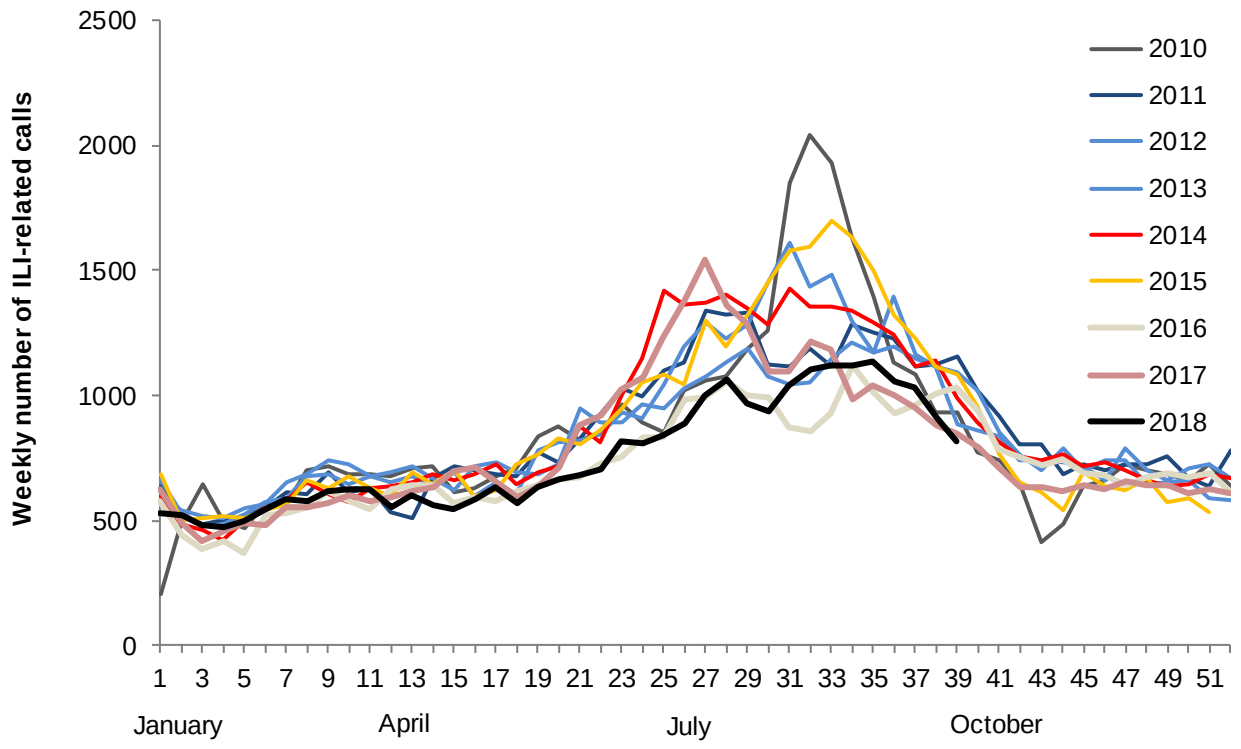
Healthline is the free national 0800 24 hour telephone health advice service funded by the Ministry of Health. Calls made to Healthline are triaged using electronic clinical decision support software. Data collected are daily counts of all symptomatic calls made to Healthline and those triaged for Influenza-Like-Illness (ILI). Note that about 70% of all calls to Healthline are symptomatic (other calls not part of this analysis include queries for information etc).

Analysis is frequency based with alarms raised by identifying statistical deviations (aberations) from previous calls. Data are reported for all ages and in five age bands (0–4, 5–14, 15–44, 45–64, 65+ years). The analysis of the call frequency is based on the cumulative summation (CUSUM) algorithm implemented in Early Aberration Reporting System (EARS) application developed by the Centres for Disease Control and Prevention (CDC), Atlanta, United States. EARS has three sensitivity thresholds (high, medium and low). If the daily call count exceeds a threshold a flag is signalled.

Cases of ILI are defined as those that are recorded in the Healthline database as having one of the following 18 guidelines: adult fever; breathing problems; breathing difficulty – severe (paediatric); colds (paediatric); cough (paediatric); cough – adult; fever (paediatric); flu-like symptoms or known/suspected influenza; flu like symptoms pregnant; influenza (paediatric); headache; headache (paediatric); muscle ache/pain; sore throat (paediatric); sore throat/hoarseness; sore throat/hoarseness pregnant; upper respiratory tract infections/colds; upper respiratory tract infections/colds – pregnant.

Figure 7 shows the weekly number of calls to Healthline for ILI during 2009–2018. Healthline calls in 2018 were in the low range, similar to the level in 2016.

Figure 7. Weekly number of ILI-related calls to Healthline, 2010–2018



HOSPITAL-BASED SURVEILLANCE

HOSPITAL-BASED SEVERE ACUTE RESPIRATORY ILLNESS (SARI) SURVEILLANCE

Inpatients with suspected respiratory infections admitted overnight to any of the four hospitals (Auckland City Hospital and the associated Starship Children's Hospital, Middlemore Hospital and the associated Kidz First Children's Hospital) in the Auckland District Health Board (ADHB) and Counties Manukau DHB, were screened by research nurses each day. Overnight admission is defined as: "*A patient who is admitted under a medical team, and to a hospital ward or assessment unit*". Case ascertainment followed a surveillance algorithm. The presence of the components of the case definition was determined through a combination of reviewing the clinician's admission diagnoses and by interviewing patients about their presenting symptoms. Records of all patients admitted overnight to medical wards were reviewed daily to identify anyone with a suspected respiratory infection. These patients were categorised into one of ten admission diagnostic syndrome groups. Research nurses then interviewed the patients and documented the components of the case definition of severe acute respiratory illness (SARI) that were present and ascertain the patients whether meeting the SARI case definition.

The case definition being used is the World Health Organisation (WHO) SARI case definition: *"an acute respiratory illness with a history of fever or measured fever of ≥38°C, and cough, and onset within the past 10 days, and requiring inpatient hospitalisation"*. If a patient with suspected respiratory infection met the SARI case definition, a respiratory sample was collected to test for influenza and other respiratory pathogens. In addition, patient information was captured via a case report form which included patient demographics, presenting symptoms and illness, pre-hospital healthcare, medication usage, influenza vaccination history, co-morbidities, disease course and outcome, including major treatments, ICU admission and mortality, epidemiologic risk factors and laboratory results.

The total numbers of all new hospital inpatient acute admissions and newly assessed and tested patients, including ICU admissions and deaths were collected. This allowed calculation of population-based incidence for SARI and associated influenza cases overall and stratified by age, sex, ethnicity and socio-economic status among the ADHB and CMDHB resident population (from 2013 census data). Incidence rates were calculated along with 95% confidence intervals (95%CI). In addition, this allowed the calculation of the proportion of SARI and associated influenza cases, including ICU admissions and deaths, by overall and stratified patients, among all acute admissions regardless of residence status. An acute admission is defined as an unplanned admission on the day of presentation at the admitting health care facility. Admission may have been from the emergency or outpatient departments of the health care facility, a transfer from another facility or a referral from primary care.

The overall impact of influenza on healthcare use in hospitals and ICU admissions was low in 2018. Severe acute respiratory illness (SARI) and influenza-associated SARI hospitalization rates in 2018 were at a low level (Figure 8 and Figure 9). From week 18 (commencing 30 April) through week 39 (ending 30 September), SARI hospitalisation rates remained below the seasonal threshold with the exception of a peak at week 33 (ending 19 August). SARI-associated influenza hospitalisation rates in 2018 were at a low level (Figure 10).

Figure 8. Weekly resident SARI and SARI-associated influenza incidence, 2018

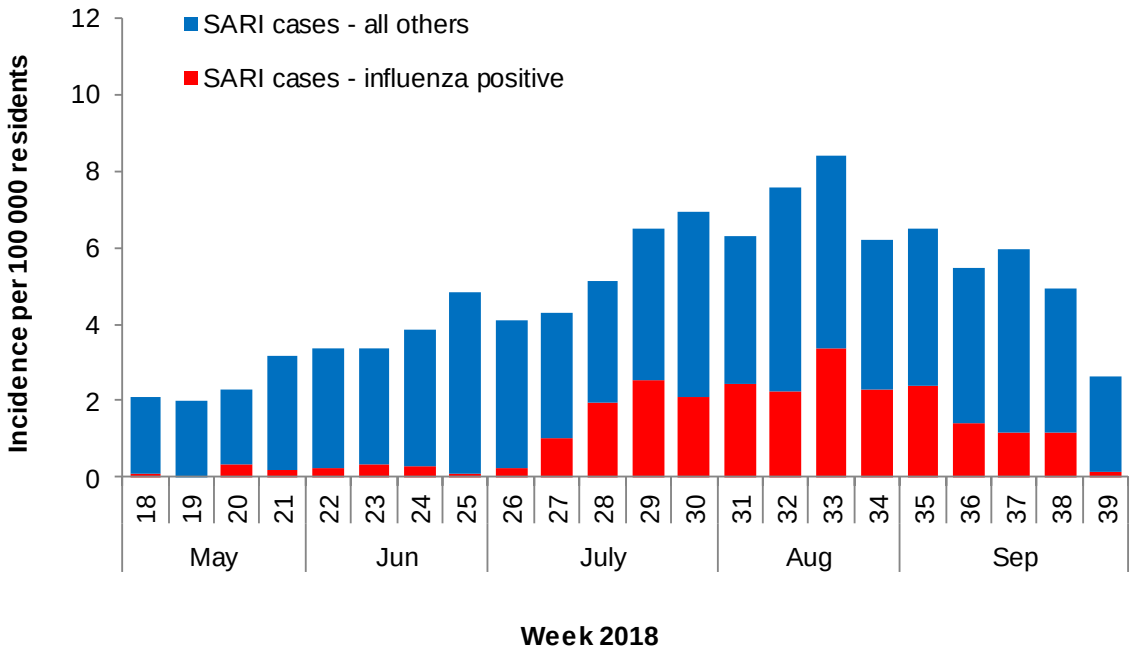


Figure 9. Weekly hospitalisation rates for SARI in 2018 compared to 2012–2017

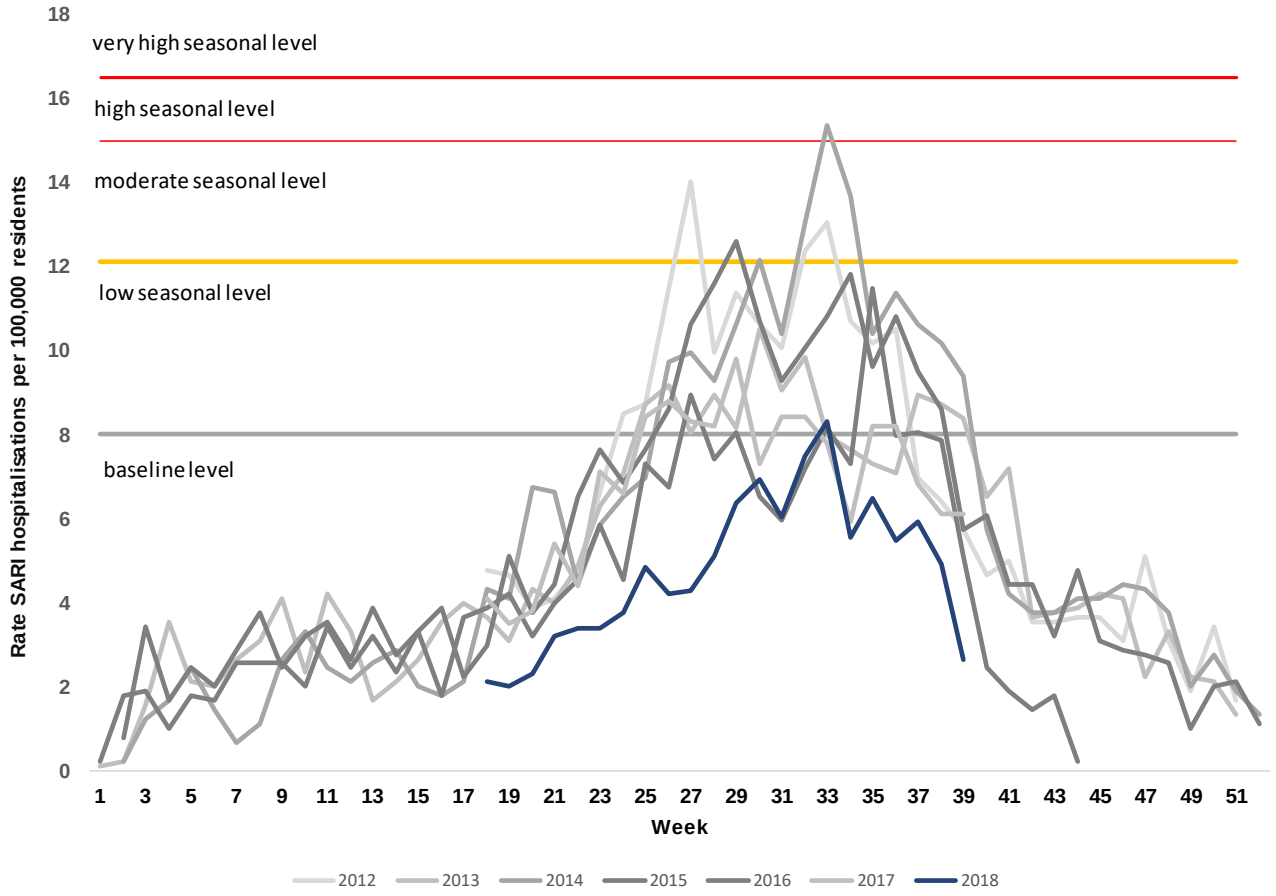
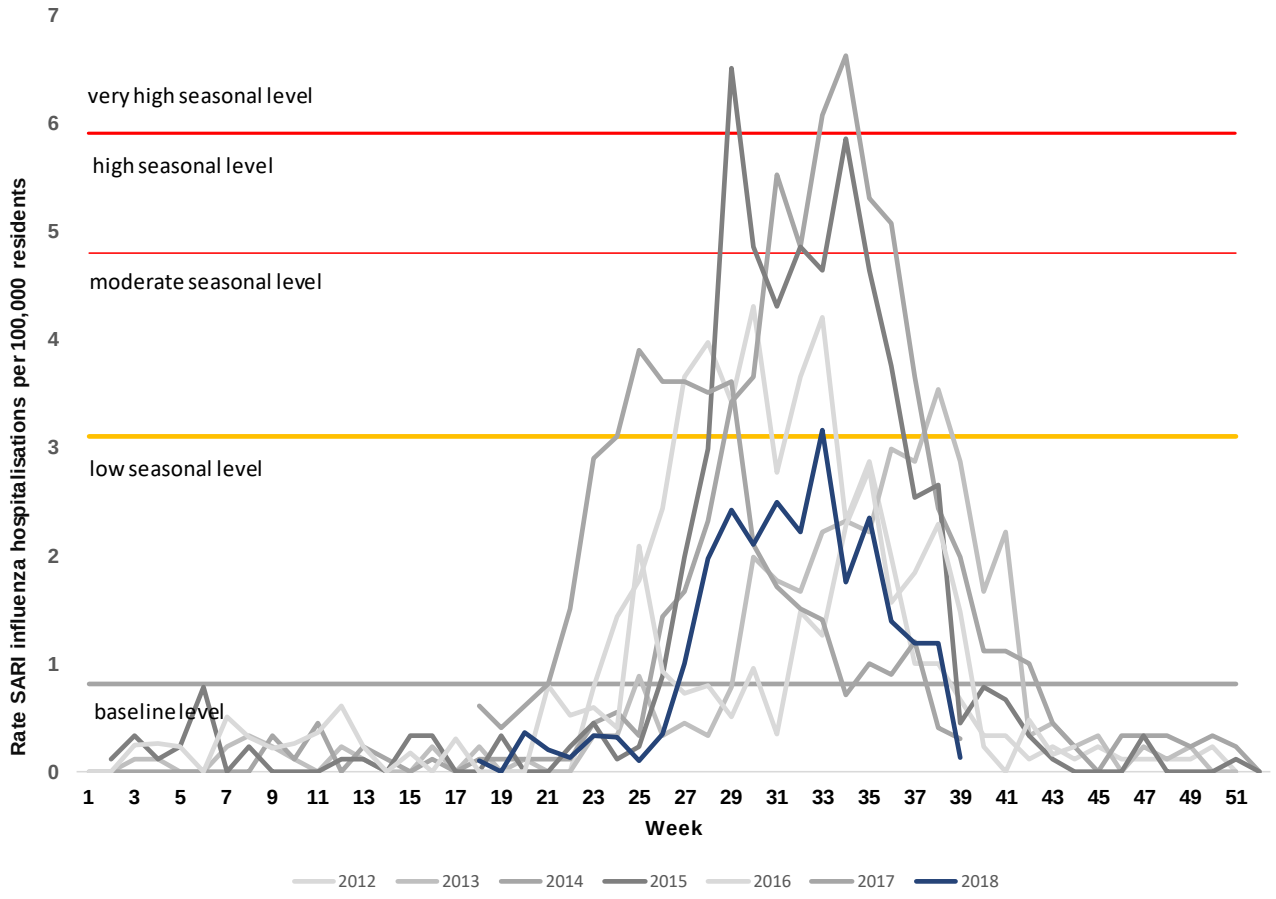
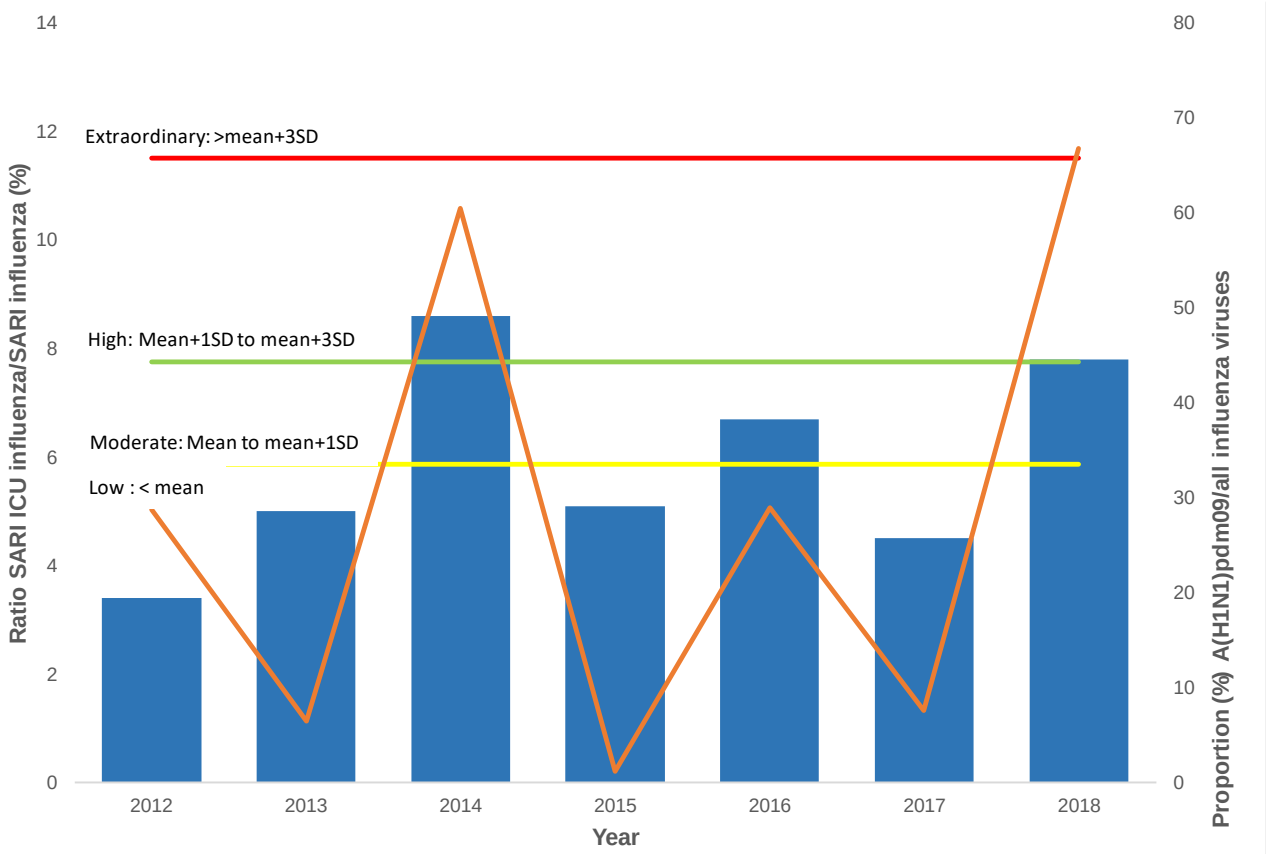


Figure 10. Weekly hospitalisation rates for SARI-associated influenza in 2018 compared to 2012–2017



Seriousness of disease (ie, severity) that indicates the extent to which individuals get sick when infected with the influenza virus was high in 2018 as measured by the ratio of influenza-associated ICU admission over influenza-associated hospitalization. It has been noticed that when influenza A(H1N1)pdm09 virus was the predominant strain in 2018, 2014, it appeared to be associated with high level of severity (Figure 11).

Figure 11. Seriousness of disease indicator in 2018 compared to 2012–2017



From 30 April to 30 September 2018, there were 62,168 acute admissions to ADHB and CMDHB hospitals. A total of 2261 patients with suspected respiratory infections were assessed in these hospitals. Of these, 1486 (65.7%) patients met the SARI case definition. Among these, 1160 were residents of ADHB and CMDHB, giving the SARI incidence rate of 105.8 per 100,000 population (Table 4). Among the 1011 tested SARI cases who were ADHB and CMDHB residents, 250 (24.7%) had positive influenza virus results. This gives a SARI related influenza incidence (adjusted for non-testing) of 26.2 per 100,000 population.

Between 30 April and 30 September 2018, the 1486 SARI cases give a SARI proportion of 23.9 per 1000 acute hospitalisations (Table 5). Of these SARI cases, 35.7% were children aged less than 5 years and 19.7% were adults 65 years and older. One hundred and fourteen SARI cases have been admitted to ICU and 16 SARI-related deaths were reported during this period.

Table 5. Demographic characteristics of SARI cases and related influenza cases, since 30 April 2018

Characteristics	SARI & influenza cases among all hospital patients		SARI & influenza cases among ADHB & CMDHB residents			
	SARI Cases (%)	Influenza positive[1] (%)	SARI cases	SARI incidence (per 100,000)	Influenza Cases	Influenza incidence (per 100,000)
Overall	**1486 (65.7)**	**275 (24.9)**	**1160**	**105.8**	**250**	**26.2**
Age group (years)						
<1	300 (62.4)	27 (10.3)	269	1850.1	25	196.0
1–4	230 (77.7)	40 (23.5)	206	383.0	33	85.4
5–19	83 (89.2)	14 (23.3)	70	33.3	12	8.0
20–34	73 (92.4)	30 (43.5)	71	23.2	30	10.4
35–49	83 (96.5)	29 (36.3)	82	39.2	28	13.9
50–64	183 (73.8)	54 (31.4)	177	99.4	53	31.7
65–79	189 (58.3)	48 (27.0)	180	185.7	43	47.3
>80	103 (53.1)	26 (27.4)	101	369.0	25	99.2
Unknown	241 (52.5)	7 (38.9)	3	0.0	1	
Ethnicity						
Māori	261 (62.4)	40 (17.6)	238	182.1	39	34.3
Pacific peoples	469 (74.1)	111 (27.5)	453	261.1	103	69.0
Asian	119 (75.8)	26 (25.2)	113	35.0	24	8.6
European and Other	395 (66.8)	90 (25.6)	352	74.9	82	19.6
Unknown	242 (52.4)	8 (42.1)	4		2	
Hospitals						
ADHB	754 (89.5)	119 (23.7)	478	88.7	99	20.5
CMDHB	732 (51.6)	156 (25.9)	682	122.3	151	31.7
Sex						
Female	611 (69.3)	143 (26.5)	569	102.5	135	27.7
Male	633 (68.9)	125 (22.9)	586	108.2	114	24.3
Unknown	242 (52.6)	7 (33.3)	5	0.0	1	0.0

[1]Proportion of cases tested which were positive for influenza viruses

From 30 April to 30 September 2016, 1190 SARI specimens have been tested and 286 (24.0%) were positive for influenza viruses with more influenza A (266) than influenza B (19) viruses (Table 6). Additionally, 1311 SARI specimens were tested for non-influenza respiratory viruses.

Table 6. Influenza and non-influenza respiratory viruses among SARI cases, 30 April to 30 September 2018

Influenza viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	1190	204	22
No. of positive specimens (%)[1]	286 (24.0)	42 (20.6)	8 (36.4)
Influenza A	266	39	7
A (not subtyped)	82	15	2
A(H1N1)pdm09	145	21	4
A(H1N1)pdm09 by PCR	142	20	4
A/Michigan/45/2015 (H1N1)pdm09 - like	3	1	0
A(H3N2)	39	3	1
A(H3N2) by PCR	39	3	1
A/Hong Kong/4801/2014 (H3N2) - like	0	0	0
A/Singapore/INFIMH-16-0019/2016 (H3N2) - like	0	0	0
Influenza B	19	2	1
B (lineage not determined)	19	2	1
B/Yamagata lineage	0	0	0
B/Yamagata lineage by PCR	0	0	0
B/Phuket/3073/2013 - like	0	0	0
B/Victoria lineage	0	0	0
B/Victoria lineage by PCR	0	0	0
B/Brisbane/60/2008 - like	0	0	0
Influenza and non-influenza co-detection (% +ve)	16 (5.6)	3 (7.1)	0 (0.0)
Non-influenza respiratory viruses	**SARI**	**SARI and non-SARI**	
	Cases (%)	**ICU (%)**	**Deaths (%)**
No. of specimens tested	1311	208	27
No. of positive specimens (%)[1]	483 (36.8)	98 (47.1)	6 (22.2)
Respiratory syncytial virus (RSV)	226	56	3
Parainfluenza 1 (PIV1)	31	4	0
Parainfluenza 2 (PIV2)	1	0	0
Parainfluenza 3 (PIV3)	37	7	0
Rhinovirus (RV)	108	30	3
Adenovirus (AdV)	151	30	1
Human metapneumovirus (hMPV)	100	4	0
Enterovirus	12	8	0
Single virus detection (% of positives)	319 (66.0)	64 (65.3)	0 (-)
Multiple virus detection (% of positives)	168 (34.8)	35 (35.7)	0 (-)

[1]Number of specimens positive for at least one of the listed viruses; note a specimen may be positive for more than one virus

The temporal distribution of the number and proportion of the influenza viruses and non-influenza respiratory viruses is shown in Figure 12 and Figure 13. Influenza A(H1N1)pdm09 was the predominant strain between 30 April to 30 September 2018.

Figure 12. Temporal distribution of the number and proportion of influenza viruses from SARI specimens, by type and week[1]

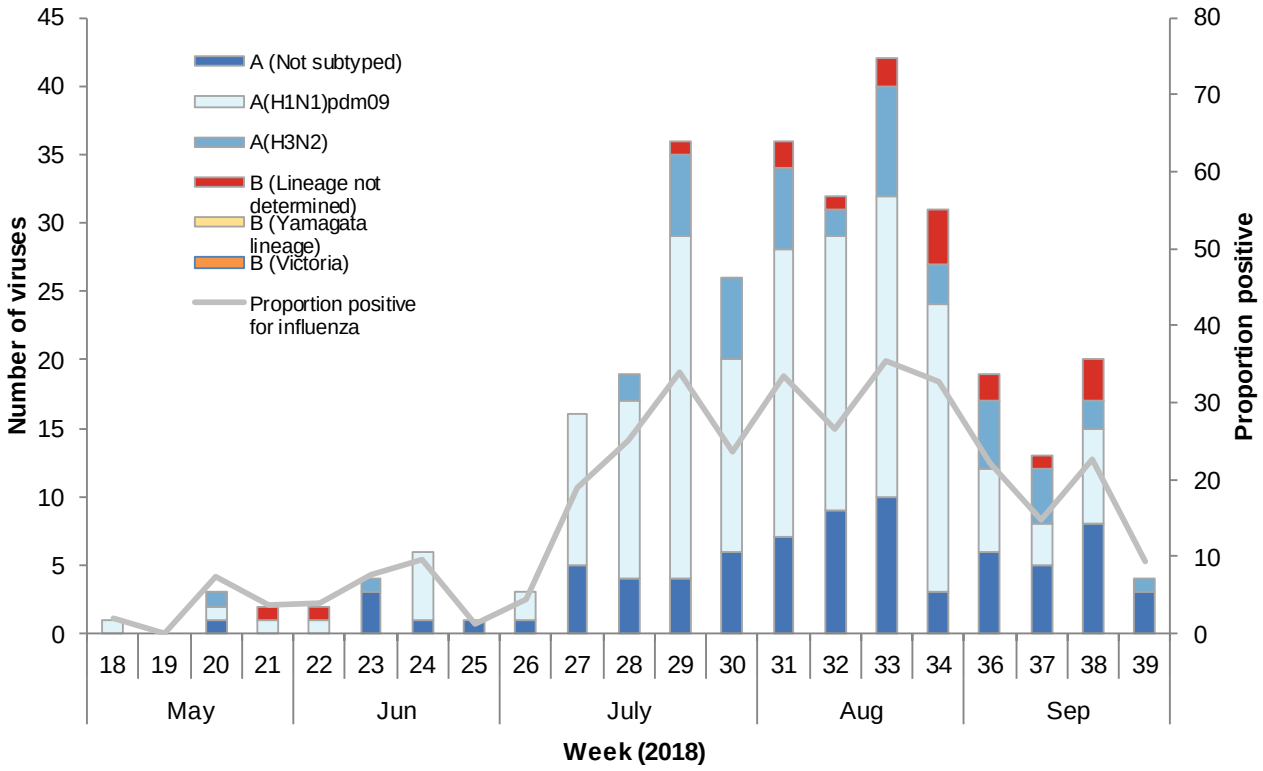
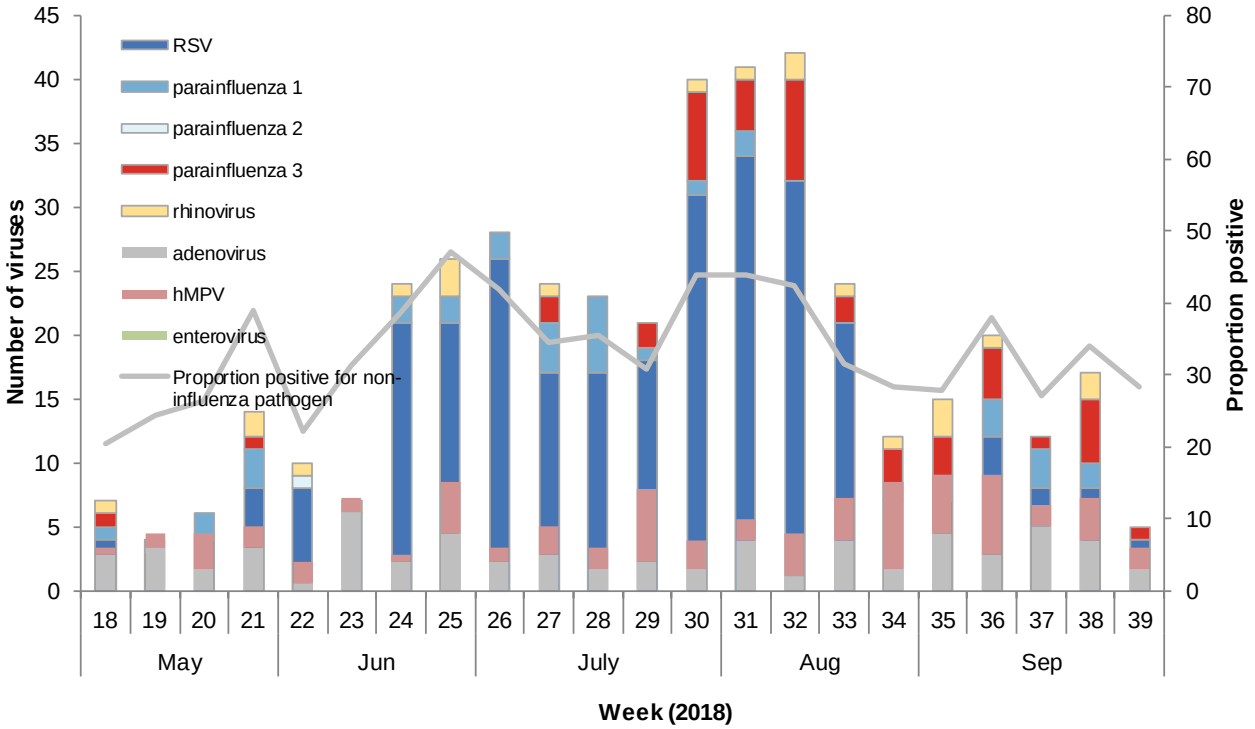


Figure 13. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1]



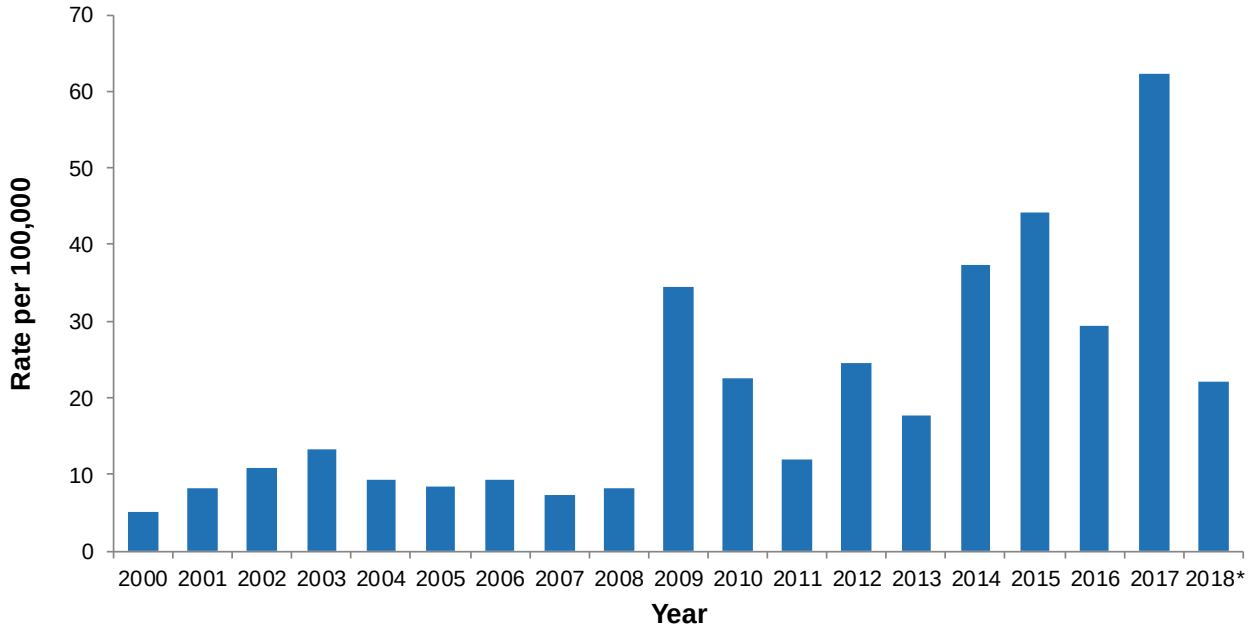
[1]Figures for recent weeks will be underestimates due to time lag in receiving laboratory test results

MINISTRY OF HEALTH DATA ON PUBLICLY FUNDED HOSPITAL DISCHARGES

Hospitalisation data for influenza (ICD-10AM-VI code I (J09-J11) for 2018 which correlate with previous versions of ICD-10AM codes J10-J11, were extracted from the New Zealand Ministry of Health's NMDS (by discharge date). In this dataset, people who received less than 1 day of hospital treatment in hospital emergency departments were excluded from any time series analysis of influenza hospitalisations during 2000–2018. Influenza-related hospitalisations were conservatively taken to include only those cases where influenza was the principal diagnosis. Repeat admissions were included, as infections with another influenza A subtype or B virus are possible.

