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

Summary

Week 5/2018 (29 January–4 February 2018)

- Influenza activity was widespread in the majority of reporting countries.
- 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. Proportions of specimens positive for influenza viruses were increasing in the eastern part of Europe.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 57% tested positive for influenza viruses, a slight increase compared to the previous week (54%).

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. Of the type A detections from sentinel sources, A(H1N1)pdm09 viruses have outnumbered A(H3N2) viruses, while in non-sentinel sources more A(H3N2) viruses were reported than A(H1N1)pdm09 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 subtype were observed across the countries in the Region, which may be due to the relative weights of information being derived from sentinel, non-sentinel and severe influenza case sources of information.
- The majority of ICU severe cases are in adults infected by influenza A(H1N1)pdm09 or type B virus.
- While low in number, 58% 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 2017–18, and 38% to subclade 3C.2a1, with mammalian cell-cultured viruses in both clades being antigenically similar.
- A situation analysis that describes the early season evolving epidemiological pattern was published by WHO Regional Office for Europe in January. A high level of influenza B virus circulation is observed during the first half of the season, compared to previous seasons.
- An early risk assessment based on data from EU/EEA countries was published by ECDC on 20 December 2017.
- Interim or real-time vaccine effectiveness estimates from Canada, Stockholm County and Finland suggest overall vaccine effectiveness of 30–42%, depending on the proportion of circulating (sub)types. Effectiveness against influenza B is in the range of 35–55%,

despite the circulating lineage not being included in the more commonly used trivalent vaccine.

- European mortality among the elderly has significantly increased over the past weeks, except in central and eastern Europe.
- Additional information on global influenza activity is available from WHO's biweekly global updates.

Primary care data

Overall, the majority of the countries reported low or medium intensity of influenza activity of respiratory infections, based on syndromic 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 5/2018.

Of 46 Member States and areas reporting on intensity, Albania, Finland and Luxembourg reported very high intensity, while Ireland, Kosovo, Sweden, Switzerland and the UK (Wales) reported high intensity; 26 Member States and the UK (England) reported medium intensity and 12 Member States and the UK (Scotland and Northern Ireland) low intensity (Fig. 1).

Of the 46 Member States and areas reporting on geographic spread, 29 Member States and the UK (Scotland and Wales) reported widespread activity, while others reported regional (n=5), local (n=4), or sporadic spread (n=6 and the UK (England and Northern Ireland)) and one reported no activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 5/2018

