

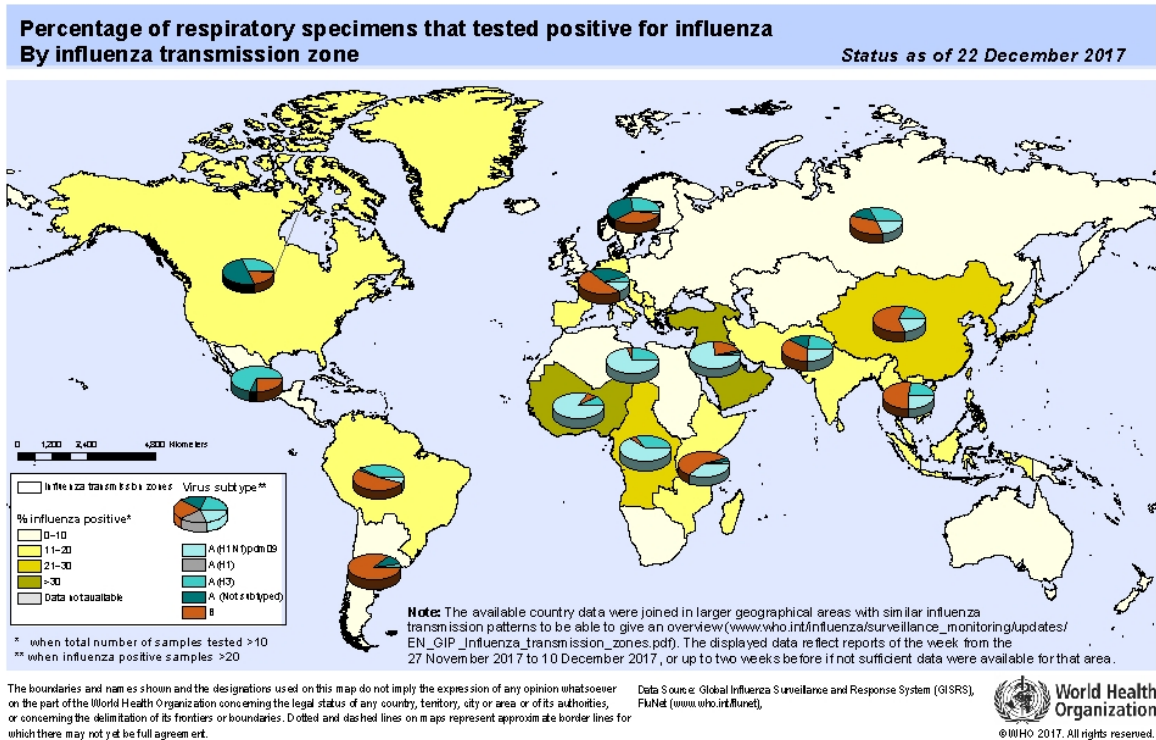


Global Influenza Hospital Surveillance Network

GLOBAL INFLUENZA SURVEILLANCE MONITORING UPDATE

January 5th, 2018

1. GLOBAL WHO SUMMARY – based on data up to Dec 22th 2017



North America: overall activity continued to increase in the region, with detections of predominantly influenza A(H3N2) viruses.

Europe: activity continued to increase, but remained low in most of the countries, with detections of predominantly influenza B followed by influenza A(H3N2) viruses.

Asia: Western Asia: elevated levels of activity were reported in recent weeks, with influenza A(H1N1)pdm09 predominantly detected. **Central Asia:** low to no activity was reported. **East Asia:** influenza activity remained low in most of the countries with the exception of China where influenza like illness (ILI) and influenza percentage positive continued to increase, with influenza B/Yamagata viruses predominantly detected. **South East Asia:** low levels of influenza activity were reported. **Southern Asia:** influenza activity remained low in general. Detections of influenza A(H1N1)pdm09 and A(H3N2) viruses were reported in India and of all seasonal subtypes in the Islamic Republic of Iran.

Africa: Northern Africa: low levels of influenza activity were reported. Detections of influenza A(H1N1)pdm09 virus increased slightly in Tunisia. **Western Africa,** influenza virus detections were reported in Burkina Faso, Ghana, and Sierra Leone, with influenza A(H1N1) pdm09 virus predominating. **Middle Africa:** sporadic detections of influenza A were reported in Cameroon. **Eastern Africa,** influenza A(H3N2) and B detections were reported in Madagascar and Mozambique.

In the Caribbean and Central American countries, respiratory illness indicators and influenza activity remained low in general but respiratory syncytial virus (RSV) activity remained high in several countries.

