

## Summary

### Week 46/2019 (11–17 November 2019)

- Influenza activity was low throughout the European Region with mixed circulation of type A and B viruses but, while numbers of influenza detections are low, there are early signs of influenza B dominance in some central Asian countries.
- Influenza viruses were detected sporadically in specimens from persons with respiratory illness presenting to medical care.
- Both influenza types A and B viruses were detected in sentinel and non-sentinel source specimens, with a higher number of detections for influenza A viruses.
- Data from the 22 countries or areas reporting to the [EuroMOMO](#) project indicated that all-cause mortality was at expected levels for this time of the year.

### 2019–2020 season overview

- As is usual for this time of year, influenza activity was low in the European Region.

## Primary care data

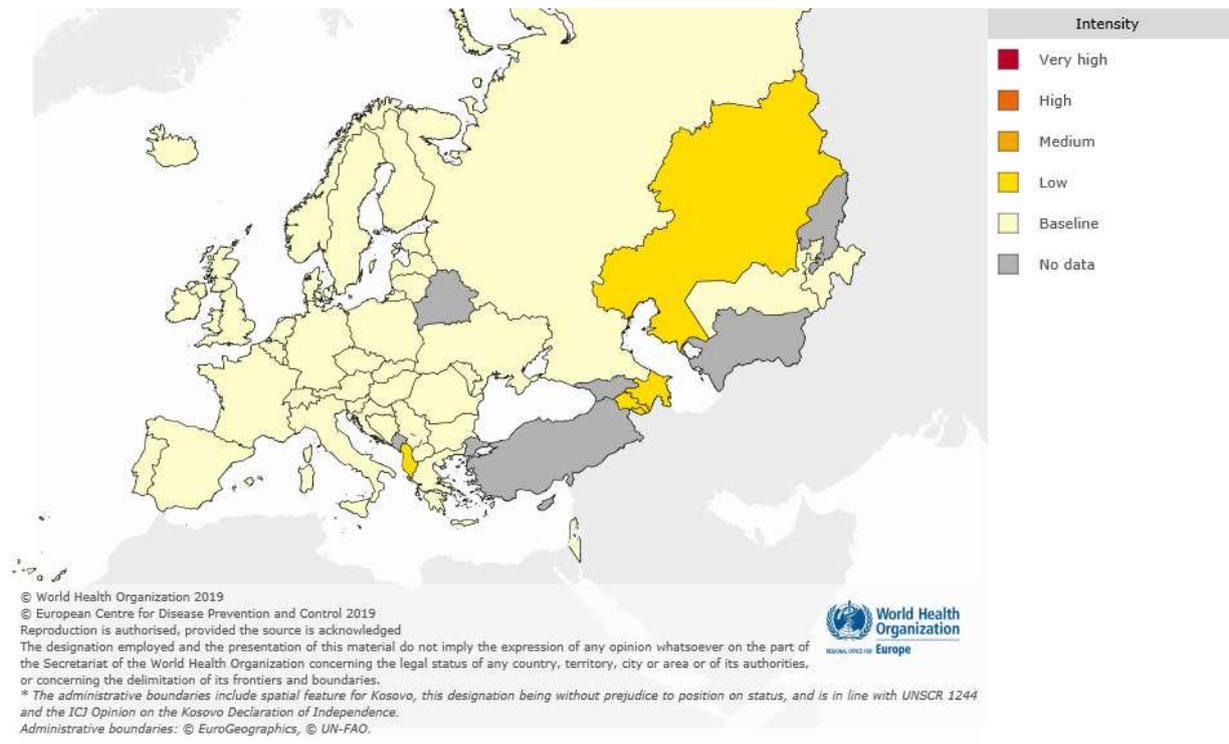
### Syndromic surveillance data

Based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI), all countries reported ILI activity within their baseline levels. Of the 11 Member States reporting acute respiratory infection (ARI) thresholds, 1 (Armenia) reported ARI above baseline levels.

