

Summary

Week 6/2019 (4–10 February 2019)

- Influenza activity is widespread in the European Region. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 53%, slightly lower than in the previous week (58%).
- Influenza type A virus detections dominated with A(H1N1)pdm09 viruses and A(H3N2) viruses co-circulating. Very few influenza B viruses were detected.
- 46% of specimens from patients hospitalized with severe acute respiratory infection (SARI) collected in week 6/2019 were positive for influenza virus, and all were type A.
- Pooled data from 24 Member States and areas reporting to the [EuroMOMO](#) project indicated excess mortality mostly among elderly aged 65 years and above, but also in adults in the age group of 15–64 years.

2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018 and has increased continuously into week 5/2019, after which it started to decrease. The positivity rate has exceeded 50% since week 3/2019.
- Both influenza A virus subtypes are circulating widely, with co-circulation in some countries while others report dominance of either A(H1N1)pdm09 or A(H3N2) viruses.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 40% of influenza A viruses were subtyped; of these 78% were A(H1N1)pdm09 virus. Among influenza virus-infected patients admitted to other wards, 28% of influenza A viruses were subtyped and 71% were A(H1N1)pdm09 virus.
- Over 90% of influenza A viruses detected from SARI surveillance since week 40/2018 were subtyped and 81% were A(H1N1)pdm09 virus.
- In general, current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses and preliminary vaccine effectiveness estimates continue to support the use of vaccines. Early data suggests the vaccines are effective and estimates vary depending on the population studied and the proportions of circulating influenza A virus subtypes (e.g., higher VE in children). See data from [Canada](#), [Finland](#), [Hong Kong](#), [Sweden](#), and the [United States](#).
- Circulating viruses remain susceptible to neuraminidase inhibitors supporting early initiation of treatment and prophylactic use according to national guidelines.

Primary care data

Syndromic surveillance data

For week 6/2019, those Member States in which thresholds for ILI activity are defined, countries in eastern (n=2; Republic of Moldova, Russian Federation), northern (n=8; Denmark, Estonia, Iceland, Ireland, Latvia, Lithuania, Norway, United Kingdom (England)), southern (n=7; Greece, Israel, Italy, Montenegro, Romania, Serbia, The Former Yugoslav Republic of Macedonia) and western (n=11; Austria, Belgium, Czech Republic, Hungary, Luxembourg, Netherlands, Poland, Portugal, Slovakia, Spain, Switzerland) areas of the European Region reported activity above baseline levels.

Of those Member States and areas in which thresholds for ARI activity are defined, countries in eastern (n=4; Armenia, Kyrgyzstan, Republic of Moldova, Russian Federation), northern (n=3; Estonia, Latvia, Lithuania), southern (n=2; Albania, Bulgaria) and (n=3; Belgium, Czech Republic, Slovakia) areas of the European Region reported activity above baseline levels.

Influenza activity

Of 49 Member States and areas reporting on intensity, 9 reported high (southern, western areas), 26 reported medium (across the region), 12 reported low (across the region) and 2 reported baseline (Austria, Kazakhstan), and intensity for week 6/2019 (Fig. 1).

Of 49 Member States and areas reporting on geographic spread, 1 reported no activity (Kyrgyzstan), 3 reported sporadic cases (Armenia, Lithuania, United Kingdom (Northern Ireland)), 3 reported local spread (Azerbaijan, Ireland, Slovakia), 5 reported regional spread (Bulgaria, Poland, Ukraine, Uzbekistan, Kosovo (in accordance with United Nations Security Council Resolution 1244 [1999])) and 37 reported widespread activity (across the region) for week 6/2019 (Fig. 2).