2. VIROLOGICAL SURVEILLANCE AND STRAIN CHARACTERIZATION

WHO GISRS laboratories: from 27 November 2017 to 10 December 2017

127006 specimens were tested during that time period. 15344 (12,0%) were positive for influenza viruses, of which 9579 (62.4%) were typed as influenza A and 5765 (37.6%) as influenza B. Of the sub-typed influenza A viruses, 1596 (30.1%) were influenza A(H1N1)pdm09 and 3698 (69.9%) were influenza A(H3N2). Of the characterized B viruses, **2640 (85.2%) belonged to the B-Yamagata lineage** and 460 (14.8%) to the B-Victoria lineage.

NB: The recommended components for the 2017-2018 Northern hemisphere Influenza vaccine includes: an A/Michigan/45/2015 (H1N1)pdm09-like virus; an A/Hong Kong/4801/2014 (H3N2)-like virus; a B/Brisbane/60/2008-like virus (Vic Lineage). and a B/Phuket/3073/2013-like virus (Yam Lineage) in QIV vaccine.

EUROPE weeks: Week 40 to 51/2017

First detections indicated circulation of A(H3N2) and B/Yamagata viruses in the highest proportions. As the A(H3N2) subtype dominated last season, a high proportion of the population should be protected.

For type B viruses from both sentinel and non-sentinel sources, B/Yamagata lineage viruses have greatly outnumbered those of the B/Victoria lineage.

While low in number, 59% of the genetically characterized A(H3N2) viruses belonged to clade 3C.2a, the vaccine virus clade as described in the WHO recommendations for vaccine composition for the NH 2017–18, and 40% to clade 3C.2a1, the viruses of which are antigenically similar to those of clade 3C.2a.

For specimens collected since week 40/2017, genetic characterization of 235 viruses has been reported. Among 107 influenza A(H3N2) viruses, 63 (59%) fell in the vaccine virus component clade (3C.2a), and 42 (40%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin. Viruses in these 2 groups are antigenically similar, but both clade and subclade are evolving rapidly with the emergence of several virus clusters defined by additional amino acid substitutions in the haemagglutinin, thereby requiring continued monitoring of antigenic characteristics. 1 A(H1N1)pdm09, 1 A(H3N2) and 3 B/Yamagata viruses were not attributed to any clade.

See also the November report from ECDC here: <https://ecdc.europa.eu/en/publications-data/influenza-virus-characterisation-summary-europe-november-2017>

Table. Viruses attributed to genetic groups, cumulative for weeks 40–51/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1) ^a	30
A(H1N1)pdm09 not attributable to any clade	1
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) ^b	63
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1) ^c	43
A(H3N2) not attributable to any clade	1
B/Brisbane/60/2008 (Victoria lineage clade 1A) ^{b, d}	8
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163) ^e	6
B/Phuket/3073/2013 (Yamagata lineage clade 3) ^{c, f}	80
B/Yamagata lineage not attributed to any clade	3

^a Vaccine component of vaccines for both northern (2017–2018 season) and southern (2018 season) hemispheres

^b Vaccine component for northern hemisphere 2017–2018 season

^c Vaccine component for southern hemisphere 2018 season

^d Vaccine component of quadrivalent vaccines for use in southern hemisphere 2018 season

^e Deletion of K162 and N163 in the HA1 subunit of the hemagglutinin and antigenically different from the vaccine component.

^f Vaccine component of quadrivalent vaccines for use in northern hemisphere 2017–2018 season

US-CDC- Until Dec 23th,2017

The most frequently identified influenza virus subtype reported by public health laboratories during week 51 was influenza A(H3N2). The percentage of respiratory specimens testing positive for influenza in clinical laboratories increased.

