

## Summary

### Week 19/2019 (6–12 May 2019)

- For week 19/2019, all countries reporting ILI or ARI thresholds reported activity at or below baseline levels, indicating a return to interseason levels.
- Few countries reported influenza virus detections. Of 79 sentinel specimens tested, only 8 were influenza virus positive.
- For week 19/2019, only one of the 54 specimens from patients with severe acute respiratory infection (SARI) tested positive for an influenza virus.
- Pooled data from 24 Member States and areas reporting to the [EuroMOMO](#) project indicated that all-cause mortality was at expected levels.

### 2018–2019 season overview

- Influenza activity in the European Region, based on sentinel sampling, reached 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 have circulated, with co-circulation in some countries, while others reported dominance of either A(H1N1)pdm09 or A(H3N2) viruses.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 99% were infected with type A viruses, with 66% of those subtyped being A(H1N1)pdm09. Among influenza virus-infected patients admitted to other wards, 99% were infected with type A viruses, with 55% of those subtyped being A(H1N1)pdm09.
- Of the patient specimens from SARI surveillance that tested positive for an influenza virus, 99% were type A viruses, with 79% of those subtyped being A(H1N1)pdm09.
- A 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. For more detail, see the [Vaccine effectiveness](#) section.
- WHO has published [recommendations](#) for the composition of influenza vaccines to be used in the 2019–2020 northern hemisphere season. The recommendation states that both type B lineage viruses should remain unchanged, while the A(H1N1)pdm09 and A(H3N2) viruses should be updated.

- The vast majority of circulating viruses in the European Region were susceptible to neuraminidase inhibitors supporting use of antiviral treatment according to national guidelines.

## Primary care data

## Syndromic surveillance data

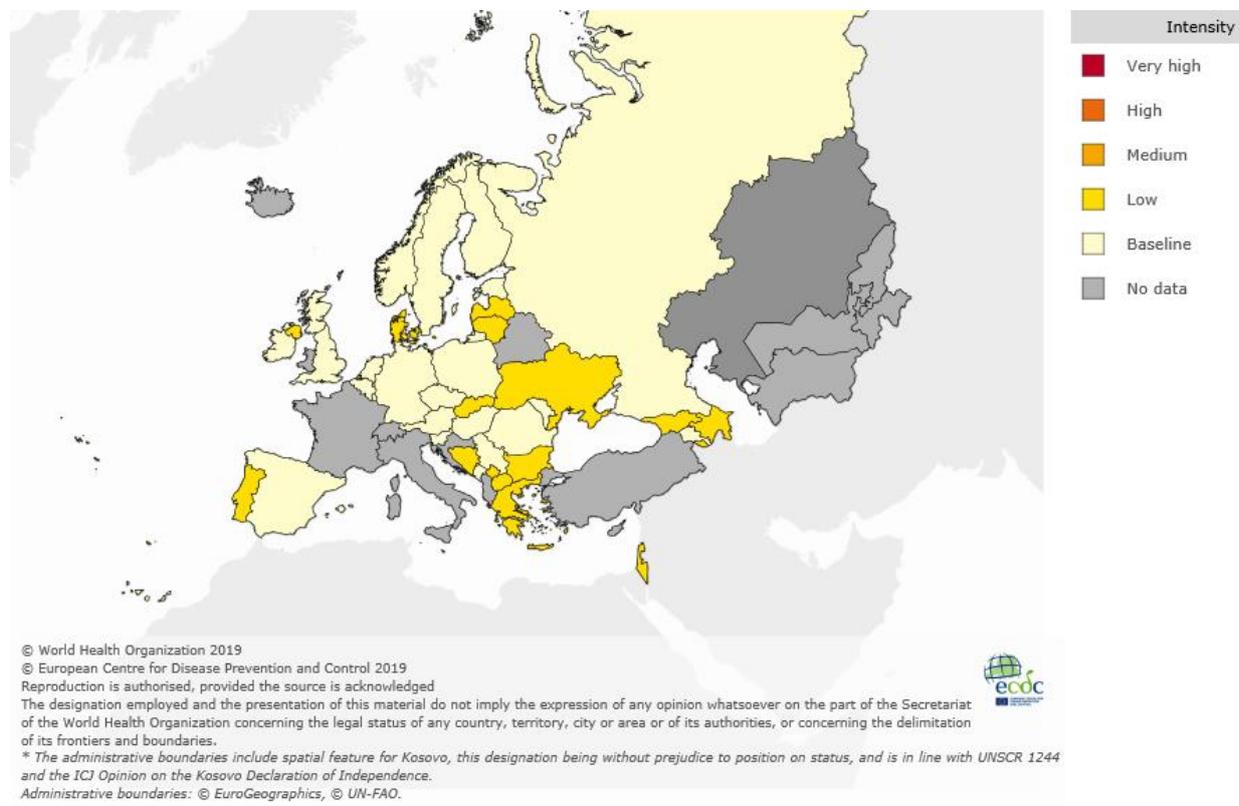
For week 19/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds and the 18 Member States reporting acute respiratory infection (ARI) thresholds, none reported activity above baseline levels.

