Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 11/2018 (12–18 March 2018)

- Influenza viruses continue to circulate widely in the Region with some eastern European countries that have only recently reported increased activity experiencing a late start to the season with increased circulation of influenza type A viruses.
- Similar to the previous week, 44% of the individuals sampled from primary healthcare settings tested positive for influenza viruses, despite the peak rate for the Region occurring in week 05/2018.
- Both influenza virus types A and B were co-circulating with the majority being type B viruses and B/Yamagata continuing to be the dominant lineage.
- Similar proportions of influenza type A and B viruses were reported in patients admitted to ICU, with the majority of severe cases reported this season being due to influenza type B and occurring in persons above the age of 15 years.
- A seasonal reassortant A(H1N2) influenza virus consisting of HA and NS genes of human seasonal A(H1N1)pdm09 influenza virus and M, NA, NP, PA, PB1 and PB2 genes of human seasonal A(H3N2) influenza virus was detected in the Netherlands. As the reassortant virus genome contains a mixture of genes from currently circulating seasonal influenza viruses, no increase in virulence is expected. Having similar HA with circulating strains, the current vaccine is expected to offer protection against this reassortant. The neuraminidase showed no evidence for reduced sensitivity to neuraminidase inhibitors. There is no evidence for extensive spread of this A(H1N2) influenza virus.

2017–2018 season overview

- For the region overall, the majority of influenza viruses detected were type B, representing a high level of circulation of influenza B viruses compared to recent seasons. B/Yamagata lineage viruses have greatly outnumbered those of the B/Victoria lineage. Click here for more information
- 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. Influenza A viruses are dominant in several eastern European countries (e.g. Russian Federation, Kazakhstan). See the maps below for more information
- 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 than A(H1N1)pdm09 viruses were reported. Click here for more information
- While low in number, 56% of A(H3N2) viruses belong to clade 3C.2a and 48% of B/Victoria viruses belong to a subclade of clade 1A viruses that are antigenically distinct from the current trivalent vaccine component. Click here for more information

- The majority of severe cases reported this season are due to influenza type B and have occured in persons above the age of 15 years. Click here for more information
- Mortality from all causes based on pooled data from 19 EU countries and regions that reported to EuroMOMO (http://www.euromomo.eu/) remained elevated in some countries, while it was declining in others. Click here for more information
- Interim results from 5 European studies indicate that influenza vaccine effectiveness was estimated to be similar to that in recent years. Click here for more information

Primary care data

Overall, the majority of countries reported low or medium 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 geographically widespread or regional detections of laboratory-confirmed influenza cases.

Influenza activity

Influenza activity was at variable levels across the region in week 11/2018.

Of 46 Member States and areas reporting on intensity, Luxembourg reported very high intensity, while Denmark, Finland and Germany reported high intensity; 22 Member States including the United Kingdom (Wales) reported medium intensity and 20 Member States including the United Kingdom (England, Northern Ireland and Scotland) low intensity (Fig. 1).

Of the 46 Member States and areas reporting on geographic spread, 22 Member States reported widespread activity, while others reported regional (n=9 including the United Kingdom (Scotland and Wales)), local (n=6) or sporadic spread (n=6 including the United Kingdom (England and Northern Ireland)) and 3 reported no activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, week 11/2018

