Flu News Europe
Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 7/2018 (12–18 February 2018)

- Influenza activity was widespread in the majority of reporting countries, with overall 51% of individuals sampled from primary healthcare testing positive for influenza. The detection rate decreased slightly compared to the previous week (53%).
- Both influenza virus types A and B were co-circulating with a higher proportion of type B viruses. Different proportions of circulating influenza virus types and A subtypes were observed between countries.
- The majority of severe cases admitted to non-ICU hospital wards were adults infected by influenza type B viruses. The majority of severe cases admitted to ICU were adults infected mostly by influenza type A viruses.

2017–2018 season overview

- For the Region overall, a higher proportion of type B compared to type A viruses has been detected in sentinel and non-sentinel sources, representing a high level of influenza B compared with previous seasons. Of the type A detections from sentinel sources, whereby the majority of viruses were subtyped, A(H1N1)pdm09 viruses have outnumbered A(H3N2) viruses. In non-sentinel sources, whereby only 35% of influenza viruses were subtyped, more A(H3N2) viruses were reported than A(H1N1)pdm09 viruses.
- The majority of severe cases reported this season are due to influenza B and occur in persons above the age of 15 years. In confirmed influenza cases in ICU, similar numbers were infected by influenza type A and B viruses, and approximately equal numbers of cases were reported in the 15–64 and >64 year age groups. In laboratory confirmed cases reported in wards other than ICU, type B viruses were detected approximately twice as frequently as type A viruses and twice as many cases occurred among those aged >64 years compared with patients in the 15–64 age group.
- Concomitant with the increase in influenza activity, mortality due to any cause among the elderly has significantly increased over the past weeks in the western parts of the Region based on data provided by 20 EU countries to EuroMOMO.
- For type B viruses from both sentinel and non-sentinel sources, B/Yamagata lineage viruses have greatly outnumbered those of the B/Victoria lineage. The current trivalent seasonal influenza vaccine does not include a virus from the B/Yamagata lineage.
- Different patterns of dominant type and A subtype were observed between the countries of the Region, which may be due to differences in relative weights of information being derived from sentinel, non-sentinel and severe influenza case sources of information.
- While low in number, 59% of the genetically characterized A(H3N2) viruses belong to clade 3C.2a, the clade of the vaccine virus described in the WHO recommendations for

vaccine composition for the northern hemisphere 2017–2018, and 37% to subclade 3C.2a1, with mammalian cell-cultured viruses in both clades being antigenically similar.

- Although low in number detected and characterised, an increasing percentage (currently 47%) of B/Victoria lineage viruses belonged to B/Norway/2409/2017, representing the Victoria lineage clade 1A with deletion Δ162-163 which is antigenically different from the current quadrivalent vaccine component B/Brisbane/60/2008-like virus.
- Interim or real-time vaccine effectiveness estimates from Canada, Finland, Germany, Spain, Stockholm County and the United States of America suggest overall vaccine effectiveness of 15–46%, depending on the proportions of circulating (sub)types. Effectiveness against influenza B is in the range of 16–67%, despite the circulating lineage not being included in the most commonly used trivalent vaccine.
- Additional information on global influenza activity is available from WHO's biweekly global updates.
- WHO convened the Vaccine Composition Meeting on 19–21 February and recommended the composition of the 2018–2019 northern hemisphere vaccine. The full report is available here.

Primary care data

Overall, the majority of countries reported medium or high intensity of activity of respiratory infections, based on sentinel surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI). The majority of countries reported widespread detections of laboratory-confirmed influenza cases.

