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

Summary

Week 8/2018 (19–25 February 2018)

- Influenza activity was widespread in the majority of reporting countries.
- Overall 49% of individuals sampled from primary healthcare settings tested positive for influenza virus, a slight decrease compared to the previous week (51%).
- Both influenza virus types A and B were co-circulating with a higher proportion of type B viruses. Differences in 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. Half of severe cases admitted to ICU were adults infected by influenza type A viruses.
- Based on data provided by 20 EU countries to EuroMOMO, excess mortality from all causes has elevated significantly over the past months in the south-western part of the European region, but this increase seems less in some countries.

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 circulation of influenza B viruses compared with previous seasons. Of the type A virus detections from sentinel sources, the majority of which were subtyped, A(H1N1)pdm09 viruses have outnumbered A(H3N2) viruses. In non-sentinel sources, 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 laboratory-confirmed influenza cases in ICU, comparable numbers were infected by influenza type A and B viruses, and the elderly were at increased risk of ICU admission. In laboratory-confirmed influenza cases reported from wards other than ICU, type B viruses were detected approximately twice as frequently as type A viruses.
- 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 subtypes 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 few B/Victoria lineage viruses have been detected, their characterization has shown an increasing percentage (currently 47%) of viruses belonging to a subclade of clade 1A viruses, represented by B/Norway/2409/2017. These viruses have a two amino acid deletion in haemagglutinin (Δ162-163) and are antigenically different from the current trivalent vaccine component, a B/Brisbane/60/2008-like virus.
- Interim results from 5 European studies indicate that, in all age groups, influenza vaccine effectiveness was 25 to 52% against any influenza, 55 to 68% against influenza A(H1N1)pdm09, -42 to 7% against influenza A(H3N2) and 36 to 54% against influenza B, which is consistent with previous estimates from Canada, Finland, Germany, Spain, Stockholm County and the United States of America.
- Additional information on global influenza activity is available from WHO's biweekly global updates.
- 19–21 February 2018, WHO-HQ convened the Vaccine Composition Meeting, which made recommendations for 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

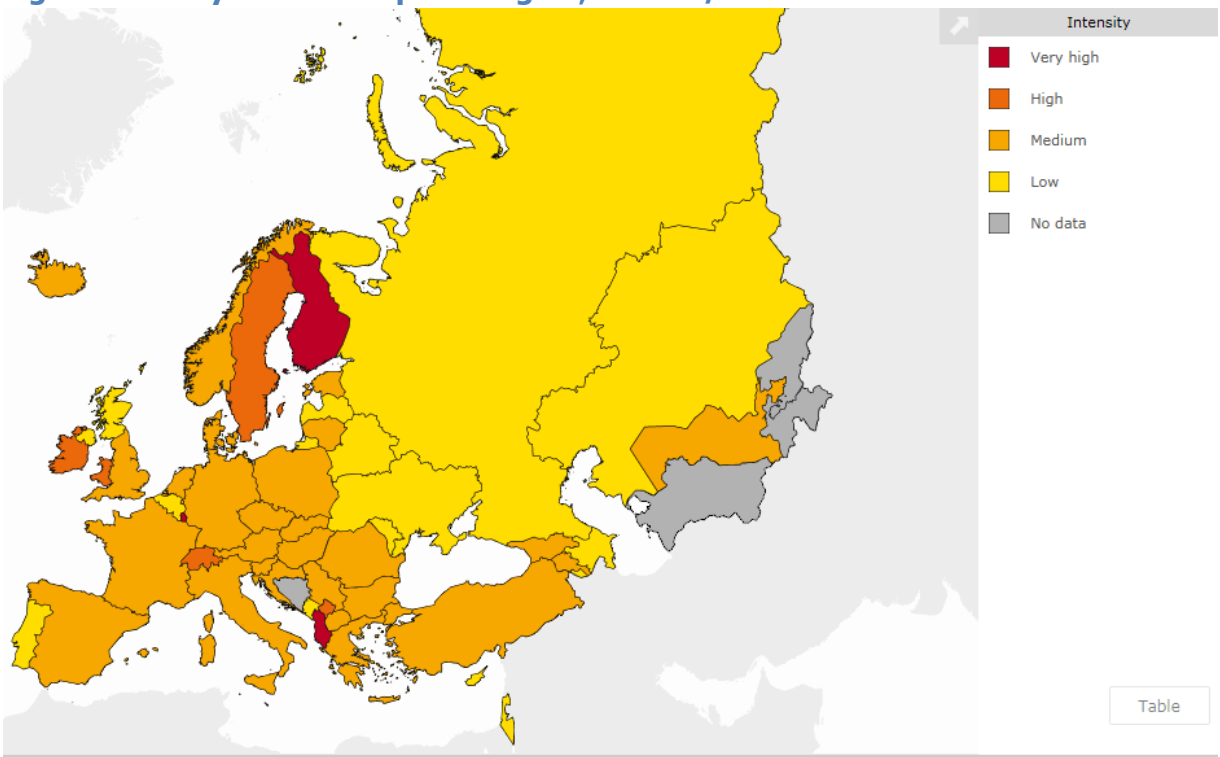
Influenza activity was at variable levels across the region in week 8/2018.

