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

Summary

Week 11/2019 (11–17 March 2019)

- Influenza activity was widespread in one-third of the countries of the European Region. Widespread activity was located in northern, southern, and western areas of 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 34%, a decrease compared to 43% during the previous week.

- Influenza type A virus detections dominated with slightly more A(H1N1)pdm09 than A(H3N2) viruses. Very few influenza B viruses were detected.

- Of the specimens from patients with severe acute respiratory infection (SARI) collected in week 11/2019 that were tested for influenza viruses, 31% were positive and almost all were type A.

- Pooled data from 24 Member States and areas reporting to the EuroMOMO project indicated that the excess mortality observed in previous weeks continued to decline. Excess mortality was seen in persons aged 65 years and in persons 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, exceeded 50% between weeks 3/2019 and 7/2019, and peaked in week 5/2019.

- 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, 41% of influenza A viruses were subtyped; of these 71% were A(H1N1)pdm09 viruses. Among influenza virus-infected patients admitted to other wards, 37% of influenza A viruses were subtyped and 61% were A(H1N1)pdm09 viruses.

- Over 90% of influenza type A viruses detected from SARI surveillance since week 40/2018 were subtyped and 80% were A(H1N1)pdm09 viruses.

- A recent summary of regional activity from October 2018 to February 2019 was published in Eurosurveillance and can be found here.

- Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. Preliminary vaccine effectiveness estimates continue to support the use of vaccines. Early data suggest the vaccines are effective, with estimates varying depending on the population studied and

the proportions of circulating influenza A virus subtypes. See data from a European study (6 countries), Canada, Finland, Hong Kong, Sweden, and the United States.

- WHO has published the recommendations for the composition of influenza vaccines to be used in the 2019–2020 northern hemisphere season. The recommendation was that type B lineages remain unchanged, and the A(H1N1)pdm09 and A(H3N2) strains were updated.

- Circulating viruses remain susceptible to neuraminidase inhibitors supporting use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

For week 11/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, 11 (34%) reported ILI activity above baseline levels.

These include countries in eastern areas of the European Region (n=2; Republic of Moldova, Russian Federation), northern areas (n=4; Estonia, Latvia, Lithuania, Norway), southern areas (n=1; Montenegro) and western areas (n=4; Belgium, Luxembourg, Netherlands, Switzerland).

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, 4 (22%) reported ARI above baseline levels. These were countries in the eastern (n=2; Armenia, Russian Federation) and northern (n=2; Estonia, Lithuania) areas of the European Region.

Influenza activity

For week 11/2019, of 47 Member States and areas reporting on intensity, 8 reported baseline (eastern, northern, western areas), 26 reported low (across the region) and 13 reported medium (across the region) intensity (Fig. 1).

Of 47 Member States and areas reporting on geographic spread, 2 reported no activity (Bulgaria, Tajikistan), 8 reported sporadic cases (across the region), 9 reported local spread (across the region), 12 reported regional spread (in eastern, southern and western areas) and 16 reported widespread activity (in northern, southern and western areas) (Fig. 2).