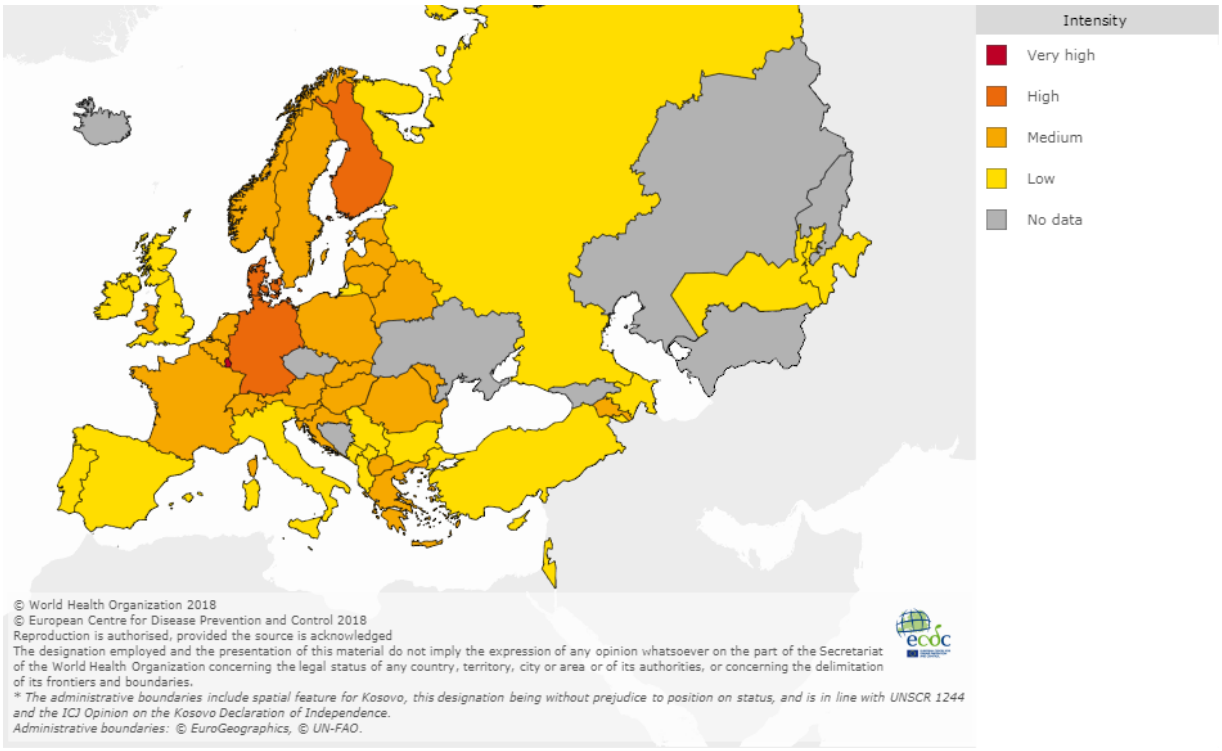
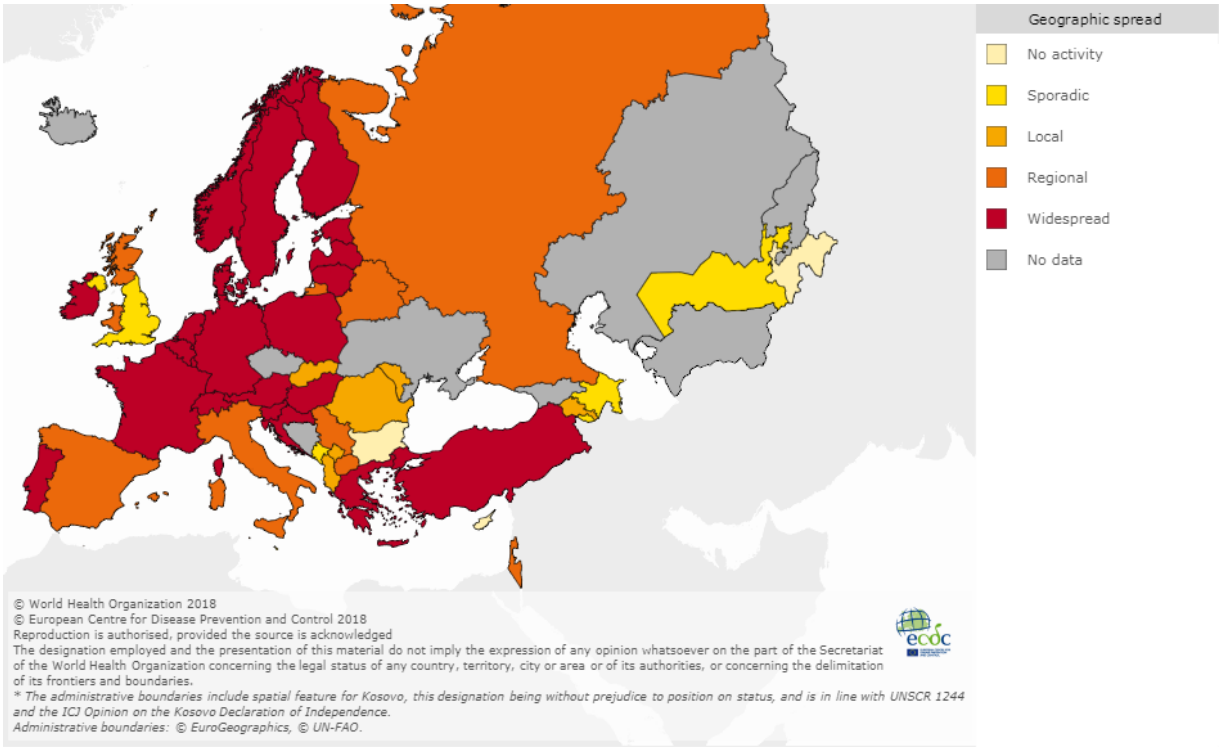


Fig. 2. Geographic spread in the European Region, week 11/2018



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 11/2018, 898 (44%) of 2 055 sentinel specimens tested positive for influenza viruses; 48% were type A and 52% were type B (Table 1).