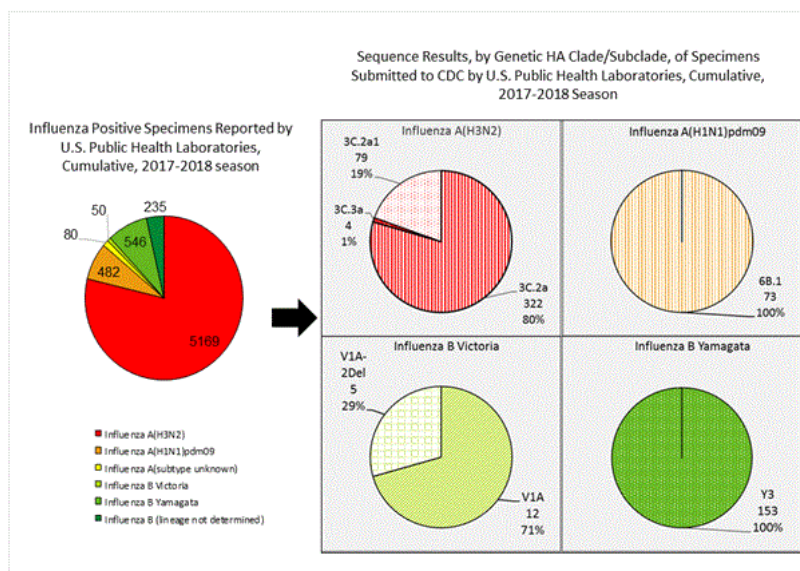
CDC has antigenically or genetically characterized 648 influenza viruses collected during October 1 – December 23, 2017 including 73 influenza A(H1N1)pdm09 viruses, 405 influenza A(H3N2) viruses, and 170 influenza B viruses.

A (H1N1)pdm09: Phylogenetic analysis of the HA genes from 73 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Forty-one A(H1N1)pdm09 viruses were antigenically characterized, and all were antigenically similar (analyzed using HI with ferret antisera) to the reference 6B.1 virus A/Michigan/45/2015, representing the recommended influenza A(H1N1)pdm09 reference virus for the 2017–18 NH vaccines.

A (H3N2): Phylogenetic analysis of the HA genes from 405 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=322), subclade 3C.2a1 (n=79) or clade 3C.3a (n=4). One hundred twenty seven influenza A(H3N2) viruses were antigenically characterized, and 126 (99.2%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within fourfold of the homologous virus titer) by ferret antisera raised against A/Michigan/15/2014 (3C.2a), a cell propagated A/Hong Kong/4801/2014-like reference virus representing the A(H3N2) component of 2017–18 NH vaccines.

B/Victoria: Phylogenetic analysis of 17 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008. However, a small number of viruses identified in 2017 had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). Four (57.1%) B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell -propagated B/Brisbane/60/2008 reference virus, representing a recommended B virus component of 2017–18 NH vaccines. Three (42.9%) B/Victoria lineage virus reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) with ferret antisera raised against cell-propagated B/Brisbane/60/2008, and these viruses had the V1A-2Del HA.

B/Yamagata: Phylogenetic analysis of 153 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 71 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell propagated B/Phuket/3073/2013, the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2017–18 NH QIV.



HPA-London until Week 01,2018

The PHE Respiratory Virus Unit has characterised 124 influenza viruses detected since week 37. Of the 43 A(H1N1)pdm09 influenza viruses that have been characterised, all belong in the genetic subgroup 6B.1, which was the predominant genetic subgroup in the 2016/17 season and to date during the current season. The 25 viruses antigenically analysed are similar to the A/Michigan/45/2015 NH 2017/18 (H1N1)pdm09 vaccine strain.

Genetic characterisation of 56 A(H3N2) influenza viruses detected since late summer, showed that they all belong to genetic subclade 3C.2a, with 32 belonging to a cluster within this genetic subclade designated as 3C.2a1. The NH 2017/18 influenza A(H3N2) vaccine strain A/HongKong/4801/2014 belongs in genetic subclade 3C.2a.