Fig. 1. Intensity in the European Region, week 6/2019

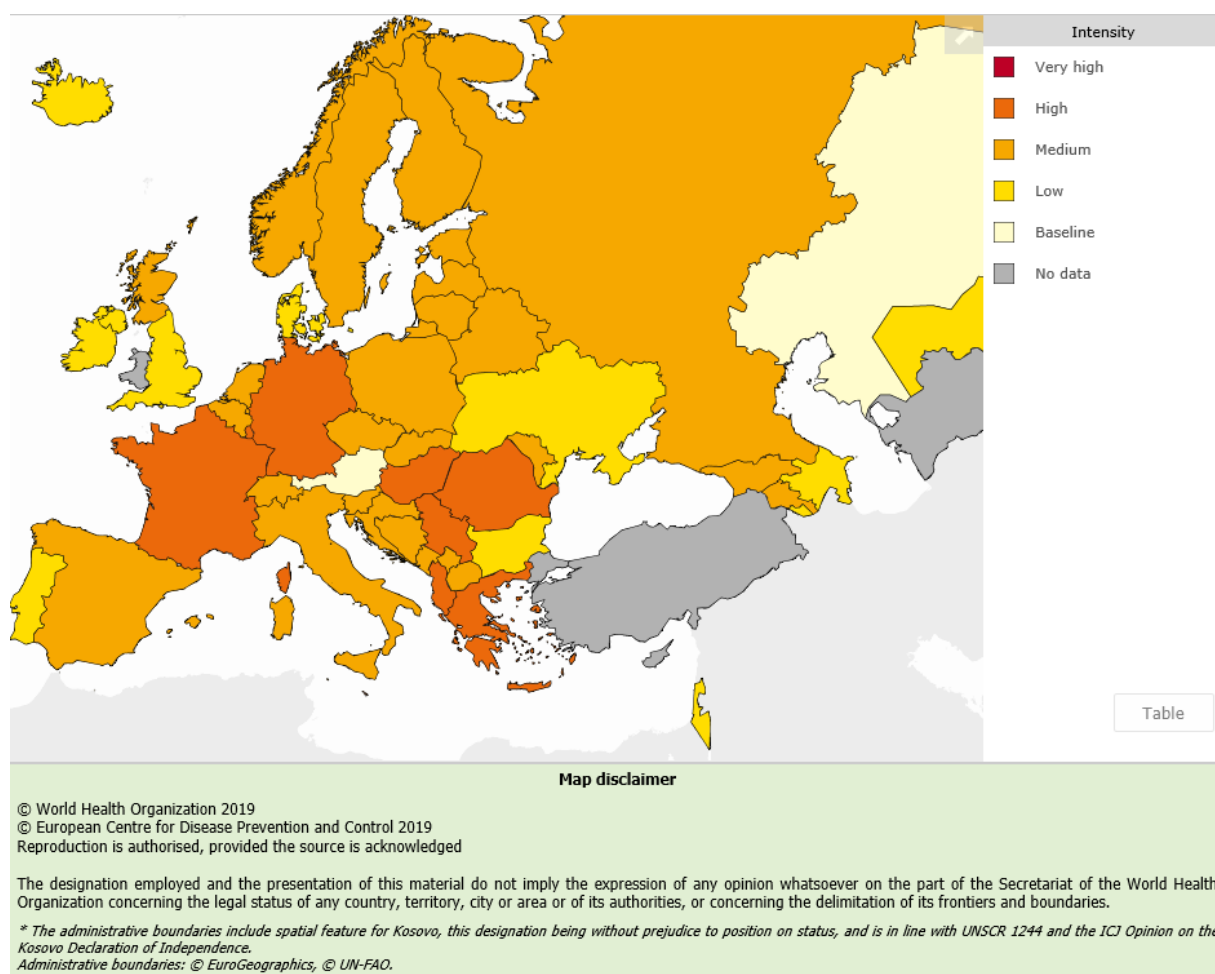
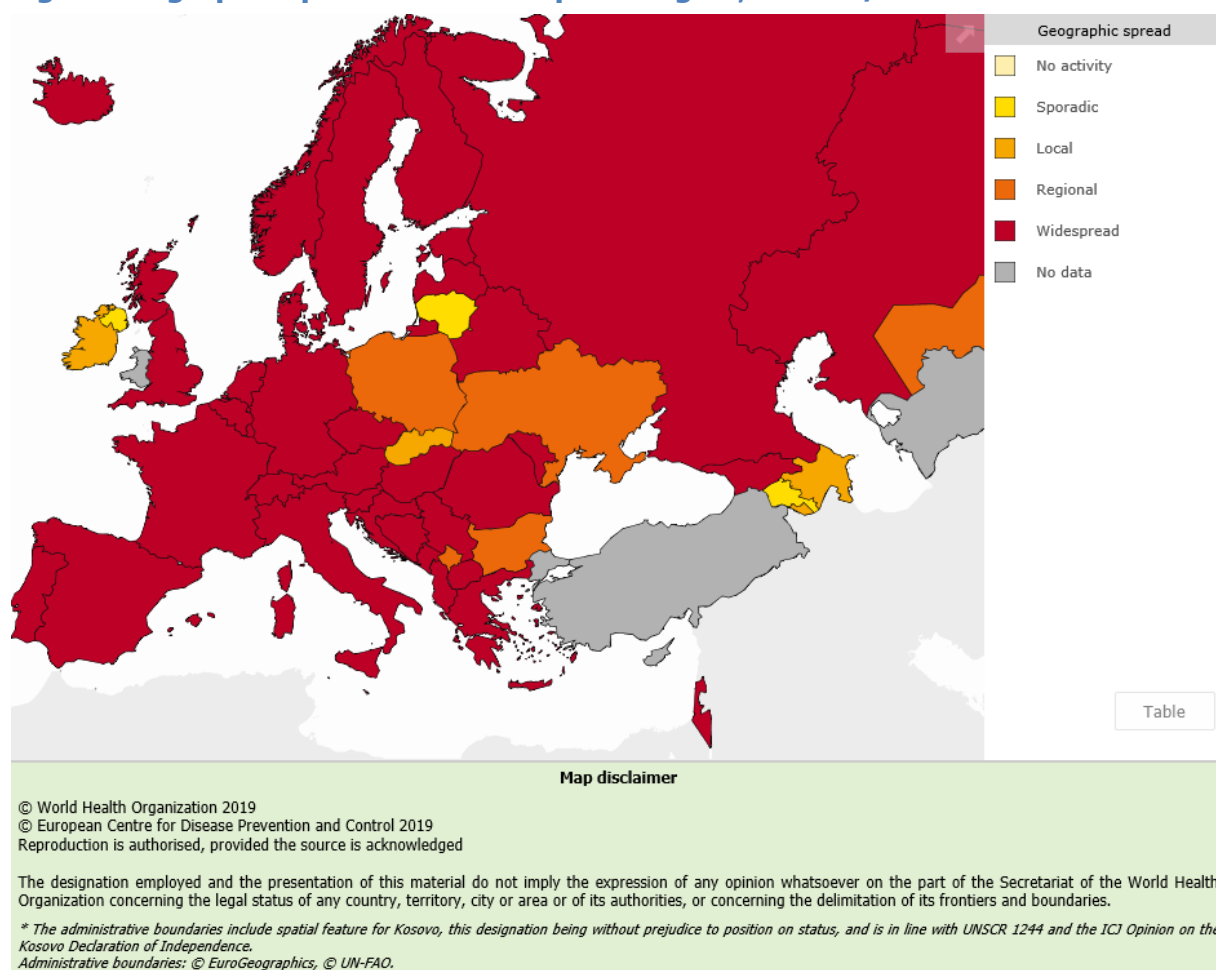