## Influenza activity

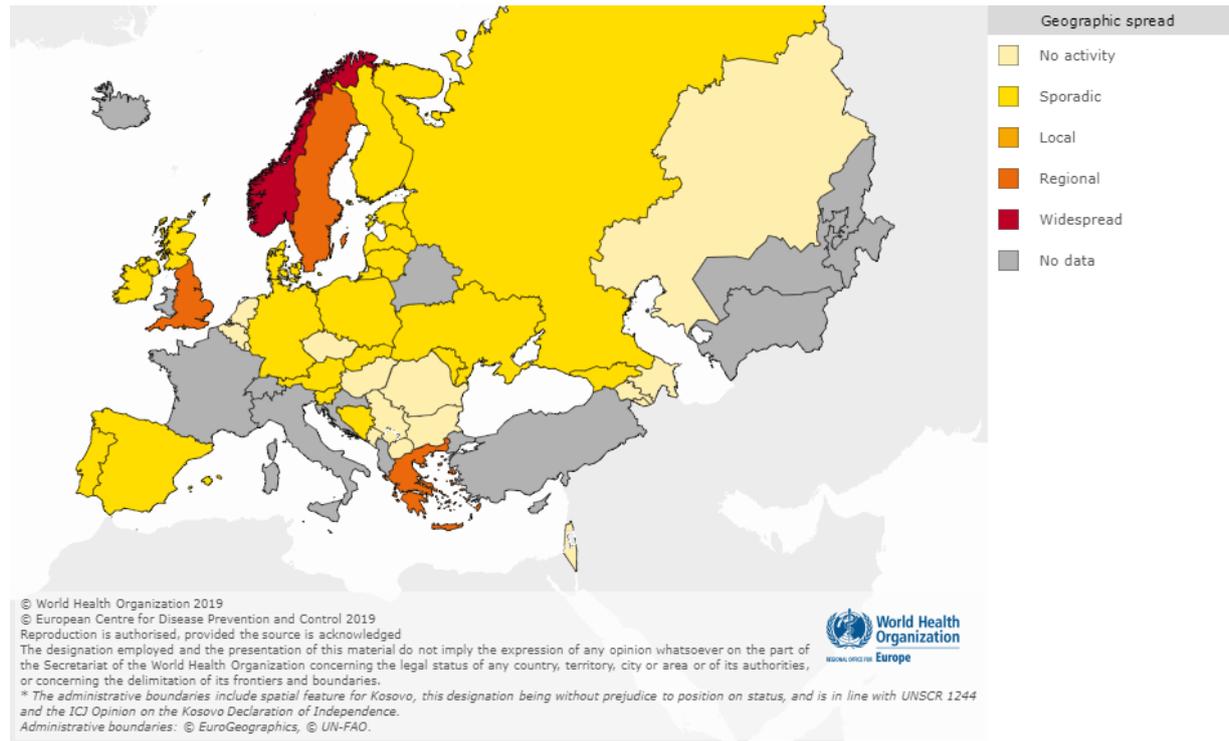
For week 19/2019, of 39 Member States and areas reporting on intensity, 23 reported baseline and 16 reported low intensity (Fig. 1).