Of 45 Member States and areas reporting on intensity, Luxembourg reported very high intensity, while Albania, the Czech Republic, Denmark, Germany, Hungary, Slovakia, Sweden, Ukraine and Kosovo (in accordance with Security Council resolution 1244 (1999)) reported high intensity; 25 Member States including the United Kingdom (England, Scotland and Wales) reported medium intensity and 11 Member States including the United Kingdom (Northern Ireland) low intensity (Fig. 1).

Of the 45 Member States and areas reporting on geographic spread, 32 Member States including the United Kingdom (Scotland) reported widespread activity, while others reported regional (n=3 including the United Kingdom (Wales)), local (n=4) or sporadic spread (n=6 including the United Kingdom (England and Northern Ireland)) and 2 reported no activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 8/2018



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.*
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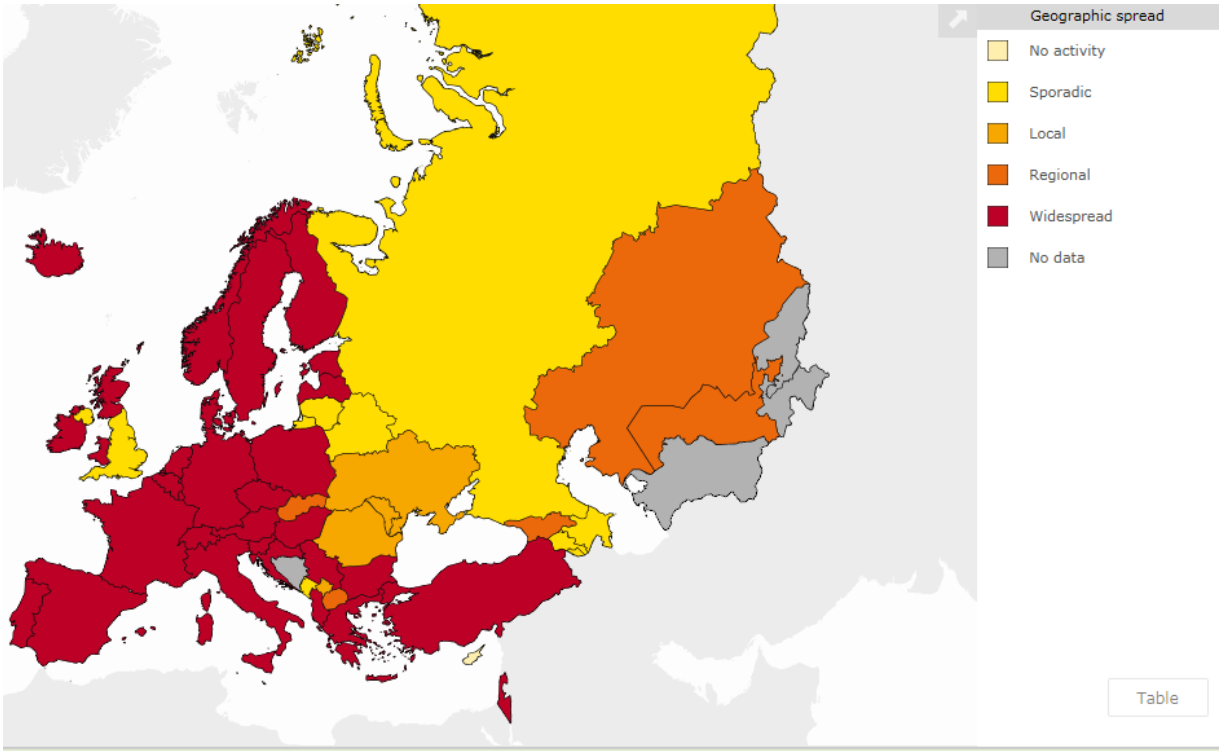
Fig. 2 Geographic spread in the European Region, week 8/2018



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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 8/2018, 1 525 (49%) of 3 116 sentinel specimens tested positive for influenza viruses; 36% were type A and 64% were type B (Table 1).