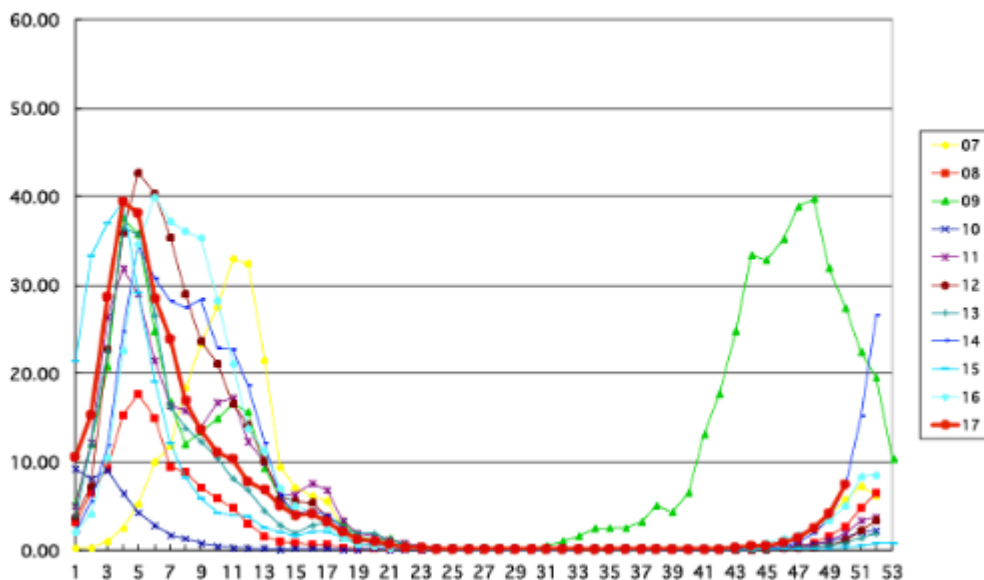
Twenty five influenza B viruses have been analysed; 21 were characterised as belonging to the B/Yamagata/16/88-lineage and 4 belonging to the B/Victoria/2/1987-lineage. Of the influenza B viruses antigenically characterised, the B/Victoria/2/87-lineage viruses were antigenically similar to B/Brisbane/60/2008, the influenza B/Victoria-lineage component of 2017/18 NH TIV trivalent and QIV. B/Yamagata/16/88-lineage viruses were antigenically similar to B/Phuket/3073/2013, the influenza B/Yamagata-lineage component of the 2017/18 NH QIV vaccine.

Table 3: Viruses characterised by PHE Reference Laboratory, 2017/18

Virus	No. viruses characterised			
	Genetic and antigenic	Genetic only	Antigenic only	Total
A(H1N1)pdm09	9	18	16	43
A(H3N2)	0	56	0	56
B/Yamagata-lineage	5	13	3	21
B/Victoria-lineage	3	1	0	4

JAPAN National infectious diseases- Until Week 51/2017

Influenza cases reported per sentinel weekly [定点当たり報告数]

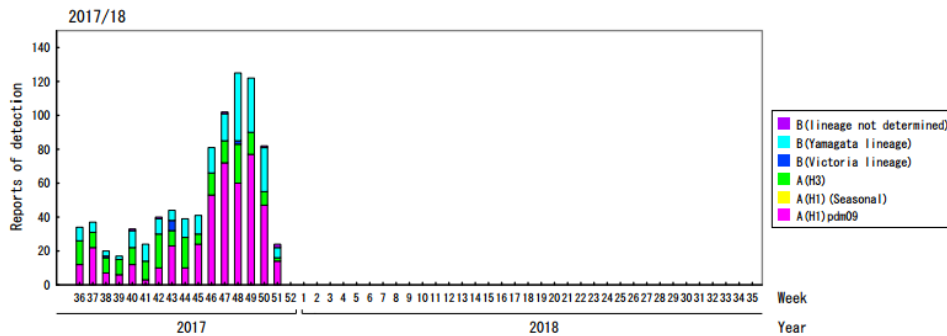


Weekly reports of influenza virus isolation/detection, 2013/14 – 2017/18

(Infectious Agents Surveillance Report: Data based on the reports received before December 27, 2017 from public health institutes)

IASR

Infectious Agents Surveillance Report



MORE DATA FROM REGIONAL OR COUNTRIES SURVEILLANCE

Canada Government, FluWatch Report <http://healthycanadians.gc.ca/diseases-conditions-maladies-affections/disease-maladie/flu-grippe/surveillance/fluwatch-reports-rapports-surveillance-influenza-eng.php>

China Chinese National Influenza Center – Influenza Weekly Report- Week <http://www.cnic.org.cn/>

Europe ECDC/ WHO Europe Weekly Influenza update – <http://flunewseurope.org/>

Hong Kong Centre for Health Protection- Flux Express Surveillance Report http://www.chp.gov.hk/en/guideline1_year/134/441/304.html

PAHO Regional Update:

http://www.paho.org/hq/index.php?option=com_content&view=article&id=3352&Itemid=2469&to=2246&lang=es

Russian Federation WHO NIC at Research Institute of Influenza and D.I Ivanovsky Institute of Virology, Integrated data of influenza morbidity and diagnosis

http://www.influenza.spb.ru/en/influenza_surveillance_system_in_russia/epidemic_situation/

Singapore Ministry of Health – weekly infectious disease bulletin

https://www.moh.gov.sg/content/moh_web/home/statistics/infectiousDiseasesStatistics/weekly_infectiousdiseasesbulletin.html

Unites States Of America Centers for Disease Control and Prevention, Weekly U.S. Influenza Surveillance Report <http://www.cdc.gov/flu/weekly/>