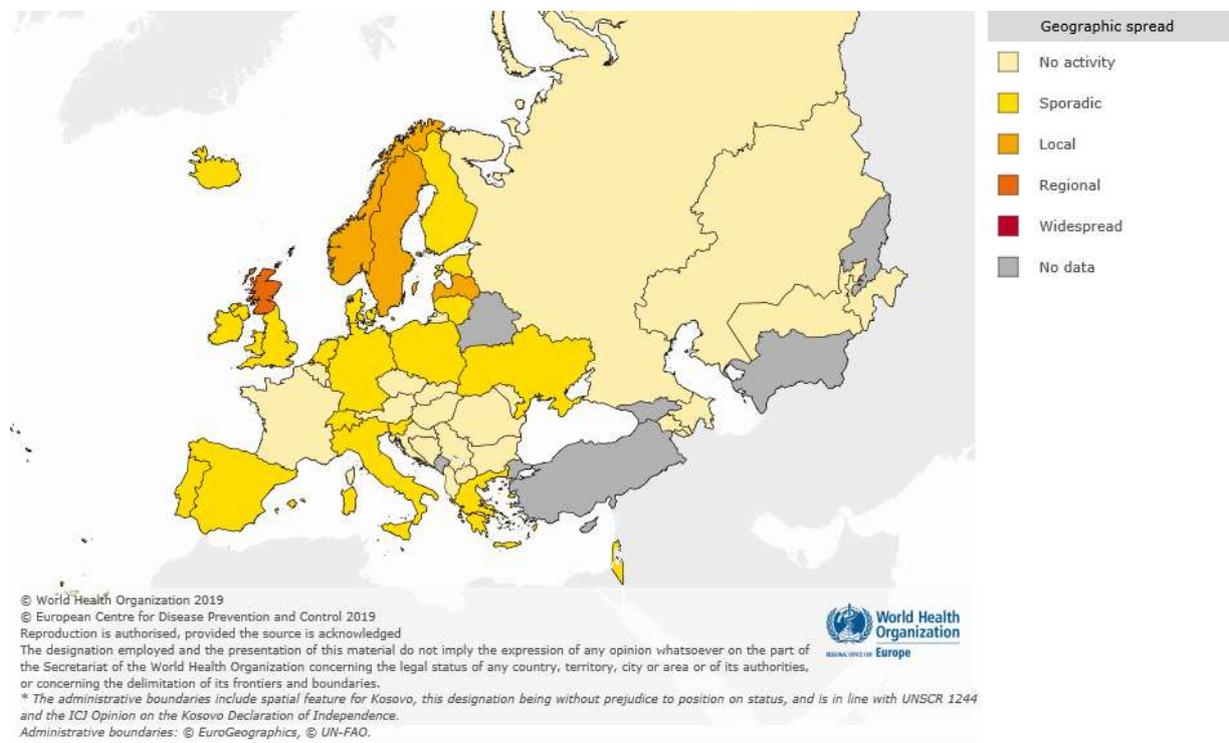
### Influenza activity

Of 47 Member States and areas reporting on intensity, 43 reported baseline, and 4 (Albania, Armenia, Azerbaijan and Kazakhstan) reported low intensity for week 46/2019 (Fig. 1). Of 47 Member States and areas reporting on geographic spread, 23 reported no activity, 20 reported sporadic cases, 3 reported local spread (Latvia, Norway and Sweden) and 1 reported regional spread (United Kingdom [Scotland]) (Fig. 2).