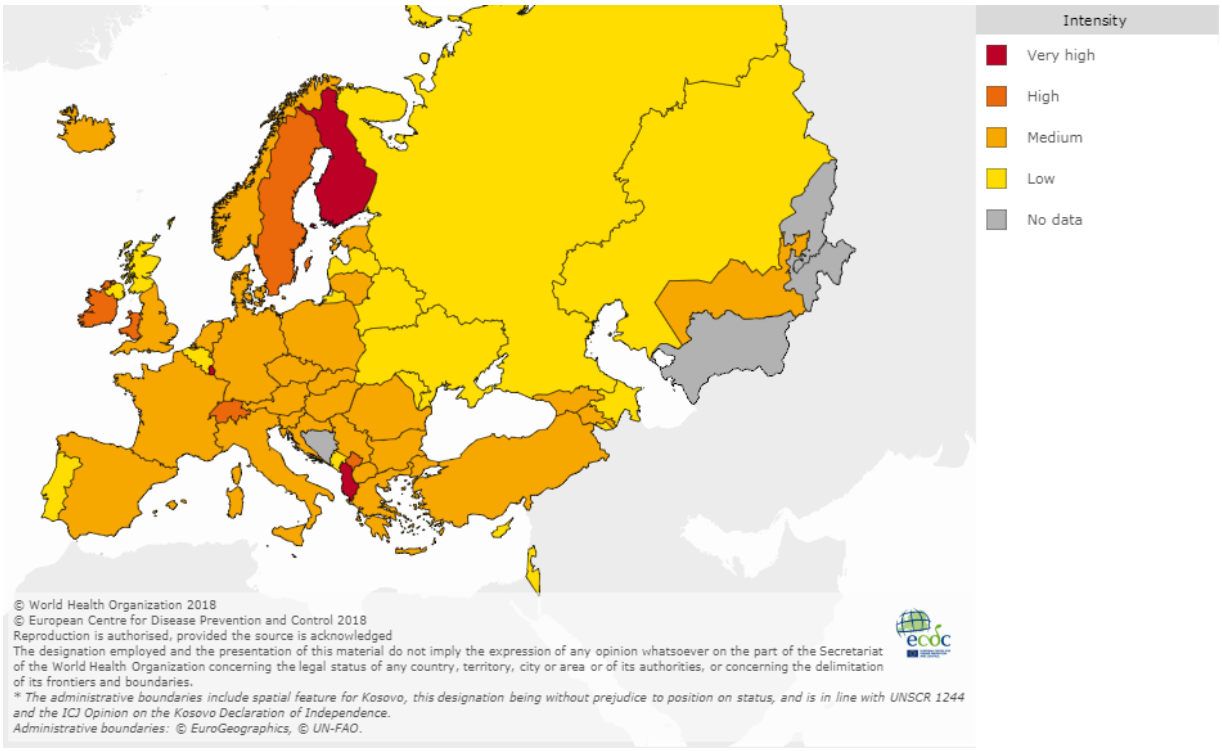
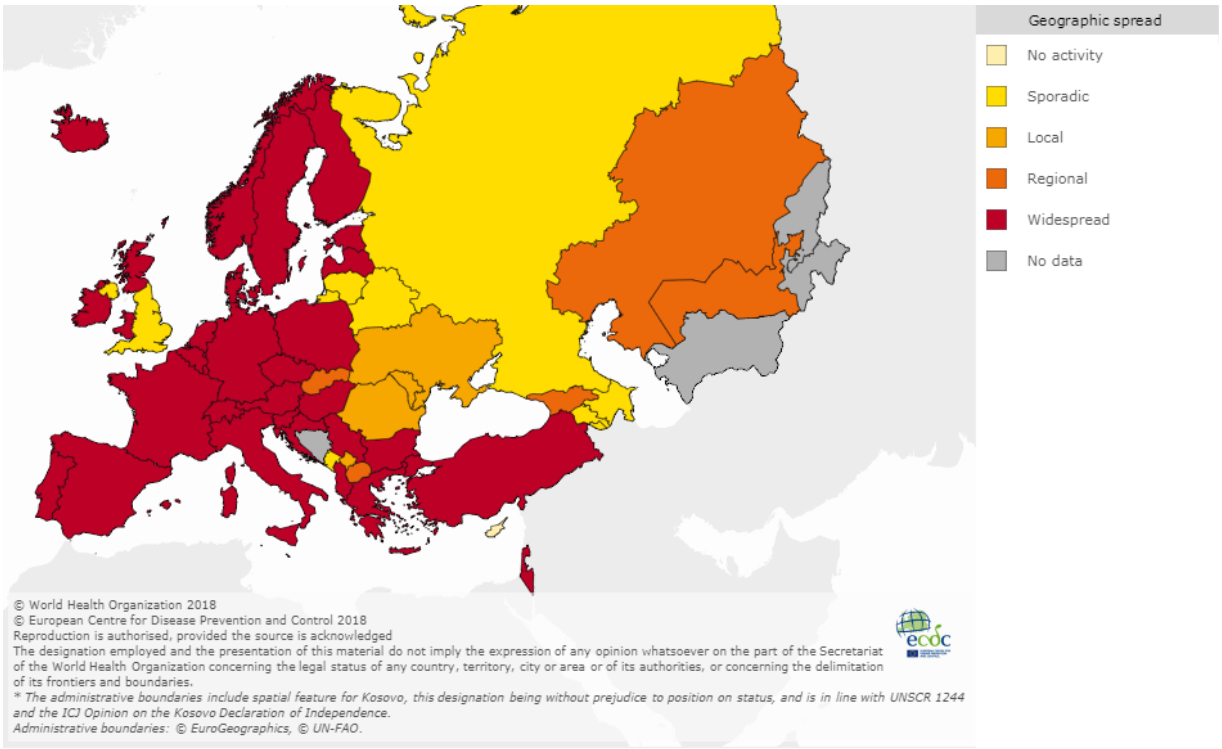


Fig. 2 Geographic spread in the European Region, week 5/2018



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)