Influenza activity

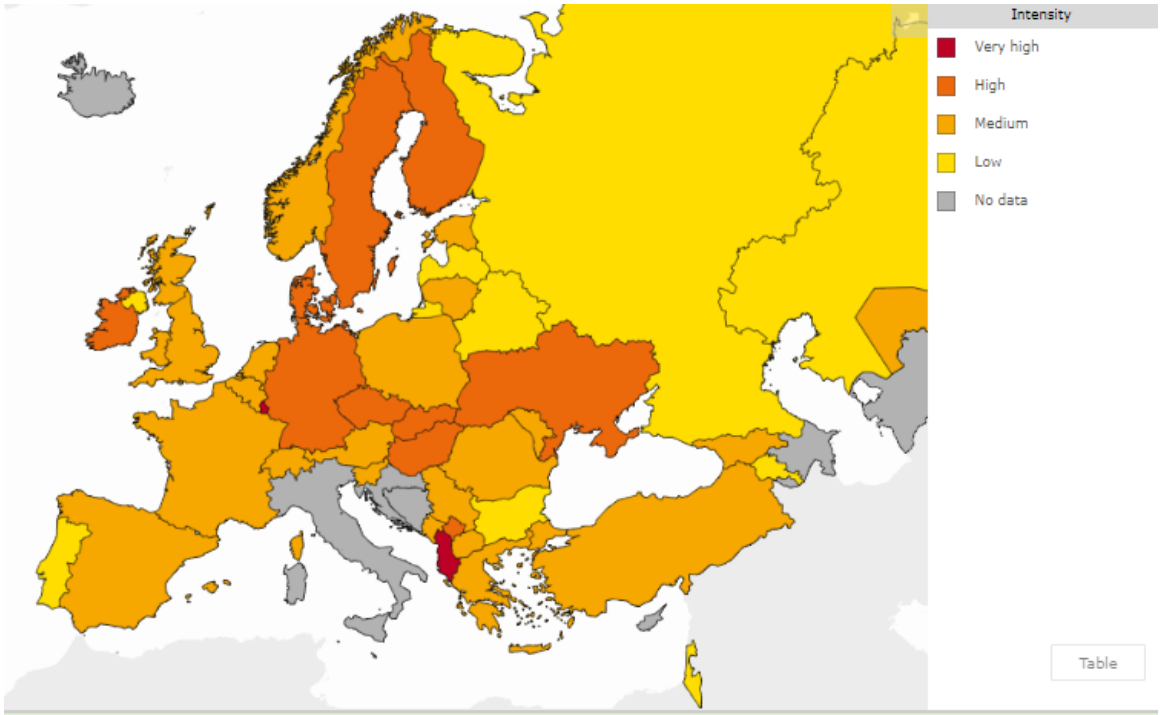
Influenza activity was at variable levels across the region in week 7/2018.

Of 41 Member States and areas reporting on intensity, Albania and Luxembourg reported very high intensity, while the Czech Republic, Denmark, Finland, Germany, Hungary, Ireland, Slovakia, Sweden, Ukraine and Kosovo (in accordance with Security Council resolution 1244 (1999)) reported high intensity; 20 Member States and the UK (England, Scotland and Wales) reported medium intensity and 8 Member States and the UK (Northern Ireland) low intensity (Fig. 1).

Of the 41 Member States and areas reporting on geographic spread, 28 Member States and the UK (Scotland and Wales) reported widespread activity, while others reported regional (n=4 and the UK (Northern Ireland)), local (n=4), or sporadic spread (n=4 and the UK (England)) (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 7/2018

