Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 13/2018 (26–31 March 2018)

- Influenza viruses continued to circulate in the Region, while all countries reported low or medium intensity of activity of respiratory infections.
- Influenza continued to circulate widely in the Region with 35% of the individuals sampled from primary healthcare settings testing positive for influenza viruses.
- Both influenza virus types A and B were co-circulating with the majority being type B viruses and the B/Yamagata lineage continuing to dominate.
- 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.

2017–2018 season overview

- Influenza has been circulating widely in the Region since week 52/2017, based on positivity rates among sentinel specimens (Fig. 1), which is longer than in previous seasons and may contribute to the severity of the season.
- 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. the 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 characterized A(H3N2) viruses belong to clade 3C.2a and 49% of B/Victoria lineage 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 occurred in persons above the age of 15 years. Click here for more information
- Mortality from all causes based on pooled data from 18 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
- 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 in March. WHO assesses the risk posed by this virus to be comparable to the risk posed by the currently circulating seasonal influenza viruses, as all the genes of this reassortant virus originate from circulating seasonal viruses. Click here for more information

Primary care data

All of the 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 sporadic or widespread detections of laboratory-confirmed influenza cases.

Influenza activity

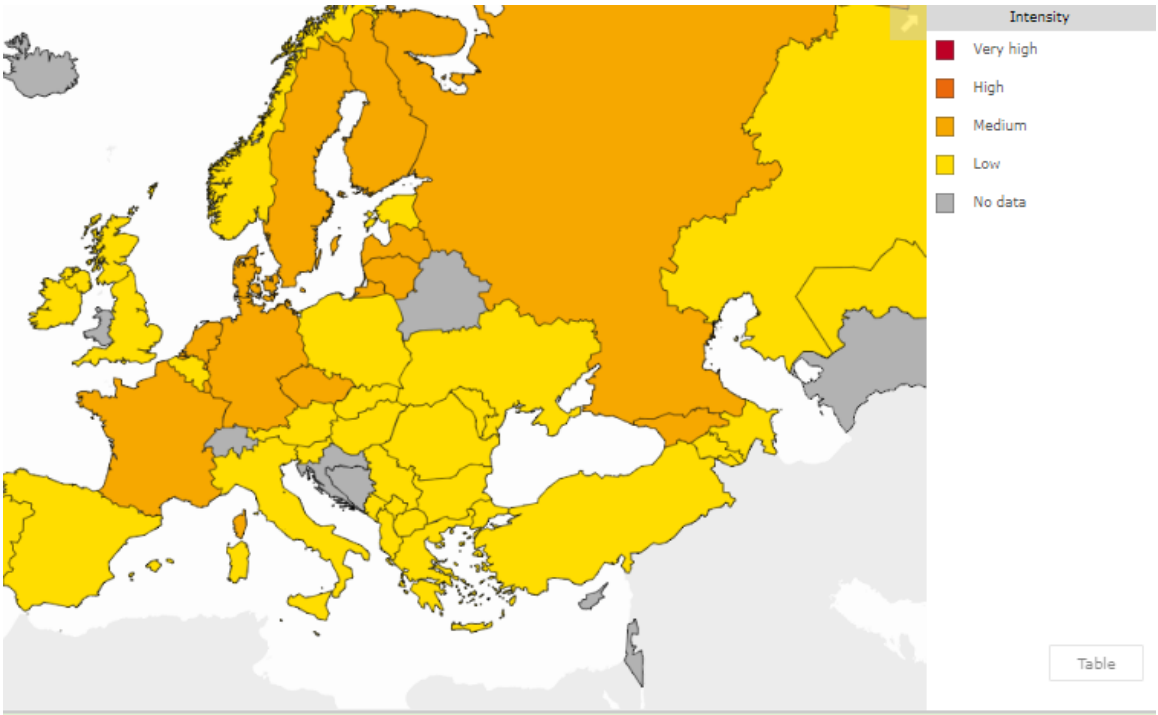
Influenza activity was at variable levels across the region in week 13/2018.

Of 45 Member States and areas reporting on intensity, 12 Member States reported medium intensity and 33 Member States including the United Kingdom (England, Northern Ireland and Scotland) reported low intensity (Fig. 1).

Of the 45 Member States and areas reporting on geographic spread, 14 Member States reported widespread activity, while others reported regional (n=6 including the United Kingdom (Scotland)), local (n=6) or sporadic (n=16 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 13/2018



