

## Summary

### Week 40/2019 (30 September–6 October 2019)

- This is the first weekly report for the 2019–2020 influenza season.
- Influenza activity was low throughout the European Region.
- Influenza viruses were detected sporadically in specimens from persons with respiratory illness presenting to medical care.
- Both influenza A and B type viruses were detected.
- For week 40/2019, data from the 21 countries or regions reporting to the [EuroMOMO](#) project indicated all-cause mortality to be at expected levels for this time of the year.

### 2019–2020 season overview

- As is usual for this time of year, influenza activity is low in the European Region.
- During the influenza [Vaccine Composition Meeting for the southern hemisphere](#) 2020 season, held in September 2019, WHO recommended the A(H1N1)pdm09 component to be an A/Brisbane/02/2018 (H1N1)pdm09-like virus, the A(H3N2) component an A/South Australia/34/2019 (H3N2)-like virus and the B/Victoria-lineage component to be a B/Washington/02/2019-like virus. The B/Yamagata-lineage component, included only in quadrivalent vaccines is a B/Phuket/3073/2013-like virus. The full report can be found [here](#).

## Primary care data

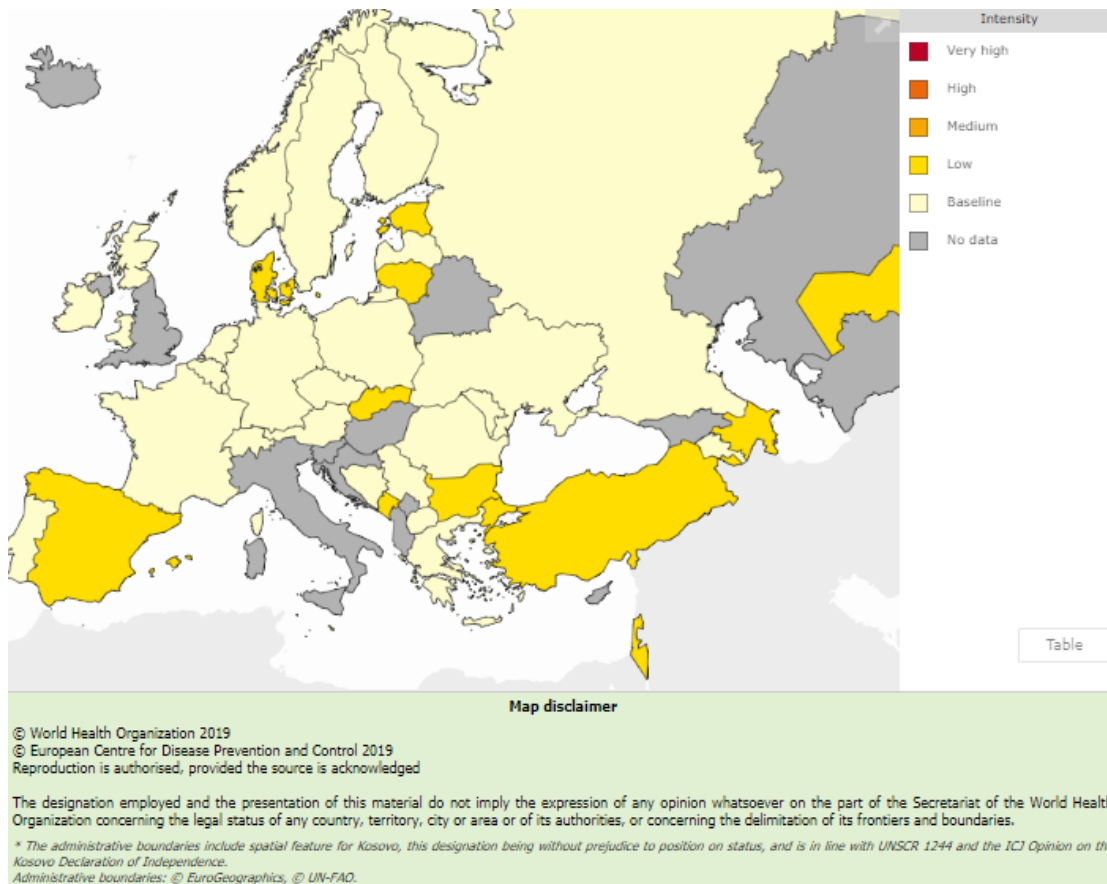
### Syndromic surveillance data

Based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI), all countries reported activity within baseline levels.