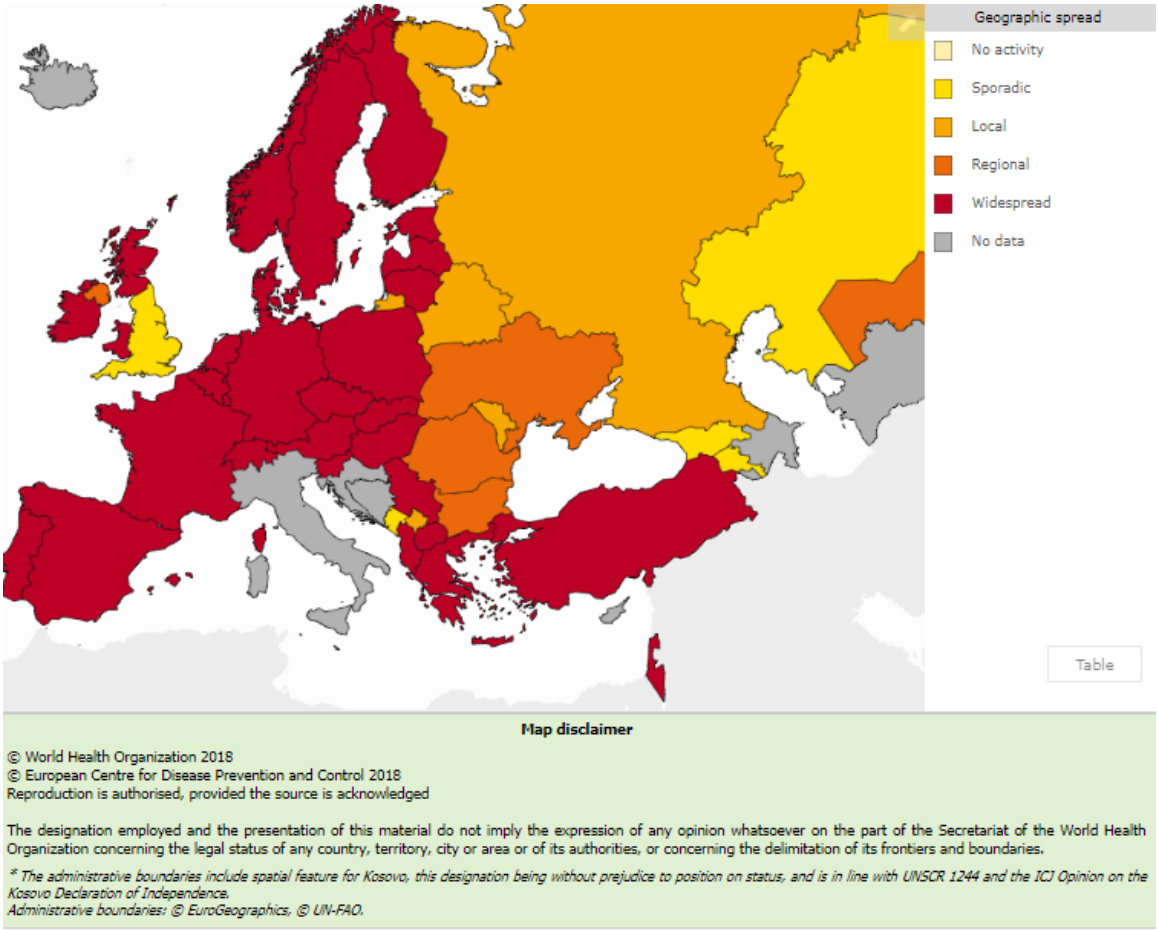


Map disclaimer

The designation employed and the presentation of this material do not imply the expression of any opinion whatsoever on the part of the Secretariat of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers and boundaries.

** The administrative boundaries include spatial feature for Kosovo, this designation being without prejudice to position on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.*
Administrative boundaries: © EuroGeographics, © UN-FAO.

Fig. 2 Geographic spread in the European Region, week 7/2018



For interactive maps of influenza intensity and geographic spread, please see the Flu News Europe website.

Viruses detected in sentinel-source specimens (ILI and ARI)

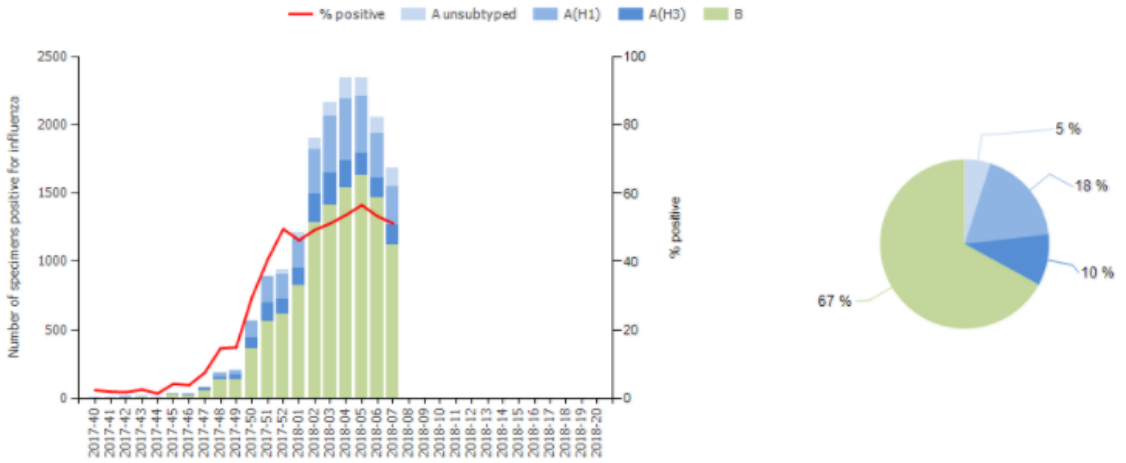
For week 7/2018, 1 683 (51%) of 3 297 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 33.3% were type A and 66.7% were type B. Of 428 subtyped A viruses, 66.4% were influenza A(H1N1)pdm09 and 33.6% A(H3N2). Of 595 type B viruses ascribed to a lineage, 96.6% were B/Yamagata and 3.4% B/Victoria (Fig. 3 and Table 1).