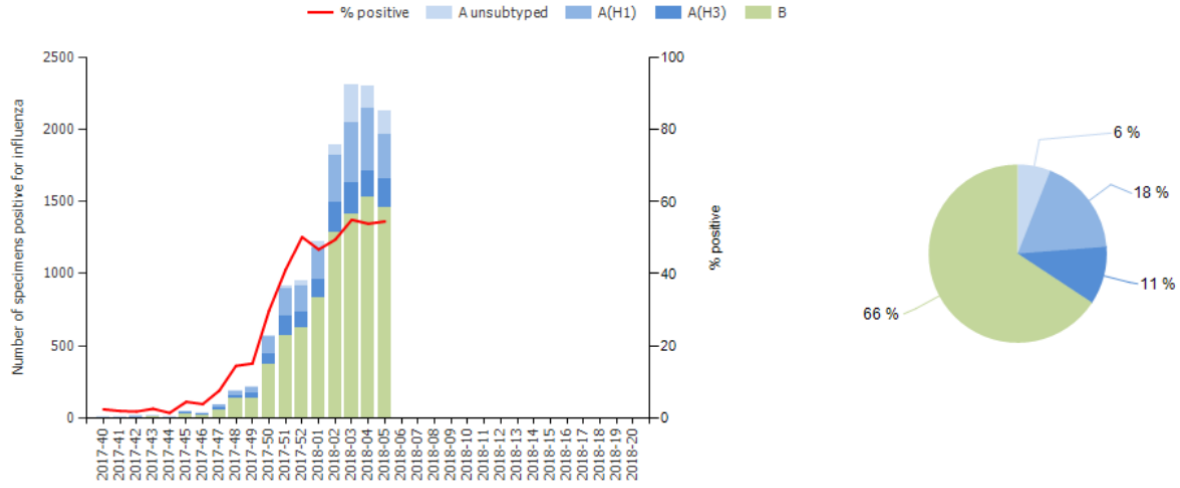
For week 5/2018, 2 122 (57.2%) of 3 710 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 31.2% were type A and 68.8% were type B. Of 503 subtyped A viruses, 61.6% were influenza A(H1N1)pdm09 and 38.4% A(H3N2). Of 650 type B viruses ascribed to a lineage, 96.5% were B/Yamagata and 3.5% B/Victoria (Fig. 3 and Table 1).

Of 40 Member States across the region that each tested at least 10 sentinel specimens in week 5/2018, 33 reported proportions of influenza virus detections above 30% (range of 17% to 92%).

Overall, since week 40/2017, more influenza type B (65.7%) than type A (34.3%) viruses have been detected. Of 3 650 subtyped A viruses, 62.8% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 3 205 ascribed to a lineage, 96.7% 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 5/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**663**	**31.2**	**4 421**	**34.3**
A(H1N1)pdm09	310	61.6	2 293	62.8
A(H3N2)	193	38.4	1 357	37.2
A not subtyped	160	-	771	-
Influenza B	**1 459**	**68.8**	**8 481**	**65.7**
B/Victoria lineage	23	3.5	107	3.3
B/Yamagata lineage	627	96.5	3 098	96.7
Unknown lineage	809	-	5 276	-
Total detections (total tested)	**2 122 (3 710)**	**57.2**	**12 902 (33 981)**	**38**

[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=11), or 2) severe acute respiratory infections (SARI; n=15). The majority of severe cases are in adults admitted to ICU and infected by influenza A(H1N1)pdm09 or type B virus.

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

Since week 40/2017, 11 countries have reported laboratory-confirmed influenza cases admitted to either all ICUs of the country or a set of sentinel ICUs (Table 2). Overall, numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs decreased in week 5/2018: compared to 484 and 333 cases reported by the same countries during weeks 3/2018 and 4/2018 respectively, 238 laboratory-confirmed influenza-infected cases from ICUs were reported, with the majority being in the United Kingdom (n=166, 70%).

Since week 40/2017, type A influenza virus was detected in 55% and type B in 45% of the cases in ICUs. Of 821 subtyped influenza A viruses, 57% were A(H1N1)pdm09 and 43% A(H3N2). Of 2 265 cases with known age, 48% were 15 to 64 years old and 45% 65 years and older.

In the age group 15–64, type A influenza virus accounted for 48% of all infections with 73% of the 467 subtyped A viruses being A(H1N1)pdm09. For patients aged 65 years and older, type A influenza virus was detected in 51% of the 1 026 cases with 22% of the subtyped A viruses being A(H1N1)pdm09.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–5/2018

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	30	7	7	1	15	4	2	14	10	0
Denmark	27	3	2	5	17	1	0	9	17	0
Finland	16	0	2	4	10	0	0	5	11	0
France	1279	705	258	22	294	37	11	661	534	36
Ireland	86	24	3	13	46	6	4	40	36	0
Netherlands	2	0	0	0	2	0	0	1	1	0
Romania	10	0	6	0	4	0	1	5	4	0
Russian Federation	4	0	1	3	0	0	0	3	1	0
Spain	727	134	75	74	444	57	13	312	345	0
Sweden	120	26	0	6	88	2	6	45	67	0
United Kingdom	1 801	557	118	221	905	0	0	0	0	1 801
TOTAL	**4 102**	**1 456**	**472**	**349**	**1 825**	**107**	**37**	**1 095**	**1026**	**1 837**

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

1.2) Hospitalized laboratory-confirmed influenza – other wards

For week 5/2018, a total of 235 cases was reported from other wards, with the majority of cases reported by Ireland (49%) and Spain (38%). Overall, numbers of cases in other wards decreased in week 5/2018 compared to week 3/2018 and 4/2018, during which 865 and 666 hospitalised cases were reported respectively by the same countries.