**Fig. 1. Intensity in the European Region, week 46/2019**



**Fig. 2. Geographic spread in the European Region, week 46/2019**



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

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

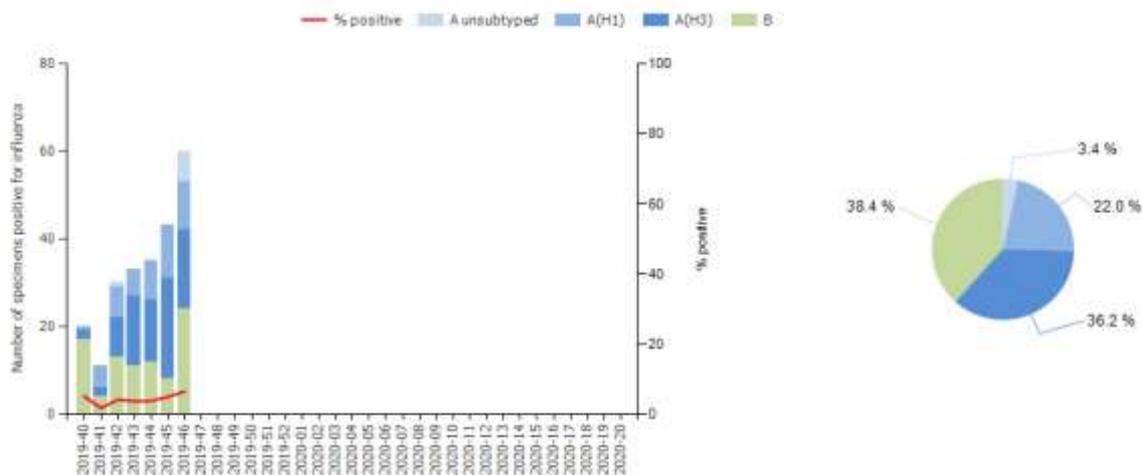
For week 46/2019, 60 (6.6%) of 910 sentinel specimens tested positive for influenza viruses: 36 were type A and 24 were type B (Fig. 3 and Table 1). Of 29 subtyped A viruses, 11 (38%) were A(H1N1)pdm09 and 18 (62%) A(H3N2) (Fig. 3 and Table 1). Of 11 type B viruses ascribed to a lineage all were B/Victoria (Table 1).

Of 21 Member States or areas across the region that each tested at least 10 sentinel specimens in week 46/2019, 8 reported a rate of influenza virus detections above 10% (median 17.1%; range 10.0%–28.6%).

For the season overall, more influenza type A (n=143, 61.6%) than type B (n=89, 38.4%) viruses have been detected (Fig. 3 and Table 1). Of 135 subtyped A viruses, 51 (37.8%) were A(H1N1)pdm09 and 84 (62.2%) were A(H3N2) (Fig. 3 and Table 1). Of 25 influenza type B viruses ascribed to a lineage, 24 (96%) were B/Victoria and 1 (4%) 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 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 46/2019 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>36</b>	<b>60</b>	<b>143</b>	<b>61.6</b>
A(H1N1)pdm09	11	37.9	51	37.8
A(H3N2)	18	62.1	84	62.2
A not subtyped	7	-	8	-
<b>Influenza B</b>	<b>24</b>	<b>40</b>	<b>89</b>	<b>38.4</b>
B/Victoria lineage	11	100	24	96
B/Yamagata lineage	0	0	1	4
Unknown lineage	13	-	64	-
<b>Total detections (total tested)</b>	<b>60 (910)</b>	<b>6.6</b>	<b>232 (5 271)</b>	<b>4.4</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, or other wards, or 2) severe acute respiratory infection (SARI; 17 Member States or areas).

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

Among laboratory-confirmed influenza cases reported in ICUs for week 46/2019 (n=29), influenza type A viruses (n=28, 96.6%) were detected more frequently than influenza type B viruses (n=1, 3.4%).

Since week 40/2019, more influenza type A (n=80, 93.0%) than type B (n=6, 7.0%) viruses were detected. Of 16 subtyped influenza A viruses, 50.0% were A(H1N1)pdm09 and 50.0% A(H3N2). None of the influenza B viruses were ascribed to a lineage.

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

Among laboratory-confirmed influenza cases reported in wards other than ICUs for week 46/2019 (n=11), all were influenza type A viruses.

Since week 40/2019 more influenza type A (n=43, 91.5%) than type B (n=4, 8.5%) viruses were detected. Of 30 subtyped influenza A viruses, all were A(H3N2). No influenza B viruses were ascribed to a lineage.

## 2. SARI surveillance

For week 46/2019, 757 SARI cases were reported by 10 countries. In total, 168 specimens were tested for influenza viruses and 7 (4.2%) were positive for influenza, 3 A(H3N2) and 4 type B.