Of 38 Member States across the region that each tested at least 10 sentinel specimens in week 7/2018, 35 reported proportions of influenza virus detections above 30% (range of 30% to 87%).

Overall, since week 40/2017, more influenza type B (67%) than type A (33%) viruses have been detected. Of 4 682 subtyped A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 4 816 ascribed to a lineage, 96.8% were B/Yamagata (Table 1).

Details of the distribution of viruses detected in non-sentinel-source specimens can be found in the virus characteristics section.

Fig. 3 Influenza virus detections in sentinel-source specimens by type and subtype, by week and cumulatively [a]



[a]Pie chart shows cumulative data.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 7/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**560**	**33.3**	**5514**	**33.0**
A(H1N1)pdm09	284	66.4	3044	65.0
A(H3N2)	144	33.6	1638	35.0
A not subtyped	132	-	832	-
Influenza B	**1 123**	**66.7**	**11215**	**67.0**
B/Victoria lineage	20	3.4	152	3.2
B/Yamagata lineage	575	96.6	4664	96.8
Unknown lineage	528	-	6399	-
Total detections (total tested)	**1 683 (3 297)**	**51.0**	**16 729 (41 790)**	**40.0**

[a]For influenza type percentage calculations, the denominator is total detections; for subtype and lineage, it is total influenza A subtyped and total influenza B lineage determined, respectively; for total detections, it is total tested.

Severity

A subset of Member States monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs or other wards (n=12), or 2) severe acute respiratory infections (SARI; n=15).

The majority of severe cases reported this season have been due to influenza B and occur in persons above the age of 15 years. In confirmed influenza cases in ICU, similar numbers of cases were infected with type A or type B viruses and approximately equal numbers of cases were reported in the 15–64 years and >64 age groups. In laboratory confirmed cases reported in wards other than ICU, influenza type B was detected approximately twice as frequently as influenza type A and twice as many cases occurred among those >64 compared with patients in the 15–64 age group.

1.1) Hospitalized laboratory-confirmed influenza cases – Intensive care units (ICU)

Since week 40/2017, 12 countries have reported laboratory-confirmed influenza cases admitted to either all ICUs in the country or a set of sentinel ICUs (

Table 2). Overall, numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs continued to decrease in week 7/2018, reflecting the fact that the season peak has passed in the mainly western European countries reporting. There were 206 laboratory-confirmed influenza cases from ICUs, with the majority being in the United Kingdom (n=150, 73%). For weeks 5/2018 and 6/2018 the same countries reported 470 and 384 cases, respectively.

Since week 40/2017, type A influenza viruses were detected in 54% and type B in 46% of the cases in ICUs. Of 1 042 subtyped influenza A viruses, 60% were A(H1N1)pdm09 and 40% A(H3N2). Of 3 033 cases with known age, 48% were 15–64 years old and 46% 65 years and older.

In the age group 15–64, type A influenza viruses accounted for 66% of all infections with 81% of the subtyped A viruses being A(H1N1)pdm09. For patients aged 65 years and older, type A influenza virus was detected in 50% of the 1 381 cases with 66% of the subtyped A viruses being A(H1N1)pdm09. In all age groups, 75% of the 621 subtyped A viruses were A(H1N1)pdm09.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–7/2018

Country	Total Cases	A unsub.	A(H1N1) pdm09	A(H3N2)	B all	0-4 yrs	5-14 yrs	15-64 yrs	>64 yrs	UNK
Czech Republic	75	13	15	2	45	6	3	34	32	0
Denmark	69	7	6	7	49	2	0	24	43	0
Finland	23	0	3	5	15	0	1	10	12	0
France	1 714	897	347	25	445	50	22	860	737	45
Ireland	122	34	7	19	62	13	7	51	51	0
Netherlands	2	0	0	0	2	0	0	1	1	0
Romania	25	0	11	0	14	2	1	10	12	0

Russian Federation	4	0	1	3	0	0	0	3	1	0
Spain	869	173	88	89	519	67	19	380	403	0
Sweden	169	38	3	7	121	3	12	65	89	0
Ukraine	6	0	0	1	5	2	2	2	0	0
United Kingdom	2 251	684	143	260	1 164	0	0	0	0	2 251
TOTAL	**5 329**	**1 846**	**624**	**418**	**2 441**	**145**	**67**	**1 440**	**1 381**	**2 296**

UNK = age unknown, *from either sentinel hospitals or all hospitals per country

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 7/2018, a total of 281 cases was reported from other wards, with the majority reported from Ireland (56%) and Spain (33%). Overall, numbers of cases in other wards decreased in week 7/2018 compared to weeks 5/2018 and 6/2018, for which 978 and 892 hospitalised cases were reported, respectively.

