

## Summary

### Week 45/2019 (4–10 November 2019)

- 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 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 23 countries or areas reporting to the [EuroMOMO](#) project indicated 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

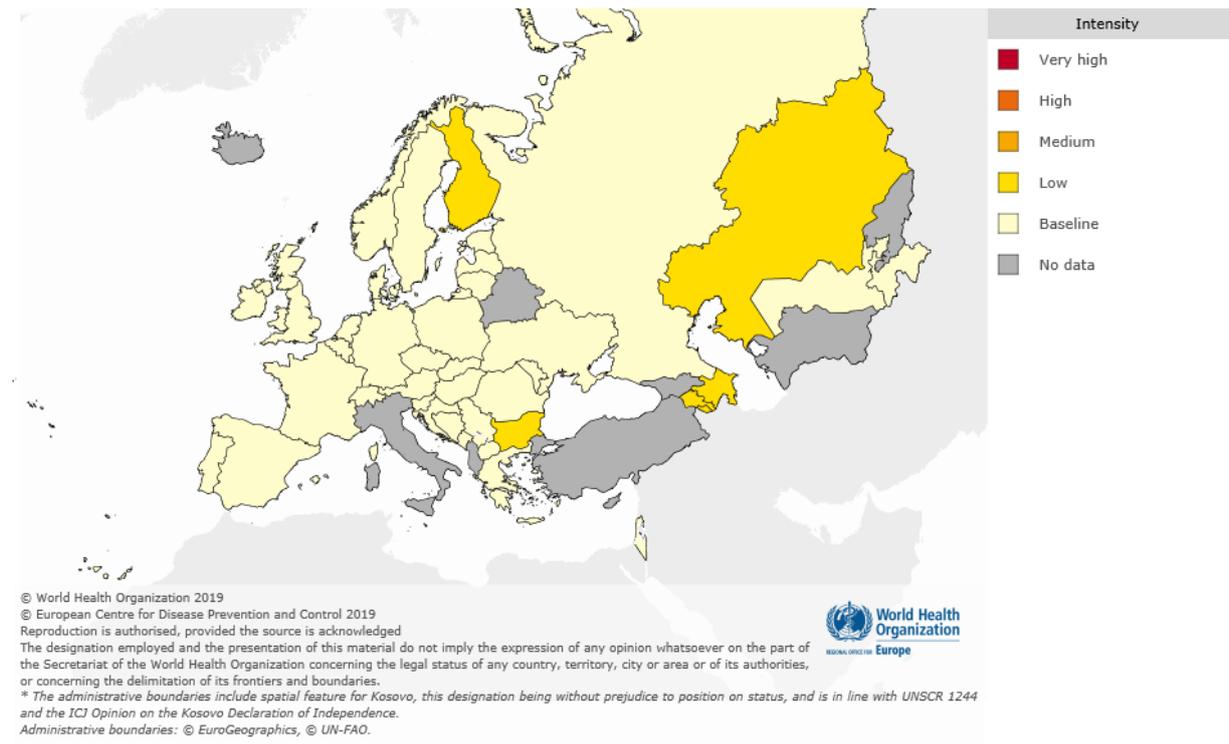
### Syndromic surveillance data

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