From 1 January to 7 September, there were a total of 1060 hospitalisations (22.1 per 100,000) for influenza (Figure 14). Influenza hospitalisation coding has not been completed for the year. This data only captured a proportion of influenza cases for the winter season of 2018.

Figure 14. Influenza hospital discharges, 2000–2018*

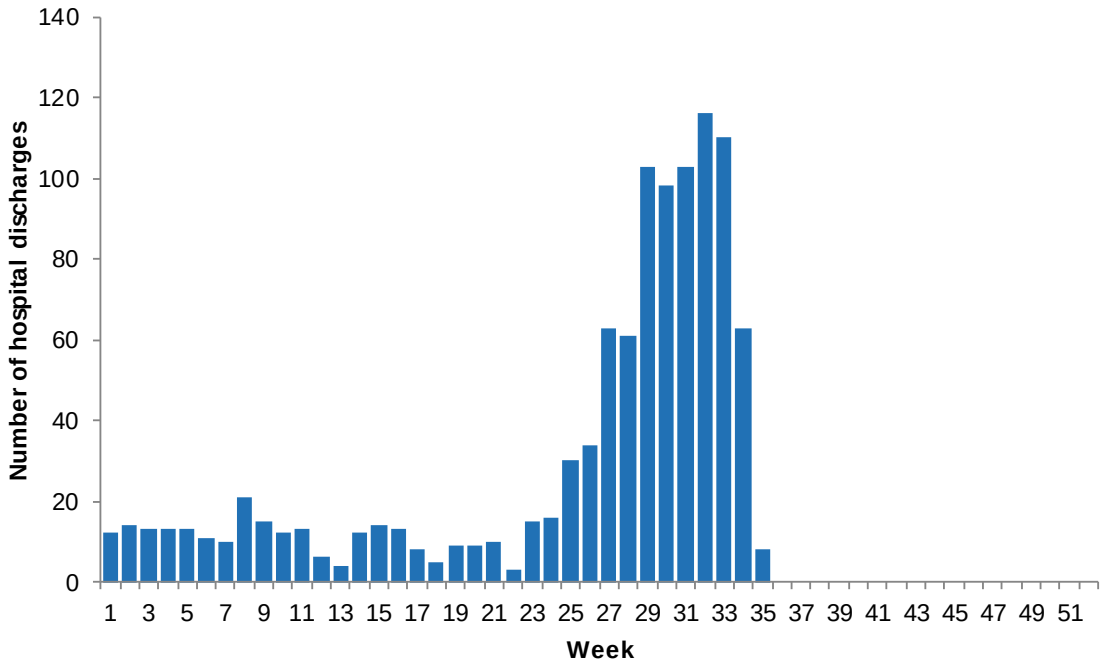


*Data from 1 Jan to 7 Sep only.

Source: Ministry of Health, NMDS (Hospital Events)

Figure 15 shows influenza hospitalisations by week discharged. The highest number of hospitalisations (392) occurred in August (weeks 31–34).

Figure 15. Influenza hospital discharges by week, 2018*

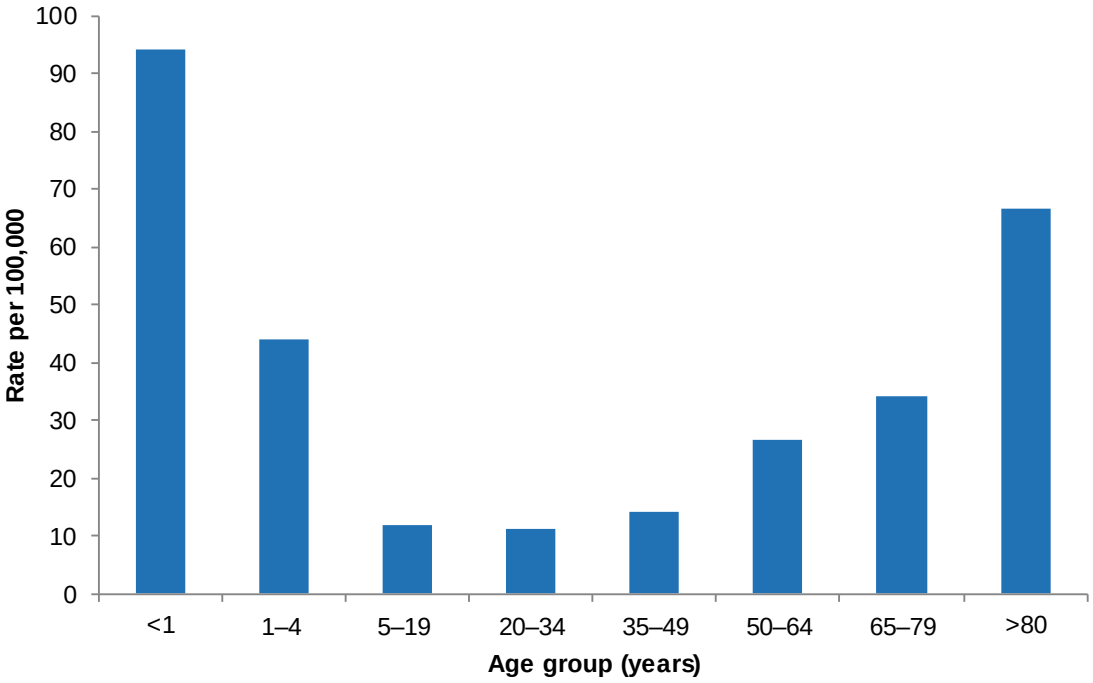


*Data from 1 Jan to 7 Sep only.

Source: Ministry of Health, NMDS (Hospital Events)

From 1 January to 7 September 2018, the highest influenza hospitalisation rates were recorded among those aged <1 year (94.1 per 100,000) followed by adults ≥80 years (66.8 per 100,000) (Figure 16).

Figure 16. Influenza hospital discharge rates by age group, 2018*

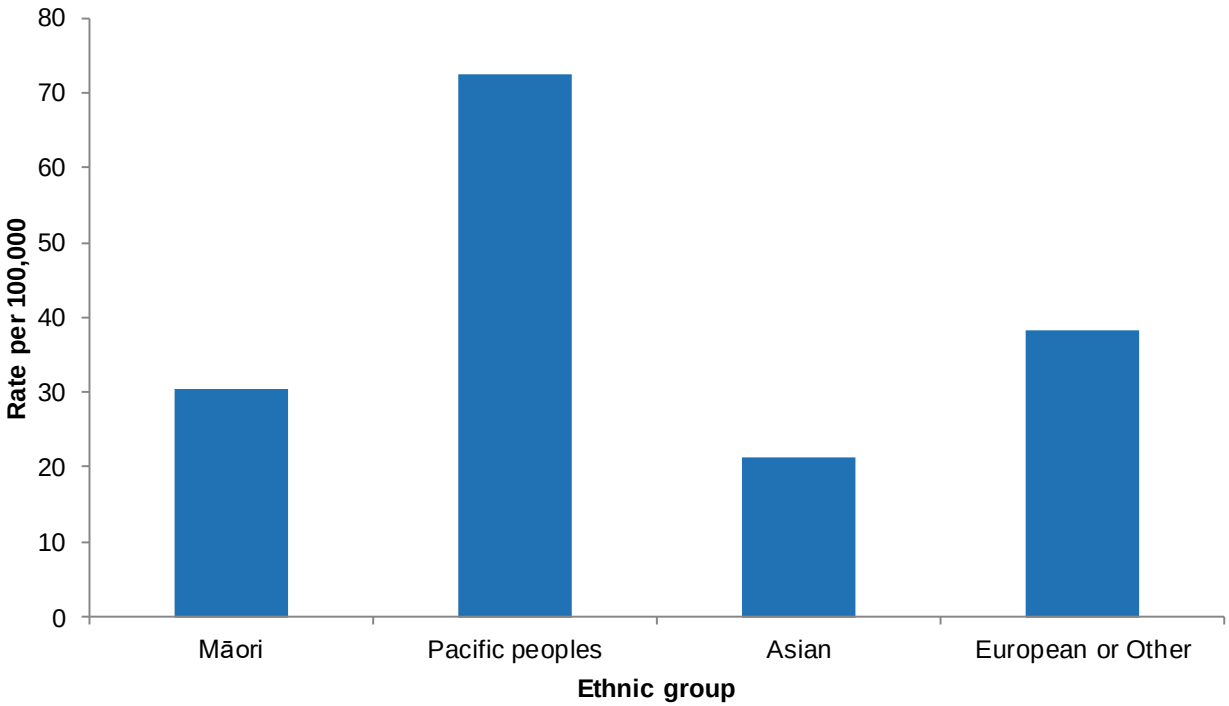


*Data from 1 Jan to 7 Sep only.

Source: Ministry of Health, NMDS (Hospital Events)

The ethnic distribution of influenza hospitalisations in 2018 is shown in Figure 17. Pacific peoples had the highest hospitalisation rate (72.4 per 100,000, 216 hospitalisations) followed by European or Other (38.3 per 100,000, 483 hospitalisations). Māori (30.4 per 100,000 populations, 216) and Asian (21.4 per 100,000 populations, 118 hospitalisations) ethnic groups had the lowest rate of hospitalisations.

Figure 17. Hospital discharge rates by prioritised ethnic group, 2018*



*Data from 1 Jan to 7 Sep only.

Source: Ministry of Health, NMDS (Hospital Events)

NEW ZEALAND STRAIN CHARACTERISATIONS

CIRCULATING STRAINS IN 2018

A total of 3433 influenza viruses were detected and reported through any surveillance system in 2018, with influenza A representing 90.4% (3103/3433) and influenza B 9.6% (330/3433) of all influenza viruses (Table 7). Among A sub-typed, 95.4% (1816/1903) were A(H1N1)pdm09 virus and 98.2% (380/387) were A(H3N2) virus. Among B lineage-typed, 96.1% (74/77) were of B/Yamagata lineage and 3.9% (3/77) B/Victoria lineage viruses.

Table 7. Influenza virus identifications by type and sub-type and lineage-typed, 2018

Viruses	All viruses (%)	Sub-typed and lineage-typed (%)
Influenza A	**3103 (90.4)**	**2290**
Influenza A (not sub-typed)	813 (23.7)	
Influenza A(H1N1)pdm09	**1903 (55.4)**	**1903**
A(H1N1)pdm09 by PCR	1816 (52.9)	1816 (95.4)
A/Michigan/45/2015 (H1N1)-like	87 (2.5)	87 (4.6)
Influenza A(H3N2)	**387 (11.3)**	**387**
A(H3N2) by PCR	380 (11.1)	380 (98.2)
A/Singapore/INFIMH-16-0019/2016 (H3N2)-like	4 (0.1)	4 (1.0)
A/Hong Kong/4801/201 (H3N2)-like	3 (0.1)	3 (0.8)
Influenza B	**330 (9.6)**	**77**
Influenza B (not lineage-typed)	253 (7.4)	
B/Yamagata lineage	**74 (2.2)**	**74**
B/Phuket/3073/2013-like	44 (1.3)	44 (59.5)
B/Yamagata lineage by PCR	30 (0.9)	30 (40.5)
B/Victoria lineage	**3 (0.1)**	**3**
B/Brisbane/60/2008-like	2 (0.1)	2 (66.7)
B/Victoria lineage by PCR	1 (0.0)	1 (33.3)
Total	**3433 (100)**	**2367**

Figure 18 shows the influenza virus identifications by type and sub-type for each week throughout 2018. A(H1N1) was the predominant type throughout the season.

Figure 18. Total influenza viruses by type and week specimen taken, 2018

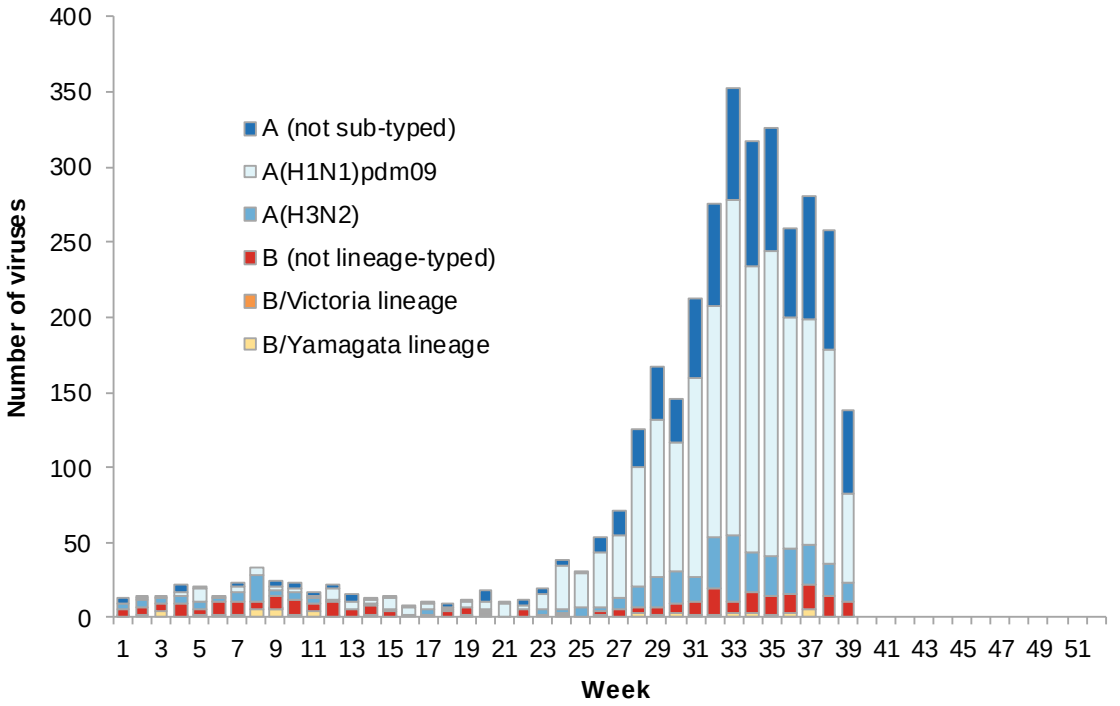
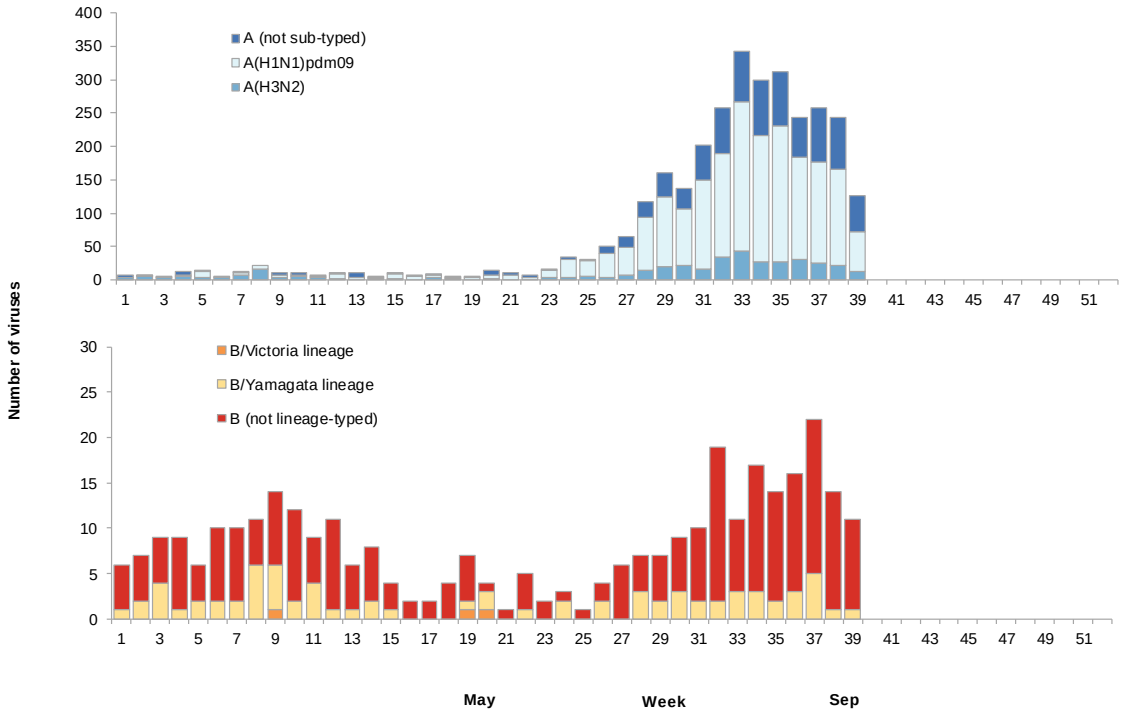


Figure 19 shows the general pattern of influenza virus identifications. Influenza A and B viruses co-circulated throughout the season.

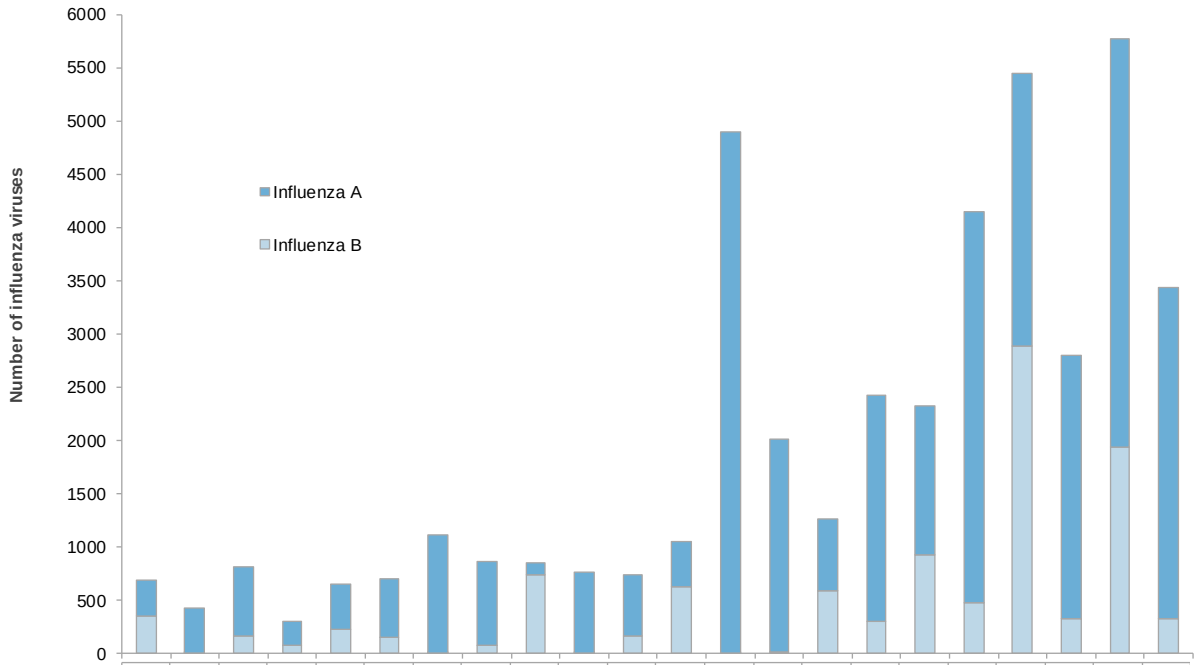
Figure 19. Total influenza A and B viruses by week specimen taken, 2018



PREDOMINANT STRAINS DURING 1997–2018

Figure 20 shows the number and percentage of typed influenza viruses from 1997 to 2018. Influenza A is the most frequent predominant influenza type. Of 22 influenza seasons during 1997–2018, influenza A predominated in 18 seasons whereas influenza B only predominated in three seasons (2005, 2008 and 2015). There was one season (1997) with equal proportion of influenza A and B circulation.

Figure 20. Influenza viruses by type, 1997–2018

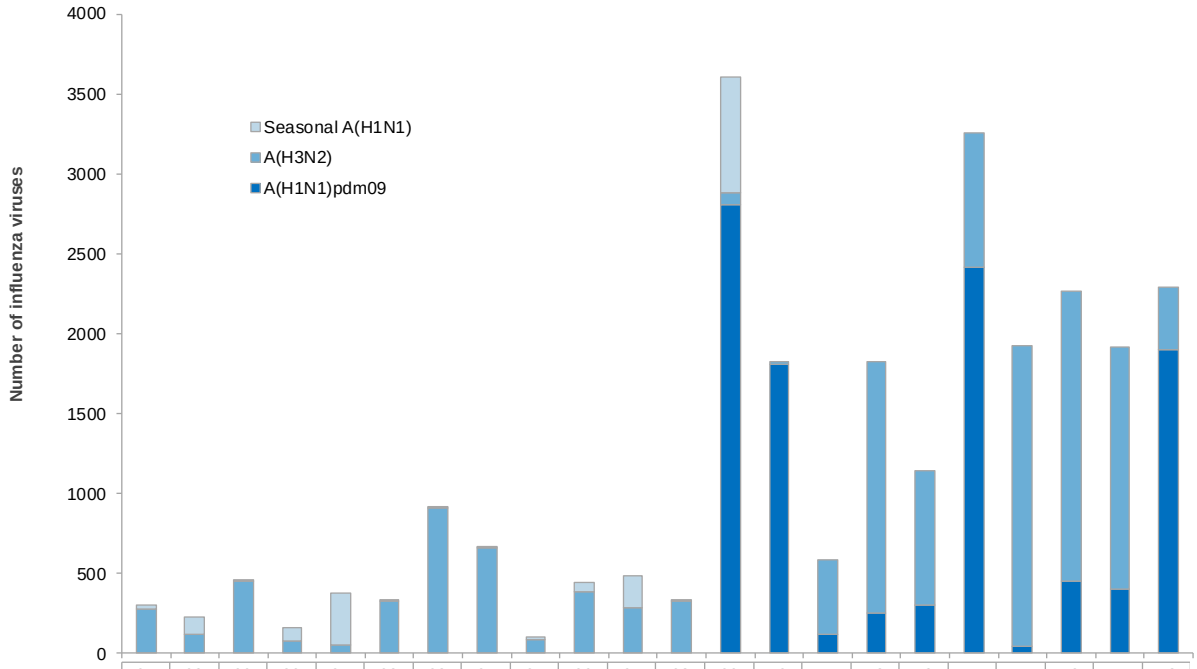


	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18
Influenza A (%)	50	100	80	76	65	78	100	91	13	99	78	40	100	100	53	87	60	89	47	88	67	90
Influenza B (%)	50	0	20	24	35	22	0	9	87	1	22	60	0	0	47	13	40	11	53	12	33	10

Figure 21 shows the number and percentage of all sub-typed influenza A viruses from 1997 to 2018 (excluding influenza A not sub-typed). Overall, the patterns of the predominant influenza A subtypes among all sub-typed A viruses during 1997–2018 are described below:

- Influenza A(H3N2) strain predominated for 16 seasons (1997–1999, 2002–2008, 2011–2013, 2015–2017).
- Influenza A(H1N1)pdm09 strain has become the predominant strain for three seasons in 2009, 2010, 2014 and 2018.
- Influenza A(H1N1) strain predominated in two seasons (2000 and 2001) with associated relatively low hospitalisations (228 in 2000 and 379 in 2001), this strain has not been detected in New Zealand since 2010.

Figure 21. Influenza A viruses by subtypes 1997–2018

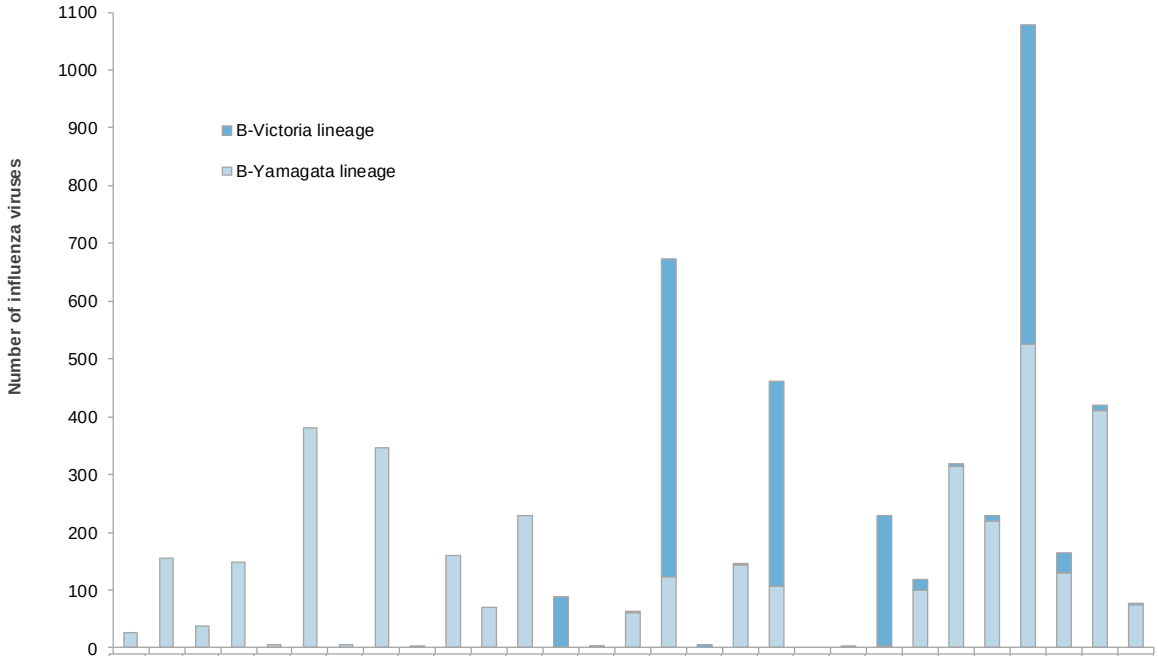


	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18
Seasonal A(H1N1)	8	48	0	52	87	1	0	0	18	13	42	2	20	0	0	0	0	0	0	0	0	0
A(H3N2)	92	52	100	48	13	99	100	100	82	87	58	98	2	1	80	86	74	26	98	80	79	17
A(H1N1)pdm09	0	0	0	0	0	0	0	0	0	0	0	0	78	99	20	14	26	74	2	20	21	83

Figure 22 shows the number and percentage of all B viruses from 1990 to 2018 (excluding influenza B not lineage-typed). Overall, the patterns of the predominant influenza B among all lineage-typed B viruses during 1990–2018 are described below:

- Influenza B/Yamagata lineage was the only lineage circulating in New Zealand during 1990–2001. Relatively high number of influenza B viruses were recorded in 1995 and 1997.
- Since the introduction of the B/Victoria lineage viruses into New Zealand in 2002, this lineage has co-circulated with B/Yamagata lineage viruses. During 2002–2011, B/Victoria lineage viruses predominated over the B/Yamagata lineage viruses in every three years in New Zealand (2002, 2005, 2008 and 2011). In 2005, the disease burden was high in children aged 5–19 years with associated deaths in 3 children.
- B/Yamagata lineage viruses was the predominant lineage over B/Victoria lineage virus during 2012–2014, 2016, 2017 and 2018.
- In 2015, there were almost equal proportions of B/Yamagata and B/Victoria lineage viruses.

Figure 22. Influenza B viruses by lineages, 1990–2018



	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18
B/Victoria lineage (%)	0	0	0	0	0	0	0	0	0	0	0	0	99	33	2	82	60	1	77	0	100	98	16	2	4	51	21	2	4
B/Yamagata lineage (%)	100	100	100	100	100	100	100	100	100	100	100	100	1	67	98	18	40	99	23	0	0	2	84	98	96	49	79	98	96

INFLUENZA A(H1N1)PDM09

Representative influenza A(H1N1)pdm09 isolates were antigenically typed at the WHO National Influenza Centre at ESR using rabbit antisera supplied by the WHO Collaborating Centre (WHOCC) in Melbourne. Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 31 August 2018, a total of 85 influenza A(H1N1)pdm09 isolates were antigenically typed using antisera A/Michigan/45/2015/A(H1N1)pdm09 at ESR. Of them, 84 (98.8%, 84/85) were antigenically related to A/Michigan/45/2015/A(H1N1)pdm09 and 1 (1.2%, 1/85) had reduced reactivity against A/Michigan/45/2015/A(H1N1)pdm09. Genetically, the NZ influenza A(H1N1)pdm09 viruses in 2018 fell into genetic subclade 6B.1 (CDC designations, Figure 23).

SEASONAL INFLUENZA A(H3N2)

Representative seasonal influenza A(H3N2) isolates were antigenically typed at the WHO National Influenza Centre at ESR using HAI typing kit supplied by the WHO Collaborating Centre (WHOCC) in Melbourne. Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 31 August 2018, a total of six influenza A(H3N2) isolates were antigenically typed at ESR using antisera against A/Singapore/INFIMH-16-0019/2016. Three (50%, 3/6) were antigenically related to the reference strain A/Singapore/INFIMH-16-0019/2016, three (50%, 3/3) had reduced reactivity against the reference vaccine strain. Genetically, the NZ influenza A(H3N2) viruses in 2018 fell into subclade 3C.2a1b and 3C.2a2 (CDC designations, Figure 24).