Since week 40/2017, 8 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (65%) of these cases were infected by influenza type B viruses and 58% of all cases were in patients aged 65 years and older.

Table 3. Laboratory-confirmed hospitalised cases in other wards* by country, cumulatively weeks 40/2017–7/2018

Country	Total Cases	A unsub.	A(H1N1) pdm09	A(H3N2)	B total	0-4 yrs	5-14 yrs	15-64 yrs	>64 yrs	UNK
Czech Republic	70	21	13	0	36	1	0	37	32	0
Denmark	1 794	254	81	124	1 335	95	70	728	901	0
Ireland	2 751	736	97	285	1 633	335	270	777	1 368	1
Romania	39	0	16	2	21	8	4	21	6	0
Russian Federation	36	0	5	19	12	8	2	22	4	0
Slovakia	4	2	1	0	1	0	0	4	0	0
Spain	3 117	682	145	236	2 054	152	33	700	2 232	0
Ukraine	27	4	2	0	21	3	6	18	0	0
TOTAL	**7 838**	**1 699**	**360**	**666**	**5 113**	**602**	**385**	**2 307**	**4 543**	**1**

UNK = age unknown, *from either sentinel hospitals or all hospitals per country

2. SARI surveillance

Since week 40/2017, SARI cases have been reported by 15 countries, the majority being located in the eastern part of the Region.

For week 7/2018, 920 SARI cases, compared to 1 651 during week 6/2018, were reported by 12 countries from which 557 specimens were tested for influenza viruses with 29.8% being positive (compared to 30.2% during week 6/2018). The positivity rate had been gradually

increasing up until week 5/2018, reflecting mainly the epidemic moving towards eastern Europe.

For SARI cases testing positive for influenza virus, type B viruses have been most common; 60.8% in week 7/2018 and 66.2% overall for weeks 40/2017–7/2018. A(H1N1)pdm09 virus was detected in 20.5% of influenza-positive SARI cases.

Mortality monitoring

Data from 20 EU/EEA Member States or regions reporting to the EuroMOMO project were received for week 7/2018 and included in the pooled analyses of excess mortality from all causes. Mortality among the elderly has increased significantly over the past weeks in the western part of the European region.

Virus characteristics

Most influenza viruses detected in sentinel surveillance systems this season were type B with those assigned to a lineage being mainly B/Yamagata viruses, while most of the type A viruses subtyped were influenza A(H1N1)pdm09 viruses. Details of the distribution of viruses detected in sentinel-source specimens can be found in the Primary care data section.

Since week 1/2018, the majority of influenza virus detections in non-sentinel systems have been type B with B/Yamagata lineage viruses predominating, as seen in sentinel systems. However, in contrast to sentinel systems, the majority of non-sentinel influenza A viruses subtyped were A(H3N2). This may be related to the higher proportion of non-sentinel specimens being derived from hospital-based settings or outbreaks in long-term care facilities for the elderly, with A(H3N2) viruses often causing more severe disease in the elderly, while A(H1N1)pdm09 viruses do so in middle-aged patients. Further details are given in the section below.

Differences in the relative contributions of sentinel and non-sentinel specimen sources to influenza surveillance between countries may lead to variation in (sub)type proportions between countries within the Region.

Viruses detected in non-sentinel-source specimens

For week 7/2018, 12 279 specimens from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, nursing homes and other institutions) tested positive for influenza viruses. Of these, 37.7% were type A and 62.3% type B viruses (Table 4), making this the seventh week in which type B viruses have predominated in non-sentinel specimens. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage.

While relatively few of the viruses detected in non-sentinel specimens since week 40/2017 have been ascribed to a subtype or lineage, 58% of all subtyped A viruses were A(H3N2) and 98.7% of influenza type B viruses ascribed to a lineage were B/Yamagata lineage (Table 4).

Table 4. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 7/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**4 626**	**37.7**	**48 028**	**41.6**
A(H1N1)pdm09	843	51.4	7 727	42.0
A(H3N2)	796	48.6	106 74	58.0
A not subtyped	2 987	-	29 627	-
Influenza B	**7 653**	**62.3**	**67 561**	**58.4**
B/Victoria lineage	5	2.1	57	1.3
B/Yamagata lineage	236	97.9	4 338	98.7
Unknown lineage	7 412	-	63 166	-
Total detections (total tested)	**12 279 (31 508)**	**-**	**115 589 (448 635)**	**-**

[a]For influenza type percentage calculations, the denominator is total detections; for subtype and lineage, it is total influenza A subtyped and total influenza B lineage determined, respectively; as not all countries have a true non-sentinel testing denominator, no percentage calculations for total tested are shown.

