

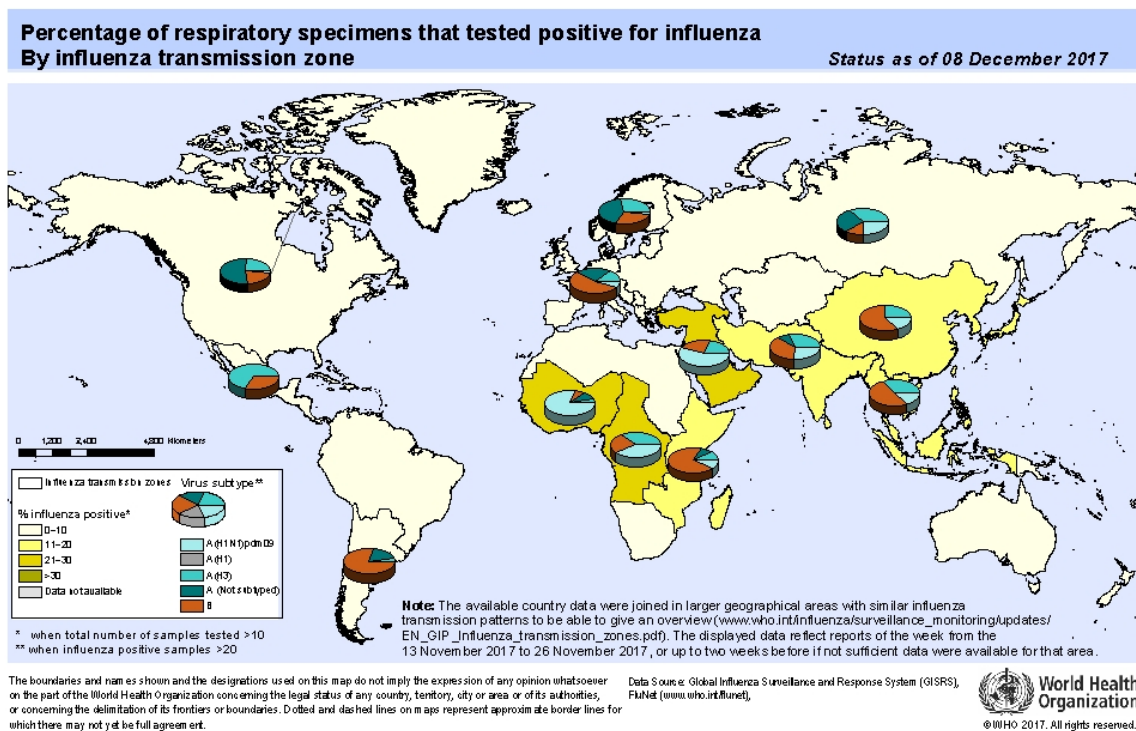


Global Influenza Hospital Surveillance Network

Global Influenza Surveillance Monitoring Update

December 15th, 2017

1. GLOBAL WHO SUMMARY – based on data up to Dec 08th 2017



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

Europe: influenza activity increased since the previous weeks, but remained low, with detections of predominantly influenza B viruses followed by influenza A(H3N2) viruses.

Northern Africa: sporadic influenza A virus detections were reported in Morocco and Tunisia.

Western Africa: influenza A(H1N1)pdm09 virus detections increased in Cote d'Ivoire and Ghana. In Middle Africa, influenza B detections were reported in Central African Republic.

In Eastern Africa: influenza B Yamagata-lineage virus detections were reported in Mozambique.

Western Asia: high levels of influenza activity were reported in Oman and Qatar in recent weeks, with detections of all seasonal influenza subtypes.

Central Asia: respiratory illness indicators appeared to increase in Kazakhstan and Uzbekistan in recent weeks.

Eastern Asia: influenza activity remained low in general. In Northern China, ILI and influenza percentage positive continued to increase, with influenza A(H3N2) and B Yamagata-lineage viruses predominantly detected.

2. VIROLOGICAL SURVEILLANCE AND STRAIN CHARACTERIZATION

WHO GISRS laboratories: from 13 November 2017 to 26 November 2017

NICs and other national influenza laboratories from 99 countries reported data to FluNet for the time period. More than 113412 specimens were tested during that time period and 8982 were positive for influenza viruses (7,9%), of which 5617 (62.5%) were typed as influenza A and 3365 (37.5%) as influenza B. Of the sub-typed influenza A viruses, 1122 (33%) were influenza A(H1N1)pdm09 and 2273 (67%) were influenza A(H3N2). Of the characterized B viruses, 1521 (80%) belonged to the B-Yamagata lineage and 381 (20%) 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 48/2017

While relatively few of the viruses detected in non-sentinel samples since week 40/2017 have been ascribed to a subtype or lineage, of all subtyped A viruses 82% were A(H3N2). Of influenza type B viruses ascribed to a lineage (n=76), 92% were B/Yamagata lineage and 8% were B/Victoria lineage.