Fig. 2. Geographic spread in the European Region, week 6/2019



For interactive maps of influenza intensity and geographic spread, see the [Flu News Europe website](#).

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

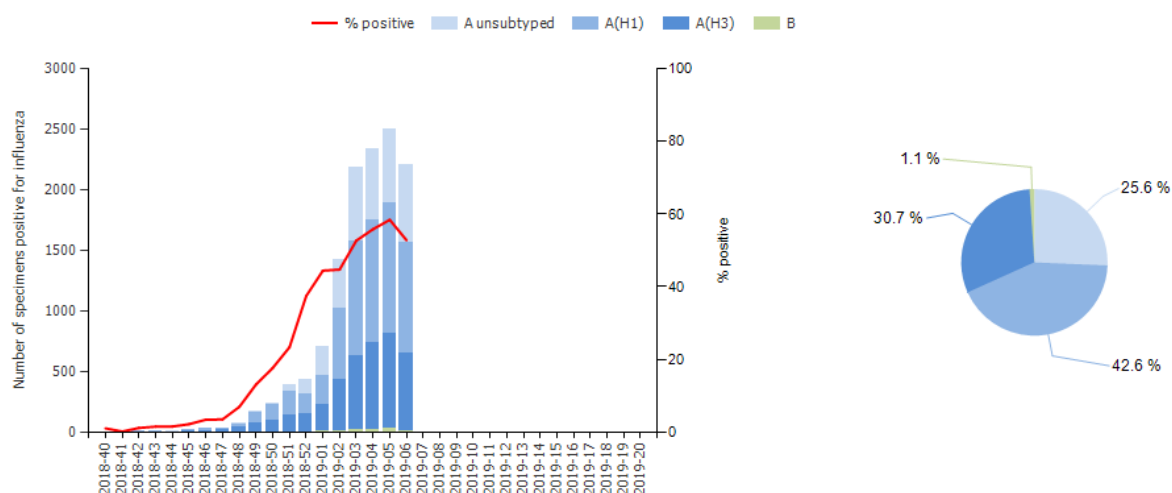
For week 6/2019, 2 209 (52.8%) of 4 181 sentinel specimens tested positive for an influenza virus; 99.3% were type A. Of 1 545 subtyped A viruses, 58.8% were A(H1N1)pdm09 and 41.2% were A(H3N2). Of 5 type B viruses ascribed to a lineage, all were Yamagata (Fig. 3 and Table 1).