Fig. 1. Intensity in the European Region, week 11/2019

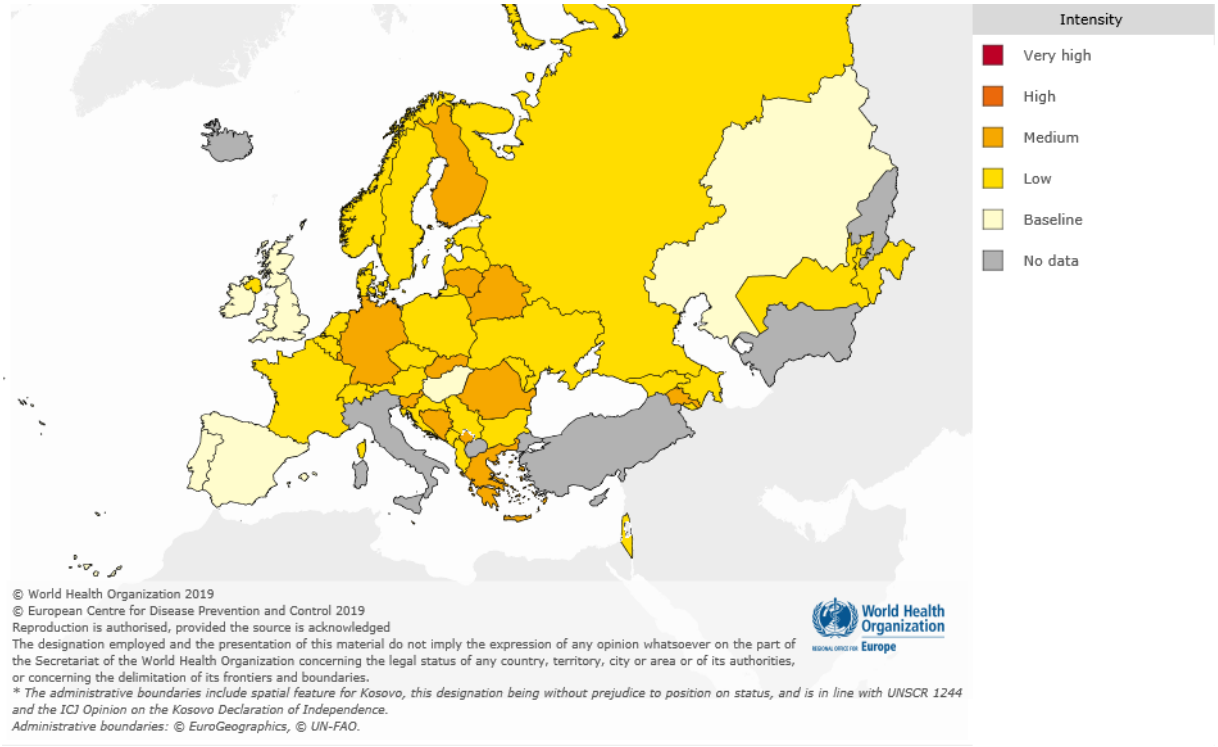
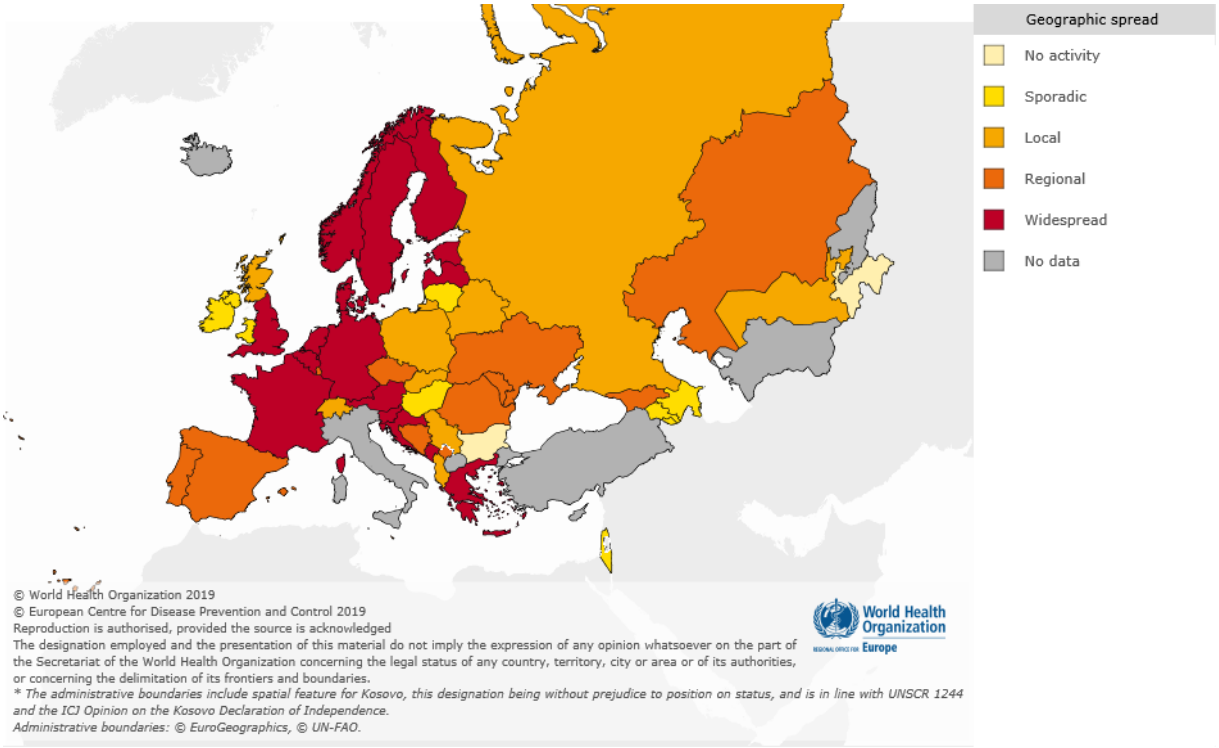