Genetic characterization of 122 viruses has been reported (see table below). Among 74 influenza A(H3N2) viruses, 45 (61%) fell in the vaccine virus component clade (3C.2a), and 29 (39%) 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. Three B/Yamagata viruses were not attributed to any clade.

Table. Viruses attributed to genetic groups, cumulative for weeks 40–48/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1) ^a	16
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) ^b	45
A(H3N2) A/Singapore/INFIMH-16-0019/2014 (clade 3C.2a1) ^c	29
B/Brisbane/60/2008 (Victoria lineage clade 1A) ^{b,d}	3
B/Phuket/3073/2013 (Yamagata lineage clade 3) ^{c, e}	26
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 Vaccine component of quadrivalent vaccines for use in Northern Northern Hemisphere 2017–2018 season

See also November report (genetic data as of week 48)

<https://ecdc.europa.eu/sites/portal/files/documents/ERLI-Net-report-Nov-2017.pdf>

US-CDC- Until Nov 25th,2017

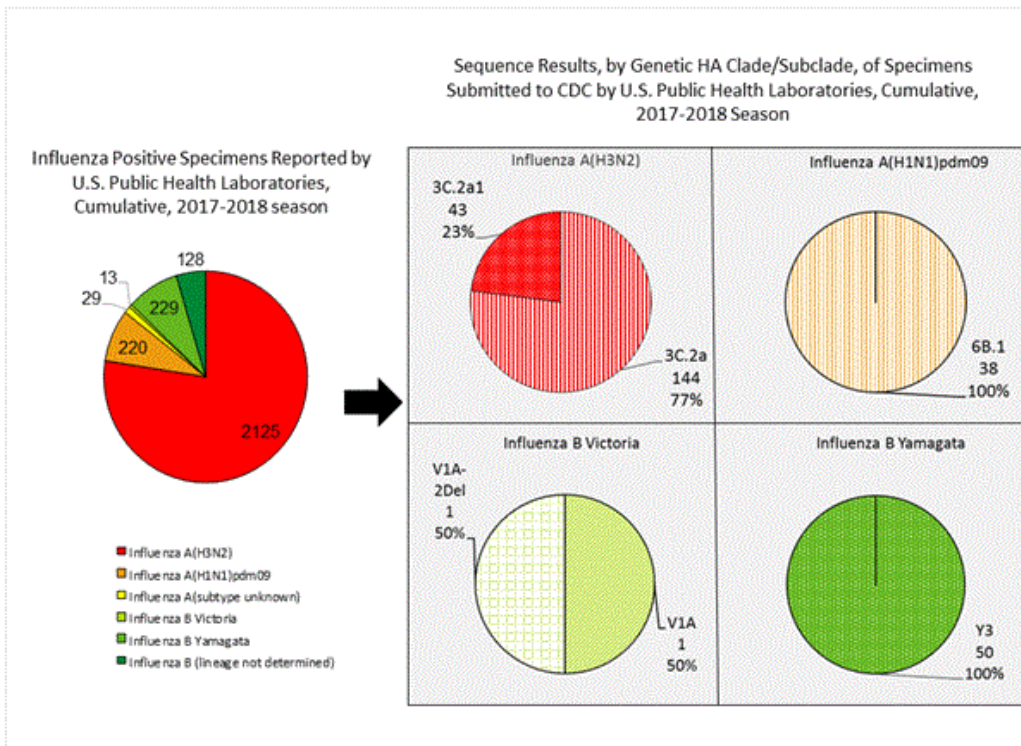
CDC has antigenically or genetically characterized 277 influenza viruses collected during October 1 – November 25, 2017 including 38 influenza A(H1N1)pdm09 viruses, 187 influenza A(H3N2) viruses, and 52 influenza B viruses.

A (H1N1)pdm09: Phylogenetic analysis of the HA genes from 38 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. 38 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 influenza vaccines.

A (H3N2): Phylogenetic analysis of the HA genes from 187 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=144) or subclade 3C.2a1 (n=43). 64 influenza A(H3N2) viruses were antigenically characterized, and 63 (98%) 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 influenza vaccines.