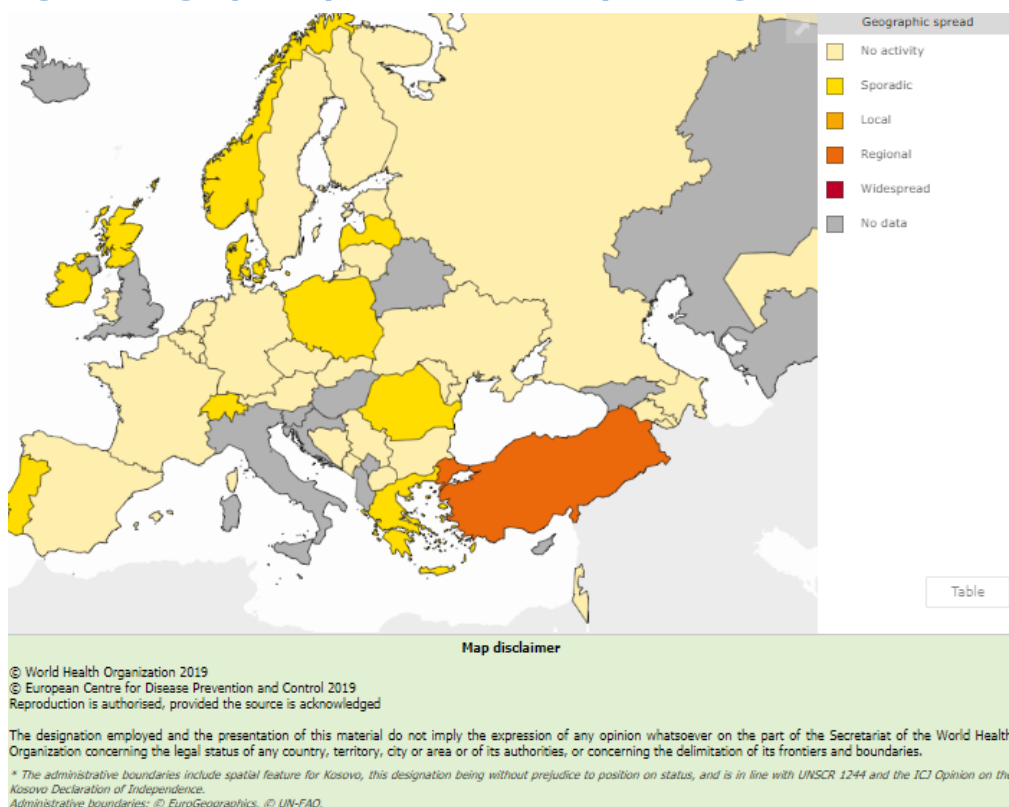
### Influenza activity

For week 40/2019, of 38 Member States and areas reporting on intensity, all reported baseline or low intensity (Fig. 1). Of 38 Member States and areas reporting on geographic spread, 27 reported no activity (across the region), 10 reported sporadic cases (in northern, southern and western areas) and 1 (Turkey) reported regional activity (Fig. 2).