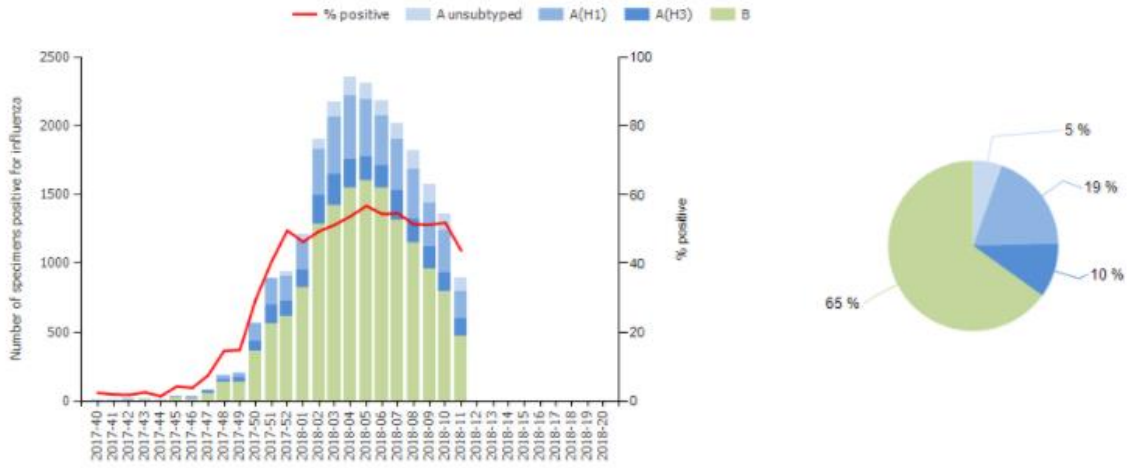
Of 326 subtyped A viruses, 60% were influenza A(H1N1)pdm09 and 40% A(H3N2). Of 275 type B viruses ascribed to a lineage, 99% were B/Yamagata and 1% B/Victoria (Fig. 3 and Table 1).

Of 24 Member States across the region including the United Kingdom (England) that each tested at least 10 sentinel specimens in week 11/2018, 21 reported proportions of influenza virus detections above 30% (range of 33% to 70%).

Overall, since week 40/2017, more influenza type B (65%) than type A (35%) viruses have been detected. Of 6 713 subtyped A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 6 979 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 11/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**431**	**48.0**	**7 966**	**34.9**
A(H1N1)pdm09	197	60.4	4 370	65.1
A(H3N2)	129	39.6	2 343	34.9
A not subtyped	105	-	1 253	-
Influenza B	**467**	**52.0**	**14 848**	**65.1**
B/Victoria lineage	2	0.7	193	2.8
B/Yamagata lineage	273	99.3	6 786	97.2
Unknown lineage	192	-	7 869	-
Total detections (total tested)	**898 (2 055)**	**43.7**	**22 814 (53 606)**	**42.6**

[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=16).

The majority of severe cases reported this season have been due to influenza type B and occur in persons above the age of 15 years. In laboratory-confirmed influenza cases in ICU, more cases were infected with influenza type A compared to type B viruses (n=4 049 and 3 782 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 years 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 11/2018, reflecting mainly the situation in countries of the western part of the Region. During week 11/2018, there were 276 laboratory-confirmed influenza cases from ICUs, with the majority being in the United Kingdom (n=114, 41%). For weeks 9/2018 and 10/2018, the same countries reported 518 and 478 cases, respectively.