B/Victoria: Phylogenetic analysis of two 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). One (50%) of two 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 Northern Hemisphere influenza vaccines. One 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 this virus had the two amino acid deletion in the HA of the V1A-2Del viruses.

B/Yamagata: Phylogenetic analysis of 50 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 14 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 Northern Hemisphere QIV.



HPA-London until Week 48

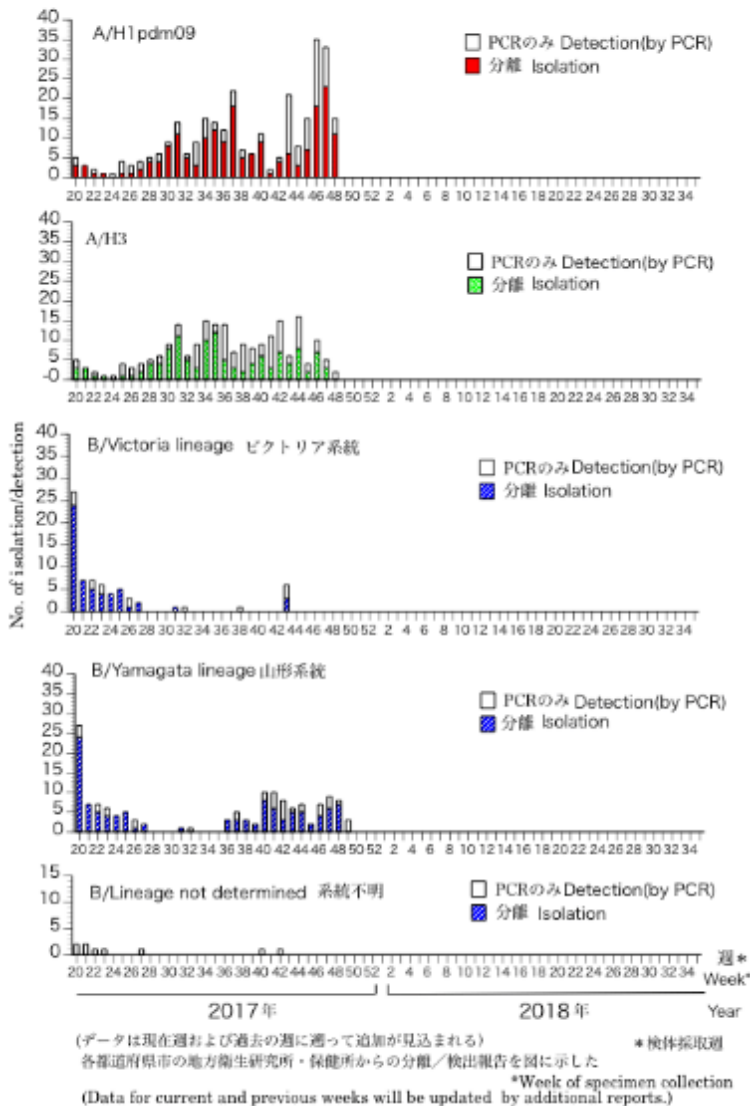
The PHE Respiratory Virus Unit has characterised 88 influenza viruses detected since week 37. Of the 19 A(H1N1)pdm09 influenza viruses that have been characterised, all belong in the genetic subgroup 6B.1, which was the predominant genetic subgroup in the 2016/17 season. The four viruses antigenically analysed are similar to the A/Michigan/45/2015 Northern Hemisphere 2017/18 (H1N1)pdm09 vaccine strain.

Genetic characterisation of 50 A(H3N2) influenza viruses detected since late summer, showed that they all belong to genetic subclade 3C.2a, with 30 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.

Nineteen influenza B viruses have been analysed; 16 were characterised as belonging to the B/Yamagata/16/88-lineage and 3 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 and QIV. B/Yamagata/16/88-lineage viruses were antigenically similar to B/Phuket/3073/2013, the influenza B/Yamagata-lineage component of 2016/17 NH QIV.