Of 40 Member States and areas reporting on geographic spread, 16 reported no activity, 20 reported sporadic, 3 reported regional and 1 (Norway) reported widespread activity (Fig. 2).

**Fig. 1. Intensity in the European Region, week 19/2019**



**Fig. 2. Geographic spread in the European Region, week 19/2019**



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

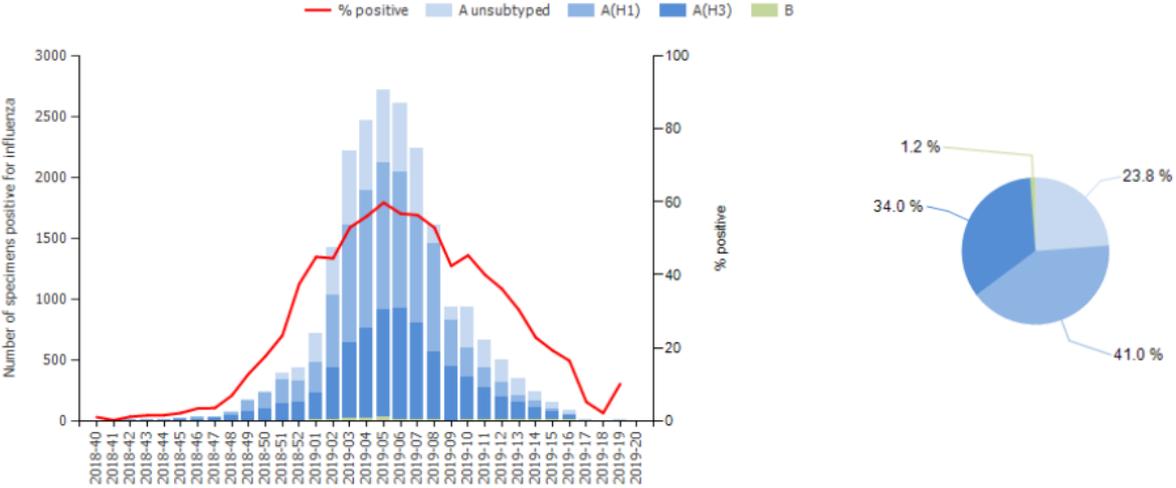
### **Viruses detected in sentinel-source specimens (ILI and ARI)**

For week 19/2019, 8 (10%) of 79 sentinel specimens tested positive for an influenza virus; 7 were type A and 1 was type B. Of subtyped influenza A viruses, 4 were A(H3N2) and 1 was A(H1N1)pdm09 (Fig. 3 and Table 1). While the percentage of specimens testing positive for influenza increased this week, this is likely due to the low number of specimens tested for influenza. Very few influenza positive viruses were reported.

For the season to date, almost all influenza viruses detected were type A (99%) with type B accounting for only 1% of detections. Of subtyped A viruses, 55% were A(H1N1)pdm09 and 45% were A(H3N2). Of 64 influenza type B viruses ascribed to a lineage, 81% were B/Yamagata (74% 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<sup>a</sup>**



<sup>a</sup> Pie chart shows cumulative data for this period.

**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 19/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>7</b>	<b>87.5</b>	<b>21 053</b>	<b>98.8</b>
A(H1N1)pdm09	1	20.0	8 741	54.7
A(H3N2)	4	80.0	7 248	45.3
A not subtyped	2	-	5 064	-
<b>Influenza B</b>	<b>1</b>	<b>12.5</b>	<b>250</b>	<b>1.2</b>
B/Victoria lineage	0	-	12	18.8
B/Yamagata lineage	0	-	52	81.3
Unknown lineage	1	-	186	-
<b>Total detections (total tested)</b>	<b>8 (79)</b>	<b>10.1</b>	<b>21 303 (53 172)</b>	<b>40.1</b>

<sup>a</sup>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 infection (SARI; 17 Member States or areas).