Of 5 346 SARI cases reported since week 40/2019, 5 326 had a recorded age and, of these, 60.1% were 0-4 years old and 19% were 15-64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=22), type B viruses were the most common (16; 72.7%). Of the 5 influenza type A infected cases for which subtyping was performed, all were infected by A(H3N2) viruses. Of those influenza B viruses that have been ascribed to a lineage (n=4), all were B/Victoria.

## **Mortality monitoring**

For week 46/2019, the [EuroMOMO](#) project received data from 22 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality were within the expected range for the time of year.

## **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 46/2019, 665 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; 83% were type A and 17% were type B. Of 110 subtyped A viruses, 20% were A(H1N1)pdm09 and 80% were A(H3N2). Of 4 influenza type B viruses ascribed to a lineage 3 were B/Victoria and 1 was B/Yamagata (Table 2).

For the season to date, more influenza type A (82%) than type B (18%) viruses have been detected. Of 563 subtyped A viruses, 126 (22.4%) were A(H1N1)pdm09 and 437 (77.6%) were A(H3N2). Of 40 influenza type B viruses ascribed to a lineage, 90% were B/Victoria and 10% B/Yamagata (Table 2).

**Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 46/2019 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>552</b>	<b>83</b>	<b>2084</b>	<b>82</b>
A(H1N1)pdm09	22	20	126	22.4
A(H3N2)	88	80	437	77.6
A not subtyped	442	-	1 521	-
<b>Influenza B</b>	<b>113</b>	<b>17</b>	<b>457</b>	<b>18</b>
B/Victoria lineage	3	75	36	90
B/Yamagata lineage	1	25	4	10
Unknown lineage	109	-	417	-
<b>Total detections (total tested)</b>	<b>665 (14 523)</b>		<b>2 541 (87 093)</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

Since the beginning of the season, there have been very few reports of influenza virus genetic characterization.

ECDC published a [report](#) in November on detailed influenza virus characterizations conducted since week 40/2019 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

Three test viruses characterized antigenically since the last report were antigenically similar to the vaccine virus used in the 2019–2020 northern hemisphere season (A/Brisbane/02/2018, clade 6B.1A1). The single virus that was genetically characterized at the WHO Collaborating Centre carried the HA1 S183P substitution and fell in the 6B.1A5B subgroup.

### A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the last characterization report, no A(H3N2) viruses have been characterised antigenically or genetically. However, viruses from EU/EEA countries with collection dates in January through August 2019 have HA genes that fall mainly in subclades 3C.2a1b+T131K and 3C.2a1b+T135K, and clade 3C.3a, with the most recently collected viruses (from Norway) falling in subclade 3C.2a1b+T131K.

### B/Victoria viruses

Two B/Victoria lineage viruses have been tested by HI in this reporting period. While genetic characterisation is pending, the profile of both viruses indicate they are of the HA triple

deletion group that originated in Africa and are designated as the  $\Delta$ 162-164, 1A( $\Delta$ 3)B subgroup, represented by B/Washington/02/2019, which was recently recommended for use in vaccines for the southern hemisphere 2020 influenza season. While relatively low numbers of B/Victoria-lineage viruses have been detected in recent months, the large majority have fallen in this genetic subgroup.

### **B/Yamagata viruses**

Two B/Yamagata lineage viruses have been characterized antigenically in this reporting period. They were similar to the vaccine virus B/Phuket/3073/2013 (clade 3) recommended for use in quadrivalent vaccines for the current northern hemisphere influenza season. While all recently circulating B/Yamagata-lineage viruses contain HA amino acid substitutions compared to B/Phuket/3073/2013, antigenic effects have been minimal based on this and earlier reports.

### **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](#).

The report from the [Vaccine Composition Meeting for the southern hemisphere](#) 2020 season can be found [here](#).

### **Antiviral susceptibility testing**

Six viruses collected in the weeks 40–46/2019 period were tested for susceptibility to neuraminidase inhibitors: 5 A(H3N2) viruses and 1 type B virus showed normal inhibition (NI) by both oseltamivir and zanamivir.

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 (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.

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