Figure 23..Phylogenetic relationships among influenza A(H1N) haemagglutinin genes

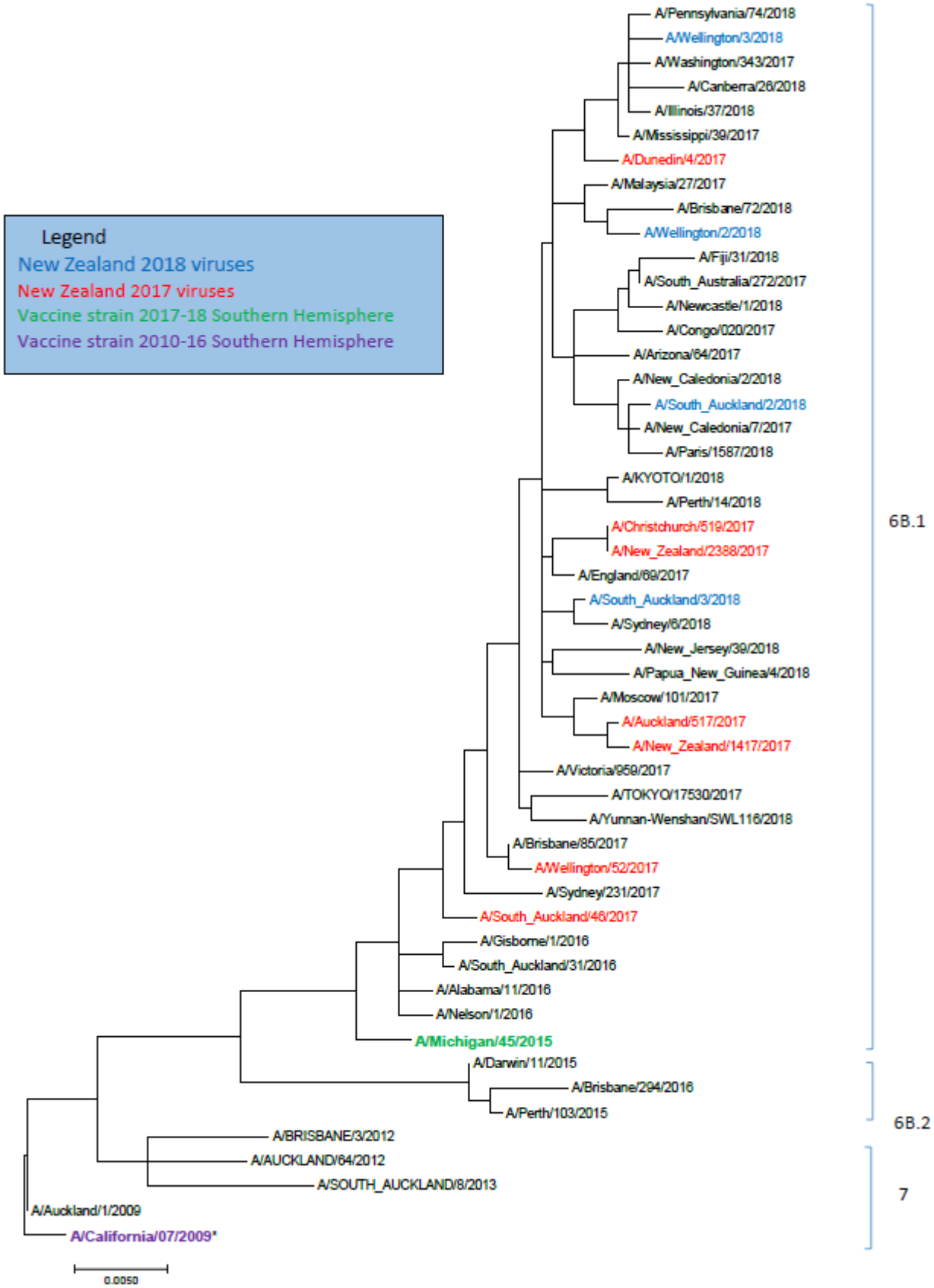


Figure 24..Phylogenetic relationships among influenza A(H3N2) haemagglutinin genes

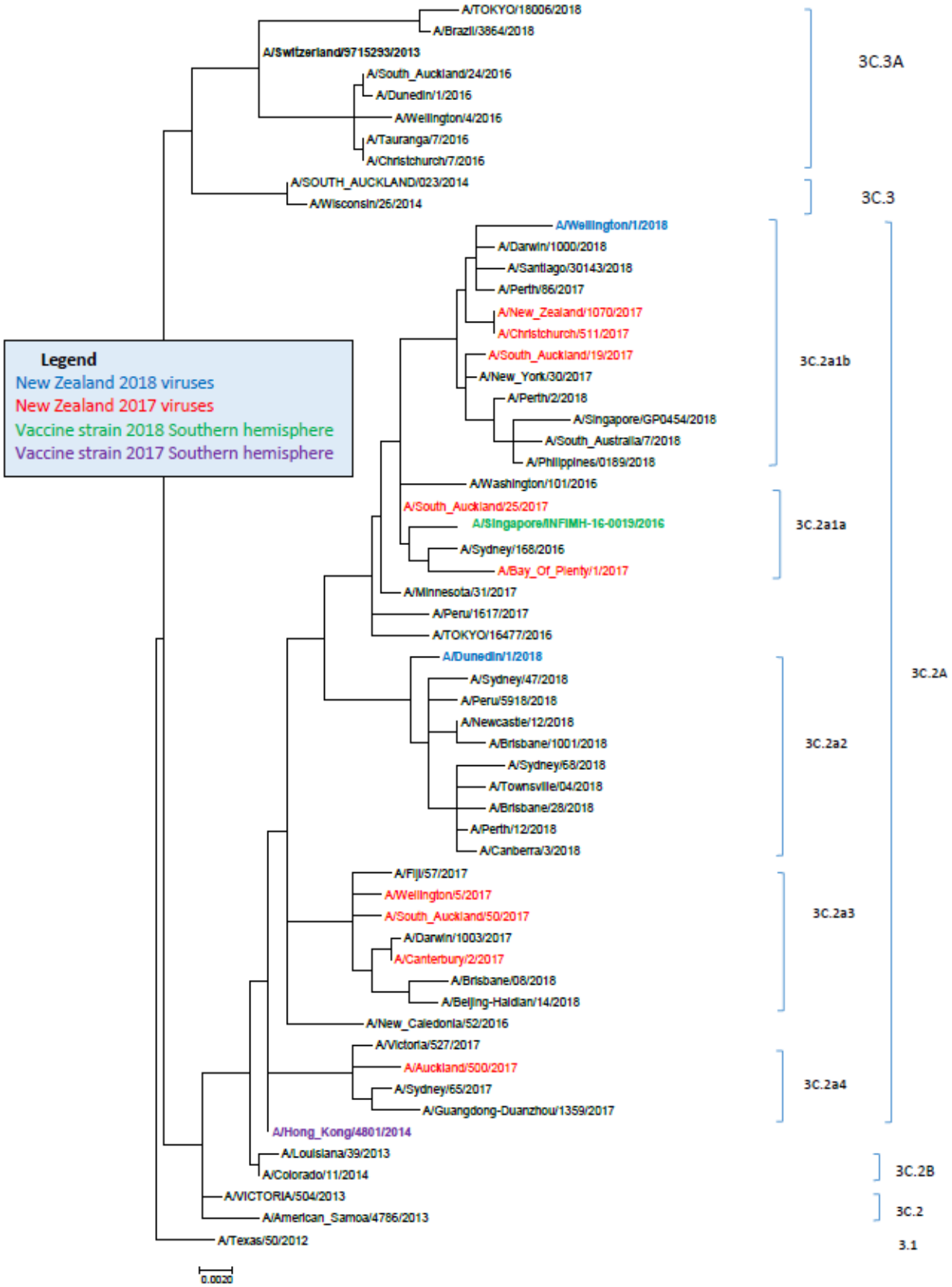
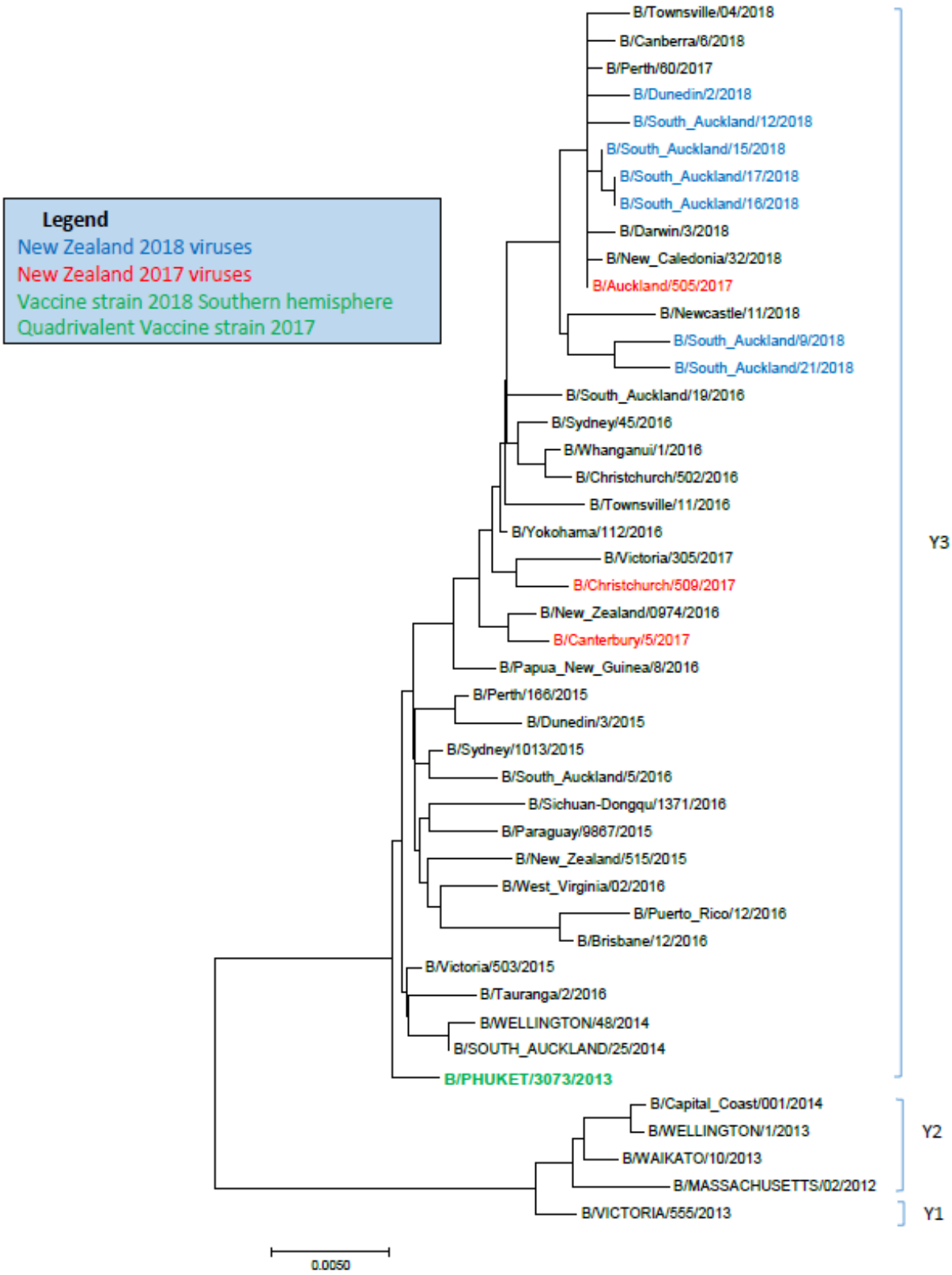


Figure 25. Phylogenetic relationships among influenza B (Yamagata) haemagglutinin genes



INFLUENZA B

Representative influenza B/Yamagata lineage isolates and B/Victoria lineage isolates were antigenically typed at the WHO National Influenza Centre at ESR using HAI typing kit supplied by the WHO Collaborating Centre (WHOCC) in Melbourne. Some of these isolates were also sent to WHOCC-Melbourne and CDC-Atlanta.

During 1 January to 31 August 2018, a total of 46 B/Yamagata lineages isolates were antigenically typed at ESR using antisera against B/Phuket/3073/2013-like virus. Of them, 46 (100%, 46/46) were antigenically related to the reference strain B/Phuket/3073/2013. Genetically, the NZ influenza B/Yamagata lineage viruses in 2018 fell into genetic clade Y3 (CDC designations, Figure 25).

In addition, a total of three B/Victoria lineage isolates were antigenically typed using antisera against B/Brisbane/60/2008-like virus. Of them, two (66.7%, 2/3) were antigenically related to the reference strain B/Brisbane/60/2008, and one (33.3%, 1/3) had reduced reactivity against the reference strain B/Brisbane/60/2008.

OSELTAMIVIR RESISTANCE

The WHO National Influenza Centre at ESR employed a phenotypic method (fluorometric neuraminidase inhibition assay) for the surveillance of anti-viral drug resistance in influenza viruses. In addition, NIC at ESR employed a molecular method (PCR and sequencing) to monitor the H275Y mutation (histidine-to-tyrosine mutation at the codon of 275 in N1 numbering) which is known to confer resistance to oseltamivir.

In 2018, fluorometric neuraminidase inhibition assay was used to test a total of 128 influenza viruses against oseltamivir and zanamivir. The preliminary results showed that all except one were sensitive to both oseltamivir and zanamivir (Table 8 and Table 9). One influenza B virus with 6-7 fold reduced inhibition against oseltamivir was isolated from a 7-year boy with unknown history of travel or antiviral medication.

Table 8. Antiviral susceptibility to oseltamivir for influenza viruses, 2014–2018^

Influenza	NA inhibition to Oseltamivir*	Fold change in IC50 of test viruses (No. of viruses)**				
		2014	2015	2016	2017	2018
A(H1N1)pdm09	Normal	0-9 (665)	0-2 (12)	0-2 (48)	0-2 (103)	0-3 (75)
	Reduced	35 (1)	-	-	-	-
	Highly reduced	356 (1)	-	-	-	-
A(H3N2)	Normal	0-8 (164)	0-5 (110)	0-2 (93)	0-2 (254)	0-2 (6)
	Reduced	-	-	-	-	-
	Highly reduced	-	-	-	-	-
Influenza B	Normal	0-4 (167)	0-5 (730)	0-2 (30)	0-2 (548)	0-2 (46)
	Reduced	-	-	-	-	6-7 (1)
	Highly reduced	-	-	-	-	-

^ Jan-Aug 2018

*Neuraminidase inhibition was defined as:

Normal inhibition = IC_{50} values which are within or close to the median IC_{50} of the type/subtype matched viruses as detailed in the table above.

Reduced inhibition = IC_{50} values which are 10 to 100 fold above the median value of viruses with normal inhibition (5 to 50 fold for influenza B viruses)

Highly reduced inhibition = IC_{50} values which are greater than 100 fold above the median value of viruses with normal inhibition (above 50 fold for influenza B viruses)

**Fold change determined by dividing IC50 of test viruses by median IC50 for virus type/subtype

Table 9. Antiviral susceptibility to zanamivir for influenza viruses, 2014–2018^

Influenza	NA inhibition to Zanamivir*	Fold change in IC50 of test viruses (No. of viruses)**				
		2014	2015	2016	2017	2018
A(H1N1)pdm09	Normal	0-6 (671)	0-2 (12)	0-3 (48)	0-3 (125)	0-1 (75)
	Reduced	-	-	-	-	-
	Highly reduced	-	-	-	-	-
A(H3N2)	Normal	0-7 (157)	0-4 (110)	0-3 (93)	0-3 (284)	0-1 (6)
	Reduced	-	-	-	-	-
	Highly reduced	-	-	-	-	-
Influenza B	Normal	0-5 (168)	0-4 (735)	0-2 (30)	0-2 (641)	0-2 (47)
	Reduced	-	-	-	-	-
	Highly reduced	-	-	-	-	-

^ Jan-Aug 2018

*Neuraminidase inhibition was defined as:

Normal inhibition = IC50 values which are within or close to the median IC50 of the type/subtype matched viruses as detailed in the table above.

Reduced inhibition = IC50 values which are 10 to 100 fold above the median value of viruses with normal inhibition (5 to 50 fold for influenza B viruses)

Highly reduced inhibition = IC50 values which are greater than 100 fold above the median value of viruses with normal inhibition (above 50 fold for influenza B viruses)

**Fold change determined by dividing IC50 of test viruses by median IC50 for virus type/subtype

INFLUENZA VACCINE EFFECTIVENESS

In New Zealand seasonal trivalent influenza vaccine is offered annually free of charge to all adults aged 65 years and over, pregnant women and all those over six months of age with chronic medical conditions that are likely to increase the severity of the infection. Since 2013, free influenza vaccines have been offered to children (6-months to 4-years) who have been hospitalised or have a history of significant respiratory illness. Influenza vaccines are also available on the private market for all others over six months of age. The influenza season usually occurs between May and September.

Using the case test-negative design to estimate propensity-adjusted VE, we estimated the effectiveness of seasonal quadrivalent inactivated influenza vaccine in preventing laboratory-confirmed influenza in patients hospitalised with severe acute respiratory infections (SARI) and in patients presenting to general practice with an influenza-like illness (ILI) during the influenza season. The influenza season was defined as starting when there were two consecutive weeks with two or more cases; The data is contributed to I-GIVE project for the WHO vaccine strain selection meeting in September for southern hemisphere countries.

Most ILI and SARI patients with laboratory-confirmed influenza are included except those with incomplete data for vaccination status, infants under 6 months of age, children under 9 years who were only given one dose of vaccine, those vaccinated less than 14 days before admission or presentation. For patients with multiple episodes, the first influenza virus-positive episode was used for the analysis or the first illness episode if there was no influenza virus-positive episode.

The proportion vaccinated did not change throughout the season. For influenza-confirmed SARI cases, after adjustment for age, week of admission and any underlying health condition, the estimated vaccine effectiveness (VE) was 35% (95% CI: 12 to 52). For influenza-confirmed ILI cases, after adjustment for age, week of presentation and any underlying health condition, the estimated VE was 38% (95% CI: 1 to 61) (Table 10).

Table 10. Estimated influenza vaccine effectiveness, by participant age group and by influenza virus type and subtype in New Zealand, 2018 influenza season

Age & Virus	Influenza Positive		Influenza Negative		Crude			Age and week adjusted*		
	Vaccinated-Yes	Vaccinated-Not	Vaccinated-Yes	Vaccinated-Not	VE%	LCL	UCL	VE%	LCL	UCL
ILI										
Overall	80	352	215	631	33.3	10.3	50.6	34.8	11.6	51.9
<18y	8	138	24	216	47.8	-24.5	80.3	66.4	18.0	86.3
18-64y	59	204	137	396	16.4	-19.9	42.1	17.7	-19.4	43.3
65+y	13	10	54	19	54.3	-38.4	84.4	48.5	-70.7	84.5
H1	49	265	246	718	46.0	23.8	62.3	45.4	22.6	61.5
<18y	5	110	27	244	58.9	-12.4	87.9	73.7	25.1	90.8
18-64y	40	152	156	448	24.4	-13.4	50.4	23.5	-15.7	49.4
65+y	4	3	63	26	NA	NA	NA	NA	NA	NA
					0.0	0.0	0.0	0.0	0.0	0.0
H3	17	40	278	943	NA	NA	NA	NA	NA	NA
<18y	1	13	31	341	15.4	-500.5	98.1	-6.0	-947.3	89.3
18-64y	8	26	188	574	6.1	-118.3	63.9	21.4	-82.3	66.1
65+y	8	1	59	28	NA	NA	NA	NA	NA	NA
B	0	2	295	981	NA	NA	NA	NA	NA	NA
<18y	0	1	32	353	NA	NA	NA	NA	NA	NA
18-64y	0	1	196	599	NA	NA	NA	NA	NA	NA
65+y	0	0	67	29	NA	NA	NA	NA	NA	NA
SARI										
Overall	35	97	179	345	30.5	-8.3	56.0	37.6	1.4	60.5
<18y	2	45	29	221	66.1	-42.6	96.2	78.2	-1.6	95.3
18-64y	14	41	56	85	48.2	-8.2	76.1	56.3	3.0	80.3
65+y	19	11	94	38	30.2	-79.1	71.6	43.7	-57.4	79.9
H1	14	56	200	386	51.8	9.4	75.8	60.8	25.1	79.5
<18y	1	36	30	230	NA	NA	NA	NA	NA	NA
18-64y	6	18	64	108	NA	NA	NA	NA	NA	NA
65+y	7	2	106	47	NA	NA	NA	NA	NA	NA
H3	10	13	204	429	NA	NA	NA	NA	NA	NA
<18y	0	1	31	265	NA	NA	NA	NA	NA	NA
18-64y	3	8	67	118	NA	NA	NA	NA	NA	NA
65+y	7	4	106	45	NA	NA	NA	NA	NA	NA
B	2	6	212	436	NA	NA	NA	NA	NA	NA
<18y	0	3	31	263	NA	NA	NA	NA	NA	NA
18-64y	1	2	69	124	NA	NA	NA	NA	NA	NA
65+y	1	1	112	48	NA	NA	NA	NA	NA	NA

*Adjusted for week in season, age group

N/A: not applicable as numbers to too low to reach any significance; CI: Confidence interval; ILI: Influenza-like illness; SARI: severe acute respiratory infections. Highlighted cells indicate low numbers

RECENT STRAIN CHARACTERISATION FOR SOUTHERN HEMISPHERE VIRUSES AND LIKELY VACCINE CANDIDATES

INFLUENZA A(H1N1)PDM09

The influenza A(H1N1)pdm09 virus was first detected in April 2009 in the United States and was responsible for outbreaks in Mexico in March and April 2009. Outbreaks subsequently occurred in all regions of the world and, by July 2009, influenza A(H1N1)pdm09 was the predominant influenza virus circulating in many countries in the Americas, Asia, Europe and Oceania.

During the 2018 influenza season, 662 A(H1N1)pdm09 viruses were received at the Melbourne WHOCC from 14 countries with most coming from Australia and New Zealand. The vast majority of A(H1N1)pdm09 viruses had HA gene sequences that belonged to phylogenetic subclade 6B.1 and encoded the additional HA1 amino acid substitutions S74R, S164T and I295V. There is increasing genetic diversification of the HA genes of 6B.1 viruses with several subgroups emerging (CDC designations, Figure 27 in Appendix 3).

The antigenic characteristics of A(H1N1)pdm09 viruses were assessed with post-infection ferret antisera in haemagglutination inhibition (HAI) assay. Most of the viruses (99%, 499/504) tested reacted well with ferret antisera raised against egg and cell-propagated A/Michigan/45/2015 (the H1 component of the 2018 southern hemisphere and 2018/2019 northern hemisphere vaccines) (Figure 26, Table 12 in Appendix 3).

Human serology studies used serum panels from children, adults and elderly adults who had received trivalent or quadrivalent inactivated vaccines, either of the composition recommended for the northern hemisphere 2017-2018 season (A/Michigan/45/2015 (H1N1) pdm09-like, A/Hong Kong/4801/2014 (H3N2)-like and B/Brisbane/60/2008-like viruses in trivalent vaccines, with B/Phuket/3073/2013-like viruses included in quadrivalent vaccines) or that recommended for the southern hemisphere 2018 season (A/Michigan/45/2015 (H1N1) pdm09-like, A/Singapore/INFIMH-16-0019/2016 (H3N2)like and B/Phuket/3073/2013-like viruses in trivalent vaccines, with B/Brisbane/60/2008-like viruses included in quadrivalent vaccines).

Haemagglutination inhibition Geometric mean titres (GMTs) of post-vaccination antibodies against the majority of recent representative A(H1N1)pdm09 viruses were not reduced significantly, although GMTs against some recent viruses were somewhat reduced when compared to GMTs with the vaccine virus. (*Abridged from the Weekly Epidemiological Record (WER), 2018 93(42):553-576 and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

In summary, influenza A(H1N1)pdm09 viruses were predominant in many countries including New Zealand and Australia. The majority of influenza A(H1N1)pdm09 viruses were antigenically indistinguishable from the current vaccine virus A/Michigan/45/2015. Based on all of the available data, the WHO consultation recommended vaccines containing an A/Michigan/45/2015 (H1N1)pdm09-like strain. The AIVC accepted this recommendation.

SEASONAL INFLUENZA A(H3N2)

Influenza A(H3N2) has frequently been associated with severe disease and excess mortality in high-risk groups. This subtype has also shown the greatest tendency for antigenic drift as illustrated by the frequency of vaccine formulation changes recommended by the WHO and AIVC (Table 13).

A(H3N2) viruses have become increasingly difficult to test with the haemagglutination inhibition assay. Some viruses have low or no HA titre with guinea pig RBC even though there is ample virus present (as detected by other methods). Particular mutations or polymorphisms in the NA of recent H3N2 viruses (especially the D151G) appear to allow some level of binding to red blood cells (RBC), thus interfering with the inhibition of viruses between HA and RBC using post-infection ferret sera. To overcome this problem a number of WHOCCs have been performing their HI assays in the presence of 20nM oseltamivir carboxylate in order to prevent this NA binding. This appears to improve the discrimination between antigenically drifted vs not-drifted viruses. However, about 35% of these viruses have a drop in HA titre to a point whereby these viruses cannot be assayed by HI anymore. Alternatively, virus neutralization assays such as the microneutralisation or plaque reduction assays or focus reduction assays (FRA) can be used where the NA binding is not relevant.

During the 2018 influenza season, 283 A(H3N2) viruses were received at the Melbourne WHOCC from 12 countries with most coming from Australia and New Zealand. The majority of A(H3N2) viruses belonged to the phylogenetic clade 3C.2a. There has continued to be considerable genetic diversification of the HA and NA genes of viruses within this clade and the 3C.2a viruses could be further subdivided into viruses falling into the 3C.2a1 or 3C.2a2 sub-clades which also had further sub-groups. Viruses in subclade 3C.2a1b or 3C.2a2 were most common with subclade 3C.2a2 predominating. Some heterogeneity within the subclade 3C.2a2 and significant heterogeneity within the subclade 3C.2a1b were observed (Figure 28 in Appendix 4).

The antigenic characterization of clade 3C.2a viruses were technically difficult because a large proportion of viruses did not agglutinate red blood cells, preventing HAI analysis. Virus neutralization assays have become the preferred method for this. Most recent A(H3N2) viruses were well inhibited by ferret antisera raised against cell culture-propagated reference viruses such as A/Singapore/ INFIMH-16-0019/2016 (the H3 component of vaccine strain for the southern hemisphere). In contrast, ferret antisera raised against egg-propagated A/Singapore/INFIMH-160019/2016-like viruses inhibited a smaller proportion of recently circulating viruses. Ferret antiserum raised against egg-propagated A/Switzerland/8060/2017 inhibited the majority of viruses tested from the predominating subclade 3C.2a2 (Table 14 in Appendix 4 and also WER's Table 1 in Appendix 6).

Human serology studies, using the serum panels described above, showed that HAI GMTs of post-vaccination antibodies against many cell culture-propagated and some egg-propagated A(H3N2) viruses were reduced significantly compared to GMTs against the egg-propagated vaccine virus A/Singapore/INFIMH-160019/2016. When compared to results for cell culture-propagated A/Singapore/INFIMH-16-0019/2016, cell culture-propagated viruses did not show significant reductions in HAI GMTs. In virus neutralisation tests, using the same serum panels, all cell culture-propagated A(H3N2) viruses tested showed significant reductions in GMTs when compared to

GMTs against egg-propagated A/Singapore/INFIMH-16-0019/2016. (*Abridged from the Weekly Epidemiological Record, 2018 93(42): 553-576 and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

In summary, influenza A(H3N2) viruses were predominant and associated with outbreaks in several countries. The majority of A(H3N2) viruses fell into the phylogenetic clades 3C.2a and the subclade 3C.2a2. The majority of recent viruses were inhibited well by ferret antisera raised against cell culture-propagated A/Singapore/INFIMH16-0019/2016-like viruses. In contrast, ferret antisera raised against egg-propagated A/Singapore/INFIMH-160019/2016-like viruses inhibited a smaller proportion of recently circulating viruses. Interestingly, ferret antiserum raised against egg-propagated A/Switzerland/8060/2017 inhibited the majority of viruses tested from the predominating subclade 3C.2a2. Based on all available data, the WHO Consultative Group recommended the H3 component of the vaccines containing an A/Switzerland/8060/2017-like strain. AIVC accepted this recommendation.

INFLUENZA B

Two distinct lines of influenza B have co-circulated in many countries during recent years. This dates from the late 1980s when the B/Panama/45/90 variant of influenza B was first observed. This strain and its further variants of the Yamagata/16/88 lineage (most recently representative strain-B/Phuket/3073/2013) spread worldwide, whereas strains of the previous B/Victoria/2/87-like viruses continued to circulate in Asia and subsequently underwent independent evolution as an antigenically distinct lineage (most recent representative strain-B/Brisbane/60/2008). For reasons not wholly understood, these remained geographically restricted to Asia until 2001. In 2002 the B/Victoria/2/87 lineage viruses were the predominant viruses worldwide.

Both B/Yamagata-like strains (B/Phuket/3073/2013 is the 2018 southern hemisphere reference strain for trivalent and quadrivalent B/Yam component) and B/Victoria-like strains (B/Brisbane/60/2008 is the 2018 southern hemisphere reference strain for quadrivalent B/Vic component) continued to be isolated worldwide in 2018 with variable proportions in different regions. More B/Yamagata than B/Victoria lineage viruses circulated in New Zealand and Australia.

324 influenza B isolates (including 231 B/Yamagata and 93 B/Victoria viruses) were received in 2018 by the Melbourne WHOCC from 14 countries. Sequence analysis of the HA1 gene of recent isolates showed that recent isolates fell into one of the two major lineages of B viruses (B/Victoria/2/87 or B/Yamagata/16/88). B/Yamagata lineage fell into the B/Phuket/3073/2013-like virus, with the majority of viruses falling in clade Y3. (Figure 31 in Appendix 5). The B/Victoria lineage viruses mostly grouped in the B/Brisbane/60/2008 group (all clade V1A) (Figure 32 in Appendix 5). A steadily increasing proportion of double deletion viruses from many countries had a 2 amino acid deletion in HA (amino acids 162 and 163). In addition, triple deletion viruses with a 3 amino acid deletion in HA (amino acids 162-164) were also identified.

The antigenic characterization of B/Yamagata-lineage viruses showed indistinguishable antigenic profiles between circulating viruses and B/Phuket/3073/2013-like reference strain (Figure 30 in Appendix 5). The majority of recent viruses were well covered by ferret sera raised to either cell-propagated and to (a lesser extent) egg propagated B/Phuket/3073/2013-like viruses (Table 16 in Appendix 5). In addition, the antigenic characterization of B/Victoria-lineage viruses showed that about 58% of the viruses were well inhibited by ferret antisera raised against cell-propagated B/Brisbane/60/2008 virus, but less well inhibited by ferret antisera against egg-propagated B/Brisbane/60/2008**-**like virus. Overall, recent viruses without double/triple HA deletion were inhibited better by post-infection ferret antisera against egg-propagated B/Brisbane/60/2008**-**like virus better than those viruses with double/triple deletions. The great majority of viruses with HA deletions reacted well with ferret sera raised to cell-propagated B/Colorado/06/2017-like virus in HAI assays (Figure 29, Table 15 in Appendix 5).

Human serology studies were performed using the same serum panels described above. Geometric mean HAI titres of post-vaccination antibodies against most recent B/Yamagata lineage viruses were similar to, or somewhat reduced, compared to those against cell-propagated B/Phuket/3073/2013-like reference viruses. In addition, geometric mean HAI titres of post-vaccination antibodies against representative recent viruses of the B/Victoria lineage with 2 or 3 amino acid deletions in HA showed moderate reductions when compared to egg- or cell-propagated B/Brisbane/60/2008-like reference viruses. (*Abridged from the Weekly Epidemiological Record, 2018 93(42): 553-576 and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

In summary, influenza B viruses of the B/Victoria/2/87 and B/Yamagata/16/88 lineages co-circulated, with viruses of the B/Yamagata lineage predominating in many countries including New Zealand and Australia. The majority of recent B/Yamagata lineage viruses were antigenically and genetically closely related to B/Phuket/3073/2013-like virus. Influenza B viruses of the B/Victoria lineage were detected in low numbers but a substantial and increasing proportion of these viruses, containing a 2 amino acid deletion in the HA, were antigenically different from B/Brisbane/60/2008-like vaccine viruses but closely related to B/Colorado/06/2017-like viruses. Based on all available data, the WHO Consultative Group recommended the B/Phuket/3073/2013-like virus (B/Yamagata/16/88-lineage) and B/Colorado/06/2017-like virus (B/Victoria/2/87-lineage) as quadrivalent vaccine strains. The AIVC accepted this recommendation. In addition, AIVC recommended B/Phuket/3073/2013-like virus as the B component of the trivalent vaccines due to the predominance of the B/Yamagata/16/88-lineage circulating in New Zealand and Australia.

SUMMARY OF VACCINE COMPOSITION RECOMMENDATION

It is recommended that the influenza vaccine formulation for New Zealand for 2019 is:

The quadrivalent vaccines:

- A(H1N1) an A/Michigan/45/2015 (H1N1)pdm09-like virus
- A(H3N2) an A/Switzerland/8060/2017 (H3N2)-like virus
- B a B/Phuket/3073/2013-like virus (belonging to B/Yamagata lineage)
- B a B/Colorado/06/2017-like virus (belonging to B/Victoria lineage)

The trivalent vaccines:

- A(H1N1) an A/Michigan/45/2015 (H1N1)pdm09-like virus
- A(H3N2) an A/Switzerland/8060/2017 (H3N2)-like virus
- B a B/Phuket/3073/2013-like virus (belonging to B/Yamagata lineage)

EXPLANATION OF "LIKE" STRAINS SUITABLE FOR INCLUSION IN VACCINE

In the past, some strains of influenza recommended for inclusion in the vaccine formulation have been unsuitable vaccine candidates due to their poor growth potential with resulting low yields or poor serological responses in vaccinees. Under the "like" strain concession in the vaccine recommendation, an antigenically similar strain can be substituted which has the qualities that are lacking in the prototype strain.