**Fig. 1. Intensity in the European Region, week 40/2019**



**Fig. 2. Geographic spread in the European Region, week 40/2019**



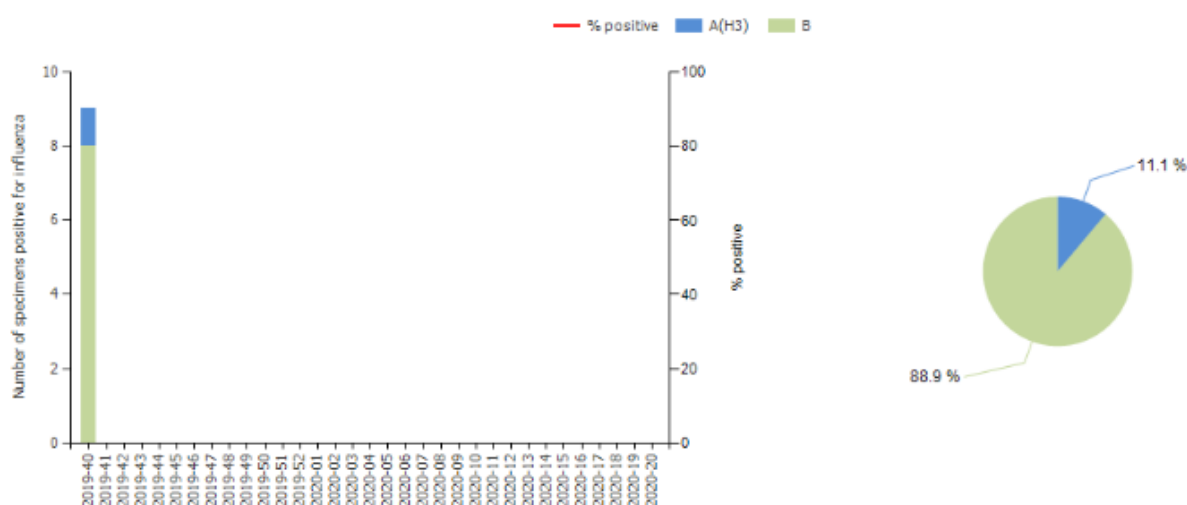
For interactive maps of influenza intensity and geographic spread, see the [Flu News Europe website](#).

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

For week 40/2019, 9 of 212 (4%) sentinel specimens tested positive for an influenza virus; 1 was influenza type A and 8 were influenza type B (Fig. 3 and Table 1). The 7 influenza B viruses genotyped were of the B/Victoria 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 for the season<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 40/2019 and cumulatively for the season**

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>1</b>	<b>11.1</b>	<b>1</b>	<b>11.1</b>
A(H1N1)pdm09	0	0.0	0	0.0
A(H3N2)	1	100.0	1	100.0
A not subtyped	0	-	0	-
<b>Influenza B</b>	<b>8</b>	<b>88.9</b>	<b>8</b>	<b>88.9</b>
B/Victoria lineage	7	100.0	7	100.0
B/Yamagata lineage	0	0.0	0	0.0
Unknown lineage	1	-	1	-
<b>Total detections (total tested)</b>	<b>9 (212)</b>	<b>4.2</b>	<b>9 (212)</b>	<b>4.2</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 monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (14 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infection (SARI; 18 Member States or areas).

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

For week 40/2019, the United Kingdom reported 2 laboratory-confirmed influenza cases in ICU, both were infected with influenza type A viruses.

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

For week 40/2019, Ireland reported 1 laboratory-confirmed influenza case from other wards that was infected with an influenza type B virus.

## 2. SARI surveillance

For week 40/2019, 149 SARI cases were reported by 6 Member States or areas. Of these cases, none were tested for influenza viruses.

## Mortality monitoring

For week 40/2019, the [EuroMOMO](#) project received data from 21 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality show mortality levels within normal 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 40/2019, 64 of 8 159 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 influenza viruses; 84% were type A and 16% were type B. Of 18 A viruses subtyped, 94% were A(H3N2), and both B viruses ascribed to a lineage were B/Victoria (Table 2).

**Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 40/2019 and cumulatively for the season**

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>54</b>	<b>84.4</b>	<b>54</b>	<b>84.4</b>
A(H1N1)pdm09	1	5.6	1	5.6
A(H3N2)	17	94.4	17	94.4
A not subtyped	36	-	36	-
<b>Influenza B</b>	<b>10</b>	<b>15.6</b>	<b>10</b>	<b>15.6</b>
B/Victoria lineage	2	100.0	2	100.0
B/Yamagata lineage	0	0.0	0	0.0
Unknown lineage	8	-	8	-
<b>Total detections (total tested)</b>	<b>64 (8 159)</b>	<b>-</b>	<b>64 (8 159)</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

One A(H3N2) influenza virus from week 40/2019 has been characterized genetically and it belonged to the 3C.2a1b subclade.

ECDC published a [report](#) in September detailing influenza virus characterizations conducted in July 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

All 103 test viruses characterized antigenically since the June 2019 characterization report were similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1). The 539 test viruses with collection dates from week 40/2018 genetically characterized at the WHO Collaborating Centre, including two A(H1N2) reassortants, all fell in a 6B.1 subclade, designated 6B.1A, defined by HA1 amino acid substitutions of S74R, S164T and I295V. Within this subclade there has been increasing genetic diversity of the HA genes and of these recently circulating viruses, 493 also have an HA1 S183P substitution, often with additional substitutions in HA1 and/or HA2 that define several emerging genetic subgroups.

### A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the June 2019 characterization report, 21 A(H3N2) viruses had sufficient HA titre to allow antigenic characterization by HI assay in the presence of oseltamivir. These viruses were poorly recognized by antisera raised against the currently used clade 3C.2a1 vaccine virus, egg-propagated A/Singapore/INFIMH-16-0019/2016, in HI assays. Of the 446 viruses with collection dates from week 40/2018 genetically characterized at the WHO Collaborating Centre,

363 were clade 3C.2a with many falling in subclades (32 3C.2a2, 13 3C.2a3, 6 3C.2a4 and 216 3C.2a1b) and 83 were clade 3C.3a.

### **B/Victoria viruses**

Four B/Victoria lineage viruses had been tested by HI since the June 2019 characterization 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 2 ( $\Delta$ 162-163, 1A( $\Delta$ 2)) or 3 ( $\Delta$ 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 4 virus groups to be antigenically distinguishable. Of a total of 12 viruses characterized from EU/EEA countries this season, 1 has been  $\Delta$ 162-163 and 11  $\Delta$ 162-164 (10 African and 1 Asian subgroup).

### **B/Yamagata viruses**

Two B/Yamagata lineage viruses had been characterized antigenically since the June characterization report and a total of 15 had been characterized from the 2018–19 season. All had 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 15 viruses remained antigenically similar to the vaccine virus.

### **Vaccine composition**

On 21 February 2019, WHO published recommendations for the components of influenza vaccines for use in the 2019–2020 northern hemisphere influenza season; the recommendations were finalized on 21 March. Vaccines should contain the following:

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus (Clade 6B.1A1);
- an A/Kansas/14/2017 (H3N2)-like virus (Clade 3C.3a);
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage) (Clade 1A\_Δ2); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage) (Clade 3).

It was 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](#).

### **Antiviral susceptibility testing**

Neuraminidase inhibitor susceptibility has not been assessed on viruses with collection dates in week 40/2019.

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, Emmanuel Robesyn, and Oksana Martinuka) and the WHO Regional Office for Europe (Caroline Brown, Sonja Olsen, James Fielding, Dmitriy Pereyaslov and Tamara Meerhoff, Temporary Advisor to WHO). It was reviewed by country experts (Ana Paula Rodrigues, National Institute of Health Dr Ricardo Jorge (INSA), Portugal and Božidarka Rakočević, Centre for Disease Control, Institute of Public Health, Montenegro) 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 40/2019.

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 40/2019.

© World Health Organization 2019.

© European Centre for Disease Prevention and Control 2019.

Reproduction is authorized, provided the source is acknowledged.