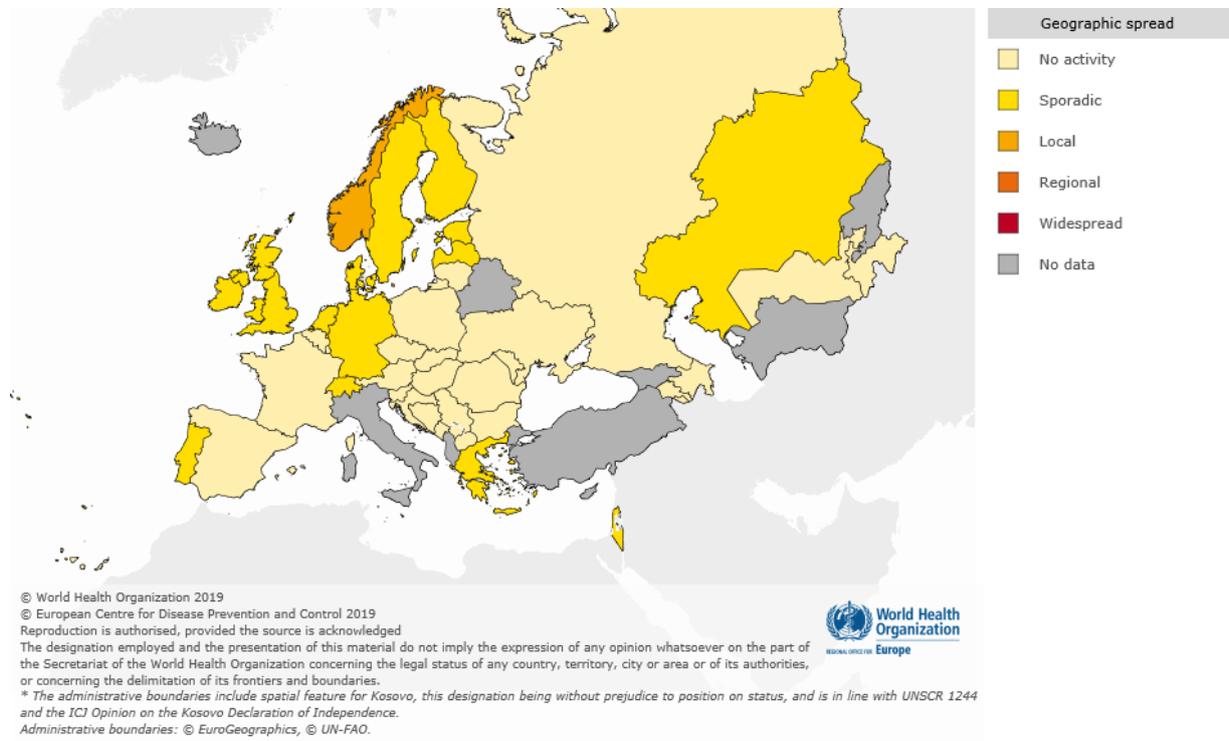
### Influenza activity

Of 45 Member States and areas reporting on intensity, 40 reported baseline and 5 reported low intensity for week 45/2019 (Fig. 1). Of 45 Member States and areas reporting on geographic spread, 27 reported no activity, 17 reported sporadic cases and 1 reported local spread (Norway) (Fig. 2).