Since week 40/2017, 7 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (65%) of these cases were infected by influenza B viruses and 60% of all cases were in patients aged 65 years and older.

Table 3. Laboratory-confirmed hospitalised cases in other wards* by country, cumulatively weeks 40/2017–5/2018

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	28	10	7	0	11	1	0	16	11	0
Denmark	720	121	37	71	491	39	25	320	336	0
Ireland	2 004	498	64	230	1212	218	158	589	1038	1
Romania	18	1	8	2	7	3	0	11	4	0
Russian Federation	36	0	5	19	12	8	2	22	4	0
Slovakia	2	2	0	0	0	0	0	2	0	0
Spain	2 432	488	107	178	1 659	103	26	557	1 746	0
TOTAL	**5 240**	**1 120**	**228**	**500**	**3 392**	**372**	**211**	**1 517**	**3 139**	**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 5/2018, 1 436 SARI cases, compared to 713 during week 4/2018, were reported by 11 countries from which 643 specimens were tested for influenza viruses with 30.4% being positive (compared to 20.7% during week 4/2018). The positivity rate has gradually increased over recent weeks.

For SARI cases testing positive for influenza virus, type B viruses have been most common; 77% in week 5/2018 and 65% overall for weeks 40/2017–5/2018. A(H1N1)pdm09 virus represented 26% of influenza–related SARI cases.

Mortality monitoring

Data from 21 Member States or regions reporting to the EuroMOMO project were received for week 5/2018 and included in the pooled analyses of excess mortality from all causes. European mortality among the elderly has increased significantly over the past weeks, except in central and eastern Europe. This observation should be interpreted with caution as this may be due to imprecise adjustments due to delays in data registration.

Virus characteristics

For reports based on sentinel surveillance systems this season, most influenza viruses detected were type B with those assigned to a lineage being mainly B/Yamagata viruses, while of the type A viruses subtyped most 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 from 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 5/2018, 12 625 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, 37.1% were type A and 62.9% type B viruses (Table 4), making this the fifth week in which more type B viruses than type A viruses were detected 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, 63% of all subtyped A viruses were A(H3N2) and 98.2% 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 5/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**4 338**	**34.4**	**37 371**	**43.2**
A(H1N1)pdm09	711	52.1	5 656	38.9
A(H3N2)	654	47.9	8 898	61.1
A not subtyped	2 973	-	22 817	-
Influenza B	**8 287**	**65.6**	**48 124**	**56.3**
B/Victoria lineage	6	2.0	50	1.7
B/Yamagata lineage	301	98.0	2 908	98.3
Unknown lineage	7 980	-	45 166	-
Total detections (total tested)	**12 625 (34 635)**	**-**	**85 495 (376 611)**	**-**

[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 1 403 viruses has been reported (Table 5).

Among 470 influenza A(H3N2) viruses attributed to a clade, 273 (58%) fell in the vaccine virus component clade (3C.2a), 179 (38%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 18 (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 173 A(H1N1)pdm09 viruses attributed to a clade, all fell in the A/Michigan/45/2015 vaccine component clade (6B.1) with the exception of one not attributed to a clade.

35 of the 81 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. 3 B/Victoria and 88 B/Yamagata viruses were not attributed to any clade. 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 40/2017–5/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	172
A(H1N1)pdm09 not attributable to any clade	1
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	273
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	179
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	18
A(H3N2) not attributable to any clade	1
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	46
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	35
B(Victoria) lineage not attributed to clade	3
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	587
B/Yamagata lineage not attributed to any clade	88

[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 28 September 2017, WHO recommended two changes, compared to the current trivalent vaccine recommended for the 2017–2018 northern hemisphere influenza season, in trivalent vaccine composition for the 2018 season in the southern hemisphere. The recommendations matched the A(H1N1)pdm09 component for the 2017–2018 northern hemisphere season, but the A(H3N2) component was changed to an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and the B component was switched to a B/Yamagata-lineage virus. These changes were made due to the emergence of numerous genetic subclades of A(H3N2) viruses – none of which showed significant antigenic drift compared to the vaccine component – while for type B viruses the B/Yamagata lineage predominated by a large margin in the course of the 2017 southern hemisphere season. See also the ECDC commentary.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 925 viruses; 483 type B, 254 A(H3N2), and 188 A(H1N1)pdm09) with collection dates since week 40/2017. 1 A(H3N2) virus showed evidence of reduced inhibition by both oseltamivir and zanamivir, 1 A(H1N1)pdm09 showed evidence of reduced inhibition by oseltamivir and 2 type B virus showed evidence of reduced inhibition by 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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