Fig. 2. Geographic spread in the European Region, week 11/2019



For interactive maps of influenza intensity and geographic spread, see the Flu News Europe website.

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

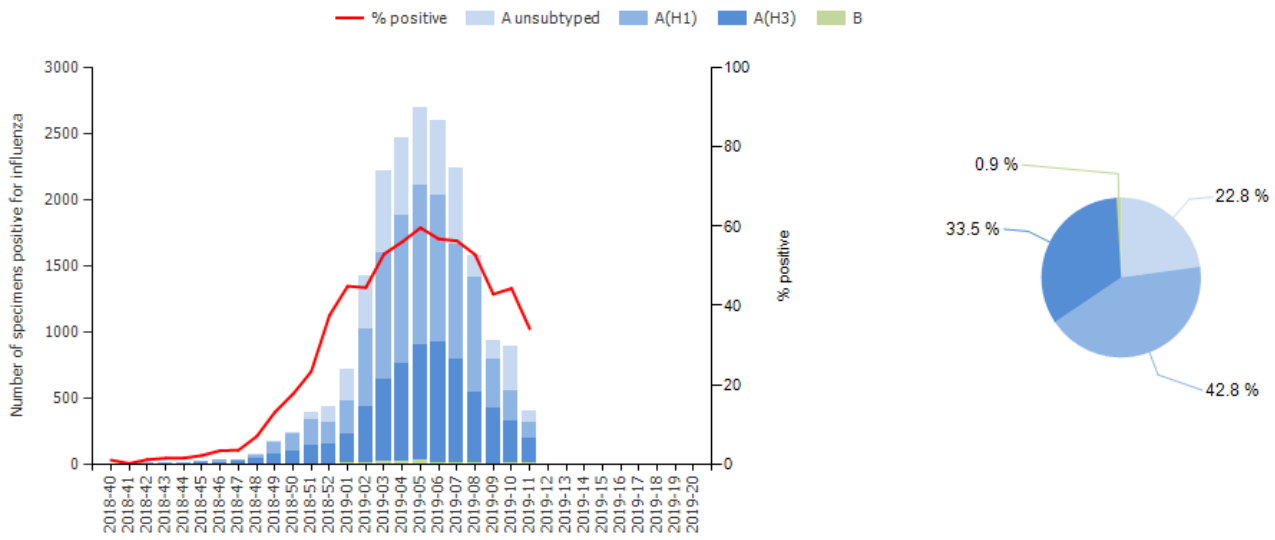
For week 11/2019, 398 (34.1%) of 1 167 sentinel specimens tested positive for an influenza virus; 391 were type A and 7 were type B. Of 309 subtyped A viruses, 39.5% were A(H1N1)pdm09 and 60.5% were A(H3N2) (Fig. 3 and Table 1).

Of 28 countries or areas across the region that each tested at least 10 sentinel specimens in week 11/2019, 14 reported a proportion of influenza virus detections above 30% (median 48.5%; range 33.3% – 70.6%).