Genetic characterization

For specimens collected since week 40/2017, genetic characterization of 1 696 viruses has been reported (Table 5).

Among 544 influenza A(H3N2) viruses attributed to a clade, 323 (59%) fell in the vaccine virus component clade (3C.2a), 202 (37%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 19 (4%) in clade 3C.3a. 1 A(H3N2) virus was not attributed to any clade. Viruses in the first two 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.

Of the 227 A(H1N1)pdm09 viruses attributed to a clade, all fell in the A/Michigan/45/2015 vaccine component clade (6B.1). 1 virus was not attributed to a clade.

42 of the 89 B/Victoria-lineage clade 1A viruses belonged to a subgroup represented by B/Norway/2409/2017, which carries the HA1 double amino acid deletion, Δ162-163, characteristic of a new antigenically distinct subgroup of viruses that has been detected in several countries. All of the 834 B/Yamagata lineage viruses belonged to clade 3 represented by B/Phuket/3073/2013. For more information on virus characterizations for EU/EEA countries, see the WHO CC London December 2017 report.

Table 5. Viruses attributed to genetic groups, cumulative for weeks 40/2017–7/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	227
A(H1N1)pdm09 not attributable to any clade	1*
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	323
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	202
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	19
A(H3N2) not attributable to any clade	1*
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	47
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	42
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	834
B/Yamagata lineage not attributed to any clade	0

[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
* These reports are under clarification with the reporting countries

The recommended composition of trivalent influenza vaccines for the 2017–2018 season in the northern hemisphere includes an A/Michigan/45/2015 (H1N1)pdm09-like virus; an A/Hong Kong/4801/2014 (H3N2)-like virus; and a B/Brisbane/60/2008-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended.

On 21 February 2018, WHO recommended two changes, compared to the current trivalent and quadrivalent vaccines recommended for the 2017–2018 season in the northern hemisphere influenza season, in the trivalent and quadrivalent vaccine composition for the 2018-2019 season in the northern hemisphere. Similar to the recommended composition for the 2018 southern hemisphere vaccine, the A(H3N2) component was changed to an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus. In trivalent vaccines the B component was switched to a B/Victoria -lineage B/Colorado/06/2017-like virus, representing the emergent strain of B/Victoria with deletion of K162 and N163 in the HA1 subunit. The A(H1N1)pdm09 component in trivalent and quadrivalent vaccines and the B/Yamagata component in quadrivalent vaccines remained the same.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 1 233 viruses; 546 type B, 407 A(H3N2), and 280 A(H1N1)pdm09) with collection dates since week 40/2017. One A(H3N2) virus carried amino acid substitution R292K in neuraminidase and showed evidence of reduced inhibition by both oseltamivir and zanamivir. One A(H1N1)pdm09 showed evidence of reduced inhibition by oseltamivir. Two type B viruses showed evidence of reduced inhibition by zanamivir and one, carrying amino acid substitution D198N in neuraminidase, to both oseltamivir and zanamivir.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, René Snacken, Pasi Penttinen, Phillip Zucs), Angeliki Melidou (ECDC Consultant from the National Influenza Centre for N. Greece) and the WHO Regional Office for Europe (Caroline Brown, Piers Mook, Dmitriy Pereyaslov and Tamara Meerhoff, Temporary Advisor to WHO). It was reviewed by country experts (Raquel Guiomar, Instituto Nacional de Saúde Doutor Ricardo Jorge, Portugal; Vladimir Mikic, Institute of Public Health, The former Yugoslav Republic of Macedonia) and by experts from the network (Adam Meijer, National Institute for Public Health and the Environment (RIVM), the Netherlands; Rod Daniels and John McCauley, WHO Collaborating Centre for Reference and Research on Influenza, Francis Crick Institute, United Kingdom; Tyra Grove Krause, Statens Serum Institut and EuroMOMO network, Denmark).

All data are up to date on the day of publication. Past this date, however, published data should not be used for longitudinal comparisons, as countries retrospectively update their databases.

The WHO Regional Office for Europe is responsible for the accuracy of the Russian translation.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 7/2018.

Tables and figures should be referenced:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 7/2018.