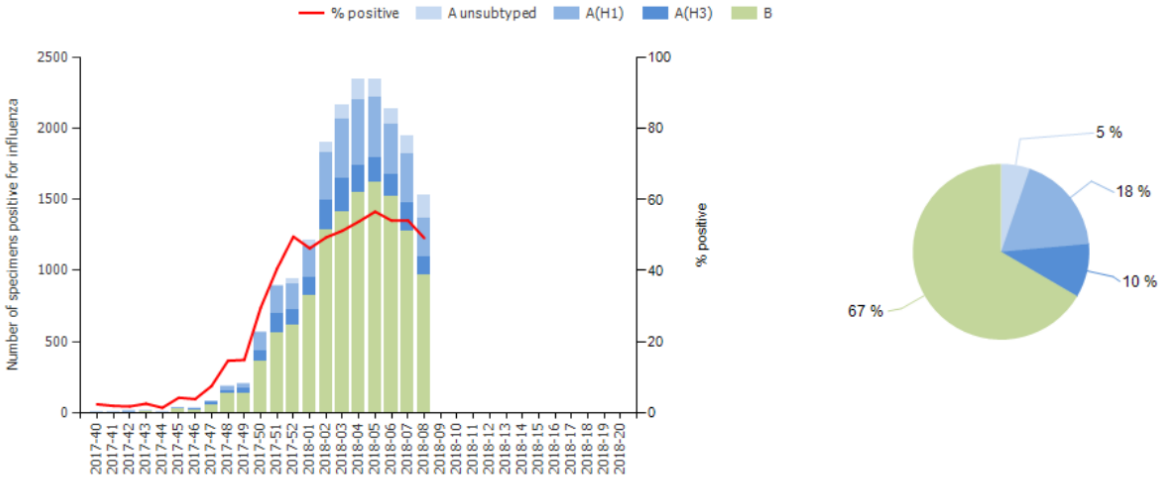
Of 392 subtyped A viruses, 68% were influenza A(H1N1)pdm09 and 32% A(H3N2). Of 486 type B viruses ascribed to a lineage, 97% were B/Yamagata and 3% B/Victoria (Fig. 3 and Table 1).

Of 31 Member States across the region and the United Kingdom (England, Northern Ireland and Wales) that each tested at least 10 sentinel specimens in week 8/2018, 23 and the UK (England) reported proportions of influenza virus detections above 30% (range of 31% to 78%).

Overall, since week 40/2017, more influenza type B (67%) than type A (33%) viruses have been detected. Of 5 239 subtyped A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 5 440 ascribed to a lineage, 97% 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 8/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**555**	**36.4**	**6 221**	**33.4**
A(H1N1)pdm09	268	68.4	3 403	65.0
A(H3N2)	124	31.6	1 836	35.0
A not subtyped	163	-	982	-
Influenza B	**970**	**63.6**	**12 389**	**66.6**
B/Victoria lineage	14	2.9	169	3.1
B/Yamagata lineage	472	97.1	5 271	96.9
Unknown lineage	484	-	6 949	-
Total detections (total tested)	**1 525 (3 116)**	**48.9**	**18 610 (45 320)**	**41.1**

[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 (n=12) or other wards (n=8), or 2) severe acute respiratory infections (SARI; n=9).

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 laboratory-confirmed influenza cases in ICU, more cases were infected with type A compared to type B viruses (n=3 464 and 2 666 respectively).

In laboratory-confirmed influenza 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 older than 64 years 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 8/2018, reflecting the fact that weekly detections have been decreasing in a number of countries, mainly in the western part of the Region. During week 08/2018, there were 234 laboratory-confirmed influenza cases from ICUs, with the majority being in the United Kingdom (n=149, 64%). For weeks 6/2018 and 7/2018 the same countries reported 431 and 298 cases, respectively, indicating a continued decline.