The AIVC considered the information about international surveillance by WHO, recent data from Australia, New Zealand, South Africa and Argentina on influenza epidemiology and virus strain characterisation, and the recommendations of the WHO annual consultation on the composition of influenza vaccine for the southern hemisphere. The AIVC agreed to adopt the WHO recommendations. The influenza quadrivalent vaccine components for year 2019 season should contain the following:

- **A (H1N1)**: an A/Michigan/45/2015 (H1N1)**-**like strain, 15 µg HA per dose
- **A (H3N2)**: an A/Hong Kong/4801/2014 (H3N2)-like strain, 15 µg HA per dose
- **B**: a B/Phuket/3073/2013 - like virus, 15 µg HA per dose
- **B**: a B/Colorado/06/2017 - like virus, 15 µg HA per dose

WHO is now listing all recommended candidate viruses and potency testing reagents for development and production of vaccines for use in specific influenza seasons at the following website: http://www.who.int/influenza/vaccines/virus/candidates_reagents/home/en/

APPENDIX 1 - COMPOSITION OF THE AUSTRALIAN INFLUENZA VACCINE COMMITTEE 2018

AIVC MEMBERS 2018

The details of the Australian Influenza Vaccine Committee Members can be accessed from the website below:

https://www.tga.gov.au/committee/australian-influenza-vaccine-committee-aivc

APPENDIX 2 – ISOLATES RECEIVED FOR ANALYSIS AT THE AUSTRALIAN WHO COLLABORATING CENTRE

Table 11. Influenza Viruses Analysed at the Melbourne WHO CC

1 February – 19 September 2018

Country	A(H1N1) pdm09	A(H3N2)	A Un-subtyped	B Yam	B Vic	Total
Australia	403	139	51	117	5	**715**
Cambodia	30	1	0	15	2	**48**
Fiji	27	24	0	12	0	**63**
Indonesia	6	9	0	0	3	**18**
Macau SAR, China	8	1	0	2	0	**11**
New Caledonia	20	2	0	21	7	**50**
New Zealand	53	8	0	36	3	**100**
Papua New Guinea	6	0	0	0	2	**8**
Philippines	8	60	0	1	1	**70**
Singapore	18	14	0	7	9	**48**
Solomon Islands	0	0	4	0	0	**4**
South Africa	36	0	0	2	0	**38**
Sri Lanka	13	5	17	2	2	**39**
Thailand	12	14	0	6	0	**32**
Timor-Leste	22	6	0	10	59	**97**
Total	**662**	**283**	**72**	**231**	**93**	**1341**
%	49.37%	21.10%	5.37%	17.23%	6.94%	100%

APPENDIX 3 – INFLUENZA A(H1N1)PDM09

Figure 26. Antigenic cartographic representation of A(H1N1)pdm09 viruses

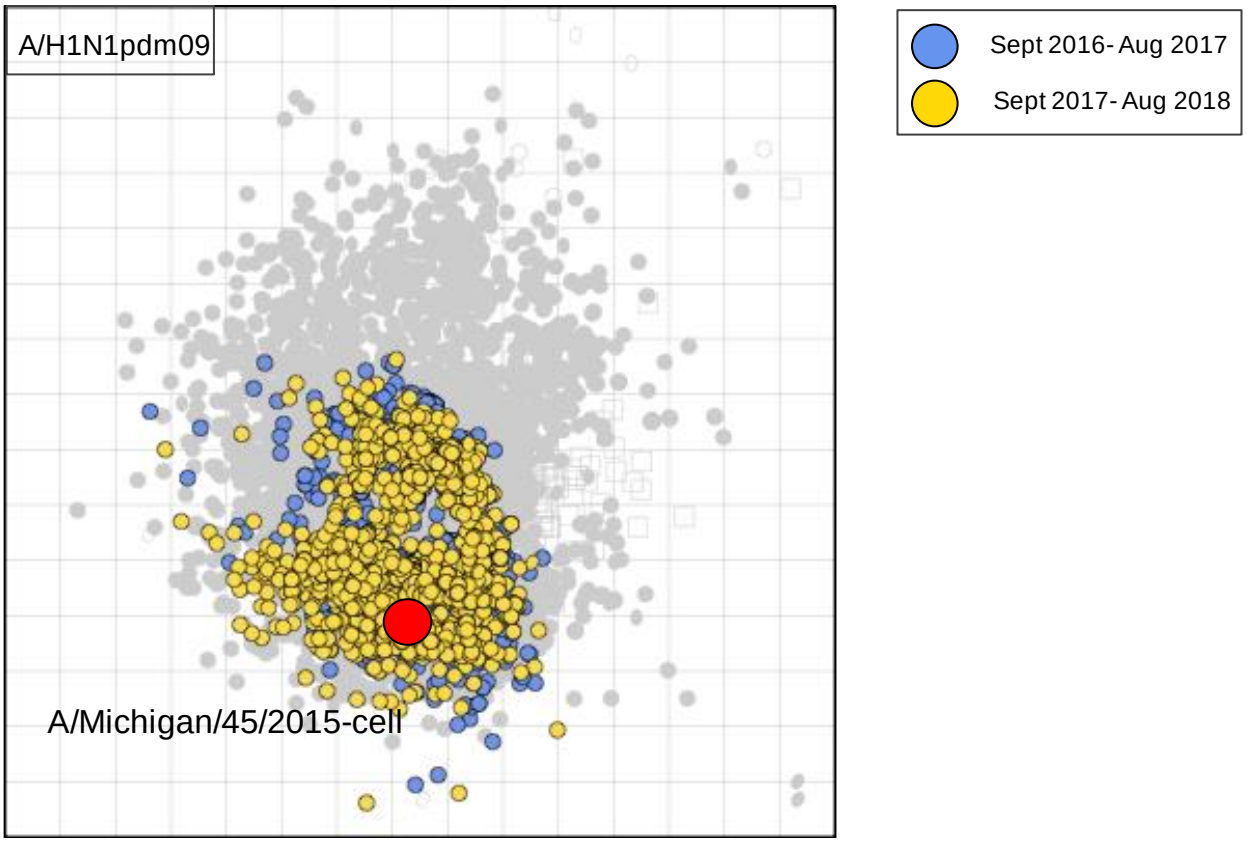


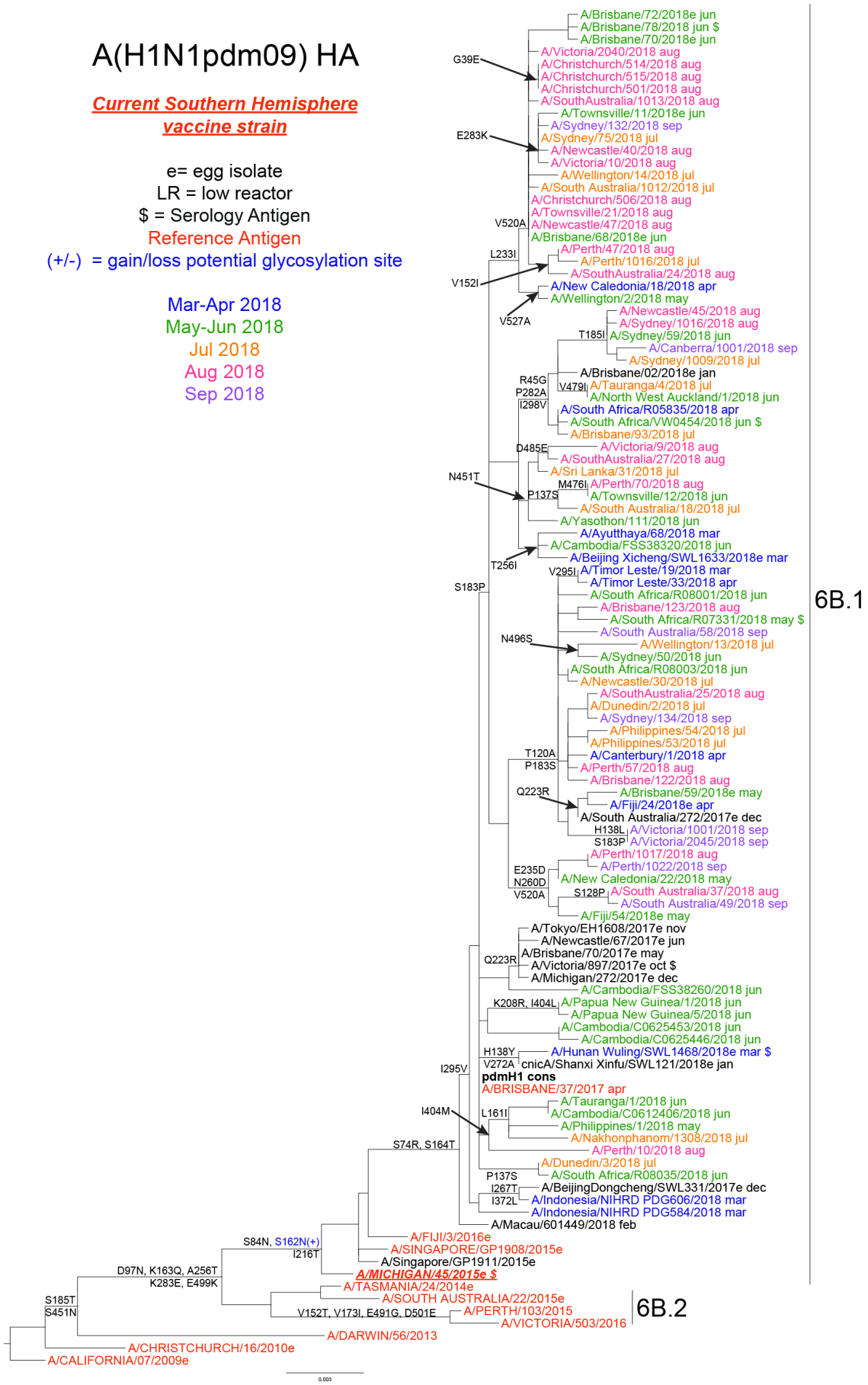
Table 12. (H1N1)pdm09 viruses (1)

			Haemagglutination Inhibition Assay - WHO Influenza Centre													
			Reference Antisera													
	Sequenced		A	B	C	D	E	F	G	H	I	J	K	L		
	September 15, 2017		F2257-13D	F2771-13D	F3647-13D	F3168-14D	F3421-21D	F3520-14D	F3809-14D	F3702-12D	F3641-13D	F3646-13D	F3492-14D	F3640-13D	Passage	Sample
			E4	E2	MDCK1	E3	E2	E4	M1/C2,M1	E3	E3	S1,M1	MX,M1	S1,M2	Details	Date
			CAL/7	CHCH/16	Dar/56	Tas/24	SA/22	Mich/45	Mich/45	Sing/GP1908	FIJI/3	FIJI/3	Pth/103	VIC/503		
	Reference Antigens	**Clade**		**4**	**7**	**6B**		**6B.1**					**6B.2**			
A	A/CALIFORNIA/7/2009		**2560**	2560	1280	2560	5120	1280	2560	5120	1280	5120	1280	2560	E6	
B	A/CHRISTCHURCH/16/2010	**4**	2560	**>10240**	1280	2560	5120	1280	2560	5120	1280	5120	640	2560	E3	
C	A/DARWIN/56/2013	**7**	80	<80	**160**	<80	<80	<80	<80	80	<80	80	<80	<80	MDCK3	
D	A/TASMANIA/24/2014	**6B**	2560	2560	640	**2560**	5120	1280	2560	5120	1280	5120	1280	2560	E3	
E	A/SOUTH AUSTRALIA/22/2015	**6B**	2560	2560	1280	2560	**5120**	1280	2560	2560	1280	2560	1280	2560	E3	
F	A/MICHIGAN/45/2015	**6B.1**	2560	2560	640	2560	5120	**1280**	2560	2560	1280	5120	1280	2560	E3, E4	
G	A/MICHIGAN/45/2015	**6B.1**	640	320	160	640	1280	320	**640**	640	320	1280	320	640	M1/C2,M2	
H	A/SINGAPORE/GP1908/2015	**6B.1**	1280	640	640	1280	2560	640	2560	**2560**	1280	2560	640	2560	E3	
I	A/FIJI/3/2016	**6B.1**	5120	5120	1280	5120	>10240	2560	5120	5120	**1280**	>10240	1280	5120	E3	
J	A/FIJI/3/2016	**6B.1**	1280	640	320	1280	2560	640	1280	2560	640	**2560**	640	1280	S1,M1	
K	A/PERTH/103/2015	**6B.2**	1280	1280	320	1280	2560	640	1280	2560	640	2560	**640**	1280	MX,M4	
L	A/VICTORIA/503/2016	**6B.2**	1280	1280	320	1280	2560	640	1280	2560	640	2560	640	**2560**	S1,M1	
	Test Antigens															
1	A/Victoria/717/2017		2560	5120	1280	5120	5120	2560	5120	5120	2560	>10240	1280	5120	SIAT1	2/09/2017
2	A/Sydney/1054/2017	**6B.1**	2560	1280	640	1280	5120	1280	2560	5120	1280	5120	1280	2560	SIAT1	7/08/2017
3	A/Sydney/1076/2017		1280	1280	640	1280	2560	1280	2560	2560	640	2560	640	2560	SIAT1	28/07/2017
4	A/Sydney/1077/2017	**6B.1**	2560	1280	640	1280	5120	1280	2560	2560	640	5120	1280	2560	SIAT1	3/08/2017
5	A/Sydney/1078/2017	**6B.1**	1280	1280	640	1280	2560	1280	2560	2560	640	5120	1280	2560	SIAT1	1/08/2017
6	A/Victoria/1013/2017		1280	1280	640	1280	5120	1280	2560	2560	1280	5120	640	2560	SIAT1	2/08/2017
7	A/Brisbane/1030/2017	**6B.1**	2560	2560	640	2560	5120	1280	5120	5120	1280	5120	1280	2560	SIAT1	4/08/2017
8	A/South Australia/1025/2017	**6B.1**	2560	1280	640	1280	5120	1280	2560	2560	1280	5120	640	2560	SIAT1	8/08/2017
9	A/South-Africa/R07191/17	**6B.1**	1280	1280	320	1280	2560	1280	2560	2560	640	5120	640	2560	MDCK1	22/07/2017
10	A/Victoria/2073/2017	**6B.1**	1280	1280	640	1280	2560	1280	2560	2560	640	5120	640	2560	SIAT1	5/08/2017
11	A/Brisbane/115/2017		640	640	320	1280	1280	1280	640	640	1280	1280	640	1280	MDCK2	26/07/2017
12	A/Victoria/638/2017		2560	1280	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	SIAT1	7/08/2017
13	A/Victoria/644/2017	**6B.1**	1280	1280	320	1280	2560	1280	1280	2560	640	5120	640	2560	SIAT1	8/08/2017
14	A/Victoria/808/2017		2560	1280	640	1280	5120	1280	2560	2560	1280	5120	1280	2560	SIAT1	17/08/2017
15	A/Sri Lanka/78/2017		1280	1280	640	1280	2560	1280	2560	2560	1280	5120	1280	2560	MDCK1	12/08/2017
16	A/Sri Lanka/82/2017	**6B.1**	2560	2560	640	1280	5120	1280	2560	2560	640	5120	1280	2560	MDCK1	14/08/2017
17	A/Perth/137/2017		1280	1280	320	1280	2560	1280	1280	2560	1280	5120	1280	2560	MDCK2	28/07/2017
18	A/Perth/169/2017		2560	1280	640	1280	5120	1280	2560	2560	1280	5120	1280	2560	MDCK2	18/08/2017
19	A/Sri Lanka/77/2017		1280	1280	640	1280	2560	1280	2560	2560	1280	5120	1280	2560	SIAT2	11/08/2017
20	A/Sri Lanka/83/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	SIAT2	22/08/2017
21	A/Victoria/698/2017		2560	1280	640	2560	5120	1280	2560	5120	1280	5120	1280	5120	SIAT1	2/09/2017
22	A/Perth/235/2017		5120	5120	640	2560	5120	1280	2560	5120	1280	5120	1280	5120	SIAT1	30/08/2017
23	A/Canberra/1002/2017	**6B.1**	1280	1280	320	1280	2560	640	2560	2560	640	2560	640	2560	SIAT1	2/08/2017
24	A/Tasmania/1005/2017	**6B.1**	1280	1280	320	1280	2560	640	1280	2560	640	2560	640	2560	SIAT1	4/08/2017
25	A/South-Africa/R05836/17	**6B.1**	640	320	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK1	3/07/2017
26	A/South-Africa/R06491/17		1280	640	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK1	10/07/2017
27	A/Brisbane/111/2017		1280	1280	320	1280	2560	640	1280	2560	640	2560	640	2560	MDCK2	18/07/2017
28	A/Tasmania/56/2017	**6B.1**	1280	1280	640	1280	5120	640	2560	2560	640	5120	640	2560	SIAT1	12/08/2017
29	A/Victoria/2058/2017	**6B.1**	1280	1280	640	1280	2560	640	2560	2560	640	2560	640	2560	SIAT1	2/08/2017
30	A/Victoria/807/2017		1280	1280	320	1280	2560	640	1280	1280	640	2560	640	2560	SIAT1	17/08/2017
31	A/Auckland/503/2017		1280	1280	320	1280	2560	640	1280	2560	640	2560	640	2560	MDCK1	4/08/2017
32	A/Auckland/517/2017	**6B.1**	640	640	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK1	17/08/2017
33	A/New castle/109/2017		640	640	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK1	11/08/2017
34	A/Sri Lanka/61/2017	**6B.1**	1280	1280	640	1280	5120	640	2560	2560	640	2560	640	2560	MDCK1	11/07/2017
35	A/Brisbane/130/2017		1280	1280	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK2	7/08/2017
36	A/Brisbane/134/2017		640	320	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK2	10/08/2017
37	A/Brisbane/145/2017		1280	640	320	1280	2560	640	1280	1280	640	2560	640	2560	MDCK2	21/08/2017
38	A/Brisbane/131/2017		640	640	320	640	1280	640	1280	1280	640	2560	640	1280	MDCK2	7/08/2017
39	A/Tow nsville/11/2017	**6B.1**	320	160	160	320	640	320	640	640	320	640	320	640	MDCK2	22/07/2017
40	A/Brisbane/114/2017		320	320	160	320	640	320	640	640	320	1280	320	640	MDCK2	25/07/2017
41	A/Brisbane/117/2017	**6B.1**	320	320	160	640	640	320	1280	640	320	1280	320	1280	MDCK2	29/07/2017

Table 13. (H1N1)pdm09 viruses (2)

			Haemagglutination Inhibition Assay - WHO Influenza Centre													
			Reference Antisera													
	Sequenced		A	B	C	D	E	F	G	H	I	J	K	L		
	August 15, 2017		E4	E2	MDCK1	E3	E2	E4	M1/C2,M1	E3	E3	S1,M1	MX,M1	S1,M2	Passage	Sample
			CAL/7	CHCH/16	Dar/56	Tas/24	SA/22	Mich/45	Mich/45	SNG/GP1908	FIJI/3	FIJI/3	Pth/103	VIC/503	Details	Date
	Reference Antigens	**Clade**		**4**	**7**	**6B**		**6B.1**					**6B.2**			
A	A/CALIFORNIA/7/2009		**2560**	2560	1280	2560	5120	1280	2560	2560	1280	5120	1280	2560	E6	
B	A/CHRISTCHURCH/16/2010	**4**	2560	**5120**	1280	2560	5120	1280	2560	2560	1280	2560	1280	2560	E3	
C	A/DARWIN/56/2013	**7**	<80	<80	**320**	<80	<80	<80	<80	<80	<80	80	<80	<80	MDCK4	
D	A/TASMANIA/24/2014	**6B**	2560	1280	1280	**1280**	2560	1280	2560	2560	1280	2560	1280	2560	E3	
E	A/SOUTH AUSTRALIA/22/2015	**6B**	1280	1280	640	1280	**2560**	1280	2560	2560	1280	2560	640	2560	E3	
F	A/MICHIGAN/45/2015	**6B.1**	2560	2560	1280	2560	5120	**1280**	2560	2560	1280	5120	1280	2560	E3, E4	
G	A/MICHIGAN/45/2015	**6B.1**	1280	640	320	1280	2560	640	**1280**	2560	640	2560	640	1280	M1/C2,M2	
H	A/SINGAPORE/GP1908/2015	**6B.1**	1280	1280	640	1280	2560	1280	2560	**2560**	1280	2560	640	2560	E3	
I	A/FIJI/3/2016	**6B.1**	2560	2560	1280	2560	5120	2560	5120	5120	**1280**	5120	1280	5120	E3	
J	A/FIJI/3/2016	**6B.1**	1280	1280	640	1280	2560	1280	2560	2560	1280	**2560**	1280	2560	S1,M1	
K	A/PERTH/103/2015	**6B.2**	1280	1280	320	1280	2560	1280	1280	2560	1280	2560	**640**	2560	MX,M4	
L	A/VICTORIA/503/2016	**6B.2**	1280	1280	640	1280	2560	1280	2560	2560	1280	2560	1280	**2560**	S1,M1	
	Test Antigens															
1	A/Victoria/36/2017		2560	2560	1280	2560	5120	2560	5120	2560	1280	5120	1280	2560	MDCK1	11/07/2017
2	A/Victoria/41/2017		2560	2560	1280	2560	5120	2560	5120	5120	2560	5120	1280	5120	MDCK1	14/07/2017
3	NYMC X-299 (hy A/Montana/50/2016)		1280	1280	640	1280	2560	1280	2560	2560	1280	2560	640	2560	X, E1	
4	A/Victoria/536/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	SIAT1	7/07/2017
5	A/Victoria/543/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	SIAT1	29/06/2017
6	A/Victoria/2021/2017		2560	1280	640	2560	5120	1280	2560	2560	2560	5120	1280	2560	SIAT1	24/05/2017
7	A/Victoria/2022/2017		2560	1280	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	SIAT1	26/05/2017
8	A/Cambodia/b0629529/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	S1,M1	13/07/2017
9	A/Cambodia/b0606516/2017		1280	1280	640	1280	2560	1280	2560	2560	640	2560	640	2560	S1,M1	29/05/2017
10	A/Cambodia/b0710501/2017	**6B.1**	2560	1280	640	1280	2560	1280	2560	2560	1280	2560	1280	2560	S1,M1	28/06/2017
11	A/Cambodia/b0620537/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	S1,M1	12/06/2017
12	A/Cambodia/b0620538/2017	**6B.1**	2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	S1,M1	14/06/2017
13	A/Cambodia/b0711506/2017		2560	1280	640	2560	2560	1280	2560	2560	1280	2560	1280	2560	S1,M1	4/07/2017
14	A/Victoria/1004/2017		2560	1280	640	1280	2560	1280	2560	2560	1280	2560	1280	2560	SIAT1	7/07/2017
15	A/Brisbane/1005/2017		2560	2560	1280	2560	5120	1280	2560	5120	1280	5120	1280	5120	SIAT1	12/07/2017
16	A/South Australia/196/2017	**6B.1**	1280	1280	640	1280	2560	1280	2560	2560	1280	2560	1280	2560	SIAT1	4/07/2017
17	A/Victoria/35/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	MDCK1	11/07/2017
18	A/Victoria/38/2017		2560	2560	640	2560	2560	1280	2560	1280	1280	2560	1280	2560	MDCK1	12/07/2017
19	A/Victoria/39/2017		2560	1280	640	2560	2560	1280	2560	2560	1280	2560	1280	2560	MDCK1	12/07/2017
20	A/Cambodia/b0509516/2017		1280	1280	640	1280	2560	1280	1280	2560	640	2560	640	1280	S1,M1	25/01/2017
21	A/Cambodia/b0629526/2017		1280	1280	1280	1280	2560	1280	2560	2560	1280	2560	1280	1280	S1,M1	6/06/2017
22	A/Cambodia/b0509545/2017		1280	640	640	1280	2560	1280	2560	2560	1280	2560	640	1280	S2,M1	4/05/2017
23	A/Cambodia/FSS35237/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	MDCK1	22/05/2017
24	A/Cambodia/AD07850/2017		1280	1280	640	1280	2560	1280	1280	2560	1280	2560	1280	2560	MDCK1	4/05/2017
25	A/Cambodia/AD08014/2017		2560	2560	640	2560	5120	1280	2560	2560	1280	5120	1280	2560	MDCK1	18/05/2017
26	A/Townsville/8/2017		1280	640	320	1280	2560	1280	2560	2560	1280	2560	640	2560	MDCK2	28/06/2017
27	A/Victoria/570/2017	**6B.1**	1280	1280	640	1280	2560	1280	2560	2560	640	2560	640	2560	SIAT1	17/07/2017
28	A/Victoria/2031/2017		1280	1280	640	1280	2560	1280	2560	2560	640	2560	640	2560	SIAT1	24/06/2017
29	A/Cambodia/b0629534/2017		1280	1280	320	1280	2560	640	1280	2560	640	2560	640	1280	S1,M1	15/06/2017
30	A/Cambodia/AD08005/2017		1280	1280	320	1280	2560	640	1280	1280	640	2560	640	1280	MDCK1	4/05/2017
31	A/Cambodia/b0629530/2017		1280	1280	320	1280	2560	640	2560	2560	640	2560	640	1280	S1,M1	13/07/2017
32	A/Cambodia/b0629535/2017	**6B.1**	1280	1280	640	1280	2560	640	1280	2560	640	2560	640	2560	S1,M1	19/06/2017
33	A/Brisbane/104/2017	**6B.1**	640	320	320	640	1280	640	1280	1280	640	1280	640	1280	MDCK2	4/07/2017
34	A/Townsville/9/2017	**6B.1**	1280	1280	640	1280	2560	640	1280	2560	640	2560	640	1280	MDCK2	8/07/2017
35	A/Victoria/551/2017		1280	640	320	1280	2560	640	1280	1280	640	2560	640	1280	SIAT1	13/07/2017

Figure 27. Phylogenetic relationships among influenza A(H1N1)pdm09 HA genes



APPENDIX 4 - INFLUENZA A (H3N2)

Table 13. Summary – HI Characterization of Influenza A(H3N2) Isolates

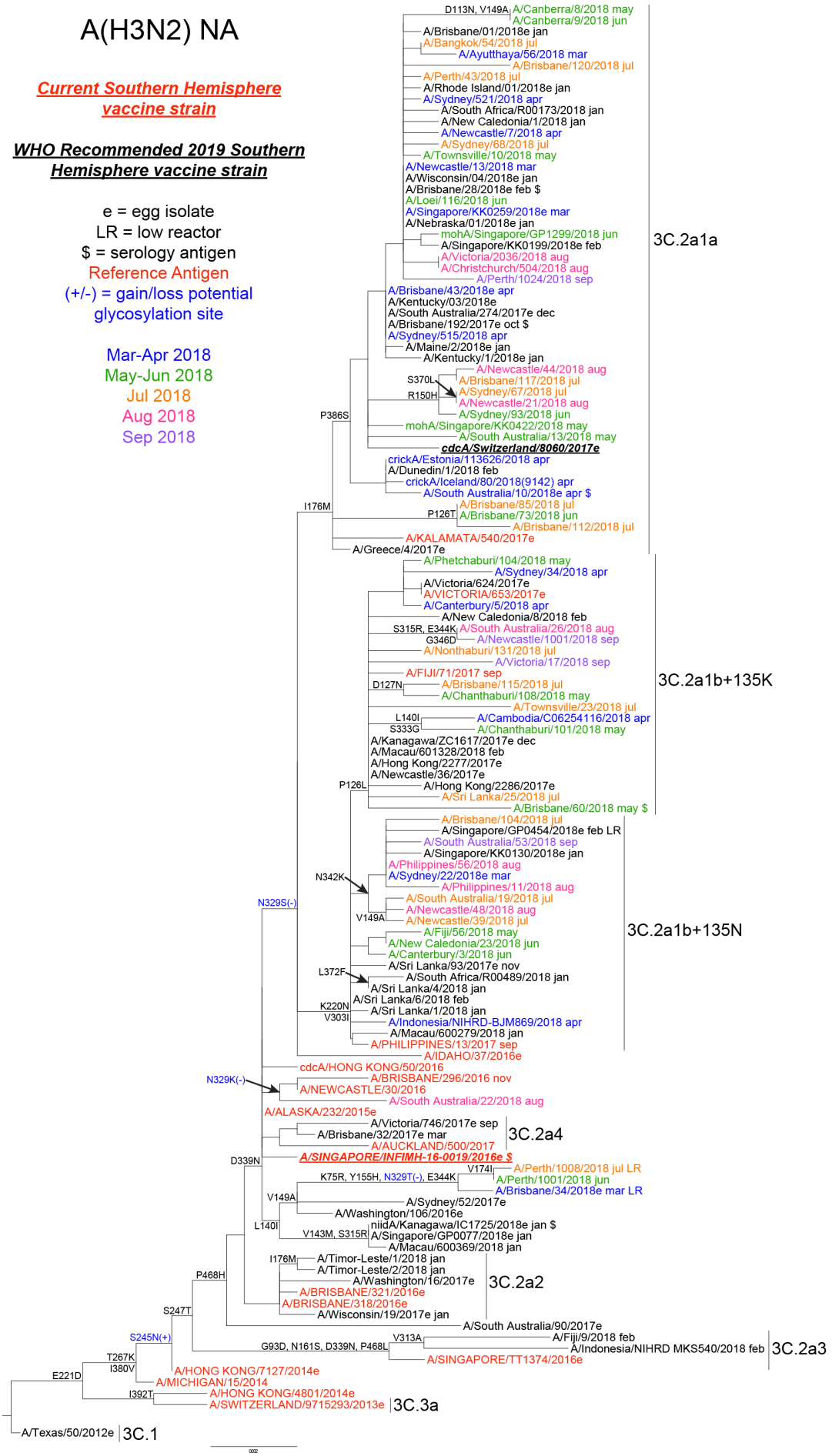
	Australia New Zealand	Pacific	SE Asia	Africa	East Asia	South Asia	Total (%)
1 September 2015 – 18 February 2016 (Based on Sample Date)							
A/Switzerland/9715293/2013-like (cell)	56	0	0	0	0	0	56 (98%)
A/Switzerland/9715293/2013 (low)* (cell)	1	0	0	0	0	0	1 (2%)
A/Switzerland/9715293/2013-like (egg)	40	0	0	0	0	0	40 (70%)
A/Switzerland/9715293/2013 (low)* (egg)	17	0	0	0	0	0	17 (30%)
A/Hong Kong/4801/2014-like (cell)	17	2	38	0	0	8	65 (100%)
A/Hong Kong/4801/2014 (low)** (cell)	0	0	0	0	0	0	0 (0%)
A/Hong Kong/4801/2014-like (egg)	10	2	32	0	0	3	47 (72%)
A/Hong Kong/4801/2014-like (low)** (egg)	7	0	6	0	0	5	18 (28%)
1 February – 22 September 2016 (Based on Sample Date)							
A/Hong Kong/4801/2014-like (cell)	294	2	25	7	0	1	329 (92%)
A/Hong Kong/4801/2014 (low)* (cell)	25	1	1	0	0	0	27 (8%)
A/Hong Kong/4801/2014-like (egg)	160	2	19	0	0	0	181 (51%)
A/Hong Kong/4801/2014-like (low)* (egg)	159	1	7	7	0	1	175 (49%)
A/Hong Kong/4801/2014-like (cell)	165	1	16	5	0	1	188 (53%)
A/Hong Kong/4801/2014 (low)** (cell)	154	2	10	2	0	0	168 (47%)
A/Hong Kong/4801/2014-like (egg)	42	0	7	0	0	0	49 (14%)
A/Hong Kong/4801/2014-like (low)** (egg)	277	3	19	7	0	1	307 (86%)
1 September 2016 – 21 February 2017 (Based on Sample Date)							
A/Hong Kong/4801/2014-like (cell)	86	0	0	0	0	0	86 (63%)
A/Hong Kong/4801/2014 (low)* (cell)	50	0	0	0	0	0	50 (37%)
A/Hong Kong/4801/2014-like (egg)	94	1	5	0	0	3	103 (37%)
A/Hong Kong/4801/2014-like (low)* (egg)	169	0	6	0	0	0	175 (63%)
A/Hong Kong/4801/2014-like (cell)	46	0	0	0	0	0	46 (34%)
A/Hong Kong/4801/2014 (low)** (cell)	90	0	0	0	0	0	90 (66%)
A/Hong Kong/4801/2014-like (egg)	14	0	0	0	0	2	16 (6%)
A/Hong Kong/4801/2014-like (low)** (egg)	249	1	11	0	0	1	262 (94%)
1 February – 19 September 2017 (Based on Sample Date)							
A/Michigan/15/2014-like* (cell)	433	13	31	10	1	3	491 (81%)
A/Michigan/15/2014-like (low)* (cell)	103	6	5	2	0	0	116 (19%)
A/Hong Kong/4801/2014-like* (egg)	340	5	27	9	1	1	383 (61%)
A/Hong Kong/4801/2014-like (low)* (egg)	216	16	9	3	0	2	246 (39%)
A/Michigan/15/2014-like** (cell)	242	9	15	7	1	0	274 (45%)
A/Michigan/15/2014-like (low)** (cell)	294	10	21	5	0	3	333 (55%)
A/Hong Kong/4801/2014-like** (egg)	112	1	9	6	0	0	128 (20%)
A/Hong Kong/4801/2014-like (low)** (egg)	444	20	27	6	1	3	501 (80%)
1 February – 19 September 2018 *(Based on Sample Date)*							
A/Singapore/INFIMH-16-0019/2016-like (cell)	78	1	30	0	1	4	114 (95%)
A/Singapore/INFIMH-16-0019/2016-like (low) (cell)	4	1	1	0	0	0	6 (5%)
A/Singapore/INFIMH-16-0019/2016-like (egg)	68	1	27	0	0	4	100 (83%)
A/Singapore/INFIMH-16-0019/2016-like (low) (egg)	14	1	4	0	1	0	20 (17%)

* 8 fold lower in HI assays
** 4 fold lower in HI assays

Table 14. A(H3) Focus Reduction Assay (3)