JAPAN National infectious diseases- Until Week 49

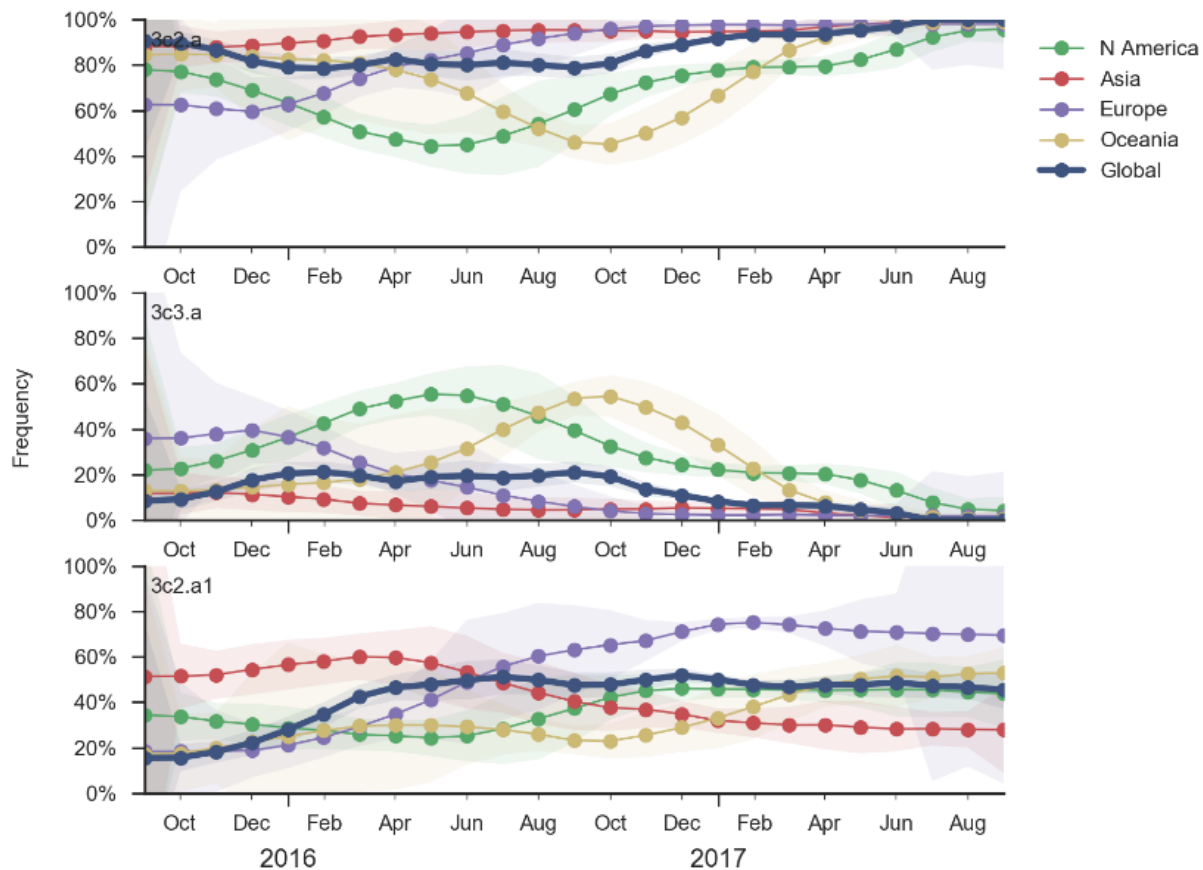
Weekly reports of influenza virus isolation/detection, week 20 of 2017 to week 49 of 2017, Japan
(Infectious Agents Surveillance Report: as of December 7, 2017 from public health institutes)



3. Real-time tracking of influenza virus evolution

Next-Flu (Sept 19th 2017 report) Neher RA, Bedford T. 2015. nextflu: real-time tracking of seasonal influenza virus evolution in humans. Bioinformatics DOI: 10.1093/bioinformatics/btv381.

H3N2 continues to diversify with many coexisting clades, all of which carry several amino acid mutations at previously characterized epitopes sites. The majority of viruses fall into the 3c2.a clade which has been dominating globally for >3 years, but 3c3.a viruses continue to persist. The common ancestor of circulating H3N2 viruses is now more than 5 years old, which is rare for H3N2. Despite extensive genetic diversity, serological assays suggest limited, but non-zero, antigenic evolution. We expect multiple competing clades within 3c2.a to persist into the future with no clear immediate winner.



A/H1N1pdm: A clade comprising mutations S74R and I295V has risen to >60% global frequency. Although it shows no antigenic distinction by ferret HI data, the rapidity of its rise suggests a selective origin.

B/Vic

A clade with a two amino acid deletion 162-/163- has altered serological properties and is increasing in frequency, albeit slowly. Two other clades (carrying mutations K209N and V87A/I175V) have increased in frequency moderately.

B/Yam

A clade comprising M251V within clade 3 viruses continues to dominate. This is little genetic differentiation within this clade and no evidence of antigenic evolution.

4. 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&language=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/>