For the season to date, almost all viruses detected were influenza type A (n=19 377, 99.1%) with type B accounting for only 0.9% of detections (n=180). Of 14 910 subtyped A viruses, 8 361 (56.1%) were A(H1N1)pdm09 and 6 549 (43.9%) were A(H3N2). Of 55 influenza type B viruses ascribed to a lineage, 85.5% were B/Yamagata (69.4% of 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 11/2019 and cumulatively

	Current Week		Season 2018–2019	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**391**	**98.2**	**19 377**	**99.1**
A(H1N1)pdm09	122	39.5	8 361	56.1
A(H3N2)	187	60.5	6 549	43.9
A not subtyped	82	-	4 467	-
Influenza B	**7**	**1.8**	**180**	**0.9**
B/Victoria lineage	0	-	8	14.5
B/Yamagata lineage	0	-	47	85.5
Unknown lineage	7	-	125	-
Total detections (total tested)	**398 (1 167)**	**34.1**	**19 557 (47 018)**	**41.6**

[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 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 11/2019 (n=99), all were influenza type A viruses.

Since week 40/2018 substantially more influenza type A (n=6 569, 99.2%) than type B viruses (n=54, 0.8%) were detected. Of 2 691 subtyped influenza A viruses, 71.3% were A(H1N1)pdm09 and 28.7% were A(H3N2). No influenza type B viruses were ascribed to a lineage. Of 3 624 cases with known age, 45.0% were 15–64 years old and 46.6% 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 11/2019 (n=92), influenza type A viruses (98.9%) were detected more frequently than influenza type B viruses (1.1%).

Since week 40/2018, substantially more influenza type A (n=8 557, 99.3%) than type B viruses (n=57, 0.7%) were detected. Of 3 166 subtyped influenza A viruses, 60.5% were A(H1N1)pdm09 and 39.5% were A(H3N2). The 1 influenza type B virus ascribed to a lineage was B/Yamagata. Of 8 614 cases with known age, 45.1% were 65 years and older and 33.4% were 15–64 years old.

2. SARI surveillance

For week 11/2019, 1 304 SARI cases were reported by 13 Member States or areas. Of 228 specimens tested for influenza viruses, 30.7% were positive. Of these, influenza type A viruses (98.6%) were detected much more frequently than influenza type B viruses (1.4%).

Of 33 023 SARI cases reported since week 40/2018, 32 967 had a recorded age and, of these, 57.6% were 0–4 years old and 23.9% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 627), almost all were type A viruses (99.5%). Of the 2 365 influenza type A virus-infected cases for which subtyping was performed, 80.4% were infected by A(H1N1)pdm09 viruses and 19.6% by A(H3N2) viruses. The 1 influenza type B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 11/2019, the EuroMOMO project received data from 24 countries or areas that were included in pooled analyses. The pooled estimates indicated that the excess mortality among persons aged 15–64 years and 65 years and older observed in recent weeks continued to decline.

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 11/2019, 5 057 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; 98.4% were type A and 1.6% were type B. Of 2 053 A viruses subtyped, 47.4% were A(H1N1)pdm09 and 52.6% were A(H3N2) (Table 2).

For the season to date, more influenza type A (n=161 013, 99.2%) than type B viruses (n= 1 300, 0.8%) have been detected. Of 54 046 A viruses subtyped, 32 929 (60.9%) were A(H1N1)pdm09 and 21 117 (39.1%) were A(H3N2). Of 41 influenza type B viruses ascribed to a lineage, 46.3% were B/Yamagata (96.8% of 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 11/2019 and cumulatively

	Current Week		Season 2018–2019	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**4 975**	**98.4**	**161 013**	**99.2**
A(H1N1)pdm09	973	47.4	32 929	60.9
A(H3N2)	1 080	52.6	21 117	39.1
A not subtyped	2 922	-	106 967	-
Influenza B	**82**	**1.6**	**1 300**	**0.8**
B/Victoria lineage	0	-	22	53.7
B/Yamagata lineage	0	-	19	46.3
Unknown lineage	82	-	1 259	-
Total detections (total tested)	**5 057 (26 877)**		**162 313 (649 340)**	