### 1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Of the laboratory-confirmed influenza cases reported in ICUs for week 19/2019 (n=13), all were influenza type A viruses. Most detections (n=10) were reported by the United Kingdom.

Since week 40/2018, almost all viruses detected were influenza type A (n=7 257, 99%). Only 1% were type B (n=63). Of 3 334 subtyped influenza A viruses, 66% were A(H1N1)pdm09 and 34% were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 4 075 cases with known age, 47% were at least 65 years old, 45% were 15-64 years old, and 6% were under 5 years old.

### 1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Among laboratory-confirmed influenza cases reported in wards other than ICUs for week 19/2019 (n=9), all were influenza type A viruses. All detections were reported by Ireland.

Since week 40/2018, almost all viruses detected have been influenza type A (n=9 856, 99%). Only 1% were type B (n=75). Of 4 053 subtyped influenza A viruses, 55% were A(H1N1)pdm09 and 45% were A(H3N2). Of 2 influenza B viruses ascribed to a lineage, 1 was B/Yamagata and 1 was B/Victoria. Of 9 931 cases with known age, 47% were at least 65 years old, 32% were 15-64 years old, and 15% were under 5 years old.

## 2. SARI surveillance

For week 19/2019, 854 SARI cases were reported by 10 Member States or areas. Of these cases, 54 specimens were tested for influenza viruses and 1 (1.9%) tested positive for A(H3N2) virus.

Of 41 865 SARI cases reported since week 40/2018, 41 770 had a recorded age and, of these, 58% were 0-4 years old and 24% were 15-64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 840), type A viruses have been predominating (99%). Of the 2 537 influenza type A infected cases for which subtyping was performed, 79% were infected by A(H1N1)pdm09 viruses and 21% were infected by A(H3N2) viruses. 1 type B virus ascribed to a lineage was B/Yamagata.

## Mortality monitoring

For week 19/2019, the [EuroMOMO](#) project received data from 24 countries or areas that were included in pooled analyses. The pooled estimates indicated that all-cause mortality was within expected ranges.

## 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 19/2019, 395 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; 92% were type A and 8% were type B. Of 91 A viruses subtyped, 29% were A(H1N1)pdm09 and 71% were A(H3N2) (Table 2).

For the season to date, the vast majority of viruses detected have been influenza type A (99%). Of A viruses subtyped, 58% were A(H1N1)pdm09 and 42% were A(H3N2). Of 61 influenza type B viruses ascribed to a lineage, 46% were B/Yamagata (97% 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 19/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>363</b>	<b>91.9</b>	<b>180 955</b>	<b>99.0</b>
A(H1N1)pdm09	26	28.6	35 236	58.3
A(H3N2)	65	71.4	25 162	41.7
A not subtyped	272	-	120 557	-
<b>Influenza B</b>	<b>32</b>	<b>8.1</b>	<b>1 838</b>	<b>1.0</b>
B/Victoria lineage	0	-	39	54.1
B/Yamagata lineage	0	-	34	45.9
Unknown lineage	32	-	1 765	-
<b>Total detections (total tested)</b>	<b>395 (7 746)</b>	<b>-</b>	<b>182 793 (782 930)</b>	<b>-</b>

<sup>a</sup> 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 3 792 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 808 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; 1 929 were A(H3) viruses, with 1 283 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 68

to the A/Switzerland/8060/2017 (3C.2a2) subclade, 33 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 57 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 9 to the A/Greece/4/2017 (3C.2a1a) subgroup, 5 to the A/Hong Kong/4801/2014 (3C.2a) clade, 467 to the A/England/538/2018 (3C.3a) clade and 7 attributed to a subgroup not listed.