			Reference Antisera												
	Sequenced on tree		A	B	C	D	E	F	G	H	I	J	K		
	Sequenced by submitting lab		F3491	F4376	F4377	A8201	A8196	F4339	F4296	F4369	A8195	F4381	F4378		
	Aug 21, 2018, Part A		X/M1/S1	SIAT4	E8	M1/S1	E4	M1/S3	E5	E5/D7,E1	E6	SIAT1	E5		
			HK4801	BRIS318	BRIS318	BRIS192	BRIS192	16-0019	16-0019	IVR-186	16-0019 (D@225)	VIC653	VIC653	Passage	Sample
	Reference Antigens	**Clade**	3c.2a	3c.2a2		3c.2a2re		3c.2a1				3c.2a1b+135K		History	Details
A	A/HONG KONG/4801/2014	**3c.2a**	**5120**	1280	640	640	1280	1280	1280	640	640	2560	320	MX,M1,S4	
B	A/BRISBANE/318/2017	**3c.2a2**	1280	**5120**	5120	640	5120	1280	1280	640	1280	2560	320	SIAT4	
C	A/BRISBANE/318/2017	**3c.2a2**	2560	10240	**10240**	1280	10240	5120	5120	1280	2560	>10240	640	E8	
D	A/BRISBANE/192/2017	**3c.2a2re**	1280	10240	5120	**1280**	5120	2560	2560	640	1280	5120	640	M1/S1	
E	A/BRISBANE/192/2017	**3c.2a2re**	2560	>10240	10240	5120	**10240**	1280	5120	5120	2560	2560	5120	E4	
F	A/SING/INFIMH-16-0019/2016	**3c.2a1**	2560	2560	1280	1280	2560	**2560**	2560	640	1280	5120	640	M1,S3	
G	A/SING/INFIMH-16-0019/2016	**3c.2a1**	640	640	1280	1280	5120	1280	**2560**	2560	640	2560	640	E5	
H	IVR-186	**3c.2a1**	1280	640	640	640	2560	640	1280	**2560**	640	640	2560	E5/D7,E1	
I	16-0019, D@225	**3c.2a1**	320	160	320	<80	640	320	640	1280	**640**	320	640	E6	
J	A/VICTORIA/653/2017	**3c.2a1b+135K**	640	320	640	640	1280	2560	2560	1280	2560	**>10240**	640	SIAT1	
K	A/VICTORIA/653/2017	**3c.2a1b+135K**	640	160	320	320	640	1280	1280	1280	1280	5120	**5120**	E5	
	Test Antigens														
1	A/Sydney/17/2018	**3c.2a2**	5120	10240	10240	2560	10240	5120	5120	2560	1280	5120	320	M-S,S1	5/03/2018
2	A/Sydney/15/2018	**3c.2a2re**	2560	10240	10240	1280	10240	2560	2560	1280	1280	5120	320	M-S,S1	3/03/2018
3	A/Newcastle/13/2018	**3C.2a2**	2560	>10240	>10240	1280	>10240	2560	2560	640	320	5120	320	SIAT1	13/03/2018
4	A/Perth/16/2018	**3c.2a1b+135K**	320	320	320	160	640	1280	640	320	320	5120	640	M1,S1	22/03/2018
5	A/Dunedin/1/2018	**3c.2a2re**	640	640	640	160	640	1280	1280	320	640	5120	160	SIAT1	24/02/2018
6	A/Sydney/34/2018	**3c.2a1b+135K**	640	320	640	320	640	1280	640	320	640	5120	1280	SIAT1	13/04/2018
7	A/Brisbane/88/2018	**3c.2a2re**	1280	5120	5120	640	5120	1280	1280	320	640	2560	160	S1,S1	2/07/2018
8	A/South Australia/1004/2018	**3c.2a1b+135N**	320	320	320	160	640	1280	320	160	640	2560	160	SIAT1	9/07/2018
9	A/Victoria/6/2018		640	640	640	320	1280	1280	1280	160	320	2560	160	SIAT1	18/07/2018
10	A/South Australia/1007/2018	**3c.2a1b+135N**	320	640	640	320	1280	1280	640	320	1280	2560	320	SIAT1	18/07/2018
11	A/South Australia/1009/2018	**3c.2a1b+135N**	320	640	640	320	640	1280	320	320	640	1280	160	SIAT1	17/07/2018
12	A/Brisbane/45/2018	**3c.2a2re**	1280	10240	5120	1280	10240	1280	1280	640	640	5120	320	SIAT2	17/04/2018
13	A/Brisbane/56/2018	**3c.2a2**	1280	10240	5120	1280	10240	1280	1280	320	640	5120	320	SIAT2	8/05/2018
14	A/South Australia/13/2018	**3c.2a2**	1280	5120	5120	640	5120	1280	1280	320	640	5120	160	SIAT1	29/05/2018
15	A/Brisbane/1001/2018	**3c.2a2**	1280	5120	5120	640	5120	1280	1280	320	640	5120	320	SIAT1	3/04/2018
16	A/Brisbane/73/2018	**3c.2a2**	1280	5120	5120	640	5120	1280	1280	640	1280	5120	320	S1,S1	11/06/2018
17	A/South Africa/R00173/2018	**3c.2a2**	160	2560	640	320	5120	1280	1280	640	640	2560	320	M2,S1	7/01/2018
18	A/Brisbane/77/2018	**3c.2a2**	640	5120	2560	640	5120	1280	1280	320	640	2560	160	S2,S1	12/06/2018
19	A/Indonesia/NIHRD-BJM869/2018	**3c.2a1b+135N**	80	320	320	320	1280	640	640	320	640	1280	320	SIAT1	26/04/2018
20	A/Singapore/GP1299/2018	**3c.2a2re**	1280	5120	5120	1280	5120	640	1280	640	640	2560	320	M1,S1	29/06/2018
21	A/Singapore/KK0259/2018	**3c.2a2re**	1280	5120	1280	1280	5120	640	1280	640	640	2560	320	M1,S1	9/03/2018
22	A/Brisbane/57/2018	**3c.2a2**	640	5120	2560	320	2560	640	640	320	320	2560	160	SIAT2	9/05/2018
23	A/Townsville/10/2018	**3c.2a2**	640	5120	2560	320	2560	640	640	320	640	2560	320	S1,S1	31/05/2018
24	A/Brisbane/85/2018	**3c.2a2**	320	2560	1280	640	2560	640	640	320	320	1280	160	M1,S1	1/07/2018
25	A/Brisbane/94/2018	**3c.2a2**	160	1280	1280	320	1280	640	640	160	160	1280	80	M1,S1	6/07/2018
26	A/Perth/1001/2018	**3c.3a**	<80	320	640	160	1280	320	640	320	320	640	80	SIAT1	7/06/2018
27	A/Brisbane/43/2018	**3c.2a2re**	160	1280	1280	320	1280	320	320	160	160	1280	80	M2, S1	7/04/2018
28	A/Brisbane/54/2018	**3c.2a2**	160	640	640	160	1280	320	320	160	160	640	80	M2,S1	26/04/2018
29	A/Brisbane/55/2018	**3c.2a2**	160	640	640	320	1280	320	640	160	320	640	80	M3,S1	20/04/2018
30	A/Brisbane/58/2018	**3C.2a2**	160	640	640	160	640	320	320	160	80	640	80	M3,S1	24/04/2018
31	A/Sydney/47/2018	**3c.2a2**	640	2560	2560	640	5120	320	640	320	320	1280	160	SIAT1	7/06/2018
32	A/Brisbane/89/2018	**3c.2a2re**	160	640	640	160	640	160	160	80	<80	640	<80	M2,S1	21/06/2018

Figure 28. Phylogenetic relationships among influenza A (H3) N2 genes



APPENDIX 5 - INFLUENZA B

Figure 29. Antigenic cartographic representation of B Victoria viruses

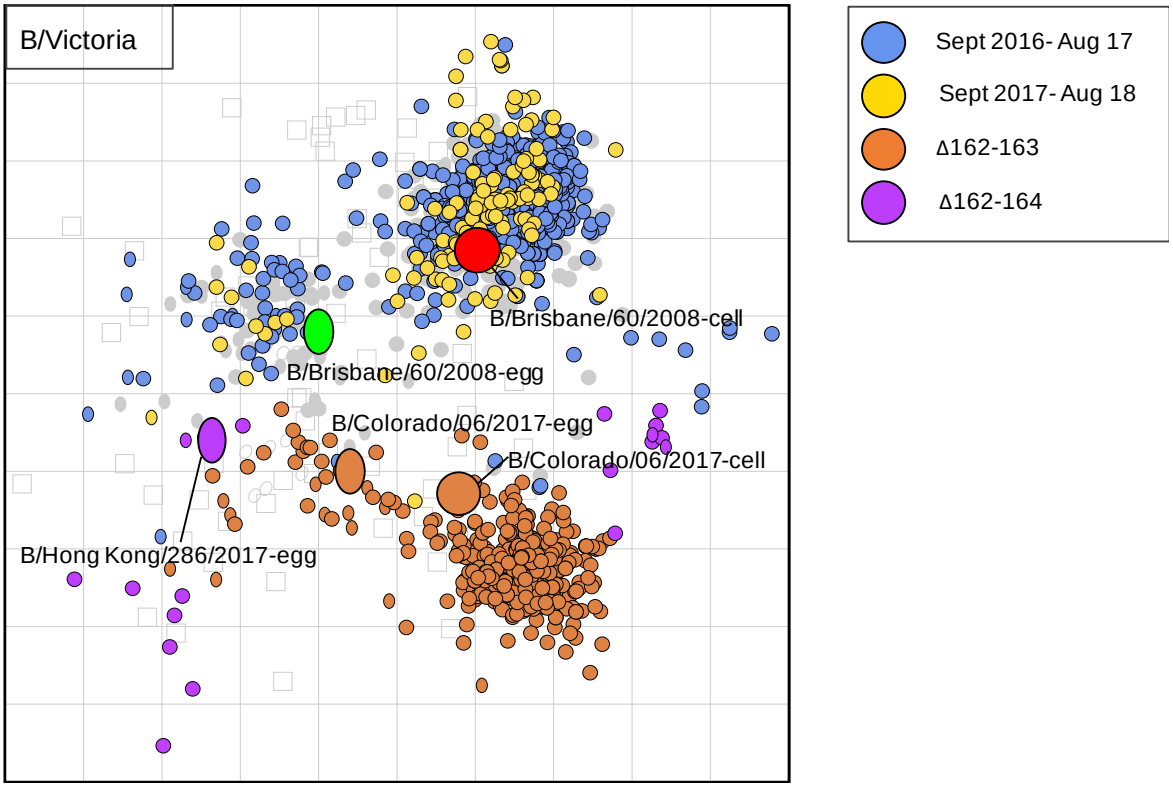


Figure 30. Antigenic cartographic representation of B Yamagata viruses

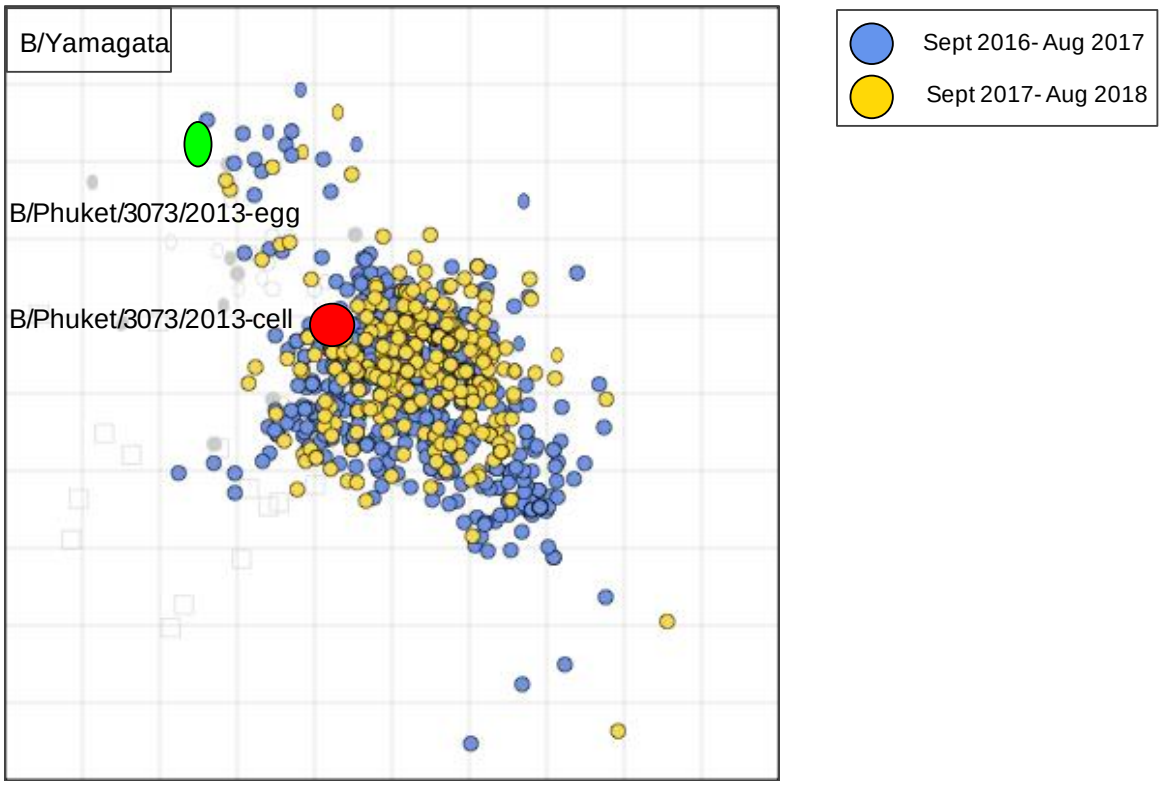


Figure 31. B viruses (B/Victoria lineage)

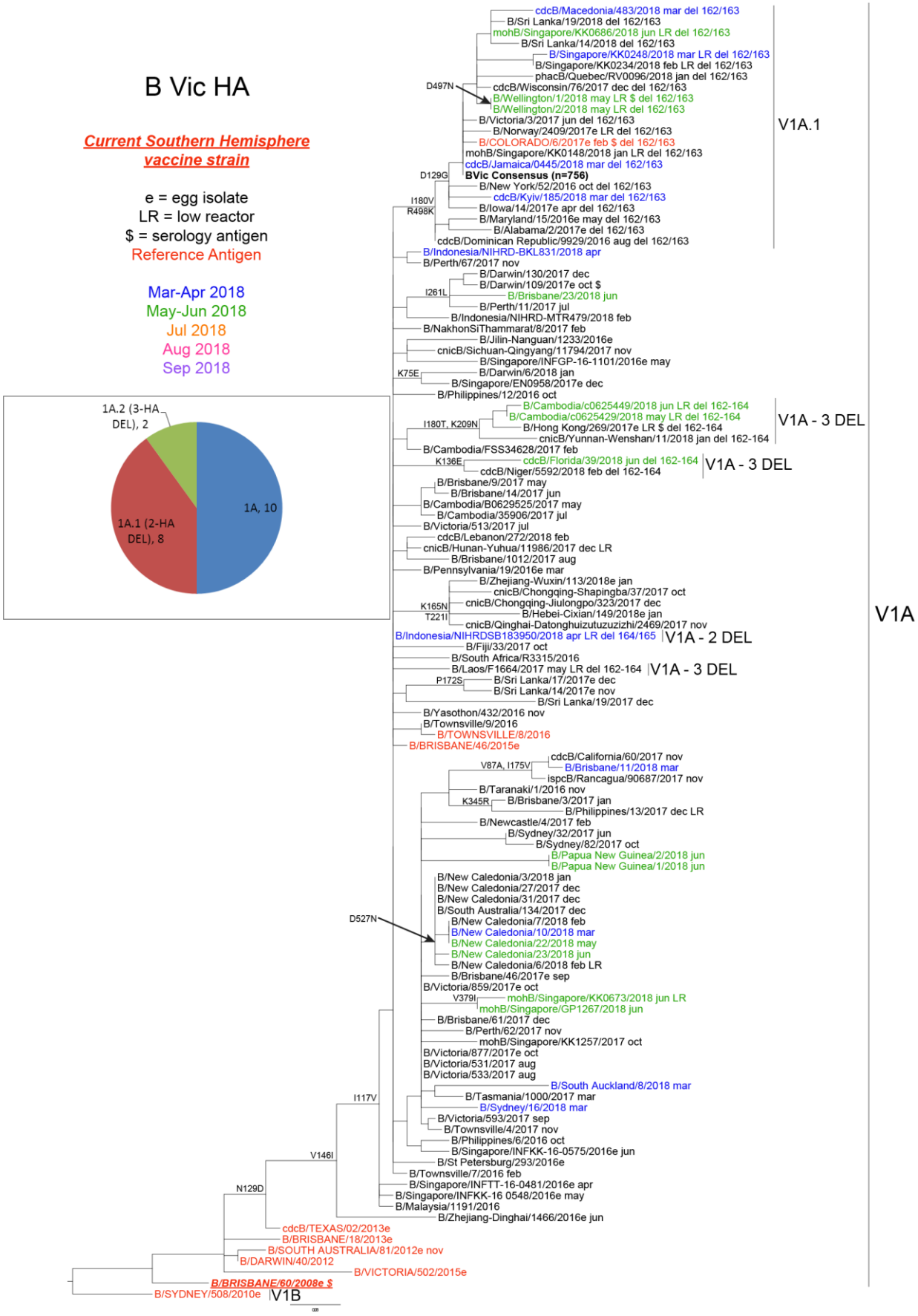


Table 15. B viruses (B/Victoria lineage)

			Reference Antisera													
	Sequenced on tree		A	B	C	D	E	F	G	H	I	J	K	L		
	Sequenced by submitting lab		F4159	F3700	F2315	F3810	F3366	F3413	F3643	F4442	F4443	F4067	F4440	F4432	Passage	Sample
	August 14, 2018		MX,M5	E6		E6	E4	MDCK2	MDCK3	C1,M2	E6	E3/D1	E7	C2,M1	Details	Date
			BRIS60	BRIS60	DAR40	TEX02	BRIS46	BRIS46	TOWNS8	COL6	COL6	Mary15	HK269	Chong1840		
	Reference Antigens		V1A							V1A.1			V1A.2	K165N,T221I		
A	B/BRISBANE/60/2008	**V1A**	**320**	80	320	160	320	320	160	<20	<20	40	20	80	MX,M5	
B	B/BRISBANE/60/2008	**V1A**	160	**1280**	320	1280	1280	160	80	20	80	320	80	80	E7	
C	B/DARWIN/40/2012	**V1A**	320	80	**640**	320	160	320	160	<20	<20	40	20	80	MDCK4	
D	B/TEXAS/02/2013	**V1A**	80	320	160	**640**	320	80	40	20	40	320	40	80	E7	
E	B/BRISBANE/46/2015	**V1A**	160	1280	320	1280	**>2560**	160	160	40	160	640	80	160	E4	
F	B/BRISBANE/46/2015	**V1A**	160	80	320	160	160	**320**	80	<20	<20	40	20	80	MDCK4	
G	B/TOWNSVILLE/8/2016	**V1A**	160	80	320	320	320	320	**160**	<20	<20	80	40	80	MDCK3	
H	B/COLORADO/6/2017	**V1A.1**	<20	20	<20	<20	<20	<20	<20	**80**	320	160	40	80	C1,M3	
I	B/Colorado/6/2017	**V1A.1**	<20	320	20	320	320	<20	<20	160	**640**	640	80	40	E6	
J	B/Maryland/15/2016	**V1A.1**	<20	320	<20	640	320	<20	<20	160	640	**>2560**	320	160	E5	
K	B/Hong Kong/269/2017	**V1A.2**	<20	640	20	640	640	20	<20	80	320	>2560	**1280**	160	E7	
L	B/Chongqing-Banan/1840/2017	**K165N,T221I**	20	80	20	80	160	40	<20	20	40	160	40	**320**	C2,M1	
	Test Antigens															
1	B/Brisbane/23/2018	**V1A**	320	80	320	160	160	160	160	<20	<20	80	20	80	M1,M1	20/06/2018
2	B/Singapore/GP0346/2018		320	80	640	160	160	320	160	<20	20	40	20	80	M1,M1	07/02/2018
3	B/Singapore/GP1267/2018	**V1A**	320	80	640	160	320	320	160	<20	<20	40	20	80	M1,M1	25/06/2018
4	B/South Auckland/8/2018	**V1A**	160	80	320	320	160	320	160	<20	<20	40	20	80	SX,M1	04/03/2018
5	B/Singapore/KK0673/2018	**V1A**	20	20	160	<20	<20	20	80	<20	<20	40	20	80	M1,M1	27/06/2018
6	B/Zhejiang-Wuxin/113/2018	**V1A**	<20	320	20	320	320	<20	<20	20	80	320	40	160	E3	02/01/2018
7	B/Hebei-Cixian/149/2018	**V1A**	<20	160	<20	320	160	<20	<20	20	40	640	80	160	E3	16/01/2018
8	B/Wellington/1/2018	**V1A.1**	<20	20	20	20	<20	<20	<20	160	160	160	20	40	SX,M1	11/05/2018
9	B/Wellington/2/2018	**V1A.1**	<20	20	40	20	<20	<20	<20	160	160	160	20	<20	SX,M1	11/05/2018
10	B/Cambodia/c0625429/2018	**V1A.2**	<20	40	20	80	40	20	<20	20	20	160	1280	80	SX,M1	18/05/2018
11	B/Cambodia/c0625449/2018	**V1A.2**	<20	80	20	80	40	20	<20	20	20	160	1280	80	SX,M1	08/06/2018
12	B/Singapore/KK0686/2018	**V1A.1**	<20	20	20	20	<20	<20	<20	160	320	160	20	<20	M1,M1	29/06/2018
13	B/Singapore/KK0148/2018	**V1A.1**	<20	20	20	20	<20	<20	<20	160	320	160	20	<20	M1,M1	29/01/2018

Table 16. B viruses (B/Yamagata lineage)

			Reference Antisera											
	Sequenced on tree		A	B	C	D	E	F	G	H	I	J		
	September 17 & 14, 2018		F3184	F3186	F3187	F4431	F4398	F3524	F3645	F4213	F4215	F4375	Passage	Sample
	Part B		E6	E4	E3,E1	M1/C2,M6	E6	mdck5	MX,M2	MDCK,M1	MDCK2	SX,M1	Details	Date
			HUBEI158	WISC01	MASS02	MASS02	PHK3073	PHK3073	SYD10	Cant5	Perth4	Well40		
	Reference Antigens	**Clade**								Y3	Y3	Y3		
A	B/HUBEI-WUJIAGANG/158/2009		**320**	<20	80	20	640	80	160	<20	<20	20	E7	
B	B/WISCONSIN/01/2010		320	80	320	40	1280	160	160	20	40	40	E5	
C	B/MASSACHUSETTS/02/2012		320	**40**	640	320	1280	40	80	<20	<20	20	E3.E2	
D	B/MASSACHUSETTS/02/2012		20	<20	**80**	320	160	80	160	<20	<20	20	M1/C2/M6	
E	B/PHUKET/3073/2013		320	40	320	**80**	1280	160	160	20	40	40	E6	
F	B/PHUKET/3073/2013		80	40	80	80	640	160	320	20	40	80	MDCK5	
G	B/SYDNEY/10/2016		20	<20	20	160	**320**	160	320	40	160	80	MX,M3	
H	B/Canterbury/5/2017	**Y3**	20	<20	20	80	160	**160**	320	40	80	80	mx,m2	
I	B/Perth/4/2017	**Y3**	<20	<20	20	160	320	320	**320**	40	80	40	mdck3	
J	B/Wellington/40/2017	**Y3**	80	40	80	160	640	320	160	**80**	160	80	SX,M2	
	Test Antigens													
1	B/Newcastle/10/2018	**Y3**	80	40	40	160	160	320	320	160	320	160	MDCK1	07/08/2018
2	B/New Caledonia/27/2018	**Y3**	<20	<20	<20	80	160	160	320	40	80	40	MDCK1	16/06/2018
3	B/New Caledonia/28/2018	**Y3**	<20	<20	<20	<20	160	160	160	20	80	40	MDCK1	18/06/2018
4	B/New Caledonia/31/2018	**Y3**	<20	<20	<20	<20	160	160	320	20	80	40	MDCK1	25/07/2018
5	B/New Caledonia/32/2018	**Y3**	<20	<20	<20	<20	80	160	160	20	80	40	MDCK1	26/07/2018
6	B/New Caledonia/33/2018	**Y3**	<20	<20	<20	<20	80	160	320	20	80	40	MDCK1	06/08/2018
7	B/New Caledonia/20/2018	**Y3**	<20	<20	<20	40	160	160	320	20	80	40	MDCK2	19/05/2018
8	B/Sydney/1005/2018		<20	<20	<20	80	160	160	320	40	160	40	MDCK1	24/07/2018
9	B/Newcastle/14/2018		<20	<20	<20	80	160	160	320	20	80	40	MDCK1	16/08/2018
10	B/Newcastle/25/2018	**Y3**	<20	20	<20	80	160	160	320	40	80	80	MDCK1	21/08/2018
11	B/Newcastle/42/2018		<20	20	<20	80	160	160	320	40	80	80	MDCK1	13/08/2018
12	B/Christchurch/500/2018	**Y3**	<20	<20	<20	40	160	160	320	20	80	40	MDCK1	25/08/2018
13	B/Christchurch/502/2018		<20	<20	<20	40	160	160	160	20	80	40	MDCK1	06/08/2018
14	B/Christchurch/503/2018		<20	<20	<20	40	80	160	320	20	80	40	MDCK1	15/07/2018
15	B/Christchurch/505/2018	**Y3**	<20	<20	<20	40	160	160	160	20	80	40	MDCK1	09/08/2018
16	B/Christchurch/506/2018		<20	<20	<20	<20	80	160	160	20	80	40	MDCK1	09/08/2018
17	B/Sydney/41/2018		<20	<20	<20	40	320	160	160	20	80	40	MDCK1	25/07/2018
18	B/Guyane/005/2018		<20	<20	<20	80	320	160	320	40	80	40	MX,M1	
19	B/Bangkok/74/2018	**Y3**	80	20	40	80	320	160	320	40	80	80	M1,M1	05/04/2018
20	B/Wellington/45/2018	**Y3**	40	20	20	80	160	160	320	40	80	80	MX,M1	17/07/2018
21	B/Wellington/7/2018		40	40	40	160	160	160	320	40	80	80	MX,M1	26/07/2018
22	B/Wellington/6/2018	**Y3**	40	20	40	80	160	160	320	40	80	80	MX,M1	25/07/2018
23	B/Newcastle/11/2018	**Y3**	40	40	20	80	160	160	320	40	80	80	MDCK1	08/08/2018
24	B/Jilin-Chaoyang/11723/2018		160	<20	160	<20	320	40	160	<20	<20	20	E4	12/03/2018
25	B/Guyane/005/2018	**Y3**	160	<20	40	20	320	<20	80	<20	<20	20	E4	

Figure 32. Phylogenetic relationships among influenza B neuraminidase genes B/Yamagata Lineage

APPENDIX 6 - WHO RECOMMENDATION FOR INFLUENZA VACCINES

World Health Organization
Organisation mondiale de la Santé

Weekly epidemiological record
Relevé épidémiologique hebdomadaire

19 OCTOBER 2018, 93th YEAR / 19 OCTOBRE 2018, 93e ANNÉE
No 42, 2018, 93, 553–576
http://www.who.int/wer

Contents

553 Recommended composition of influenza virus vaccines for use in the 2019 southern hemisphere influenza season

563 Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness

Sommaire

553 Composition recommandée des vaccins antigrippaux pour la saison grippale 2019 dans l'hémisphère Sud

563 Caractéristiques génétiques et antigéniques des virus grippaux zoonotiques et mise au point de virus vaccinaux candidats en vue de la préparation à une pandémie

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Recommended composition of influenza virus vaccines for use in the 2019 southern hemisphere influenza season

September 2018

WHO convenes technical consultations[1] in February and September each year to recommend viruses for inclusion in influenza vaccines[2] for the northern and southern hemisphere influenza seasons, respectively. This recommendation relates to the influenza vaccines for use in the southern hemisphere 2019 influenza season. A recommendation will be made in February 2019 relating to vaccines that will be used for the northern hemisphere 2019–2020 influenza season. For countries in tropical and subtropical regions, WHO recommendations on influenza vaccine composition (northern hemisphere or southern hemisphere) are available on the WHO Global Influenza Programme website.[3]

Seasonal influenza activity

Between February and September 2018, influenza activity was reported globally, with influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses co-circulating.

In the temperate zone of the northern hemisphere, influenza activity declined from February to April and remained at inter-seasonal levels in most countries. Influenza A(H1N1)pdm09 was the predominant type A in most countries in Europe, northern and western Africa and Asia. Influenza A(H3N2) was the predominant type A in northern Europe, North America and some countries in Asia. Influenza B viruses circulated in higher proportions

[1] WHO website on influenza vaccine viruses and reagents: http://www.who.int/influenza/vaccines/virus/en/

[2] Description of the process of influenza vaccine virus selection and development available at: http://www.who.int/gb/pip/pdf_files/Fluvaccvirusselection.pdf

[3] Influenza in the tropics and subtropics: http://www.who.int/influenza/vaccines/tropics/en/

Composition recommandée des vaccins antigrippaux pour la saison grippale 2019 dans l'hémisphère Sud

Septembre 2018

L'OMS convoque chaque année des consultations techniques[1] en février et septembre pour recommander les virus devant entrer dans la composition des vaccins[2] contre la grippe qui seront utilisés pendant les saisons grippales dans l'hémisphère Nord et l'hémisphère Sud, respectivement. La présente recommandation s'applique aux vaccins contre la grippe à utiliser pendant la saison grippale 2019 dans l'hémisphère Sud. Une recommandation concernant les vaccins devant servir pendant la saison grippale 2019-2020 dans l'hémisphère Nord sera formulée en février 2019. Pour les pays des régions tropicales et subtropicales, des recommandations de l'OMS sur la composition des vaccins antigrippaux (hémisphère Nord ou hémisphère Sud) sont disponibles sur le site Web du Programme mondial de lutte contre la grippe de l'OMS.[3]

Activité grippale saisonnière

De février à septembre 2018, une activité grippale a été signalée dans le monde entier, avec une cocirculation des virus grippaux A(H1N1) pdm09, A(H3N2) et B.

Dans la zone tempérée de l'hémisphère Nord, l'activité grippale a diminué de février à avril et est restée à des niveaux intersaisonniers dans la plupart des pays. La grippe de type A prédominante dans la plupart des pays d'Europe, d'Afrique du Nord et de l'Ouest et d'Asie était la grippe A(H1N1)pdm09. La grippe de type A prédominante en Europe du Nord, en Amérique du Nord et dans certains pays d'Asie était la grippe A(H3N2). Dans de nombreux pays d'Europe, les virus de la grippe

[1] Site Web de l'OMS sur les virus et les réactifs des vaccins antigrippaux: http://www.who.int/influenza/vaccines/virus/en/

[2] La description du processus de sélection et de mise au point des virus grippaux vaccinaux est disponible à l'adresse: http://www.who.int/gb/pip/pdf_files/Fluvaccvirusselection.pdf

[3] La grippe dans les régions tropicales et subtropicales: http://www.who.int/influenza/vaccines/tropics/en/

than influenza A viruses in many countries in Europe. Influenza activity in northern Africa was high in several countries in February and March with widespread A(H1N1)pdm09 outbreaks in Algeria and A(H3N2) in Morocco.

Influenza activity in the tropical and subtropical region of Asia was high with regional/widespread outbreaks reported in South-East Asia. Influenza activity in tropical regions of South America was generally high with A(H1N1)pdm09, A(H3N2) and B outbreaks reported.

In the temperate zone of the southern hemisphere, influenza activity increased from March to June. In the southern cone of South America there was co-circulation of influenza A and B viruses, and in South Africa A(H1N1)pdm09 virus predominated with regional activity of influenza B virus reported later in the winter season. Influenza activity was low in Australia and New Zealand throughout this period (*Map 1*).

Influenza A

Influenza A viruses were predominant in most countries during this period, including countries in Africa, North America, central America, temperate and tropical South America and Oceania. Globally, co-circulation of both A(H1N1)pdm09 and A(H3N2) viruses was evident in all countries, areas and territories. Influenza A(H1N1)pdm09 viruses circulated in higher proportions in most countries in Africa, central, south-eastern and western Asia, tropical South America, central America, Oceania and the Caribbean. Influenza A(H3N2) viruses circulated in higher proportions in some countries in temperate regions of South America, southern Asia, North America and northern Europe.

Influenza B

Influenza B viruses circulated in a higher proportion than influenza A viruses in most countries in Europe and western Asia, and in Canada. Globally, influenza B/Yamagata/16/88 lineage viruses predominated and B/Victoria/2/87 lineage viruses also circulated during this period.

Detailed information by country of the extent and type of seasonal influenza activity worldwide is available on the WHO website.[4]

Zoonotic influenza infections caused by A(H5), A(H7N9), A(H9N2), A(H1N2)v and A(H3N2)v viruses

From 20 February to 24 September 2018, one human case of highly pathogenic avian influenza A(H5N6) virus infection was reported by China, where the virus is present in poultry. Since December 2003 a total of 880 human cases of avian influenza A(H5) virus infection with 460 deaths have been confirmed in 16 countries. To date there has been no evidence of sustained human-to-human transmission.

B ont circulé dans des proportions plus élevées que les virus de la grippe A. L'activité grippale en Afrique du Nord a été soutenue dans plusieurs pays en février et mars, avec des épidémies étendues de grippe A(H1N1)pdm09 en Algérie et de grippe A(H3N2) au Maroc.

L'activité grippale dans les régions tropicale et subtropicale d'Asie a été soutenue, des épidémies régionales ou étendues ayant été signalées en Asie du Sud-Est. Dans les régions tropicales d'Amérique du Sud, elle a été généralement soutenue, avec des épidémies de grippe A(H1N1)pdm09, A(H3N2) et B.

Dans la zone tempérée de l'hémisphère Sud, l'activité grippale a augmenté de mars à juin. Dans le Cône austral de l'Amérique du Sud, il y a eu cocirculation des virus de la grippe A et de la grippe B, et en Afrique du Sud, le virus A(H1N1)pdm09 a prédominé, avec une activité régionale du virus B signalée plus tard dans la saison hivernale. L'activité grippale a été faible en Australie et en Nouvelle-Zélande tout au long de cette période (*Carte 1*).

Grippe A

Les virus de la grippe A étaient prédominants dans la plupart des pays au cours de cette période, notamment en Afrique, en Amérique du Nord, en Amérique centrale, dans les régions tempérées et tropicales d'Amérique du Sud et en Océanie. Globalement, la cocirculation des virus A(H1N1)pdm09 et A(H3N2) était clairement établie dans tous les pays, régions et territoires. Les virus de la grippe A(H1N1)pdm09 ont circulé dans des proportions plus élevées dans la plupart des pays d'Afrique, d'Asie centrale, du Sud-Est et occidentale, des régions tropicales d'Amérique du Sud, d'Amérique centrale, en Océanie et dans les Caraïbes. Les virus de la grippe A(H3N2) ont circulé dans des proportions plus élevées dans certains pays des régions tempérées d'Amérique du Sud, d'Asie méridionale, d'Amérique du Nord et d'Europe septentrionale.

Grippe B

Les virus de la grippe B ont circulé dans des proportions plus élevées que les virus de la grippe A dans la plupart des pays d'Europe et d'Asie occidentale, ainsi qu'au Canada. À l'échelle mondiale, les virus de la lignée B/Yamagata/16/88 prédominaient et les virus de la lignée B/Victoria/2/87 ont également circulé pendant cette période.