Of 41 Member States or areas across the region that each tested at least 10 sentinel specimens in week 6/2019, 35 reported a percentage of influenza virus detections 30% or above (median 53.1%; range 30.0% - 92.3%)

For the season to date, more influenza type A (n=12 660, 98.9%) than type B (n=136, 1.1%) viruses have been detected. Of 9 378 subtyped A viruses, 5 454 (58.2%) were A(H1N1)pdm09 and 3 924 (41.8%) were A(H3N2). Of 46 influenza type B viruses ascribed to a lineage, 82.6% were B/Yamagata (66.2% type B viruses were reported without a lineage) (Fig. 3 and 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 for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 6/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	2 193	99.3	12 660	98.9
A(H1N1)pdm09	909	58.8	5 454	58.2
A(H3N2)	636	41.2	3 924	41.8
A not subtyped	648	-	3 282	-
Influenza B	16	0.7	136	1.1
B/Victoria lineage	0	0.0	8	17.4
B/Yamagata lineage	5	100.0	38	82.6
Unknown lineage	11	-	90	-
Total detections (total tested)	2 209 (4 181)	52.8	12 796 (33 840)	37.8

^aFor 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 and areas monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (12

Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infections (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs in week 6/2019 (n=512), influenza type A viruses (n=509, 99.4%) were detected more frequently than influenza type B viruses (n=3, 0.6%).

Since week 40/2018, more influenza type A (n=4 155, 99.0%) than type B viruses (n=41, 1%) were detected. Of 1 613 subtyped influenza A viruses, 77.5% were A(H1N1)pdm09 and 22.5% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 2 014 cases with known age, 47.2% were 15-64 years old and 43.5% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Among laboratory-confirmed influenza cases reported in wards other than ICUs in week 6/2019 (n=320), all were influenza type A viruses.

Since week 40/2018, more influenza type A (n=5 360, 99.2%) than type B (n=45, 0.8%) viruses were detected. Of 1 497 subtyped influenza A viruses, 70.5% were A(H1N1)pdm09 and 29.5% A(H3N2). One influenza B virus ascribed to a lineage was B/Yamagata. Of 5 405 cases with known age, 41.1% were 65 years and older and 35.9% were 15-64 years old.

2. SARI surveillance

For week 6/2019, 2 111 SARI cases were reported by 15 Member States or areas. Of 683 specimens tested for influenza viruses, 46.1% were positive. Only influenza type A viruses were detected.

Of 25 145 SARI cases reported since week 40/2018, 24 734 had a recorded age and, of these, 60.2% were 0-4 years old and 22.5% were 15-64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=1 837), type A viruses have been the most common (99.8%). Of the 1 706 influenza type A cases for which subtyping was performed, 81.4% were infected by A(H1N1)pdm09 viruses and 18.6% were infected by A(H3N2) viruses. One B virus that has been ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 6/2019, the [EuroMOMO](#) project received data from 24 Member States or areas that were included in pooled analyses. The pooled estimates indicated excess mortality mostly among elderly aged 65 years and above, but also in adults in the age group of 15-64 years.

Virus characteristics

Details of the distribution of viruses detected in sentinel-source specimens can be found in the [Primary care data](#) section.

Viruses detected in non-sentinel source specimens

For week 6/2019, 17 630 specimens from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, or nursing homes and other institutions) tested positive for an influenza virus; 99.6% were type A. Of 5 821 subtyped A viruses, 63.9% were A(H1N1)pdm09 and 36.1% were A(H3N2) (Table 2).