Of the 52 genetically characterized influenza B viruses, 27 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). All 25 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 15 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 40/2018–19/2019**

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 <sup>a</sup>	1 808
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	1 283
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup <sup>b</sup>	68
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	33
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	467
A(H3) clade 3c.2a1 representative A/Singapore/INFIMH-16-0019/2016 subgroup <sup>d</sup>	57
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	5
A(H3) attributed to recognized group in current guidance but not listed here	7
A(H3) clade 3C.2a1a representative A/Greece/4/2017 subgroup	9
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	5
B(Vic)-lineage clade 1A representative B/Colorado/06/2017 <sup>a</sup>	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	15
B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>c</sup>	27

<sup>a</sup> Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

<sup>b</sup> Vaccine component for 2019 southern hemisphere season.

<sup>c</sup> Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

<sup>d</sup> Vaccine component for 2018-2019 northern hemisphere season

ECDC recently published a [report](#) detailing influenza virus characterizations conducted in April 2019 by the WHO Collaborating Centre, London (the Francis Crick Institute), on influenza-positive specimens received from European Union/European Economic Area countries. A summary is given below.

### **A(H1N1)pdm09 viruses**

The vast majority (126/129) of A(H1N1)pdm09 viruses characterized overall and all 59 test viruses characterised antigenically since the March 2019 were similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1) and all fell in subclade 6B.1A. Within this subclade, there has been increasing genetic diversity of the HA genes with several emerging genetic subgroups. The 391 test viruses with collection dates

from week 40/2018 genetically characterised at the WIC, including an A(H1N2) reassortant, all fell in a 6B.1 subclade, designated 6B.1A, defined by HA1 amino acid substitutions of S74R, S164T and I295V. Of these recently circulating viruses, 355 also have HA1 S183P substitution, often with additional substitutions in HA1 and/or HA2.

### **A(H3N2) viruses**

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the previous report published in March 2019, only 26 A(H3N2) viruses successfully recovered had sufficient HA titre to allow antigenic characterisation by HI assay in the presence of oseltamivir. These viruses were poorly recognised by antisera raised against the currently used vaccine virus, egg-propagated A/Singapore/INFIMH-16-0019/2016, in HI assays. Of the 321 viruses with collection dates from week 40/2018 genetically characterised at the WIC, 267 were clade 3C.2a (with 32 3C.2a2, 13 3C.2a3, six 3C.2a4 and 216 3C.2a1b) and 54 were clade 3C.3a.

### **B/Victoria viruses**

No B/Victoria lineage virus has been tested by HI since the March 2019 report. All recent viruses carry HA genes that fall in clade 1A but encode HA1 amino acid substitutions of I117V, N129D and V146I compared to a previous vaccine virus, B/Brisbane/60/2008. Groups of viruses defined by deletions of two ( $\Delta$ 162-163, 1A( $\Delta$ 2)) or three ( $\Delta$ 162-164, 1A( $\Delta$ 3)) amino acids in HA1 have emerged, with the triple deletion group having subgroups of Asian and African origin. HI analyses with panels of post-infection ferret antisera have shown these virus groups to be antigenically distinguishable. Of a total of five viruses characterised from EU/EEA countries this season, one has been  $\Delta$ 162-163 and four  $\Delta$ 162-164 (three African and one Asian subgroup).

### **B/Yamagata viruses**

Only 2 B/Yamagata lineage viruses have been characterized antigenically since the March report and a total of 11 from the 2018–19 season. All have HA genes that fell into clade 3 and encoded 2 HA amino acid substitutions not present in the virus recommended for inclusion in quadrivalent vaccines for the current and subsequent northern hemisphere influenza seasons, B/Phuket/3073/2013. However, all remain antigenically similar to the vaccine virus recommended for use in quadrivalent vaccines for current and subsequent northern hemisphere influenza seasons.

### **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 finalized. 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” for the 21 February decision and the 21 March addendum are available on the [WHO website](#).

### Vaccine effectiveness

Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. Early data suggest that vaccines are moderately 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 \(China\)](#), [Sweden](#), and the [United States of America](#).

### Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 2 575 viruses with collection dates since week 40/2018 [1 527 A(H1N1)pdm09, 1 016 A(H3N2), and 32 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 type B virus showed evidence of reduced inhibition (RI) by 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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 19/2019.

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 19/2019.

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