Des informations détaillées par pays sur l'étendue et le type d'activité grippale saisonnière dans le monde sont disponibles sur le site Web de l'OMS.[4]

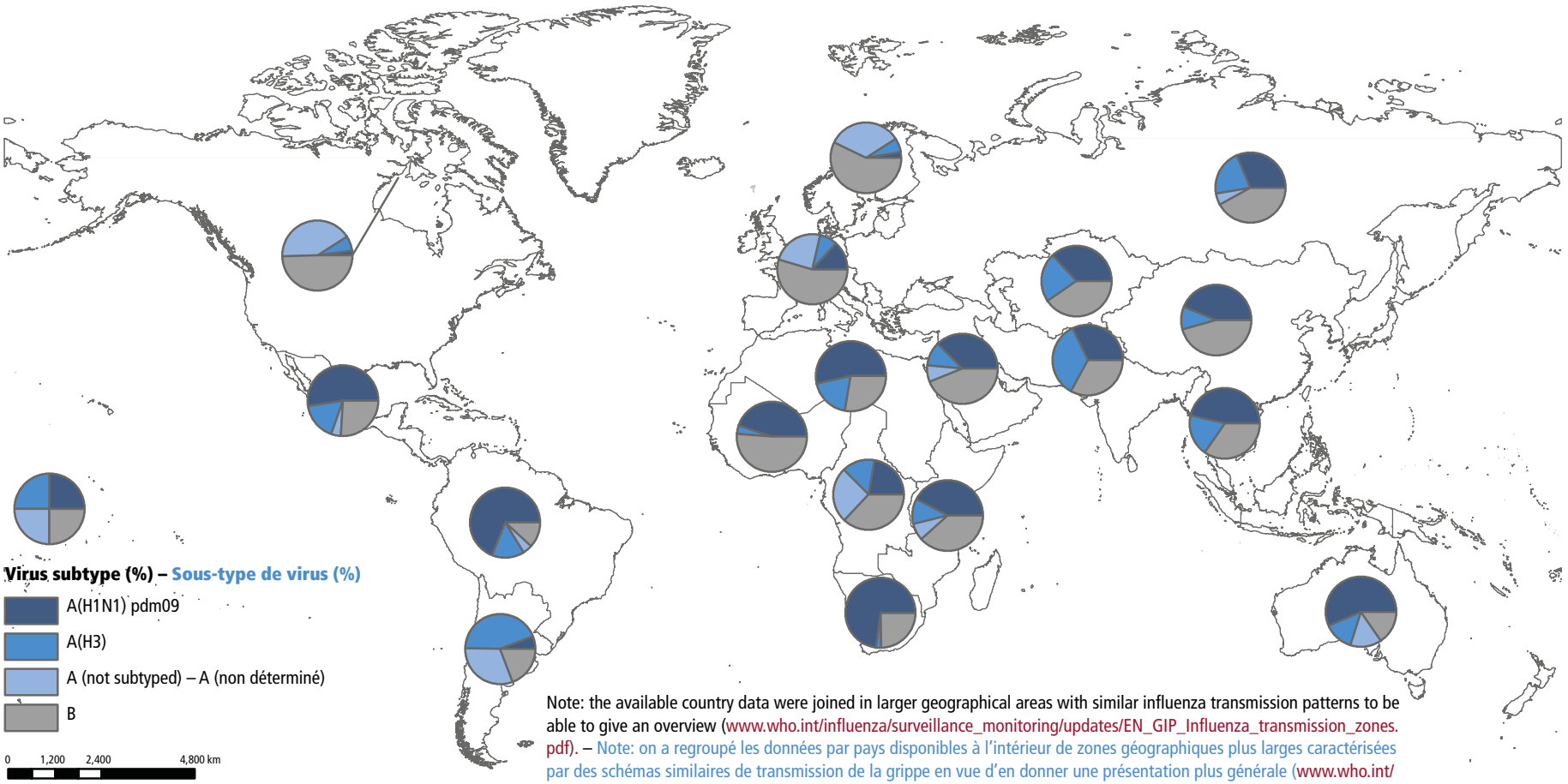
Infections grippales zoonotiques causées par les virus A(H5), A(H7N9), A(H9N2), A(H1N2)v et A(H3N2)v

Du 20 février au 24 septembre 2018, un cas humain d'infection par le virus de la grippe aviaire A(H5N6) hautement pathogène a été notifié en Chine, où le virus est présent chez les volailles. Depuis décembre 2003, 880 cas humains d'infection par le virus de la grippe aviaire A(H5), dont 460 décès, ont été confirmés dans 16 pays. À ce jour, il n'existe aucune preuve de transmission interhumaine durable.

[4] FluNet and FluID influenza surveillance data and outputs: http://www.who.int/influenza/resources/charts/en/

[4] Données et résultats de la surveillance de la grippe par FluNet et FluID: http://www.who.int/influenza/resources/charts/en/

Map 1 **Distribution of influenza-virus subtypes by influenza transmission zone, February to September 2018**
Carte 1 **Répartition des sous-types de virus grippaux par zone de transmission de la grippe, février à septembre 2018**



Note: the available country data were joined in larger geographical areas with similar influenza transmission patterns to be able to give an overview (www.who.int/influenza/surveillance_monitoring/updates/EN_GIP_Influenza_transmission_zones.pdf). – Note: on a regroupé les données par pays disponibles à l'intérieur de zones géographiques plus larges caractérisées par des schémas similaires de transmission de la grippe en vue d'en donner une présentation plus générale (www.who.int/influenza/surveillance_monitoring/updates/EN_GIP_Influenza_transmission_zones.pdf).

Source: WHO Global Influenza Programme/ Flunet (www.who.int/flunet), 17 September 2018. – Programme mondial de lutte contre la grippe de l'OMS/Flunet (www.who.int/flunet), 17 septembre 2018.

During this period, no human cases of avian influenza A(H7N9) virus infection were reported. Since February 2013, a total of 1567 cases with 615 deaths have been reported.

One human case of avian influenza A(H9N2) virus infection was reported by China during this period.

During this period, 13 cases of A(H1N2)v virus infection and one case of A(H3N2)v virus infection were reported by the United States of America.

Antigenic and genetic characteristics of recent seasonal influenza viruses

Influenza A(H1N1)pdm09 viruses

The vast majority of A(H1N1)pdm09 viruses had HA gene sequences that belonged to phylogenetic subclade 6B.1 and encoded the additional HA1 amino acid substitutions S74R, S164T and I295V. There is increasing genetic diversification of the HA genes of 6B.1 viruses with several genetic subgroups emerging, including those with HA1 amino acid substitutions of S183P, T120A or H138Y. The antigenic characteristics of A(H1N1)pdm09 viruses were assessed with post-infection ferret antisera in haemagglutination inhibition (HI) assays, which indicated that almost all recent A(H1N1)pdm09 viruses were antigenically indistinguishable from the vaccine virus, egg-propagated A/Michigan/45/2015, and its cell culture-propagated equivalent.

Human serology studies used serum panels from children, adults and elderly adults who had received trivalent or quadrivalent inactivated vaccines, either of the composition recommended for the northern hemisphere 2017-2018 season (A/Michigan/45/2015 (H1N1) pdm09-like, A/Hong Kong/4801/2014 (H3N2)-like and B/Brisbane/60/2008-like viruses in trivalent vaccines, with B/Phuket/3073/2013-like viruses included in quadrivalent vaccines) or that recommended for the southern hemisphere 2018 season (A/Michigan/45/2015 (H1N1) pdm09-like, A/Singapore/INFIMH-16-0019/2016 (H3N2)-like and B/Phuket/3073/2013-like viruses in trivalent vaccines, with B/Brisbane/60/2008-like viruses included in quadrivalent vaccines).

Haemagglutination inhibition geometric mean titres (GMTs) of post-vaccination antibodies against some recent representative cell culture-propagated A(H1N1) pdm09 viruses were significantly reduced compared to HI titres to the cell culture- or egg-propagated reference virus A/Michigan/45/2015; however, for the majority of viruses tested post-vaccination GMTs were not reduced significantly.

Influenza A(H3N2) viruses

The majority of A(H3N2) viruses collected from February to September 2018 belonged to the phylogenetic clade 3C.2a. There has continued to be considerable genetic diversification of the HA and NA genes of viruses within this clade. Viruses in subclades 3C.2a1b or 3C.2a2 were most common, with subclade 3C.2a2 predominating. Viruses in clade 3C.3a continued to be detected at low levels in several parts of the world.

Pendant cette période, aucun cas humain d'infection par le virus de la grippe aviaire A(H7N9) n'a été rapporté. Depuis février 2013, 1567 cas au total, dont 615 décès, ont été notifiés.

Un cas humain d'infection par le virus de la grippe aviaire A(H9N2) a été notifié par la Chine pendant cette période.

Pendant cette même période, 13 cas d'infection par le virus A(H1N2)v et 1 cas d'infection par le virus A(H3N2)v ont été notifiés par les États-Unis d'Amérique.

Caractéristiques antigéniques et génétiques des virus grippaux saisonniers récents

Virus grippaux A(H1N1)pdm09

La grande majorité des virus A(H1N1)pdm09 présentaient des séquences géniques de l'hémagglutinine (HA) appartenant au sous-clade phylogénétique 6B.1 et codant pour les substitutions d'acides aminés de la sous-unité HA1 supplémentaires S74R, S164T et I295V. On observe une diversification génétique croissante des gènes HA parmi les virus 6B.1 avec plusieurs sous-groupes génétiques émergents, notamment ceux présentant les substitutions d'acides aminés de HA1 S183P, T120A ou H138Y. Les caractéristiques antigéniques des virus A(H1N1)pdm09 ont été déterminées par des épreuves d'inhibition de l'hémagglutination (IH) réalisées avec des antisérums de furet postinfection qui ont révélé que presque tous les virus A(H1N1)pdm09 récents étaient indiscernables sur le plan antigénique du virus vaccinal propagé sur œufs A/Michigan/45/2015 et de ses équivalents propagés en culture cellulaire.

Les études sérologiques chez l'homme ont utilisé des panels de sérums prélevés sur des enfants, des adultes et des personnes âgées ayant reçu des vaccins inactivés trivalents ou quadrivalents, respectant la composition recommandée pour la saison 2017-2018 dans l'hémisphère Nord (virus de type A/Michigan/45/2015 (H1N1)pdm09, A/Hong Kong/4801/2014 (H3N2) et B/Brisbane/60/2008) dans les vaccins trivalents, avec le virus de type B/Phuket/3073/2013 en plus dans les vaccins quadrivalents) ou celle recommandée pour la saison 2018 dans l'hémisphère Sud (virus de type A/Michigan/45/2015 (H1N1)pdm09, A/Singapore/INFIMH-16-0019/2016 (H3N2) et B/Phuket/3073/2013) dans les vaccins trivalents, avec le virus de type B/Brisbane/60/2008 en plus dans les vaccins quadrivalents).

La moyenne géométrique des titres (MGT) d'anticorps après la vaccination inhibant l'hémagglutination, dirigés contre certains virus A(H1N1)pdm09 représentatifs récents propagés en culture cellulaire, était significativement inférieure à la MGT d'anticorps dirigés contre le virus de référence A/Michigan/45/2015 propagé en culture cellulaire ou sur œufs; cependant, pour la majorité des virus testés, la MGT après la vaccination n'a pas significativement diminué.

Virus grippaux A(H3N2)

La majorité des virus A(H3N2) collectés de février à septembre 2018 appartenaient au clade phylogénétique 3C.2a. On constate toujours une diversification génétique considérable des gènes de l'hémagglutinine et de la neuraminidase au sein de ce clade. Les virus des sous-clades 3C.2a1b ou 3C.2a2 étaient les plus courants, le sous-clade 3C.2a2 étant prédominant. On continue de détecter des virus du clade 3C.3a à de faibles niveaux dans plusieurs parties du monde.

Antigenic characterisation of clade 3C.2a viruses continued to be technically difficult because a large proportion of viruses did not agglutinate red blood cells, preventing HI analysis of such viruses. Virus neutralisation assays have become the preferred method for determining the antigenic characteristics of A(H3N2) viruses.

Most recent A(H3N2) viruses were well inhibited by ferret antisera raised against cell culture-propagated reference viruses in clade 3C.2a including A/Singapore/INFIMH-16-0019/2016. In contrast, a significantly lower proportion of A(H3N2) viruses was inhibited well by ferret antisera raised against egg-propagated A/Singapore/INFIMH-16-0019/2016. HI and virus neutralisation assays with ferret antiserum panels showed that viruses in clades 3C.2a and 3C.3a were antigenically distinguishable and those in subclades 3C.2a1b and 3C.2a2 were also antigenically distinct (*Table 1*).

Human serology studies, using the serum panels described above, showed that HI GMTs of post-vaccination antibodies against many cell culture-propagated and some egg-propagated A(H3N2) viruses were reduced significantly compared to GMTs against the egg-propagated vaccine virus A/Singapore/INFIMH-16-0019/2016. When compared to results for cell culture-propagated A/Singapore/INFIMH-16-0019/2016, cell culture-propagated viruses did not show significant reductions in HI GMTs. In virus neutralisation tests, using the same serum panels, all cell culture-propagated A(H3N2) viruses tested showed significant reductions in GMTs when compared to GMTs against egg-propagated A/Singapore/INFIMH-16-0019/2016. Some of these viruses also showed significant reductions in GMTs when compared to GMTs against cell culture-propagated A/Singapore/INFIMH-16-0019/2016.

Influenza B viruses

Influenza B viruses of the B/Victoria/2/87 and the B/Yamagata/16/88 lineages co-circulated but those of the B/Yamagata lineage predominated globally. All available HA gene sequences of B/Yamagata lineage viruses belonged to genetic clade 3. In HI assays the vast majority of recently circulating B/Yamagata lineage viruses were well inhibited by post-infection ferret antisera raised against cell culture- and egg-propagated B/Phuket/3073/2013 viruses.

The HA gene sequences of the B/Victoria lineage viruses characterised belonged to genetic clade 1A; a steadily increasing proportion of viruses from many countries had a 2 amino acid deletion in HA (amino acids 162 and 163). During this period, 13 viruses from 5 countries were identified with a 3 amino acid deletion in HA (amino acids 162-164). Recent viruses without HA amino acid deletions were well inhibited by post-infection ferret antisera raised against B/Brisbane/60/2008-like cell culture-propagated viruses in HI assays, but viruses with HA amino acid deletions were poorly inhibited by these antisera. The great majority of viruses with the deletion of 2 amino acids in HA reacted well with ferret

La caractérisation antigénique des virus du clade 3C.2a demeure techniquement difficile car une grande proportion de virus n'a pas engendré d'agglutination des globules rouges, empêchant ainsi toute analyse par IH des virus en question. L'épreuve de neutralisation virale est devenue la méthode de choix pour déterminer les caractéristiques antigéniques des virus A(H3N2).

La plupart des virus A(H3N2) récents étaient bien inhibés par les antisérums de furet dirigés contre les virus de référence du clade 3C.2a propagés en culture cellulaire, notamment le virus A/Singapore/INFIMH-16-0019/2016. En revanche, une proportion sensiblement inférieure de virus A(H3N2) était bien inhibée par les antisérums de furet dirigés contre les virus A/Singapore/INFIMH-16-0019/2016 propagés sur œufs. Les épreuves d'inhibition de l'hémagglutination et de neutralisation virale utilisant des panels d'antisérums de furet ont montré que les virus des clades 3C.2a et 3C.3a étaient discernables sur le plan antigénique, de même que ceux des sous-clades 3C.2a1b et 3C.2a2 (*Tableau1*).

Des études sérologiques chez l'homme utilisant les panels de sérums décrits ci-dessus ont mis en évidence une diminution significative de la MGT d'anticorps après la vaccination inhibant l'hémagglutination dirigés contre de nombreux virus A(H3N2) propagés en culture cellulaire et contre certains virus A(H3N2) propagés sur œufs par rapport à la MGT obtenue contre le virus vaccinal propagé sur œufs A/Singapore/INFIMH-16-0019/2016. Comparés aux résultats obtenus pour le virus A/Singapore/INFIMH-16-0019/2016 propagé en culture cellulaire, les virus propagés en culture cellulaire n'ont pas engendré de réduction significative de la MGT d'anticorps inhibant l'hémagglutination. Dans les épreuves de neutralisation virale utilisant les mêmes panels de sérums, tous les virus A(H3N2) propagés en culture cellulaire testés ont montré des diminutions significatives de la MGT par rapport à la MGT contre le virus A/Singapore/INFIMH-16-0019/2016 propagé sur œufs. Certains de ces virus ont également engendré des baisses significatives de la MGT par rapport à la MGT contre le virus A/Singapore/INFIMH-16-0019/2016 propagé en culture cellulaire.

Virus de la grippe B

Une cocirculation des virus de la grippe B des lignées B/Victoria/2/87 et B/Yamagata/16/88 a été observée, avec une prédominance de la lignée B/Yamagata dans le monde. Toutes les séquences géniques disponibles de l'hémagglutinine des virus de la lignée B/Yamagata appartenaient au clade génétique 3. Lors des épreuves d'IH, la grande majorité des virus de cette lignée récemment en circulation était bien inhibée par des antisérums de furet postinfection dirigés contre les virus B/Phuket/3073/2013 propagés sur œufs et en culture cellulaire.

Les séquences géniques de l'hémagglutinine des virus de la lignée B/Victoria caractérisés appartenaient au clade génétique 1A; une proportion régulièrement croissante de virus provenant de nombreux pays présentait une délétion de 2 acides aminés dans la séquence de l'hémagglutinine (acides aminés 162 et 163). Au cours de cette période, 13 virus provenant de 5 pays ont été identifiés avec une délétion de 3 acides aminés dans la séquence de l'hémagglutinine (acides aminés 162 à 164). Les virus récents sans délétion d'acides aminés étaient bien inhibés par des antisérums de furet postinfection dirigés contre les virus de la souche B/Brisbane/60/2008 propagés en culture cellulaire lors des épreuves d'inhibition de l'hémagglutination, tandis que les virus présentant des délétions étaient faiblement

Table 1 **Antigenic analysis of influenza A(H3N2) viruses – Plaque reduction neutralisation (MDCK-SIAT)**
Tableau 1 **Analyse antigénique des virus de la grippe A(H3N2) – Neutralisation par réduction des plages de lyse (MDCK-SIAT)**

			Neutralisation titre – Titre de neutralisation			
				Post-infection ferret antisera – Antisérums de furet postinfection		
Viruses – Virus	**Passage history – Historique des passages**		A/Singapore/ INFIMH-16-0019/16	A/Singapore/ INFIMH-16-0019/16	A/Hong Kong/ 656/18	A/Switzerland/ 8060/17
			EGG 10^{-4}	SIAT	SIAT	Egg
	Ferret number – Numéro de furet		F41/17	F45/17	F25/18	
	Genetic group – Groupe génétique		3C.2a1	3C.2a1	3C.2a2	3C.2a2 F27/18
			2-fold	2-fold	2-fold	2-fold
Reference viruses – Virus de référence	**Passage history – Historique des passages**					
A/Singapore/INFIMH-16-0019/2016	3C.2a1	E5/E2 10^{-4}	2560	160	160	160
A/Singapore/INFIMH-16-0019/2016	3C.2a1	MDCK1/SIAT3/SIAT3	80	1280	160	80
A/Hong Kong/656/2018	3C.2a2	MDCK1/SIAT1 10^{-1}	40	640	2560	2560
A/Switzerland/8060/2017	3C.2a2	E6(Am2Al4)c57 10^{-5}	1280	320	5120	5120
Test viruses – Virus testés						
A/Belgium/S0846/2018	3C.2a1b	SIATx/SIAT1	<[1]	320	40	<
A/Vologda/RII-01/2018	3C.2a1b	MDCK1/SIAT1	40	160	40	<
A/Madrid/2172/2018	3C.2a1b	SIAT1	<	640	40	<
A/Iceland/90/2018	3C.2a1b	MDCK1/SIAT1	<	320	40	<
A/Belgium/S0428/2018	3C.2a2	SIATx/SIAT1	<	320	1280	1280
A/Belgium/G0278/2018	3C.2a2	SIATx/SIAT1	<	640	2560	2560
A/Lisboa/20/2018	3C.2a2	MDCK1/SIAT1	40	1280	2560	1280
A/Iceland/71/2018	3C.2a2	MDCK1/SIAT1	40	640	1280	1280
A/Mauritius/2263/2018	3C.2a2	SIAT1	80	1280	2560	2560
			Vaccine southern hemisphere 2018 – Vaccin hémisphère Sud 2018			

[1] Titres <10

antisera raised against both egg- and cell culture-propagated B/Colorado/06/2017-like viruses. However, viruses with the 3 amino acid deletion in HA reacted poorly with these ferret antisera.

Human serology studies, using the serum panels described above, showed moderate reductions in post-vaccination HI GMTs against representative recent viruses of the B/Victoria lineage with 2 or 3 amino acid deletions in HA when compared to egg- or cell culture-propagated B/Brisbane/60/2008-like reference viruses. Post-vaccination HI GMTs against most recent B/Yamagata lineage viruses were similar to, or somewhat reduced compared to those against cell culture-propagated B/Phuket/3073/2013-like reference viruses.

inhibés par ces antisérums. La grande majorité des virus avec délétion de 2 acides aminés dans la séquence de l'hémagglutinine a bien réagi avec les antisérums de furets dirigés contre les virus de type B/Colorado/06/2017 propagés sur œufs et en culture cellulaire. En revanche, les virus présentant la délétion des 3 acides aminés ont faiblement réagi avec ces antisérums.

Des études sérologiques chez l'homme utilisant les panels de sérums décrits ci-dessus ont mis en évidence des diminutions modérées de la GMT d'anticorps inhibant l'hémagglutination après la vaccination, dirigés contre des virus récents représentatifs de la lignée B/Victoria avec 2 ou 3 délétions d'acides aminés dans la séquence de l'hémagglutinine, comparativement aux virus de référence de type B/Brisbane/60/2008 propagés sur œufs ou en culture cellulaire. Les MGT d'anticorps après la vaccination dirigés contre les virus de la lignée B/Yamagata les plus récents étaient identiques à celles des anticorps dirigés contre les virus de référence de type B/Phuket/3073/2013 propagés en culture cellulaire, ou légèrement inférieures à celles-ci.

Resistance to influenza antiviral drugs

NA inhibitors

The detection of viruses with reduced susceptibility to the NA inhibitors was very rare among the 4801 viruses tested by the WHO Collaborating Centres[5] during this reporting period.

A(H1N1)pdm09

Of 1874 influenza A(H1N1)pdm09 viruses tested, 13 showed highly reduced inhibition (HRI) by one or more NA inhibitors. All 13 viruses, from Bosnia and Herzegovina, China, France, Mexico or the United States of America, carried an NA H275Y amino acid substitution.

A(H3N2)

Of 936 influenza A(H3N2) viruses tested, 4 showed reduced inhibition by one or more NA inhibitors. One was from Canada and carried an NA E119V amino acid substitution resulting in HRI by oseltamivir, one from Estonia showed an NA S334R substitution resulting in reduced inhibition (RI) by oseltamivir, one from Australia showed polymorphism at NA residue 224 (R224X: RI by 4 NA inhibitors) and another from Australia carried 2 substitutions in the NA (V303I, N342K) resulting in RI by oseltamivir and zanamivir.

Influenza B

Of the 485 influenza B/Victoria lineage viruses tested, 7 viruses demonstrated reduced inhibition by NA inhibitors. One virus from Canada carried an NA A245T amino acid substitution that conferred HRI by zanamivir. Four viruses from the United States of America contained NA D197E or G247D amino acid substitutions and 2 viruses from Ukraine contained an NA D197N substitution, all of which conferred RI by one or more of the NA inhibitors.

Of the 1506 B/Yamagata lineage viruses tested, 8 viruses demonstrated RI by NA inhibitors. Three viruses from the United States of America and one each from Australia, Belgium, China, China Hong Kong Special Administrative Region and Russian Federation carried NA I221T, R154K, D197N, R150K or T436P amino acid substitutions, all of which conferred RI by one or more of the NA inhibitors.

Polymerase inhibitor

Sensitivity to baloxavir marboxil, now licensed for use in Japan, was assessed for representative viruses collected there. Of 10 influenza A(H1N1)pdm09, 15 A(H3N2), one B/Victoria lineage and 16 B/Yamagata lineage viruses, none showed reduced susceptibility to baloxivir marboxil.

[5] See http://www.who.int/influenza/gisrs_laboratory/collaborating_centres/list/en/

Résistance aux antiviraux utilisés contre la grippe

Inhibiteurs de la NA

Parmi les 4801 virus testés par les centres collaborateurs de l'OMS[5] au cours de cette période, très rares étaient ceux qui présentaient une sensibilité réduite aux inhibiteurs de la neuraminidase.

A(H1N1)pdm09

Parmi les 1874 virus grippaux A(H1N1)pdm09 testés, 13 présentaient une sensibilité fortement réduite à un ou plusieurs inhibiteurs de la NA. Les 13 virus provenant de Bosnie-Herzégovine, de Chine, de France, du Mexique ou des États-Unis d'Amérique portaient tous une substitution d'acides aminés H275Y dans la séquence de la NA.

A(H3N2)

Parmi les 936 virus grippaux A(H3N2)pdm09 testés, 4 présentaient une sensibilité réduite à un ou plusieurs inhibiteurs de la NA. L'un provenait du Canada et portait la substitution d'acides aminés E119V dans la séquence de la NA entraînant une sensibilité fortement réduite à l'oseltamivir, un autre d'Estonie portait la substitution S334R engendrant une sensibilité réduite à l'oseltamivir, et deux autres d'Australie dont un présentait un polymorphisme au niveau du résidu 224 de la séquence de la NA (R224X : sensibilité réduite à 4 inhibiteurs de la NA) et l'autre 2 substitutions dans la séquence de la NA (V303I, N342K) entraînant une sensibilité réduite à l'oseltamivir et au zanamivir.

Grippe B

Parmi les 485 virus grippaux de la lignée B/Victoria testés, 7 ont montré une sensibilité réduite aux inhibiteurs de la NA. Un virus canadien était porteur de la substitution d'acides aminés A245T dans la séquence de la NA qui a engendré une sensibilité fortement réduite au zanamivir. Quatre virus aux États-Unis d'Amérique contenaient les substitutions d'acides aminés D197E ou G247D et deux virus en Ukraine la substitution D197N, tous entraînant une sensibilité réduite à un ou plusieurs inhibiteurs de la NA.

Parmi les 1506 virus de la lignée B/Yamagata testés, 8 ont montré une sensibilité réduite aux inhibiteurs de la NA. Trois virus aux États-Unis d'Amérique et un virus en Australie, en Belgique, en Chine, dans la Région administrative spéciale de Hong Kong (Chine) et en Fédération de Russie portaient les substitutions d'acides aminés I221T, R154K, D197N, R150K ou T436P dans la séquence de la NA, qui ont toutes engendré une sensibilité réduite à un ou plusieurs inhibiteurs de la NA.

Inhibiteur de polymérase

Au Japon, la sensibilité des virus représentatifs collectés sur place au baloxavir marboxil, dont l'utilisation est maintenant autorisée dans le pays, a été évaluée. Sur 10 virus grippaux A(H1N1)pdm09, 15 virus A(H3N2), 1 virus de la lignée B/Victoria et 16 virus de la lignée B/Yamagata, aucun n'a montré de sensibilité réduite au baloxivir marboxil.

[5] Voir http://www.who.int/influenza/gisrs_laboratory/collaborating_centres/list/en/

Recommended composition of influenza virus vaccines for use in the 2019 southern hemisphere influenza season

There was considerable variation in the predominant virus type circulating in different regions during the period February to September 2018. Influenza A(H1N1) pdm09 viruses predominated in many countries, while A(H3N2) viruses predominated in some and influenza B viruses circulated widely in most parts of the world.

The vast majority of influenza A(H1N1)pdm09 viruses belonged to genetic subclade 6B.1 and were antigenically indistinguishable from the vaccine virus A/Michigan/45/2015.

Influenza A(H3N2) viruses were associated with outbreaks in several countries. The majority of recent viruses were inhibited well by ferret antisera raised against cell culture-propagated A/Singapore/INFIMH-16-0019/2016-like viruses. In contrast, ferret antisera raised against egg-propagated A/Singapore/INFIMH-16-0019/2016-like viruses inhibited a smaller proportion of recently circulating viruses. Ferret antiserum raised against egg-propagated A/Switzerland/8060/2017 inhibited the majority of viruses tested from the predominating subclade 3C.2a2.

Influenza B viruses of the B/Yamagata lineage predominated in most regions of the world. Recent B/Yamagata lineage viruses were antigenically and genetically closely related to the vaccine virus B/Phuket/3073/2013. Influenza B viruses of the B/Victoria lineage were detected in low numbers but a substantial and increasing proportion of these viruses, containing a 2 amino acid deletion in the HA, were antigenically different from B/Brisbane/60/2008-like vaccine viruses but closely related to B/Colorado/06/2017-like viruses.

Lists of egg- or cell culture-propagated candidate vaccine viruses (CVVs) suitable for use in human vaccine production are available on the WHO website.[6] A list of reagents for vaccine standardisation, including those for this recommendation, can also be found on the WHO website. CVVs for zoonotic influenza viruses are listed on the same website.

As in previous years, national or regional authorities approve the composition and formulation of vaccines used in each country. National public health authorities are responsible for making recommendations regarding the use of the vaccine. WHO has published recommendations on the prevention of influenza.[7]

CVVs (including reassortants) and reagents for use in the laboratory standardization of inactivated vaccines may be obtained from:

(i) Immunobiology, Laboratories Branch, Medical Devices and Product Quality Division, Therapeutic Goods Administration, P.O. Box 100, Woden, ACT,

[6] Availability of CVVs and reagents: http://www.who.int/influenza/vaccines/virus/candidates_reagents/home

[7] See No. 47, 2012, pp. 461–476 (http://www.who.int/wer/2012/wer8747.pdf, accessed September 2018).

Composition recommandée des vaccins antigrippaux pour la saison grippale 2019 dans l'hémisphère Sud

Il y a eu des variations considérables dans le type de virus prédominant circulant dans différentes régions entre février et septembre 2018. Les virus grippaux A(H1N1)pdm09 prédominaient dans de nombreux pays, tandis que les virus A(H3N2) étaient majoritaires dans certains seulement, et les virus grippaux B circulaient largement dans la plupart des régions du monde.

La grande majorité des virus grippaux A(H1N1)pdm09 appartenait au sous-clade génétique 6B.1 et étaient indiscernables sur le plan antigénique du virus vaccinal A/Michigan/45/2015.

Des virus grippaux A(H3N2) ont été associés à des flambées épidémiques dans plusieurs pays. La majorité des virus récents étaient bien inhibés par les antisérums de furet dirigés contre les virus de type A/Singapore/INFIMH-16-0019/2016 propagés en culture cellulaire. En revanche, les antisérums de furet dirigés contre les virus de type A/Singapore/INFIMH-16-0019/2016 propagés sur œufs inhibaient une moindre proportion de virus circulants. L'antisérum de furet dirigé contre les virus A/Switzerland/8060/2017 propagés sur œufs inhibait la majorité des virus testés appartenant au sous-clade prédominant 3C.2a2.

Les virus grippaux B de la lignée B/Yamagata prédominaient dans la plupart des régions du monde. Les virus récents de la lignée B/Yamagata étaient étroitement apparentés sur les plans antigénique et génétique au virus vaccinal B/Phuket/3073/2013. Les virus grippaux B de la lignée B/Victoria ont été détectés en faible nombre, mais une proportion substantielle et croissante de ces virus, contenant une délétion de 2 acides aminés dans la séquence de l'hémagglutinine, était différente sur le plan antigénique des virus vaccinaux de type B/Brisbane/60/2008 mais étroitement apparentée aux virus de type B/Colorado/06/2017.

Le site Web[6] de l'OMS fournit la liste des virus vaccinaux candidats, propagés sur œufs ou en culture cellulaire, se prêtant à la production de vaccins humains. Une liste des réactifs destinés à la standardisation des vaccins, y compris ceux qui sont concernés par la présente recommandation, est également disponible sur le site Web de l'OMS. Les virus vaccinaux candidats pour les virus grippaux zoonotiques y sont également répertoriés.

Comme les années précédentes, les autorités nationales ou régionales approuvent la composition et la formulation des vaccins utilisés dans chaque pays. Les autorités nationales de santé publique sont chargées de formuler des recommandations concernant l'utilisation de ces vaccins. L'OMS a publié des recommandations relatives à la prévention de la grippe.[7]

Les virus vaccinaux candidats (y compris réassortis) et les réactifs nécessaires à la standardisation en laboratoire des vaccins inactivés peuvent être obtenus auprès des organismes suivants:

i) Immunobiology, Laboratories Branch, Medical Devices and Product Quality Division, Therapeutic Goods Administration, P.O. Box 100, Woden ACT, 2606 Australie (télécopie:

[6] Disponibilité des virus vaccinaux candidats et des réactifs: http://www.who.int/influenza/vaccines/virus/candidates_reagents/home

[7] Voir N° 47, 2012, pp. 461-476. Disponible à l'adresse: http://www.who.int/wer/2012/wer8747.pdf, consulté en septembre 2018.

It is recommended that egg based quadrivalent vaccines for use in the 2019 southern hemisphere influenza season contain the following:

- **an A/Michigan/45/2015 (H1N1)pdm09-like virus;**
- **an A/Switzerland/8060/2017 (H3N2)-like virus;**
- **a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and**
- **a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).**

It is recommended that egg based trivalent vaccines for use in the 2019 southern hemisphere influenza season contain the following:

- **an A/Michigan/45/2015 (H1N1)pdm09-like virus;**
- **an A/Switzerland/8060/2017 (H3N2)-like virus; and**
- **a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage).**

It is recommended that the A(H3N2) component of non-egg based vaccines for use in the 2019 southern hemisphere influenza season be an A/Singapore/INFIMH-16-0019/2016-like virus together with the other vaccine components as indicated above.

Il est recommandé que les vaccins quadrivalents préparés sur œufs destinés à être utilisés pendant la saison grippale 2019 dans l'hémisphère Sud contiennent :

- **un virus de type A/Michigan/45/2015 (H1N1)pdm09;**
- **un virus de type A/Switzerland/8060/2017 (H3N2);**
- **un virus de type B/Colorado/06/2017 (lignée B/Victoria/2/87); et**
- **un virus de type B/Phuket/3073/2013 (lignée B/Yamagata/16/88).**

Il est recommandé que les vaccins trivalents préparés sur œufs destinés à être utilisés pendant la saison grippale 2019 dans l'hémisphère Sud contiennent:

- **un virus de type A/Michigan/45/2015 (H1N1)pdm09;**
- **un virus de type A/Switzerland/8060/2017 (H3N2); et**
- **un virus de type B/Colorado/06/2017 (lignée B/Victoria/2/87).**

Il est recommandé que le composant A(H3N2) des vaccins non préparés sur œufs destinés à être utilisés pendant la saison grippale 2019 dans l'hémisphère Sud soit un virus de type A/Singapore/INFIMH-16-0019/2016 utilisé avec les autres composants vaccinaux indiqués ci-dessus.