Map disclaimer

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** 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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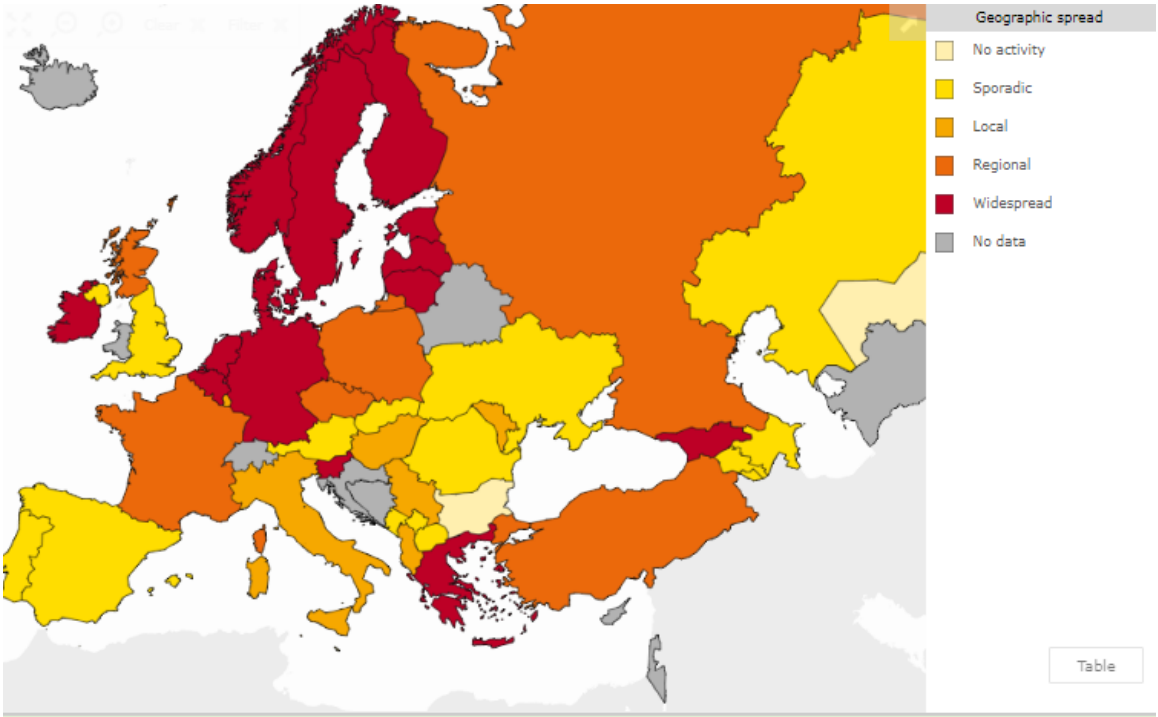
Fig. 2. Geographic spread in the European Region, week 13/2018



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 13/2018, 257 (35%) of 725 sentinel specimens tested positive for influenza viruses; 52% were type A and 48% were type B (Table 1).

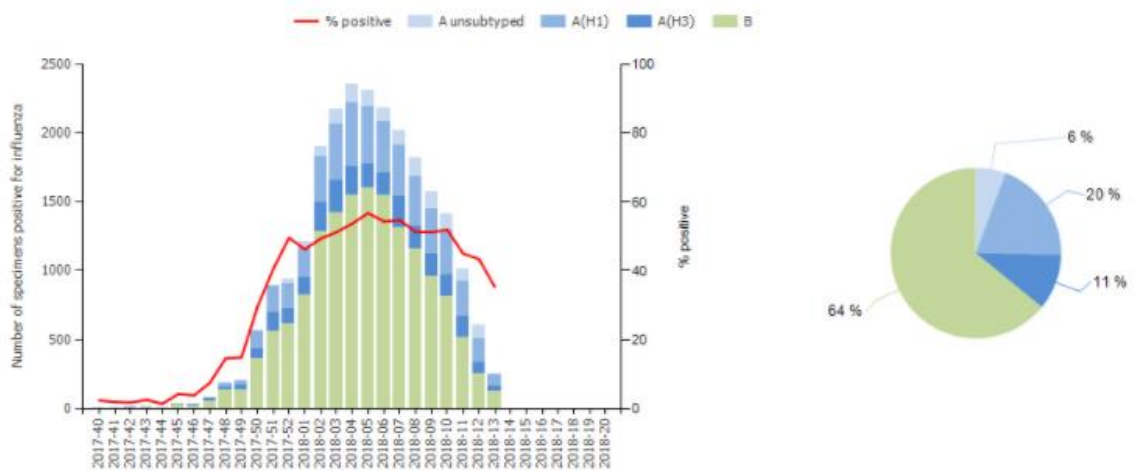
Of 117 subtyped A viruses, 68% were influenza A(H1N1)pdm09 and 32% A(H3N2). Of 65 type B viruses ascribed to a lineage, all were B/Yamagata (Fig. 3 and Table 1).

Of 20 Member States across the region that each tested at least 10 sentinel specimens in week 13/2018, 11 reported proportions of influenza virus detections above 30% (range of 37% to 60%).