Since week 40/2017, type A influenza viruses have been detected in 53% and type B in 47% of cases in ICUs. Of 1 857 subtyped influenza A viruses, 90% were A(H1N1)pdm09 and 10% A(H3N2). Of 3 284 cases with known age, 47% were 15–64 years old and 46% 65 years and older.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–8/2018

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	92	17	16	3	56	7	3	39	43	0
Denmark	145	19	9	14	103	2	0	54	89	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	129	36	9	20	64	14	9	53	53	0
Netherlands	8	0	0	0	8	0	0	3	5	0
Romania	34	1	15	0	18	2	1	12	19	0
Russian Federation	4	0	1	3	0	0	0	3	1	0
Spain	932	197	95	99	541	73	22	416	421	0
Sweden	242	52	4	9	177	7	16	93	126	0
Ukraine	6	0	0	1	5	2	2	2	0	0
United Kingdom	2 401	743	153	271	1 234	0	0	0	0	2 401
TOTAL	**5 730**	**1 962**	**652**	**450**	**2 666**	**157**	**76**	**1 545**	**1 506**	**2 446**

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

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 8/2018, a total of 721 cases was reported from other wards, with the majority reported from Denmark (63%) and Ireland (21%). Numbers of cases in other wards decreased in week 8/2018 (n = 721) compared to week 7/2018 (n = 1 317).

Since week 40/2017, 8 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (67%) 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 40/2017–8/2018

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	105	22	24	0	59	2	0	49	54	0
Denmark	3 405	451	152	192	2 610	179	135	1 261	1 830	0
Ireland	3 121	844	117	319	1 841	386	304	885	1 545	1
Romania	47	2	18	3	24	9	4	26	8	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	3 351	765	162	260	2 164	165	36	749	2 401	0
Ukraine	27	4	2	0	21	3	6	18	0	0
TOTAL	**10 096**	**2 090**	**481**	**793**	**6 732**	**752**	**487**	**3 014**	**5 842**	**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 8/2018, 1 682 SARI cases, compared to 920 during week 7/2018, were reported by 6 countries from which 140 specimens were tested for influenza viruses with 35% being positive. The positivity rate had been gradually increasing up until week 5/2018, reflecting the west to east spread of influenza across Europe.

For SARI cases testing positive for influenza virus, type B viruses have been most common; 58% in week 8/2018 and 67% overall for weeks 40/2017–8/2018. A(H1N1)pdm09 viruses were detected in 22% of influenza virus-positive SARI cases.

Mortality monitoring

Data from 20 EU/EEA Member States or regions reporting to the EuroMOMO project were received for week 8/2018 and included in pooled analyses.
Excess mortality from all causes has been significantly elevated over the past months in the south-western part of the European region. This increase seems less in some countries, but it is still too early to conclude that mortality has peaked, because the decline may be due to insufficient adjustment for delay in registration.

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 8/2018, 11 339 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, 39% were type A and 61% 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, 57% of all subtyped A viruses were A(H3N2) and 99% 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 8/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**4 433**	**39**	**54 054**	**41**
A(H1N1)pdm09	742	50	8 716	43
A(H3N2)	753	50	11 596	57
A not subtyped	2 938	-	33 742	-
Influenza B	**6 906**	**61**	**78 630**	**59**
B/Victoria lineage	4	1	61	1
B/Yamagata lineage	274	99	5 256	99
Unknown lineage	6 628	-	73 313	-
Total detections (total tested)	**11 339 (28 408)**	**-**	**132 684 (485 278)**	**-**

[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 1 715 viruses has been reported (Table 5).

Among 550 influenza A(H3N2) viruses attributed to a clade, 329 (60%) 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 (6%) in clade 3C.3a. One 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 230 A(H1N1)pdm09 viruses attributed to a clade, all fell in the A/Michigan/45/2015 vaccine component clade (6B.1). One virus was not attributed to a clade.

42 (45%) of the 93 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 842 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 40/2017–8/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	230
A(H1N1)pdm09 not attributable to any clade	1*
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	329
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]	51
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]	842
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 published influenza vaccine recommendations for the 2018-2019 season in the northern hemisphere. Two changes were recommended compared to the current trivalent and quadrivalent vaccines recommended for the 2017–2018 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 1 256 viruses; 563 type B, 413 A(H3N2), and 280 A(H1N1)pdm09) with collection dates since week 40/2017. 1 A(H3N2) virus carried amino acid substitution R292K in neuraminidase and showed evidence of reduced inhibition by both oseltamivir and zanamivir. 1 A(H1N1)pdm09 showed evidence of reduced inhibition by oseltamivir. 3 type B viruses showed evidence of reduced inhibition by zanamivir and 1, carrying amino acid substitution D198N in neuraminidase, to both oseltamivir and zanamivir.

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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 8/2018.

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 8/2018.