2606, Australia (fax: +61 2 6232 85 64; email: influenza.reagents@health.gov.au; website: http://www.tga.gov.au);

(ii) Division of Virology, National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), Blanche Lane, South Mimms, Potters Bar, Hertfordshire, EN6 3QG, UK (fax: +44 17 0764 1050; email: enquiries@nibsc.org; website: http://www.nibsc.org/science_and_research/virology/influenza_resource_.aspx);

(iii) Division of Biological Standards and Quality Control, Center for Biologics Evaluation and Research, Food and Drug Administration, 10903 New Hampshire Avenue, Silver Spring, Maryland, 20993, USA (fax: +1 301 480 9748; email: cbershippingrequests@fda.hhs.gov);

(iv) Influenza Virus Research Center, National Institute of Infectious Diseases, 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japan (fax: +81 425 616 156; email: flu-vaccine@nih.go.jp);

Requests for reference viruses should be addressed to:

(i) WHO Collaborating Centre for Reference and Research on Influenza, VIDRL, Peter Doherty Institute, 792 Elizabeth Street, Melbourne, Victoria 3000,

+61 2 6232 85 64; courriel: influenza.reagents@health.gov.au; site Web: http://www.tga.gov.au);

ii) Division of Virology, National Institute for Biological Standards and Control, a centre of the Medecine and Healthcare products Regulatory Agency (MHRA), Blanche Lane, South Mimms, Potters Bar, Hertfordshire, EN6 3QG, Royaume-Uni (télécopie: +44 17 0764 1050; courriel: enquiries@nibsc.hpa.org.uk; site Web: http://www.nibsc.org/science_and_research/virology/influenza_resource_.aspx);

iii) Division of Biological Standards and Quality, Center for Biologics Evaluation and Research, Food and Drug Administration, 10903 New Hampshire Avenue, Silver Spring, Maryland, 20993, États-Unis d'Amérique (télécopie: +1 301 480 9748; courriel: cbershippingrequests@fda.hhs.gov);

iv) Centre de recherche sur le virus grippal, Institut national des maladies infectieuses, 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japon (télécopie: +81 425 616 156; courriel: flu-vaccine@nih.go.jp).

Les souches de référence peuvent être obtenues en s'adressant aux organismes suivants:

i) Centre collaborateur OMS de référence et de recherche pour la grippe, VIDRL, Peter Doherty Institute, 792 Elizabeth Street, Melbourne, Victoria 3000, Australie (télécopie:

Australia (fax: +61 3 9342 93 29; email: whoflu@influenzacentre.org; website: http://www.influenzacentre.org);

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WHO provides fortnightly updates[8] of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website.[9]

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+61 3 9342 93 29; courriel: whoflu@influenzacentre.org; site Web: http://www.influenzacentre.org);

ii) Centre collaborateur OMS de référence et de recherche pour la grippe, Institut national des maladies infectieuses, Gakuen 4-7-1, Musashi-Murayama, Tokyo 208-0011, Japon (télécopie: +81 425 616 149 ou +81 425 652 498; courriel: whocc-flu@nih.go.jp);

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L'OMS actualise les informations sur l'activité grippale dans le monde toutes les 2 semaines.[8] D'autres informations relatives à la surveillance de la grippe peuvent être obtenues sur le site Web du Programme mondial de lutte contre la grippe de l'OMS.[9]

Remerciements

Les recommandations sur la composition des vaccins formulées par l'OMS reposent sur le travail accompli tout au long de l'année par le Système mondial OMS de surveillance de la grippe et de riposte (GISRS). Nous remercions les centres nationaux de lutte contre la grippe du GISRS, ainsi que les laboratoires non-membres du GISRS, notamment ceux du Réseau d'experts sur la grippe animale (OFFLU) de l'OIE/FAO, qui ont fourni des informations, des échantillons cliniques, des virus et d'autres données associées; les centres collaborateurs du GISRS de l'OMS pour leur caractérisation détaillée et leur analyse complète des virus; l'Université de Cambridge pour son travail de cartographie antigénique et d'analyse phylogénétique; les laboratoires essentiels de réglementation OMS du GISRS pour leurs analyses complémentaires des virus et leurs contributions d'ordre réglementaire; et les laboratoires participant à la production de virus réassortis à forte capacité de croissance/rendement destinés à servir de virus vaccinaux candidats. Nous tenons également à remercier l'Initiative mondiale d'échange des données sur la grippe aviaire (GISAID) pour la base de données EpiFlu et d'autres banques de données qui ont permis le partage des séquences génétiques et d'informations associées; les groupes de modélisation produisant des prévisions sur l'adéquation des virus; et le consortium Global Influenza Vaccine Effectiveness (GIVE) qui a fourni à titre confidentiel des estimations sur l'efficacité des vaccins antigrippaux. ■

[8] See http://www.who.int/influenza/surveillance_monitoring/updates/en/

[9] Website of the WHO Global Influenza Programme: http://www.who.int/influenza

[8] Voir http://www.who.int/influenza/surveillance_monitoring/updates/en/

[9] Site Web du Programme mondial de lutte contre la grippe: http://www.who.int/influenza/fr

Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness

September 2018

The development of influenza candidate vaccine viruses (CVVs), coordinated by WHO, remains an essential component of the overall global strategy for pandemic preparedness.

Selection and development of CVVs are the first steps towards timely vaccine production and do not imply a recommendation for initiating manufacture. National authorities may consider the use of one or more of these CVVs for pilot lot vaccine production, clinical trials and other pandemic preparedness purposes based on their assessment of public health risk and need.

Zoonotic influenza viruses continue to be identified and evolve both genetically and antigenically, leading to the need for additional CVVs for pandemic preparedness purposes. Changes in the genetic and antigenic characteristics of these viruses relative to existing CVVs, and their potential risks to public health, justify the need to select and develop new CVVs.

This document summarizes the genetic and antigenic characteristics of recent zoonotic influenza viruses and related viruses circulating in animals[1] that are relevant to CVV updates. Institutions interested in receiving these CVVs should contact WHO at gisrs-whohq@who.int or the institutions listed in announcements published on the WHO website.[2]

(1) Influenza A(H5)

Since their emergence in 1997, highly pathogenic avian influenza (HPAI) A(H5) viruses of the A/goose/Guangdong/1/96 haemagglutinin (HA) lineage have become enzootic in some countries, have infected wild birds and continue to cause outbreaks in poultry and sporadic human infections. These viruses have diversified genetically and antigenically, including the emergence of viruses with replacement of the N1 gene segment by N2, N3, N5, N6, N8 or N9 gene segments, leading to the need for multiple CVVs. This summary provides updates on the characterisation of A/goose/Guangdong/1/96-lineage A(H5) viruses and the current status of the development of influenza A(H5) CVVs.

[1] For information relevant to other notifiable influenza virus infections in animals refer to: http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home

[2] See http://www.who.int/influenza/vaccines/virus/candidates_reagents/home/en/

Caractéristiques génétiques et antigéniques des virus grippaux zoonotiques et mise au point de virus vaccinaux candidats en vue de la préparation à une pandémie

Septembre 2018

La mise au point de virus vaccinaux candidats contre la grippe, coordonnée par l'OMS, demeure une composante essentielle de la stratégie mondiale globale de préparation aux pandémies.

La sélection et la mise au point de virus vaccinaux candidats représentent les premières étapes vers la production en temps utile de vaccins, mais n'impliquent pas qu'il soit recommandé d'en démarrer la fabrication. Les autorités nationales peuvent envisager d'utiliser un ou plusieurs de ces virus vaccinaux candidats pour la production de lots pilotes de vaccins, la réalisation d'essais cliniques et d'autres opérations de préparation à une pandémie, en fonction de leur évaluation des risques et des besoins pour la santé publique.

On continue d'identifier des virus grippaux zoonotiques, qui évoluent aussi bien sur le plan génétique qu'antigénique, entraînant la nécessité de mettre au point des virus vaccinaux candidats supplémentaires pour se préparer à une éventuelle pandémie. L'évolution des caractéristiques génétiques et antigéniques de ces virus par rapport aux virus vaccinaux candidats existants et les risques potentiels qui en résultent pour la santé publique justifient la sélection et la mise au point de nouveaux virus vaccinaux candidats.

Le présent document récapitule les caractéristiques génétiques et antigéniques des virus grippaux zoonotiques récents, ainsi que des virus apparentés circulant chez les animaux,[1] utiles pour l'actualisation des virus vaccinaux candidats. Les institutions souhaitant recevoir ces virus vaccinaux candidats devront prendre contact avec l'OMS, à l'adresse gisrs-whohq@who.int, ou avec les institutions dont les noms figurent dans les communiqués publiés sur le site Web de l'OMS.[2]

1) Grippe A(H5)

Depuis leur émergence en 1997, des virus de la grippe aviaire A(H5) hautement pathogènes présentant le gène de l'hémagglutinine (HA) de la lignée A/goose/Guangdong/1/96 sont devenus enzootiques dans certains pays, ont infecté les oiseaux sauvages et continuent de provoquer des flambées épidémiques parmi les volailles, ainsi que des infections sporadiques chez l'homme. Ces virus se sont diversifiés sur le plan génétique et antigénique, notamment par l'apparition de virus porteurs d'une substitution du segment génique N1 par des segments N2, N3, N5, N6, N8 ou N9, ce qui impose de mettre au point plusieurs virus vaccinaux candidats. Le présent résumé fait le point sur la caractérisation des virus A(H5) de la lignée A/goose/Guangdong/1/96 et sur l'état d'avancement actuel de la préparation des virus vaccinaux candidats contre la grippe A(H5).

[1] Pour toute information relative à la notification d'autres infections par les virus grippaux chez l'animal, consulter: http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home/index/newlang/fr?

[2] Voir http://www.who.int/influenza/vaccines/virus/candidates_reagents/home/en/

Influenza A(H5) activity from 20 February to 24 September 2018

One A(H5N6) human infection in China, where A(H5) infections have also been detected in birds, was reported to WHO. Since 2003 there have been 860 and 20 confirmed human infections with A(H5N1) and A(H5N6) viruses, respectively. A/goose/Guangdong/1/96-lineage A(H5) viruses were detected in poultry and wild birds in many countries (*Table 1*).

Antigenic and genetic characteristics of influenza A(H5) viruses

The nomenclature for phylogenetic relationships among the HA genes of A/goose/Guangdong/1/96-lineage A(H5) viruses is defined in consultation with representatives of WHO, the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE) and academic institutions.[3]

A(H5) viruses circulating and characterised from 20 February to 24 September 2018 belong to the following clades:

Clade 2.3.2.1a viruses were detected in birds in Bangladesh, Bhutan, India and Nepal (*Figure 1*). An increasing proportion of viruses with HA1 amino acid substitutions at positions 154 and 189, which are both within known antigenic sites, reacted poorly with post-infection ferret antiserum raised against the CVVs derived from A/duck/Bangladesh/19097/2013 (*Table 2*).

Clade 2.3.2.1c viruses were detected in birds in Cambodia, Indonesia, Myanmar, Nigeria, Togo and Viet Nam. Representative viruses from these countries were genetically similar to viruses detected in previous periods and reacted with post-infection ferret antisera raised against available CVVs, albeit with reduced titres in some instances.

Clade 2.3.4.4 viruses were detected in a human, birds and environmental samples in China and in birds in an additional 22 countries in Africa, Asia and Europe (*Table 1*). Recently characterised clade 2.3.4.4 viruses showed considerable genetic diversity, similar to what has been seen in previous periods, but the majority of viruses tested remained well inhibited by ferret antisera raised against A/chicken/Viet Nam/NCVD-15A59/2015, A/Hubei/29578/2016, A/duck/Hyogo/1/2016, their corresponding CVVs or closely related viruses. The human A(H5N6) case was a 42-year-old male who reported exposure to poultry and recovered from the infection. Sequence information on the virus from this individual was not available at the time of the consultation and clade designation was inferred based on virus subtype.

Activité de la grippe A(H5) du 20 février au 24 septembre 2018

La Chine a notifié à l'OMS une infection humaine par la grippe A(H5N6) et également signalé des infections par la grippe A(H5) chez les oiseaux. Depuis 2003, il y a eu 860 et 20 infections humaines confirmées par les virus A(H5N1) et A(H5N6), respectivement. Des virus A(H5) de la lignée A/goose/Guangdong/1/96 ont été détectés parmi les volailles et les oiseaux sauvages dans de nombreux pays (*Tableau 1*).

Caractéristiques antigéniques et génétiques des virus grippaux A(H5)

La nomenclature des liens de parenté phylogénétiques existant entre les gènes de l'hémagglutinine des virus grippaux A(H5) de la lignée A/goose/Guangdong/1/96 est définie en consultation avec des représentants de l'OMS, de l'Organisation des Nations Unies pour l'alimentation et l'agriculture (FAO), de l'Organisation mondiale de la Santé animale (OIE) et d'établissements universitaires.[3]

Les virus A(H5) circulant et caractérisés entre le 20 février et le 24 septembre 2018 appartenaient aux clades suivants:

Clade 2.3.2.1a: des virus de ce clade ont été détectés chez des oiseaux au Bangladesh, au Bhoutan, en Inde et au Népal (*Figure 1*). Une proportion croissante de virus présentant des substitutions d'acides aminés au niveau du gène HA1 aux positions 154 et 189, qui se trouvent toutes deux dans des sites antigéniques connus, ont mal réagi avec l'antisérum de furet post-infection dirigé contre les virus vaccinaux candidats dérivés de la lignée A/duck/Bangladesh/19097/2013 (*Tableau 2*).

Clade 2.3.2.1c: des virus de ce clade ont été détectés chez des oiseaux au Cambodge, en Indonésie, au Myanmar, au Nigéria, au Togo et au Viet Nam. Les virus représentatifs de ces pays étaient génétiquement similaires aux virus détectés au cours des périodes précédentes et ont réagi avec des antisérums de furets post-infection dirigés contre les virus vaccinaux candidats disponibles, mais avec des titres réduits dans certains cas.

Clade 2.3.4.4: des virus de ce clade ont été détectés dans des échantillons prélevés chez l'homme, les oiseaux et dans l'environnement en Chine et chez les oiseaux dans 22 autres pays en Afrique, en Asie et en Europe (*Tableau 1*). Les virus du clade 2.3.4.4 récemment caractérisés présentaient une diversité génétique considérable, comme ce qui a été observé au cours des périodes précédentes, mais la majorité des virus testés demeuraient bien inhibés par les antisérums de furets dirigés contre les lignées A/chicken/Viet Nam/NCVD-15A59/2015, A/Hubei/29578/2016, A/duck/Hyogo/1/2016, les virus vaccins candidats correspondants, ou les virus étroitement apparentés. Le cas humain A(H5N6) était un homme âgé de 42 ans qui a déclaré avoir été exposé à de la volaille et qui a guéri de l'infection. Les données sur la séquence virale provenant de cette personne n'étaient pas disponibles au moment de la consultation et la désignation du clade a été déduite d'après le sous-type de virus.

[3] See http://onlinelibrary.wiley.com/doi/10.1111/irv.12324/epdf

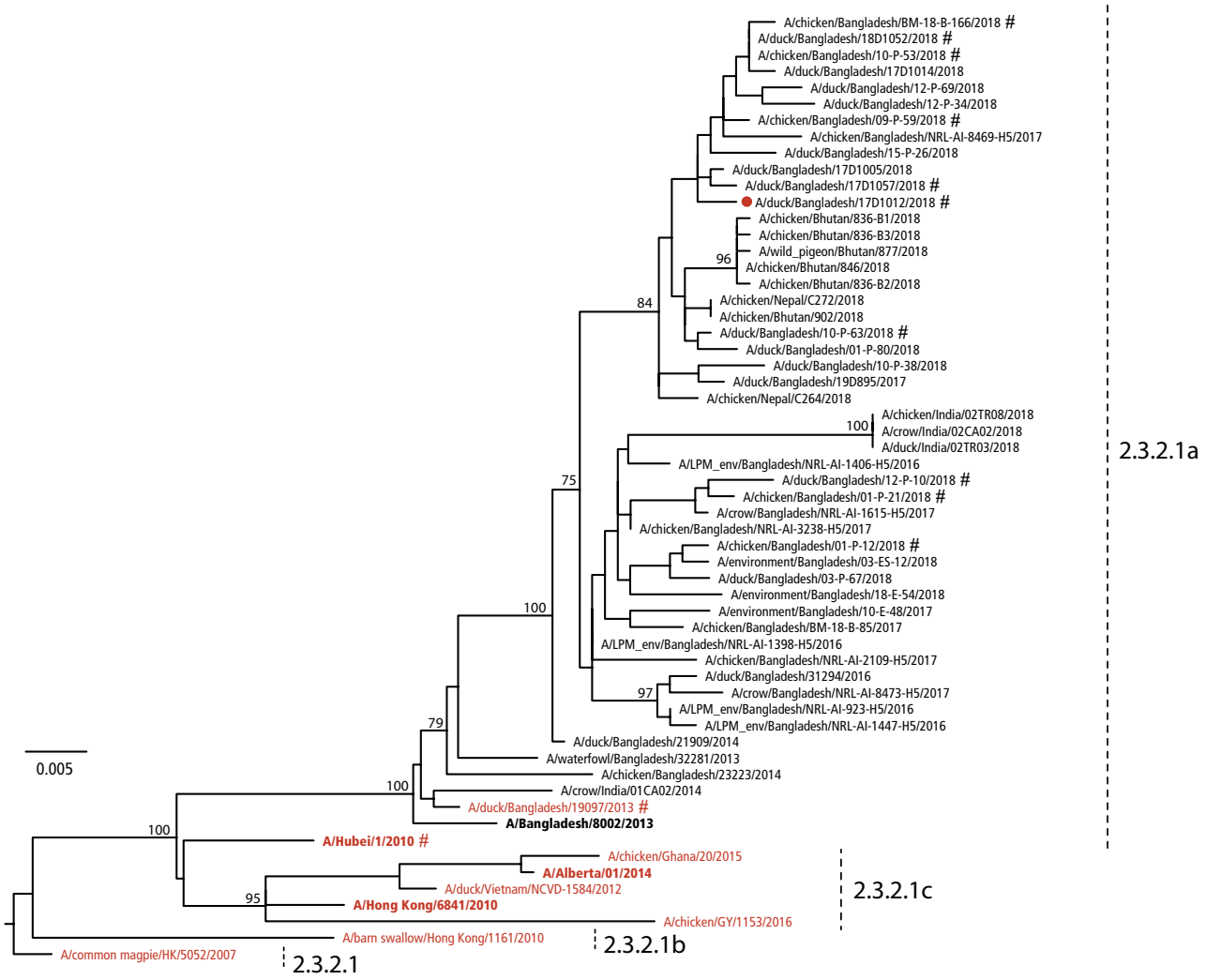
[3] Voir http://onlinelibrary.wiley.com/doi/10.1111/irv.12324/epdf

Table 1 **Recent A(H5) activity reported**
Tableau 1 **Activité récente de la grippe A(H5)**

Country, area or territory – Pays, zone ou territoire	Host – Hôte	Genetic clade (subtype) – Clade génétique (sous-type)
Bangladesh	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.2.1a (H5N1) 2.3.2.1a (H5N1/N2)
Bhutan – Bhoutan	Poultry – Volaille	2.3.2.1a
Bulgaria – Bulgarie	Poultry – Volaille	2.3.4.4 (H5N8)
Cambodia – Cambodge	Poultry – Volaille	2.3.2.1c (H5N1)
China – Chine	Human (1)[a] – Humain (1)[a] Poultry – Volaille	Unknown (H5N6) – Inconnu (H5N6) 2.3.4.4 (H5N6); unknown (H5N1) – 2.3.4.4 (H5N6); inconnu (H5N1)
China, Hong Kong SAR – Chine, RAS de Hong Kong	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
China, Taiwan – Chine, Taïwan	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N2)
Denmark – Danemark	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
Egypt – Égypte	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
Finland – Finlande	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
Germany – Allemagne	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N6) 2.3.4.4 (H5N6)
India – Inde	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.2.1a (H5N1) 2.3.2.1a (H5N1)
Indonesia – Indonésie	Poultry – Volaille	2.3.2.1c (H5N1)
Iran (Islamic Republic of) – Iran (République islamique d')	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N8) 2.3.4.4 (H5N6/8)
Iraq	Poultry – Volaille	2.3.4.4 (H5N8)
Ireland – Irlande	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
Italy – Italie	Poultry – Volaille	2.3.4.4 (H5N8)
Japan – Japon	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N6) 2.3.4.4 (H5N6)
Malaysia – Malaisie	Poultry – Volaille	Unknown (H5) – Inconnu (H5)
Myanmar	Poultry – Volaille	2.3.2.1c (H5N1); 2.3.4.4 (H5N6)
Nepal – Népal	Poultry – Volaille	2.3.2.1a (H5N1)
Netherlands – Pays-Bas	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N6) 2.3.4.4 (H5N6)
Nigeria – Nigéria	Poultry – Volaille	2.3.2.1c (H5N1)
Republic of Korea – République de Corée	Poultry – Volaille	2.3.4.4 (H5N6)
Russian Federation – Fédération de Russie	Poultry – Volaille	2.3.4.4 (H5N2/8)
Saudi Arabia – Arabie saoudite	Poultry – Volaille	2.3.4.4 (H5N8)
Slovakia – Slovaquie	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
South Africa – Afrique du sud	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N8) 2.3.4.4 (H5N8)
Sweden – Suède	Wild birds – Oiseaux sauvages Poultry – Volaille	2.3.4.4 (H5N6) 2.3.4.4 (H5N6)
Togo	Wild birds – Oiseaux sauvages	2.3.2.1c (H5N1)
United Kingdom – Royaume-Uni	Wild birds – Oiseaux sauvages	2.3.4.4 (H5N6)
Viet Nam	Poultry – Volaille	2.3.2.1c (H5N1); 2.3.4.4 (H5N6)

[a] Numbers in parentheses denote the number of human cases reported to WHO within reporting period (20 February to 24 September 2018). – Les chiffres entre parenthèses indiquent le nombre de cas humains notifiés à l'OMS au cours de cette période (du 20 février au 24 septembre 2018).

Figure 1 **Phylogenetic relationships of A(H5) clade 2.3.2.1 haemagglutinin genes**
Figure 1 **Classification phylogénétique des gènes de l'hémagglutinine des virus grippaux A(H5) appartenant au clade 2.3.2.1**



The candidate vaccine viruses (CCV) that are available or in preparation appear in red. The proposed CCV is indicated by (•); all human viruses are in **bold font**. The viruses tested in haemagglutination inhibition assay are indicated by hashes (#). The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes. – Les virus vaccinaux candidats disponibles ou en préparation apparaissent en rouge. Le virus vaccinal candidat proposé est indiqué par (•); tous les virus humains sont indiqués en **caractères gras**. Les virus testés au moyen de l'épreuve d'inhibition de l'hémagglutination sont indiqués par le symbole (#). La barre d'échelle représente le nombre de substitutions par site. Les valeurs de boostrap supportant la topologie de l'arbre sont indiquées au-dessus des nœuds sélectionnés.

Influenza A(H5) candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, a new A/duck/Bangladesh/17D1012/2018-like A(H5N1) CVV is proposed. The available and pending A(H5) CVVs are listed in *Table 3*.

Virus candidats destinés à la préparation d'un vaccin contre la grippe A(H5)

Au vu des données antigéniques, génétiques et épidémiologiques actuelles, un nouveau virus vaccinal candidat de type A/duck/Bangladesh/17D1012/2018 est proposé. Les virus vaccinaux candidats A(H5) disponibles et en attente sont recensés dans le *Tableau 3*.

(2) Influenza A(H7)

Human infections with avian influenza A(H7N9) viruses were first reported to WHO on 31 March 2013. A(H7N9) viruses are enzootic in poultry in China, and reassortment with A(H9N2) and other viruses has generated multiple genotypes. This summary provides updates on the characterisation of A/Anhui/1/2013 HA lineage

2) Grippe A(H7)

Les premiers cas d'infection humaine par des virus grippaux aviaires A(H7N9) ont été notifiés à l'OMS le 31 mars 2013. Les virus A(H7N9) sont enzootiques parmi les volailles en Chine et leur réassortiment avec les virus A(H9N2) et d'autres virus a continué de produire de nombreux génotypes. Le présent résumé fait le point sur la caractérisation des virus A(H7) de

Table 2 **Haemagglutination inhibition assays of clade 2.3.2.1a influenza A(H5N1) viruses**
Tableau 2 **Épreuves d'inhibition de l'hémagglutination obtenues avec les virus grippaux A(H5N1) appartenant au clade 2.3.2.1a**

	Clade	VN/1203	RG30	SJ001
Reference antigens – Antigènes de référence				
A/Viet Nam/1203/2004	1	**160**	40	<10
A/Hubei/1/2010 PR8 IDCDC-RG30	2.3.2.1a	<10	**160**	80
A/duck/Bangladesh/19097/2013 SJ001	2.3.2.1a	<10	40	**160**
Test antigens – Antigènes d'épreuve				
A/duck/Bangladesh/12-P-10/2018	2.3.2.1a	<10	20	10
A/chicken/Bangladesh/01-P-12/2018	2.3.2.1a	<10	<10	<10
A/chicken/Bangladesh/01-P-21/2018	2.3.2.1a	<10	20	20
A/chicken/Bangladesh/10-P-53/2018	2.3.2.1a	<10	<10	<10
A/chicken/Bangladesh/09-P-59/2018	2.3.2.1a	<10	10	<10
A/duck/Bangladesh/10-P-63/2018	2.3.2.1a	<10	<10	<10
A/duck/Bangladesh/17D1012/2018	2.3.2.1a	<10	10	<10
A/duck/Bangladesh/17D1057/2018	2.3.2.1a	<10	<10	<10
A/duck/Bangladesh/18D1052/2018	2.3.2.1a	<10	<10	<10
A/chicken/Bangladesh/BM-18-B-166/2018	2.3.2.1a	<10	<10	<10

Numbers in **bold** indicate homologous antiserum/antigen titres. – Les chiffres en caractères **gras** indiquent les titres d'antigènes/d'antisérum homologue.

A(H7) viruses and the current status of the development of corresponding CVVs.

Influenza A(H7) activity from 20 February to 24 September 2018

No human infections with A(H7N9) viruses were reported in this period. The total number of human cases reported since 2013 is 1567, with a case fatality rate of 39%. A(H7) viruses were detected in birds and environmental samples in China, albeit at low levels, and in duck meat smuggled into Japan.

Antigenic and genetic characteristics of influenza A(H7) viruses

Both highly pathogenic (HP) and low pathogenic (LP) avian influenza viruses were detected in birds and environmental samples in China. The HP viruses have accumulated a number of HA amino acid substitutions relative to viruses detected in previous periods and one HP virus has replaced the N9 NA with an N6 NA. The virus detected in Japan was a HP virus that has replaced the N9 NA with an N3 NA. Antigenic characterisation of recent A(H7N9) viruses suggests that they are well covered by existing CVVs; however, the A(H7N3) virus from Japan had reduced reactivity with post-infection ferret antisera raised against available CVVs.

la lignée A/Anhui/1/2013 et sur l'état d'avancement actuel de la préparation des virus vaccinaux candidats correspondants.

Activité de la grippe A(H7) du 20 février au 24 septembre 2018

Aucun cas humain d'infection par un virus A(H7N9) n'a été notifié pendant cette période. Au total, depuis 2013, 1567 cas humains ont été notifiés avec un taux de létalité de 39%. Des virus A(H7) ont été détectés dans des échantillons prélevés chez les oiseaux et dans l'environnement en Chine, bien qu'à de faibles taux, et dans de la viande de canard introduite clandestinement au Japon.

Caractéristiques antigéniques et génétiques des virus grippaux A(H7)

Des virus de la grippe aviaire hautement pathogènes et faiblement pathogènes ont été détectés dans des échantillons prélevés chez les oiseaux et dans l'environnement en Chine. Les virus hautement pathogènes ont accumulé un certain nombre de substitutions d'acides aminés dans le gène HA par rapport aux virus détectés lors les périodes précédentes et un virus hautement pathogène a remplacé la noradrénaline (NA) N9 par une NA N6. Le virus détecté au Japon était un virus hautement pathogène qui a remplacé la NA N9 par une NA N3. La caractérisation antigénique des virus A(H7N9) récents suggère qu'ils sont bien couverts par les virus vaccinaux candidats existants; cependant, le virus A(H7N3) du Japon montrait une réactivité réduite avec les antisérums de furet post-infection dirigés contre les virus vaccinaux candidats disponibles.

Table 3 **Status of influenza A(H5) candidate vaccine virus development**
Tableau 3 **État d'avancement dans la mise au point des virus vaccinaux candidats A(H5)**

Candidate vaccine viruses (like viruses) – Virus vaccinaux candidats (similaires aux virus)	**Clade**	**Institution***	**Available – Disponible**
CDC-RG (A/Viet Nam/1203/2004)	1	CDC	Yes – Oui
SJRG-161052 (A/Viet Nam/1203/2004)	1	SJCRH	Yes – Oui
NIBRG-14 (A/Viet Nam/1194/2004)	1	NIBSC	Yes – Oui
NIBRG-88 (A/Cambodia/R0405050/2007)	1.1	NIBSC	Yes – Oui
IDCDC-RG34B (A/Cambodia/X0810301/2013)	1.1.2	CDC	Yes – Oui
SJRG-166614 (A/duck/Hunan/795/2002)	2.1.1	SJCRH/HKU	Yes – Oui
CDC-RG2 (A/Indonesia/5/2005)	2.1.3.2	CDC	Yes – Oui
NIIDRG-9 (A/Indonesia/NIHRD11771/2011)	2.1.3.2a	NIID	Yes – Oui
SJRG-163222 (A/bar-headed goose/Qinghai/1A/2005)	2.2	SJCRH/HKU	Yes – Oui
IBCDC-RG7 (A/chicken/India/NIV33487/2006)	2.2	CDC/NIV	Yes – Oui
SJRG-163243 (A/whooper swan/Mongolia/244/2005)	2.2	SJCRH	Yes – Oui
IDCDC-RG11 (A/Egypt/2321-NAMRU3/2007)	2.2.1	CDC	Yes – Oui
NIBRG-23 (A/turkey/Turkey/1/2005)	2.2.1	NIBSC	Yes – Oui
IDCDC-RG29 (A/Egypt/N03072/2010)	2.2.1	CDC	Yes – Oui
IDCDC-RG13 (A/Egypt/3300-NAMRU3/2008)	2.2.1.1	CDC	Yes – Oui
NIBRG-306 (A/Egypt/N04915/2014)	2.2.1.2	NIBSC	Yes – Oui
SJRG-166615 (A/common magpie/Hong Kong/5052/2007)	2.3.2.1	SJCRH/HKU	Yes – Oui
IDCDC-RG30 (A/Hubei/1/2010)	2.3.2.1a	CDC	Yes – Oui
SJ007 (A/duck/Bangladesh/19097/2013)	2.3.2.1a	SJCRH	Yes – Oui
SJ003 (A/barn swallow/Hong Kong/D10-1161/2010)	2.3.2.1b	SJCRH/HKU	Yes – Oui
NIBRG-301 (A/duck/Viet Nam/NCVD-1584/2012)	2.3.2.1c	NIBSC	Yes – Oui
SJ002 (A/chicken/Hong Kong/AP156/2008)	2.3.4	SJCRH/HKU	Yes – Oui
IBCDC-RG6 (A/Anhui/1/2005)	2.3.4	CDC	Yes – Oui
CBER-RG1 (A/duck/Laos/3295/2006)	2.3.4	FDA	Yes – Oui
SJRG-164281 (A/Japanese white eye/Hong Kong/1038/2006)	2.3.4	SJCRH/HKU	Yes – Oui
IDCDC-RG36 (A/chicken/Bangladesh/11rs1984-30/2011)	2.3.4.2	CDC	Yes – Oui
IDCDC-RG35 (A/Guizhou/1/2013)	2.3.4.2	CDC/CCDC	Yes – Oui
IDCDC-RG42A (A/Sichuan/26221/2014) (H5N6)	2.3.4.4	CDC/CCDC	Yes – Oui
CNIC-29578 (A/Hubei/29578/2016) (H5N6)	2.3.4.4	CCDC	Yes – Oui
IDCDC-RG43A (A/gyrfalcon/Washington/41088-6/2014) (H5N8)	2.3.4.4	CDC	Yes – Oui
NIID-001 (A/duck/Hyogo/1/2016) (H5N6)	2.3.4.4	NIID	Yes – Oui
CNIC-21099 (A/Fujian-Sanyuan/21099/2017) (H5N6)	2.3.4.4	CCDC	Yes – Oui
SJRG-165396 (A/goose/Guiyang/337/2006)	4	SJCRH/HKU	Yes – Oui
IDCDC-RG12 (A/chicken/Viet Nam/NCVD-016/2008)	7.1	CDC	Yes – Oui
IDCDC-RG25A (A/chicken/Viet Nam/NCVD-03/2008)	7.1	CDC	Yes – Oui
Candidate vaccine viruses in preparation – Virus vaccinaux candidats en préparation	**Clade**	**Institution**	**Available – Disponible**
A/duck/Bangladesh/17D1012/2018-like	2.3.2.1a	CDC	Pending – En attente
A/chicken/Guiyang/1153/2016-like	2.3.2.1c	SJCRH/HKU	Pending – En attente
A/chicken/Ghana/20/2015-like	2.3.2.1c	CDC	Pending – En attente
A/chicken/Viet Nam/NCVD-15A59/2015 (H5N6)-like	2.3.4.4	SJCRH	Pending – En attente
A/environment/Hubei/950/2013-like	7.2	CCDC	Pending – En attente

* Institutions developing and/or distributing the candidate vaccine viruses: – Institutions distribuant les virus vaccins candidats:
CCDC: Chinese Center for Disease Control and Prevention, China – CCDC: Centre chinois de contrôle et de prévention des maladies, Chine
CDC: Centers for Disease Control and Prevention, USA – CDC: Centers for Disease Control and Prevention, États-Unis
FDA: Food and Drug Administration, USA – FDA: Food and Drug Administration, États-Unis
HKU: University of Hong Kong, Hong Kong Special Administrative Region, China – HKU: Université de Hong Kong, Hong Kond, Région administrative spéciale de la Chine
NIBSC: National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom – NIBSC: National Institute for Biological Standards and Control, un centre du Medicines and Healthcare products Regulatory Agency (MHRA), Angleterre
NIID: National Institute of Infectious Diseases, Japan – NIID: Institut national des maladies infectieuses, Japon
NIV: National Institute of Virology, India – NIV: National Institute of Virology, Inde
SJCRH: St Jude Children's Research Hospital, USA – SJCRH: St. Jude Children's Research Hospital, États-Unis

Influenza A(H7N9) candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, no new CVVs are proposed. The available A(H7N9) CVVs are listed in *Table 4*.