**Fig. 1. Intensity in the European Region, week 45/2019**



**Fig. 2. Geographic spread in the European Region, week 45/2019**



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

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

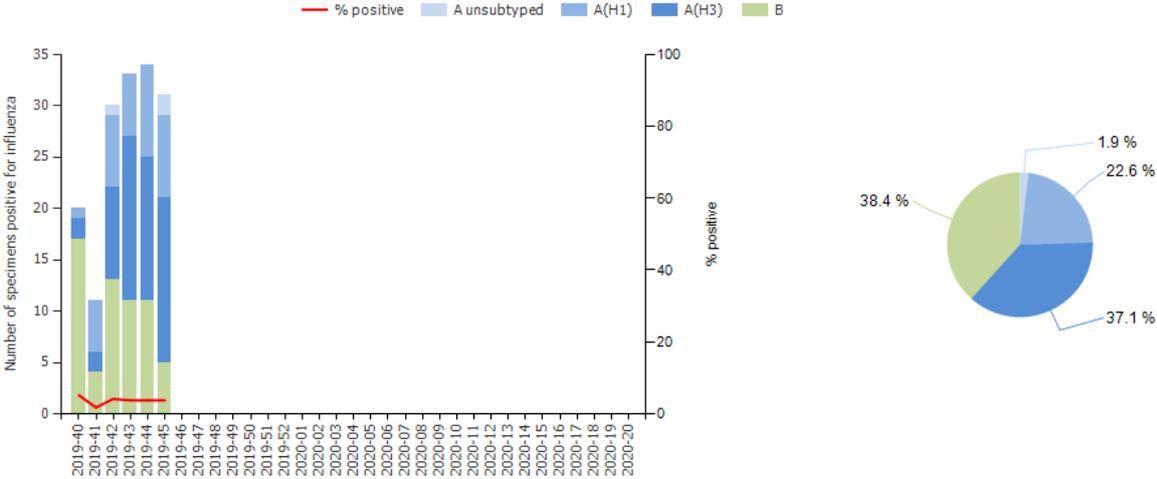
For week 45/2019, 31 (4%) of 784 sentinel specimens tested positive for influenza viruses: 26 were type A and 5 were type B. Of 24 subtyped A viruses, 33.3% were A(H1N1)pdm09 and 66.7% A(H3N2). Only 1 type B virus was ascribed to a lineage and it was B/Victoria (Fig. 3 and Table 1).

Of 18 Member States or areas across the region that each tested at least 10 sentinel specimens in week 45/2019, 3 reported a rate of influenza virus detections above 10%: Switzerland (20.0%), United Kingdom (Northern Ireland: 36.4%) and United Kingdom (Scotland: 20.8%).

For the season overall, more influenza type A (n=98, 61.6%) than type B (n=61, 38.4%) viruses have been detected. Of 95 subtyped A viruses, 36 (37.9%) were A(H1N1)pdm09 and 59 (62.1%) were A(H3N2). Of 13 influenza type B viruses ascribed to a lineage, 12 were B/Victoria (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 45/2019 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>26</b>	<b>83.9</b>	<b>98</b>	<b>61.6</b>
A(H1N1)pdm09	8	33.3	36	37.9
A(H3N2)	16	66.7	59	62.1
A not subtyped	2	-	3	-
<b>Influenza B</b>	<b>5</b>	<b>16.1</b>	<b>61</b>	<b>38.4</b>
B/Victoria lineage	1	100	12	92.3
B/Yamagata lineage	0	0	1	7.7
Unknown lineage	4	-	48	-
<b>Total detections (total tested)</b>	<b>31 (784)</b>	<b>4</b>	<b>159 (4 304)</b>	<b>3.7</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, or other wards, or 2) severe acute respiratory infection (SARI; 17 Member States or areas).

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

For week 45/2019, the United Kingdom reported 9 laboratory-confirmed influenza cases in ICUs: 8 were infected with influenza type A viruses, of which one was subtyped as A(H1N1)pdm09 and one as A(H3N2), and 1 was infected with an influenza type B virus.

Since week 40/2019, Ireland and the United Kingdom have reported respectively 1 and 51 cases of laboratory-confirmed influenza from ICU. Of the 52 cases, 47 were infected with influenza type A and 5 with influenza type B. Of 8 subtyped influenza A viruses, 5 were A(H1N1)pdm09 and 3 A(H3N2). None of the influenza B viruses were ascribed to a lineage.

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

For week 45/2019, 4 laboratory-confirmed influenza cases in other wards were reported by Ireland.

Since week 40/2019, a total of 25 laboratory-confirmed influenza cases from other wards have been reported by Ireland and Ukraine; of these 22 were infected by influenza type A viruses, with 11 subtyped as A(H3N2), and 3 by influenza type B viruses.

## 2. SARI surveillance

For week 45/2019, 956 SARI cases were reported by 11 countries. In total, 124 specimens were tested for influenza viruses and 2 (1.6%) were positive for influenza type B.