Overall, since week 40/2017, more influenza type B (64%) than type A (36%) viruses have been detected. Of 7 210 subtyped A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 7 299 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 13/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**134**	**52.1**	**8 563**	**35.9**
A(H1N1)pdm09	80	68.4	4 698	65.2
A(H3N2)	37	31.6	2 512	34.8
A not subtyped	17	-	1 353	-
Influenza B	**123**	**47.9**	**15 303**	**64.1**
B/Victoria lineage	0	0,0	206	2.8
B/Yamagata lineage	65	100.0	7 093	97.2
Unknown lineage	58	-	8 004	-
Total detections (total tested)	**257 (725)**	**35.4**	**23 866 (56 068)**	**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=4 398 and 4 079 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 13/2018, reflecting the decreasing influenza activity especially in the western parts of the Region. During week 13/2018, there were 106 laboratory-confirmed influenza cases from ICUs, with the majority being in the United Kingdom (n=69, 65%). For weeks 11/2018 and 12/2018, the same countries reported 404 and 246 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 1 644 subtyped influenza A viruses, 59% were A(H1N1)pdm09 and 41% A(H3N2). Of 5 204 cases with known age, 45% were 15–64 years old and 48% were 65 years and older.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–13/2018

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	288	40	57	6	185	12	10	116	150	0
Denmark	343	46	24	24	249	6	6	117	214	0
Finland	57	0	3	25	29	1	1	17	38	0
France	2 749	1 194	492	44	1 019	71	47	1 303	1 273	55
Ireland	157	41	13	26	77	16	12	61	68	0
Netherlands	15	5	0	0	10	0	0	8	7	0
Romania	52	2	23	1	26	4	1	23	24	0
Russian Federation	6	0	1	5	0	0	0	3	3	0
Spain	1 180	289	137	137	617	100	35	518	527	0
Sweden	383	101	5	10	267	9	18	158	198	0
Ukraine	29	1	0	1	27	9	10	10	0	0
United Kingdom	3 218	1 035	216	394	1 573	0	0	0	0	3 218
TOTAL	**8 477**	**2 754**	**971**	**673**	**4 079**	**228**	**140**	**2 334**	**2 502**	**3 273**

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

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 13/2018, 129 cases were reported from other wards, with the majority being in Ireland (64%). Numbers of cases in other wards decreased in week 13/2018 compared to week 12/2018 (n=537).

Since week 40/2017, 8 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (64%) of these cases were infected by influenza type B viruses and 57% of all cases were in patients aged 65 years and older.

Table 3. Laboratory-confirmed hospitalised cases in other wards* by country, cumulatively weeks 40/2017–13/2018

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	314	53	81	4	176	6	3	119	186	0
Denmark	6 402	887	317	422	4776	335	237	2168	3662	0
Ireland	4 165	1 178	188	444	2355	546	407	1193	2017	2
Romania	92	3	41	4	44	21	13	45	13	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	4 413	1 195	239	447	2532	234	48	991	3140	0
Ukraine	130	6	2	3	119	18	26	85	1	0
TOTAL	**15 749**	**3 324**	**898**	**1 449**	**10 078**	**1 203**	**753**	**4 752**	**9 039**	**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 13/2018, 1 264 SARI cases were reported by 11 countries, the majority of which were reported by Kazakhstan (58%); 244 specimens were tested for influenza viruses with 31% being positive, similar to week 12/2018 but decreased compared to week 11/2018 (33%).

For SARI cases testing positive for influenza virus, type B viruses have been the most common; 59% overall for weeks 40/2017–13/2018, but only 40% in week 13/2018. A(H1N1)pdm09 viruses were detected in 37% of influenza virus-positive SARI cases in week 13/2018, a lower proportion compared to week 12/2018 (46%).

Mortality monitoring

Data from 18 EU/EEA Member States or regions reporting to the EuroMOMO project were received for week 13/2018 and included in pooled analyses. Excess mortality from all causes has been significantly elevated over recent months, especially in the elderly. 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 13/2018, 5 708 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, 60% were type A and 40% 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, 52% 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 13/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**3 431**	**60.1**	**81 998**	**42.3**
A(H1N1)pdm09	938	57.9	14 834	47.6
A(H3N2)	682	42.1	16 336	52.4
A not subtyped	1 811	-	50 828	-
Influenza B	**2 277**	**39.9**	**111 637**	**57.7**
B/Victoria lineage	0	0	91	1.2
B/Yamagata lineage	26	100.0	7 357	98.8
Unknown lineage	2 251	-	104 189	-
Total detections (total tested)	**5 708 (22 228)**	**-**	**193 635 (662 166)**	**-**

[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 characterisation of 2 302 viruses has been reported (Table 5).

Among 784 influenza A(H3N2) viruses attributed to a clade, 437 (56%) fell in the vaccine virus component clade (3C.2a), 328 (42%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 19 (2%) 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. 3 A(H3N2) viruses were not attributed to any clade.

All 354 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

49 (49%) of the 100 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 1 061 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 February 2018 report.

Table 5. Viruses attributed to genetic groups, cumulative for weeks 40/2017–13/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	354
A(H1N1)pdm09 not attributable to any clade	0
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	437
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	328
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	19
A(H3N2) not attributable to any clade	3*
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	51
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	49
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	1061
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
* A(H3) attributed to recognised group in current guidance but not listed in TESSy

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. 2 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, -47 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.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 1 436 viruses with collection dates since week 40/2017, up to week 10/2018: 667 type B, 449 A(H3N2), and 320 A(H1N1)pdm09). 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 virus 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, by 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.

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