Virus candidats destinés à la préparation d'un vaccin contre la grippe A(H7N9)

Au vu des données antigéniques, génétiques et épidémiologiques actuelles, aucun nouveau virus vaccinal candidat n'est proposé. Les virus vaccinaux candidats A(H7N9) disponibles sont recensés dans le *Tableau 4*.

(3) Influenza A(H9N2)

Influenza A(H9N2) viruses are enzootic in poultry in parts of Africa, Asia and the Middle East. The majority of viruses sequenced from these regions belong to the A/quail/Hong Kong/G1/97 (G1) and A/chicken/Beijing/1/94 (Y280/G9) lineages. Since 1998, when the first human infection was identified, the detection of A(H9N2) viruses from humans and swine has been reported infrequently. In most human cases the associated illness has been mild and there has been no evidence of human-to-human transmission.

3) Grippe A(H9N2)

Les virus grippaux A(H9N2) sont enzootiques parmi les populations de volailles de certaines parties de l'Afrique, de l'Asie et du Moyen-Orient. La majorité des virus issus de ces régions qui ont été séquencés appartiennent aux lignées A/quail/Hong Kong/G1/97 (G1) et A/chicken/Beijing/1/94 (Y280/G9). Depuis 1998, date de la détection du premier cas d'infection humaine, on a rarement isolé chez l'homme ou chez le porc des virus A(H9N2). Pour la majorité des personnes touchées, les symptômes de la maladie associée ont été bénins et aucune transmission interhumaine n'a été mise en évidence.

Influenza A(H9N2) activity from 20 February to 24 September 2018

One human case of A(H9N2) virus infection was reported in China in this period. The Y280/G9 lineage A(H9N2) viruses continue to predominate in birds in China and were detected in birds in the Russian Feder-

Activité de la grippe A(H9N2) du 20 février au 24 septembre 2018

Un cas humain d'infection par le virus A(H9N2) a été signalé en Chine pendant cette période. Les virus de la lignée A(H9N2) Y280/G9 continuent à prédominer chez les oiseaux en Chine et ont été détectés chez les oiseaux en Fédération de Russie, au

Table 4 **Status of influenza A(H7N9) candidate vaccine virus development**
Tableau 4 **État d'avancement dans la mise au point des virus vaccinaux candidats A(H7N9)**

Candidate vaccine viruses (like viruses) – Virus vaccinaux candidats (similaires aux virus)	Type	Institution*	Available – Disponible
IDCDC-RG33A (A/Anhui/1/2013)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
NIBRG-268 (A/Anhui/1/2013)	Reverse genetics – Génétique inverse	NIBSC	Yes – Oui
NIIDRG-10.1 (A/Anhui/1/2013)	Reverse genetics – Génétique inverse	NIID	Yes – Oui
SJ005 (A/Anhui/1/2013)	Reverse genetics – Génétique inverse	SJCRH	Yes – Oui
NIBRG-267 (A/Shanghai/2/2013)	Reverse genetics – Génétique inverse	NIBSC	Yes – Oui
CBER-RG4A (A/Shanghai/2/2013)	Reverse genetics – Génétique inverse	FDA	Yes – Oui
IDCDC-RG32A (A/Shanghai/2/2013)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
IDCDC-RG32A.3 (A/Shanghai/2/2013)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
IDCDC-RG56B (A/Hong Kong/125/2017)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
CNIC-GD003 (A/Guangdong/17SF003/2016)	Reverse genetics – Génétique inverse	CCDC	Yes – Oui
IDCDC-RG56N (A/Guangdong/17SF003/2016)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
NIBRG-375 (A/Guangdong/17SF003/2016)	Reverse genetics – Génétique inverse	NIBSC	Yes – Oui
CBER-RG7C (A/Guangdong/17SF003/2016)	Reverse genetics – Génétique inverse	FDA	Yes – Oui
CNIC-HN02650 (A/Hunan/02650/2016)	Reverse genetics – Génétique inverse	CCDC	Yes – Oui

* Institutions distributing the candidate vaccine viruses: – Institutions distribuant les virus vaccins candidats:

CCDC: Chinese Center for Disease Control and Prevention, China – CCDC: Centre chinois de contrôle et de prévention des maladies, Chine

CDC: Centers for Disease Control and Prevention, USA – CDC: Centers for Disease Control and Prevention, États-Unis

FDA: Food and Drug Administration, USA – FDA: Food and Drug Administration, États-Unis

NIBSC: National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom – NIBSC: National Institute for Biological Standards and Control, un centre du Medicines and Healthcare products Regulatory Agency (MHRA), Angleterre

NIID: National Institute of Infectious Diseases, Japan – NIID: Institut national des maladies infectieuses, Japon

SJCRH: St Jude Children's Research Hospital, USA – SJCRH: St. Jude Children's Research Hospital, États-Unis

ation, Myanmar and Viet Nam. As in previous reporting periods, G1-lineage viruses were detected in birds in a number of countries in Africa and Asia.

Antigenic and genetic characteristics of influenza A(H9N2) viruses

The reported human A(H9N2) case was a 24-year-old female who fully recovered from the infection. As no virus was recovered from this case antigenic information is not available. All recent A(H9N2) human and poultry infections in China have been caused by viruses of the Y280/G9 lineage (*Figure 2*) with an increasing proportion showing reduced reactivity to post-infection ferret antiserum raised against A/Hong Kong/308/2014 (*Table 5*) or its associated CVV.

The majority of poultry viruses from the G1 lineage were antigenically and/or genetically similar to those detected in previous periods and to available CVVs.

Influenza A(H9N2) candidate vaccine viruses

Based on the current antigenic, genetic and epidemiologic data, a new A/Anhui-Lujiang/39/2018-like A(H9N2) CVV is proposed. The available A(H9N2) CVVs are listed in *Table 6*.

(4) Influenza A(H1) variants (v)[4]

Influenza A(H1) viruses circulate in swine populations in many regions of the world. Depending on geographic location, the genetic and antigenic characteristics of these viruses differ. Human infections with swine A(H1) viruses have been documented for many years.

Influenza A(H1)v activity from 20 February to 24 September 2018

Thirteen cases of A(H1N2)v infection were identified in the United States of America (USA). Twelve of the 13 cases reported either exposure to swine or attendance of an agricultural fair during the week preceding illness onset. All but one of these individuals were less than 18 years of age. One individual did not attend a fair and reported no swine exposure, suggesting limited human-to-human transmission. All patients recovered fully.

Antigenic and genetic characteristics of influenza A(H1)v viruses

The A(H1N2)v viruses detected had HA gene segments from the delta 2 sublineage (clade 1B.2) of the swine H1 HA lineage (*Figure 3*). The HA and NA gene segments of these viruses were closely related to those of the A(H1N2) influenza viruses circulating in the USA swine population. The delta 2 lineage A(H1N2)v viruses possessed 21 HA1 amino acid substitutions relative to the recommended delta 2 lineage CVV derived from A/Ohio/35/2017. All recent A(H1N2)v viruses possessed

[4] See http://www.who.int/influenza/gisrs_laboratory/terminology_variant/en/

Myanmar et au Viet Nam. Comme lors des périodes précédentes, des virus de la lignée G1 ont été détectés chez les oiseaux dans un certain nombre de pays d'Afrique et d'Asie.

Caractéristiques antigéniques et génétiques des virus grippaux A(H9N2)

Le cas humain A(H9N2) était une femme de 24 ans qui a complètement guéri de l'infection. Comme aucun virus n'a été retrouvé chez ce cas, aucune information antigénique n'est disponible. En Chine, toutes les infections à virus A(H9N2) récentes chez l'homme et parmi la volaille ont été causées par des virus de la lignée Y280/G9 (*Figure 2*) dont une proportion croissante montre une réactivité réduite à l'antisérum de furet post-infection dirigé contre la lignée A/Hong Kong/308/2014 (*Tableau 5*) ou le virus vaccinal candidat correspondant.

La majorité des virus aviaires de la lignée G1 étaient similaires sur le plan antigénique et/ou génétique à ceux détectés au cours des périodes précédentes et aux virus vaccinaux candidats disponibles.

Virus candidats destinés à la préparation d'un vaccin contre la grippe A(H9N2)

Au vu des données antigéniques, génétiques et épidémiologiques actuelles, un nouveau virus vaccinal candidat A(H9N2) de type A/Anhui-Lujiang/39/2018 est proposé. Les virus vaccinaux candidats A(H9N2) disponibles sont recensés dans le *Tableau 6*.

4) Variants des virus grippaux A(H1) (v)[4]

Des virus grippaux A(H1) circulent parmi les populations porcines de nombreuses régions du monde. Les caractéristiques génétiques et antigéniques de ces virus diffèrent selon le lieu géographique. Les infections humaines par des virus porcins A(H1) existent depuis de nombreuses années.

Activité de la grippe A(H1)v du 20 février au 24 septembre 2018

Treize cas d'infection humaine par un virus A(H1N2)v ont été identifiés aux États-Unis d'Amérique. Douze des 13 cas ont déclaré avoir été exposés à des porcs ou avoir assisté à une foire agricole au cours de la semaine précédant l'apparition de la maladie. Toutes ces personnes, sauf une, étaient âgées de moins de 18 ans. Une personne n'a pas assisté à une foire et n'a signalé aucune exposition à des porcs, ce qui laisse supposer une transmission interhumaine limitée. Tous les patients se sont complètement rétablis.

Caractéristiques antigéniques et génétiques des virus grippaux A(H1)v

Les virus A(H1N2)v détectés présentaient des segments du gène HA provenant de la sous-lignée delta 2 (clade 1B.2) de la lignée de HA porcine H1 (*Figure 3*). Les segments des gènes HA et NA de ces virus étaient étroitement apparentés à ceux des virus grippaux A(H1N2) circulant dans la population porcine aux États-Unis d'Amérique. Les virus de la lignée delta 2 A(H1N2)v présentaient 21 substitutions d'acides aminés dans le gène HA1 par rapport aux virus vaccinaux candidats recommandés de la lignée delta 2 dérivée de A/Ohio/35/2017. Tous les virus A(H1N2)v

[4] Voir http://www.who.int/influenza/gisrs_laboratory/terminology_variant/en/

Figure 2 **Phylogenetic relationships of A(H9) Y280-like haemagglutinin genes**

Figure 2 **Classification phylogénétique des gènes de l'hémagglutinine des virus grippaux similaires à A(H9) Y280**

The candidate vaccine viruses (CCV) that are available or in preparation appear in red. The proposed CCV is indicated by (•); all human viruses are in **bold font**. The viruses tested in haemagglutination inhibition assay are indicated by hashes (#). The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes. – Les virus vaccinaux candidats disponibles ou en préparation apparaissent en rouge. Le virus vaccinal candidat proposé est indiqué par (•); tous les virus humains sont indiqués en **caractères gras**. Les virus testés au moyen de l'épreuve d'inhibition de l'hémagglutination sont indiqués par le symbole (#). La barre d'échelle représente le nombre de substitutions par site. Les valeurs de boostrap supportant la topologie de l'arbre sont indiquées au-dessus des nœuds sélectionnés.

Table 5 **Haemagglutination inhibition assays of assays of Y280/G9 lineage influenza A(H9N2) viruses**
Tableau 5 **Épreuves d'inhibition de l'hémagglutination obtenues avec les virus grippaux A(H9N2) appartenant à la lignée Y280/G9**

	Lineage – Lignée	HK/G9	HK/308	GD/01747	SCBZ/1453	HK/G1
Reference antigens – Antigènes de référence						
A/chicken/Hong Kong/G9/97	Y280	**640**	40	40	<40	<40
A/Hong Kong/308/2014	Y280	40	**5120**	2560	1280	<40
A/Guangdong/01747/2014	Y280	40	2560	**2560**	1280	<40
A/Sichuan-Bazhou/1453/2014	Y280	40	2560	5120	**2560**	<40
A/quail/Hong Kong/G1/97	G1	<40	40	<40	<40	**1280**
Test antigens – Antigènes d'épreuve						
A/Anhui-Lujiang/39/2018	Y280	<40	320	640	320	40
A/environment/Hunan/29028/2018	Y280	40	1280	1280	640	<40
A/environment/Hunan/28910/2018	Y280	40	640	1280	640	<40
A/environment/Hunan/28975/2018	Y280	40	640	640	640	<40
A/environment/Chongqing/30179/2018	Y280	<40	640	640	640	<40
A/environment/Jiangxi/27377/2018	Y280	<40	640	1280	640	<40
A/environment/Xinjiang/27373/2018	Y280	<40	320	640	320	40
A/environment/Gansu/25274/2018	Y280	<40	160	320	160	<40
A/environment/Shandong/28173/2018	Y280	<40	2560	2560	1280	<40
A/environment/Guangdong/27994/2018	Y280	<40	320	640	640	<40
A/environment/Guangdong/29635/2018	Y280	<40	320	640	320	<40
A/environment/Guangdong/27987/2018	Y280	<40	640	80	80	<40
A/environment/Heilongjiang/30617/2018	Y280	<40	640	80	80	<40
A/environment/Fujian/30649/2018	Y280	<40	320	640	640	<40
A/environment/Guangxi/13640/2018	Y280	<40	640	640	1280	<40
A/environment/Guangxi/29429/2018	Y280	<40	640	640	640	<40
A/environment/Guangdong/29641/2018	Y280	<40	640	640	640	<40
A/environment/Fujian/04960/2017	Y280	<40	160	320	320	<40
A/environment/Guangxi/40960/2017	Y280	<40	320	320	320	<40
A/environment/Hunan/04908/2017	Y280	<40	160	320	320	<40

Numbers in **bold** indicate homologous antiserum/antigen titres. – Les chiffres en caractères **gras** indiquent les titres d'antigènes/d'antisérum homologue.

an NA gene derived from the 1998 lineage of swine influenza viruses, which is distinct from that of A/Ohio/35/2017 (2002 NA lineage). Ferret antiserum raised against A/Ohio/35/2017 reacted well with all of the 2018 A(H1N2)v viruses (*Table 7*). HI reactivity of pooled post-vaccination sera from children or adults vaccinated with the 2017–2018 vaccine was below the limit of detection for all viruses tested (*Table 7*).

Influenza A(H1)v candidate vaccine viruses

Based on the current genetic and epidemiologic data, a new A/Michigan/383/2018-like A(H1N2)v CVV is proposed. The available A(H1)v CVVs are listed in *Table 8*.

récents possédaient un gène NA dérivé de la lignée de virus grippaux porcins de 1998, qui est distinct de celui de A/Ohio/35/2017 (lignée NA 2002). L'antisérum de furet dirigé contre A/Ohio/35/2017 a bien réagi avec tous les virus A(H1N2)v de 2018 (*Tableau 7*). La réaction d'inhibition de l'hémagglutination des sérums post-vaccination groupés provenant d'enfants ou d'adultes ayant reçu le vaccin 2017-2018 était inférieure à la limite de détection pour tous les virus testés (*Tableau 7*).

Virus candidats à la préparation d'un vaccin contre la grippe A(H1)v

Au vu des données génétiques et épidémiologiques actuelles, un nouveau virus vaccinal candidat A(H1N2)v de type A/Michigan/383/2018 est proposé. Les virus vaccinaux candidats A(H1)v disponibles sont recensés dans le *Tableau 8*.

Table 6 **Status of influenza A(H9N2) candidate vaccine virus development**
Tableau 6 **État d'avancement dans la mise au point des virus vaccinaux candidats A(H9N2)**

Candidate vaccine viruses (like viruses) – Virus vaccinaux candidats (similaires aux virus)	Type	Clade	Institution*	Available – Disponible
A/Hong Kong/1073/99	Wild type – Type sauvage	G1	NIBSC	Yes – Oui
NIBRG-91 (A/chicken/Hong Kong/G9/97)	Reverse genetics – Génétique inverse	Y280/G9	NIBSC	Yes – Oui
IBCDC-2 (A/chicken/Hong Kong/G9/97)	Conventional – Classique	Y280/G9	CDC	Yes – Oui
IDCDC-RG26 (A/Hong Kong/33982/2009)	Reverse genetics – Génétique inverse	G1	CDC	Yes – Oui
IDCDC-RG31 (A/Bangladesh/994/2011)	Reverse genetics – Génétique inverse	G1	CDC	Yes – Oui
SJ008 (A/Hong Kong/308/2014)	Reverse genetics– Génétique inverse	Y280/G9	SJCRH	Yes – Oui
Candidate vaccine viruses in preparation – Virus vaccinaux candidats en préparation	**Type**	**Clade**	**Institution***	**Available – Disponible**
A/Anhui-Lujiang/39/2018-like	Reverse genetics – Génétique inverse Conventional – Classique	Y280/G9 Y280/G9	CCDC NIBSC	Pending – En attente Pending – En attente

* Institutions distributing the candidate vaccine viruses: – Institutions distribuant les virus vaccins candidats:
CCDC: Chinese Center for Disease Control and Prevention, China – CCDC: Centre chinois de contrôle et de prévention des maladies, Chine
CDC: Centers for Disease Control and Prevention, USA – CDC: Centers for Disease Control and Prevention, États-Unis
NIBSC: National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom – NIBSC: National Institute for Biological Standards and Control, un centre du Medicines and Healthcare products Regulatory Agency (MHRA), Angleterre
SJCRH: St Jude Children's Research Hospital, USA – SJCRH: St. Jude Children's Research Hospital, États-Unis

(5) Influenza A(H3N2)v[4]

Influenza A(H3N2) viruses are enzootic in swine populations in most regions of the world. Depending on geographic location, the genetic and antigenic characteristics of these viruses differ. Human infections with swine influenza A(H3N2) viruses have been documented in Asia, Europe and North America.[5]

Influenza A(H3N2)v activity from 20 February to 24 September 2018

One A(H3N2)v virus infection was reported in a child from the United States of America. The child, who recovered from mild illness, had exposure to swine at an agricultural fair where swine were found to be infected with closely related viruses.

Antigenic and genetic characteristics of influenza A(H3N2)v viruses

The A(H3N2)v virus isolated from the reported case was closely related genetically to viruses that have circulated in swine in the USA for a number of years and previously been identified in humans in 2016 and 2017. These viruses have HA gene segments derived from a seasonal human A(H3) virus that was likely transmitted to swine from humans in 2010. Reactivity of antisera raised to A/Ohio/13/2017, from which a CVV has been proposed, to the A(H3N2)v virus was reduced 8-fold compared to the homologous virus titre despite the viruses being genetically similar. Pooled adult post-vaccination antisera reacted with the virus at titres that were within 4-fold to those against the homologous reference virus, A/Michigan/15/2014, representing the A(H3N2) compo-

5) Grippe A(H3N2)v[4]

Les virus grippaux A(H3N2) sont enzootiques dans les populations porcines de la plupart des régions du monde. Les caractéristiques génétiques et antigéniques de ces virus diffèrent selon le lieu géographique. Des infections humaines par des virus grippaux porcins A(H3N2) ont été enregistrées en Asie, en Europe et en Amérique du Nord.[5]

Activité de a grippe A(H3N2)v du 20 février au 24 septembre 2018

Une infection par le virus A(H3N2)v a été signalé chez un enfant aux États-Unis d'Amérique. L'enfant, qui s'est remis d'une maladie bénigne, avait été exposé à des porcs lors d'une foire agricole où l'on a découvert que des porcs étaient infectés par des virus étroitement apparentés.

Caractéristiques antigéniques et génétiques des virus grippaux A(H3N2)v

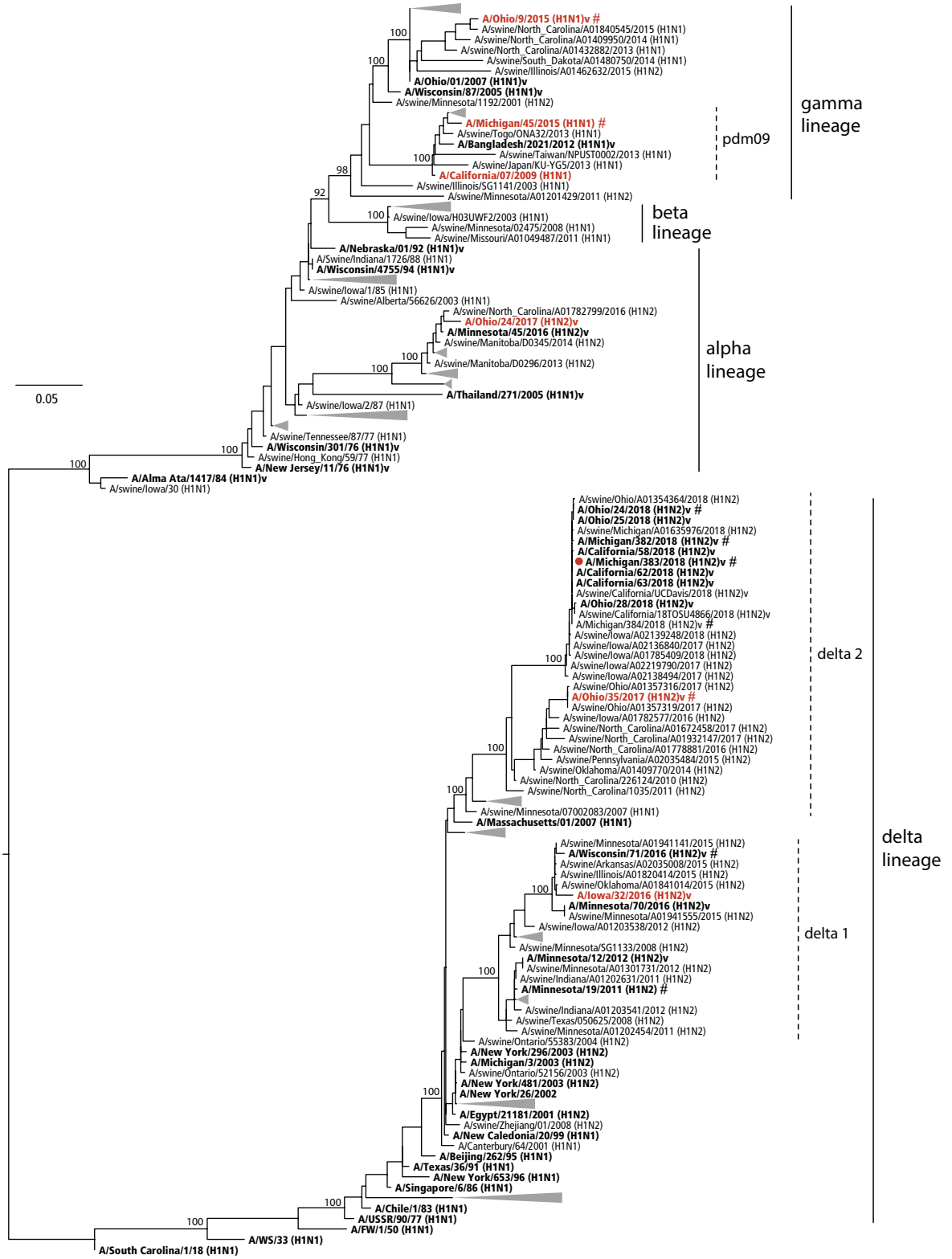
Le virus A(H3N2)v isolé à partir du cas signalé était étroitement apparenté sur le plan génétique aux virus qui circulent dans les populations porcines aux États-Unis d'Amérique depuis un certain nombre d'années et qui ont été identifiés chez les humains en 2016 et 2017. Ces virus présentent des segments du gène HA dérivés d'un virus A(H3) humain saisonnier qui a probablement été transmis aux porcs par les humains en 2010. En présence du virus A(H3N2)v, la réactivité des antisérums dirigés contre la lignée A/Ohio/13/2017, à partir de laquelle un virus vaccinal candidat a été proposé, a été réduite d'un facteur 8 par rapport au titre du virus homologue, bien que ces virus soient génétiquement similaires. Les antisérums d'adultes recueillis après vaccination et regroupés ont réagi avec ce virus à des titres allant jusqu'à 4 fois ceux utilisés contre le virus vaccinal homologue,

[5] See http://www.eurosurveillance.org/images/dynamic/EE/V19N18/art20793.pdf

[5] Voir http://www.eurosurveillance.org/images/dynamic/EE/V19N18/art20793.pdf

Figure 3 **Phylogenetic relationships of A(H1) haemagglutinin genes**

Figure 3 **Classification phylogénétique des gènes de l'hémagglutinine des virus grippaux A(H1)**



The candidate vaccine viruses (CCV) that are available or in preparation appear in red. The proposed CCV is indicated by (•); all human viruses are in **bold font**. The viruses tested in haemagglutination inhibition assay are indicated by hashes (#). The scale bar represents the number of substitutions per site. Bootstrap supports of topology are shown above selected nodes. Some branches of the virus strains are collapsed into grey triangles for clarity.–Les virus vaccinaux candidats disponibles ou en préparation apparaissent en rouge. Le virus vaccinal candidat proposé est indiqué par (•); tous les virus humains sont indiqués en **caractères gras**. Les virus testés au moyen de l'épreuve d'inhibition de l'hémagglutination sont indiqués par le symbole (#). La barre d'échelle représente le nombre de substitutions par site. Les valeurs de boostrap supportant la topologie de l'arbre sont indiquées au-dessus des nœuds sélectionnés. Certaines branches des souches virales sont condensées dans les triangles gris pour plus de clarté.

Table 7 **Haemagglutination inhibition assays of influenza A(H1)v viruses**
Tableau 7 **Épreuves d'inhibition de l'hémagglutination obtenues avec les virus grippaux A(H1)v**

		pdm09	H1N1v (gamma)	H1N1v (gamma)	H1N2v (delta 1)	H1N2v (delta 1)	H1N2v (delta 2)	2017/ 2018	2017/ 2018
	Lineage – Lignée	MI/45	Ohio/9	RG48A	MN/19	WI/71	OH/35	Post-vaccsera (children)[a] – Sérums post-vaccinaux (enfants)[a]	Post-vacc sera (adults)[b] – Sérums post-vaccinaux (adultes)[b]
Reference antigens – Antigènes de référence									
A/Michigan/45/2015 H1N1	pdm09	**5120**	80	<10	<10	<10	<10	80	1280
A/Ohio/9/2015 H1N1v	gamma	40	**2560**	640	<10	<10	<10	<10	40
A/Ohio/9/2015 IDCDC-RG48A	gamma	80	5120	**1280**	<10	<10	<10	<10	160
A/Minnesota/19/2011 H1N2v	delta 1	<10	<10	<10	**2560**	1280	10	<10	20
A/Wisconsin/71/2016 H1N2v	delta 1	<10	<10	<10	160	**2560**	10	<10	10
A/Ohio/35/2017 H1N2v	delta 2	<10	<10	<10	<10	80	**320**	<10	<10
Test antigens – Antigènes d'épreuve									
A/Michigan/382/2018	delta 2	<10	<10	<10	<10	40	160	<10	<10
A/Michigan/383/2018	delta 2	<10	<10	<10	<10	40	320	<10	<10
A/Ohio/24/2018	delta 2	<10	<10	<10	<10	20	160	<10	<10
A/Michigan/384/2018	delta 2	<10	<10	<10	<10	20	160	<10	<10

[a] 2017–2018 post-vaccine immune serum pool from children (0–3 years) vaccinees (A/Michigan/45/2015 vaccine). – Pool d'immunsérums postvaccinaux recueillis sur la période 2017-2018 chez des enfants (0 à 3 ans) ayant été vaccinés (vaccin A/Michigan/45/2015).

[b] 2017–2018 post-vaccine immune serum pool from adult (19–49 years) vaccinees (A/Michigan/45/2015 vaccine). – Pool d'immunsérums postvaccinaux recueillis sur la période 2017-2018 chez des adultes (19 à 49 ans) ayant été vaccinés (vaccin A/Michigan/45/2015).

nent of the 2017–2018 seasonal influenza vaccines. Pooled post-vaccination antisera collected from young children had highly reduced titres to the 2018 virus as compared to the A/Michigan/15/2014 homologous virus titre.

Influenza A(H3N2)v candidate vaccine viruses

Based on the available antigenic, genetic and epidemiologic data, no new CVVs are proposed. The available A(H3N2)v CVVs are listed in *Table 9*.

Acknowledgements

We acknowledge the WHO Global Influenza Surveillance and Response System (GISRS) which provides the mechanism for detection and monitoring of emerging zoonotic influenza viruses. We thank the National Influenza Centres (NICs) of GISRS who contributed information, clinical specimens and viruses, and associated data; WHO Collaborating Centres of GISRS for their in-depth characterization and comprehensive analysis of viruses; and WHO H5 Reference Laboratories for their complementary analyses. We thank the OIE/FAO Network of Expertise on Animal Influenza (OFFLU)

A/Michigan/15/2014, qui représente la composante A(H3N2) des vaccins grippaux saisonniers 2017-2018. Les titres des antisérums post-vaccination recueillis chez de jeunes enfants et regroupés étaient fortement réduits en présence du virus de 2018 par rapport au titre du virus homologue A/Michigan/15/2014.

Virus candidats à la préparation d'un vaccin contre la grippe A(H3N2)v

Au vu des données antigéniques, génétiques et épidémiologiques disponibles, aucun nouveau virus vaccinal candidat n'est proposé. Les virus vaccinaux candidats A(H3N2)v disponibles sont recensés dans le *Tableau 9*.

Remerciements

Nous saluons la contribution du système mondial de surveillance de la grippe et de riposte (GISRS) de l'OMS, qui offre un moyen de détecter et de surveiller les virus grippaux zoonotiques émergents. Nous remercions également: les centres nationaux de lutte contre la grippe du GISRS, qui ont fourni des informations, des échantillons cliniques, des virus et d'autres données associées; les centres collaborateurs du GISRS de l'OMS pour leur caractérisation détaillée et leur analyse complète des virus; et les laboratoires de référence H5 de l'OMS pour leurs études complémentaires. Nous sommes reconnaissants aux laboratoires du Réseau d'experts sur la grippe animale (OFFLU)

Table 8 **Status of influenza A(H1)v candidate vaccine virus development**
Tableau 8 **État d'avancement dans la mise au point des virus vaccinaux candidats A(H1)v**

Candidate vaccine viruses (like viruses) – Virus vaccinaux candidats (similaires aux virus)	**Type**	**Institution***	**Available – Disponible**
IDCDC-RG48A (A/Ohio/9/2015) (H1N1)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
CNIC-1601 (A/Hunan/42443/2015) (H1N1)	Conventional and reverse genetics – Génétique classique et inverse	CCDC	Yes – Oui
Candidate vaccine viruses in preparation – Virus vaccinaux candidats en préparation	**Type**	**Institution***	**Available – Disponible**
A/Iowa/32/2016-like (H1N2)	Reverse genetics – Génétique inverse	CDC	Pending – En attente
A/Netherlands/3315/2016-like (H1N1)	Conventional – Classique	NIBSC	Pending – En attente
A/Ohio/24/2017-like (H1N2)	Reverse genetics – Génétique inverse	CDC	Pending – En attente
A/Ohio/35/2017-like (H1N2)	Reverse genetics – Génétique inverse	NIBSC	Pending – En attente
A/Michigan/383/2018-like (H1N2)	Reverse genetics – Génétique inverse	CDC	Pending – En attente

* Institutions distributing the candidate vaccine viruses: – Institutions distribuant les virus vaccins candidats:
CCDC: Chinese Center for Disease Control and Prevention, China – CCDC: Centre chinois de contrôle et de prévention des maladies, Chine
CDC: Centers for Disease Control and Prevention, USA – CDC: Centers for Disease Control and Prevention, États-Unis
NIBSC: National Institute for Biological Standards and Control, a centre of the Medicines and Healthcare products Regulatory Agency (MHRA), United Kingdom – NIBSC: National Institute for Biological Standards and Control, un centre du Medicines and Healthcare products Regulatory Agency (MHRA), Angleterre

Table 9 **Status of influenza A(H3N2)v candidate vaccine virus development**
Tableau 9 **État d'avancement dans la mise au point des virus vaccinaux candidats A(H3N2)v**

Candidate vaccine viruses (like viruses) – Virus vaccinaux candidats (similaires aux virus)	**Type**	**Institution***	**Available – Disponible**
NYMC X-203 (A/Minnesota/11/2010)	Conventional – Classique	CDC	Yes – Oui
NYMC X-213 (A/Indiana/10/2011)	Conventional – Classique	CDC	Yes – Oui
IDCDC-RG55C (A/Ohio/28/2016)	Reverse genetics – Génétique inverse	CDC	Yes – Oui
Candidate vaccine viruses in preparation – Virus vaccinaux candidats en préparation	**Type**	**Institution***	**Available – Disponible**
A/Ohio/13/2017-like	Reverse genetics – Génétique inverse	CDC	Pending – En attente

* Institutions distributing the candidate vaccine viruses: – Institutions distribuant les virus vaccins candidats:
CDC: Centers for Disease Control and Prevention, USA – CDC: Centers for Disease Control and Prevention, États-Unis

laboratories and other national institutions for contributing information and viruses. We also acknowledge the Global Initiative on Sharing All Influenza Data (GISAID) for the EpiFlu database, and other sequence databases which were used to share gene sequences and associated information. ■

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