Of 4 516 SARI cases reported since week 40/2019, 4 502 had a recorded age and, of these, 60.2% were 0-4 years old and 18.3% were 15-64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=15), 12 were type B viruses and 3 were type A. Both influenza type A infected cases, for which subtyping was performed, were infected by A(H3N2) viruses. No influenza B viruses were ascribed to a lineage.

## Mortality monitoring

For week 45/2019, the [EuroMOMO](#) project received data from 23 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality were within the normal 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 45/2019, 451 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; 82.7% were type A and 17.3% were type B. Of 78 subtyped A viruses, 23.1% were A(H1N1)pdm09 and 76.9% were A(H3N2). Both type B viruses ascribed to a lineage were B/Victoria (Table 2).

For the season to date, more influenza type A (82%) than type B (18%) viruses have been detected. Of 411 subtyped A viruses, 91 (22%) were A(H1N1)pdm09 and 320 (78%) were A(H3N2). Of 31 influenza type B viruses ascribed to a lineage, 90% were B/Victoria lineage (Table 2).

**Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 45/2019 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>373</b>	<b>82.7</b>	<b>1 499</b>	<b>81.8</b>
A(H1N1)pdm09	18	23.1	91	22.1
A(H3N2)	60	76.9	320	77.9
A not subtyped	295	-	1 088	-
<b>Influenza B</b>	<b>78</b>	<b>17.3</b>	<b>334</b>	<b>18.2</b>
B/Victoria lineage	2	100	28	90.3
B/Yamagata lineage	0	0	3	9.7
Unknown lineage	76	-	303	-
<b>Total detections (total tested)</b>	<b>451 (12 895)</b>		<b>1 833 (71 060)</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 no reports of influenza virus genetic characterization.

ECDC published a [report](#) in October on detailed influenza virus characterizations conducted in September 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 85 test viruses characterized antigenically since the July 2019 characterization report were antigenically similar to the vaccine viruses used in the 2018–2019 (A/Michigan/45/2015, clade 6B.1) and 2019–2020 (A/Brisbane/02/2018, clade 6B.1A1) northern hemisphere seasons. All 613 viruses with collection dates from week 40/2018 that were genetically characterized at the WHO Collaborating Centre, including two A(H1N2) reassortants, fell in a 6B.1 subclade, designated as 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, 564 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 last characterization report, 37 A(H3N2) viruses had sufficient HA titre to allow antigenic characterization by HI assay in the presence of oseltamivir. All 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. Of the 505 viruses with collection dates from week 40/2018 that were genetically characterized at the WHO Collaborating Centre, 399 were in clade 3C.2a with many falling in subclades (43 in 3C.2a2, 17 in 3C.2a3, 8 in 3C.2a4 and 331 in 3C.2a1b) and 106 were clade 3C.3a.

### **B/Victoria viruses**

Ten B/Victoria lineage viruses have been tested by HI since the last characterization report. All recent viruses carry HA genes that fall in clade 1A but encode HA1 amino acid substitutions of I117V, N129D and V146I when compared to 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 [1A( $\Delta$ 3A)] and African [1A( $\Delta$ 3B)] origin. HI analyses with panels of post-infection ferret antisera have shown these 4 virus groups to be antigenically distinguishable. Of a total of 20 viruses genetically characterized from EU/EEA countries this season, 1 has been 1A( $\Delta$ 2) and 17 1A( $\Delta$ 3) [16 1A( $\Delta$ 3B) and 1 1A( $\Delta$ 3A) subgroup].

### **B/Yamagata viruses**

Nine B/Yamagata lineage viruses have been characterized antigenically since the last characterization report and 23 have been characterized from the 2018–2019 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 2018–2019 and 2019–2020

northern hemisphere influenza seasons, B/Phuket/3073/2013. However, all 23 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](#).

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

### **Antiviral susceptibility testing**

One A(H3N2) virus, collected in the weeks 40–45/2019 period, tested for susceptibility to neuraminidase inhibitors showed normal inhibition (NI).

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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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