Since week 40/2017, type A influenza viruses have been detected in 52% and type B in 48% of cases in ICUs. Of 1 482 subtyped influenza A viruses, 59% were A(H1N1)pdm09 and 41% A(H3N2). Of 4 796 cases with known age, 46% were 15–64 years old and 47% 65 years and older.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–11/2018

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	242	38	43	4	157	12	8	100	122	0
Denmark	256	29	18	17	192	4	5	93	154	0
Finland	48	0	3	18	27	1	1	14	32	0
France	2 614	1 176	449	41	948	69	43	1 254	1 196	52
Ireland	141	38	10	23	70	15	9	59	58	0
Netherlands	14	4	0	0	10	0	0	8	6	0
Romania	48	1	22	1	24	3	1	21	23	0
Russian Federation	6	0	1	5	0	0	0	3	3	0
Spain	1 119	274	125	121	599	93	31	491	504	0
Sweden	331	79	5	10	237	8	18	133	172	0
Ukraine	29	1	0	1	27	9	10	10	0	0
United Kingdom	2 983	927	200	365	1 491	0	0	0	0	2 983
TOTAL	**7 831**	**2 567**	**876**	**606**	**3 782**	**214**	**126**	**2 186**	**2 270**	**3 035**

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

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 11/2018, a total of 225 cases were reported from other wards, with the majority being in Denmark (50%). Numbers of cases in other wards decreased in week 11/2018 compared to week 10/2018 (n=876).

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 40/2017–11/2018

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	245	42	62	3	138	4	2	96	143	0
Denmark	5 363	659	270	335	4 099	267	204	1 833	3 059	0
Ireland	3 602	986	151	376	2 089	452	350	1 026	1 772	2
Romania	82	5	34	3	40	17	9	44	12	0
Russian Federation	229	0	29	125	75	43	19	147	20	0
Slovakia	4	2	1	0	1	0	0	4	0	0
Spain	4 151	1 104	214	374	2 459	217	45	938	2 951	0
Ukraine	130	6	2	3	119	18	26	85	1	0
TOTAL	**13 806**	**2 804**	**763**	**1 219**	**9 020**	**1 018**	**655**	**4 173**	**7 958**	**2**

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 16 countries, the majority being located in the eastern part of the Region.

For week 11/2018, 670 SARI cases were reported by 13 countries; 288 specimens were tested for influenza viruses with 33% being positive, an increase compared to week 10/2018 (28%). The positivity rate had been gradually increasing up until week 8/2018 and decreased in weeks 9/2018 and 10/2018.

For SARI cases testing positive for influenza virus, type B viruses have been most common; 61% overall for weeks 40/2017–11/2018, but only 27% in week 11/2018. A(H1N1)pdm09 viruses were detected in 53% of influenza virus-positive SARI cases in week 11/2018, a higher proportion compared to week 10/2018 (33%).

Mortality monitoring

Data from 19 EU/EEA Member States or regions reporting to the EuroMOMO project were received for week 11/2018 and included in pooled analyses. Excess mortality from all causes has been significantly elevated over recent months in the south-western part of the European region. However, mortality seems to be declining in some countries.

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 type 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 11/2018, 10 497 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, 49% were type A and 51% type B viruses (Table 4). 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, 54% 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 11/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**5 136**	**48.9**	**72 894**	**41.3**
A(H1N1)pdm09	1 041	56.7	12 563	46.2
A(H3N2)	796	43.3	14 639	53.8
A not subtyped	3 299	-	45 692	-
Influenza B	**5 361**	**51.1**	**103 795**	**58.7**
B/Victoria lineage	1	0.8	79	1.1
B/Yamagata lineage	132	99.2	6 986	98.9
Unknown lineage	5 228	-	96 730	-
Total detections (total tested)	**10 497 (31 798)**	**-**	**176 689 (603 364)**	**-**

[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 2 175 viruses has been reported (Table 5).

Among 733 influenza A(H3N2) specimens, 412 (56%) fell in the vaccine virus component clade (3C.2a), 302 (41%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 19 (3%) in clade 3C.3a. Viruses in the first 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.

All 311 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

48 (48%) of the 99 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 1032 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 40/2017–11/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	311
A(H1N1)pdm09 not attributable to any clade	0
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	412
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	302
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	19
A(H3N2) not attributable to any clade	0
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	51
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	48
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	1032
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

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/Colorado/06/2017-like virus, representing the emergent strain of B/Victoria-lineage viruses 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.

Vaccine effectiveness

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, 7 to 42% 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. It is encouraging that trivalent vaccine with lineage-mismatched influenza B virus has an estimated 36 to 54% effectiveness against the dominant B/Yamagata influenza virus circulating.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 1 436 viruses up to week 10/2018; 667 type B, 449 A(H3N2), and 320 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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Maps and commentary do not represent a statement on the legal or border status of the countries and territories shown.

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.

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