[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 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 2 737 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 399 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade with a further 3 attributed to a subgroup not listed; 1 293 were A(H3) viruses, with 881 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 58 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 25 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 306 to the A/England/538/2018 (3C.3a) clade, 12 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 4 to the A/Hong Kong/4801/2014 (3C.2a) clade, and 7 attributed to a subgroup not listed.

Of the 42 genetically characterized influenza B viruses, 22 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). All 20 B/Victoria viruses characterized belonged to clade 1A (represented by B/Brisbane/60/2008); but of these, 5 fell in a subclade with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 10 fell in a subclade 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 40/2018–11/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015[a]	1 399
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	3
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	881
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup[b]	58
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	25
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	306
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup[d]	12
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	4
A(H3) attributed to recognized group in current guidance but not listed here	7
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	5
B(Vic)-lineage clade 1A representative B/Colorado/06/2017[a]	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	10
B(Yam)-lineage clade representative B/Phuket/3073/2013[c]	22

[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 report detailing influenza virus characterization data through Febrauary 2019 from the WHO European Region was published by the European centre for Disease Prevention and Control. A summary is given below.

A(H1N1pdm09) Viruses

The great majority (203/204) of A(H1N1)pdm09 viruses characterized this season were antigenically similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1) and fell in subclade 6B.1A. Within this subclade, there has been increasing genetic diversity of the HA genes with several emerging genetic subgroups. Most viruses carried the HA1 amino acid substitution of S183P.

A(H3N2) Viruses

Antigenic characteriszation of A(H3N2) viruses remains technically difficult. Since the previous report published in December 2018, only 33 A(H3N2) viruses have had a sufficient HA titre to allow antigenic characteriszation by hemagluttinin inhibition (HI) assay. By HI assay, all viruses belonging to 3C.2a and 3C.3a subgroups were poorly recognized by antisera raised against egg-propagated A/Singaport/INFM-16-0019/2015, the current vaccine virus.

B/Victoria Viruses

Only 5 B/Victoria viruses were characterized antigenically during this season. Of these, 2 were antigenically similar to the current vaccine virus, B/Colorado/06/2017, which belongs to a subclade with a two amino acid deletion in HA (Δ 162-163, 1A.Δ2). The other 3 were

antigenically similar to a virus of African origin with a three amino acid deletion in HA1 (Δ 162-164, 1A.Δ3).

B/Yamagata Viruses

Only 7 B/Yamagata viruses were characterized antigenically during this season. HI analyses with post-infection ferret antisera raised against B/Phuket/3072/2013, the virus recommended for inclusion in the quadrivalent virus for the current and subsequent northern hemisphere influenza seasons, indicated that all 7 viruses were antigenically similar to the vaccine virus.

Vaccine composition

The recommended composition of the trivalent influenza vaccine for the current 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.

On 21 February 2019, WHO published recommendations for the components of influenza vaccines for use in the 2019–2020 northern hemisphere influenza season, and on 21 March it was updated. Vaccines should contain the following

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;
- an A/Kansas/14/2017 (H3N2)-like virus;
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).

It is recommended that the influenza B virus component of trivalent vaccines for use in the 2019-2020 northern hemisphere influenza season be a B/Colorado/06/2017-like virus of the B/Victoria/2/87-lineage.

The full report and "Frequently Asked Questions" are available for the 21 February decision and the 21 March addendum on the WHO website.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 1 901 viruses with collection dates since week 40/2018 [1 154 A(H1N1)pdm09, 720 A(H3N2), and 27 type B]. 8 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 3 of them were confirmed by phenotypic testing. 1 A(H3N2) virus showed evidence of reduced inhibition (RI) by oseltamivir only. 1 type B virus showed evidence of RI by zanamivir only.

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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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