For the season to date, more influenza type A (n=86 750, 99%) than type B viruses (n=836, 1%) have been detected. Of 30 029 subtyped A viruses, 19 809 (66%) were A(H1N1)pdm09 and 10 220 (34%) were A(H3N2). Of 32 influenza type B viruses ascribed to a lineage, 53.1% were B/Yamagata (96.2% type B viruses were reported without a lineage) (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 6/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	17 559	99.6	86 750	99.0
A(H1N1)pdm09	3 718	63.9	19 809	66.0
A(H3N2)	2 103	36.1	10 220	34.0
A not subtyped	11 738	-	56 721	-
Influenza B	71	0.4	836	1.0
B/Victoria lineage	0	-	15	46.9
B/Yamagata lineage	0	-	17	53.1
Unknown lineage	71	-	804	-
Total detections (total tested)	17 630 (45 090)	-	87 586 (430 029)	-

^a For 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 and antigenic characterization

Genetic and antigenic characterization of influenza viruses is routinely performed to understand how similar currently circulating influenza viruses are to the viruses used in influenza vaccines for an ongoing season.

Since week 40/2018, genetic characterizations of 1 503 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 897 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 575 were A(H3) viruses, with 371 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 38 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 14 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 83 to the A/England/538/2018 (3C.3a) clade, 37 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 3 to the A/Hong Kong/4801/2014 (3C.2a) clade, 3 attributed to a subgroup not listed, and 26 not attributed to a clade. Of the 31 genetically characterized influenza B viruses, 18 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 13 B/Victoria viruses characterized, 1 was not attributed to a clade. All others belonged to clade

1A, but 5 fell in subclades with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 5 fell in subclades with a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–6/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	897
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	371
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	38
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	14
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	83
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup ^d	37
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	3
A(H3) attributed to recognized group in current guidance but not listed here	3
A(H3) not attributed to a clade	26
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	2
B(Vic)-lineage clade 1A representative B/Colorado/06/2017	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	5
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	18

^a Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^b Vaccine component for 2019 southern hemisphere season.

^c Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^d Vaccine component for 2018–2019 northern hemisphere season.

A summary of recent antigenic characterization data for type A influenza viruses from the WHO collaborating centres in the WHO Global Influenza Surveillance and Response System (GISRS) is given below. A summary for influenza type B viruses is not included as very low numbers have been detected globally.

A(H1N1)pdm09 Viruses

The great majority of A(H1N1)pdm09 viruses characterized so far were antigenically similar to the vaccine virus for use in the 2018–2019 northern hemisphere and 2019 southern hemisphere influenza seasons, A/Michigan/45/2015 (clade 6B.1), as assessed in HI assays using post-infection ferret antisera.

A(H3N2) Viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult, requiring the use of modified HI and/or virus neutralization assays for analysis. In virus neutralization assays or HI assays using post-infection ferret antisera, the majority of recent A(H3N2) viruses have shown similarity to cell culture-propagated A/Singapore/INFIMH-16-0019/2016 (subclade

3C.2a1) vaccine virus, but those falling in the re-emerging 3C.3a clade have shown poor reactivity with the antisera.

The recommended composition of the trivalent influenza vaccine for the northern hemisphere 2018–2019 season included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and a B/Colorado/06/2017-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. The full report can be found [here](#). A comment by ECDC can be seen [here](#). The majority of influenza vaccines used in Europe are egg-based.

On 27 September 2018, WHO announced the recommended vaccine composition for the southern hemisphere 2019 season. The recommendations matched the A(H1N1)pdm09 and B components for the 2018–2019 northern hemisphere season, but the A(H3N2) component was changed for egg-based vaccines. The full report can be found [here](#).

The northern hemisphere Vaccine Composition Meeting for 2019–2020 has been planned for 18–20 February 2019 in Beijing, China. More information can be found [here](#).

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 966 viruses with collection dates since week 40/2018 [649 A(H1N1)pdm09, 304 A(H3N2), and 13 type B]. 3 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 2 of them were confirmed by phenotypic test. 1 A(H3N2) virus showed evidence of reduced inhibition (RI) by oseltamivir only. 1 type B virus showed evidence of RI by zanamivir only.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, Angeliki Melidou, Pasi Penttinen, Phillip Zucs and Emmanuel Robesyn) and the WHO Regional Office for Europe (Caroline Brown, Sonja Olsen, Dmitriy Pereyaslov, Hannah Segaloff and Tamara Meerhoff, Temporary Advisor to WHO). It was reviewed by country experts (Iris Hasibra [Hatibi], Institute of Public Health, Albania; Joan O'Donnell, Health Protection Surveillance Centre, Ireland) 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).

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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 6/2019.

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 6/2019.

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