

## Summary

### Week 49/2019 (2–8 December 2019)

- Influenza activity continued to increase across the region, with several countries reporting increases in intensity and geographic spread, including 2 countries with medium level intensity.
- The majority of reported influenza virus detections across the region was type A, although 6 countries reported type B virus dominance and 2 other countries co-dominance of types A and B virus.
- Data from the 23 countries or regions reporting to the [EuroMOMO](#) project indicated that all-cause mortality was at expected levels for this time of the year.

### 2019–2020 season overview

- Influenza activity is increasing in the European Region, although most countries still reported influenza activity rates below baselines or at low levels.
- Influenza activity in the European Region, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019.
- Type A viruses dominate across the European Region, although a number of countries have reported influenza type B virus dominance or co-dominance of types A and B virus.

## Primary care data

### Syndromic surveillance data

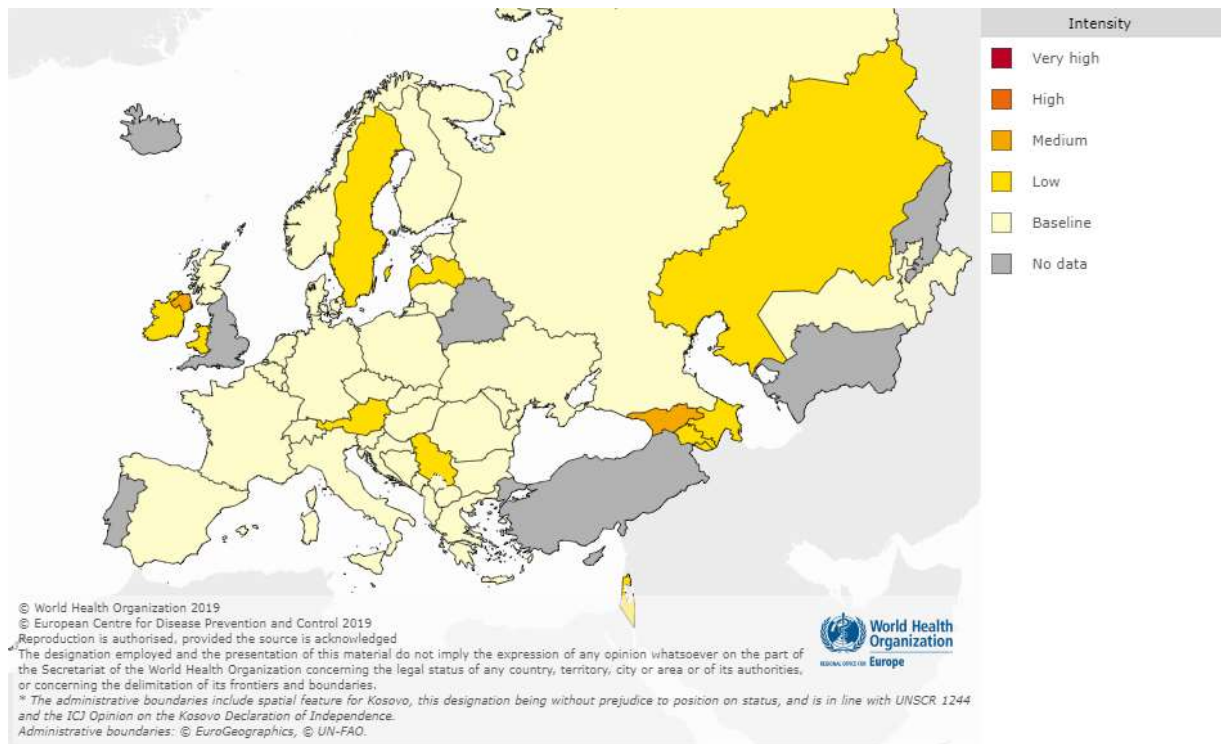
For week 49/2019, of the 34 Member States with influenza-like illness (ILI) thresholds, 6 (18%) reported ILI activity above baseline levels; 3 countries (Ireland, Latvia and United Kingdom (Northern Ireland)) were in northern and 3 (Croatia, Israel and Italy) in southern areas of the European Region. Of the 17 Member States reporting acute respiratory infection (ARI) thresholds, 1 (6%) (Armenia) reported ARI above baseline levels.

### Influenza activity

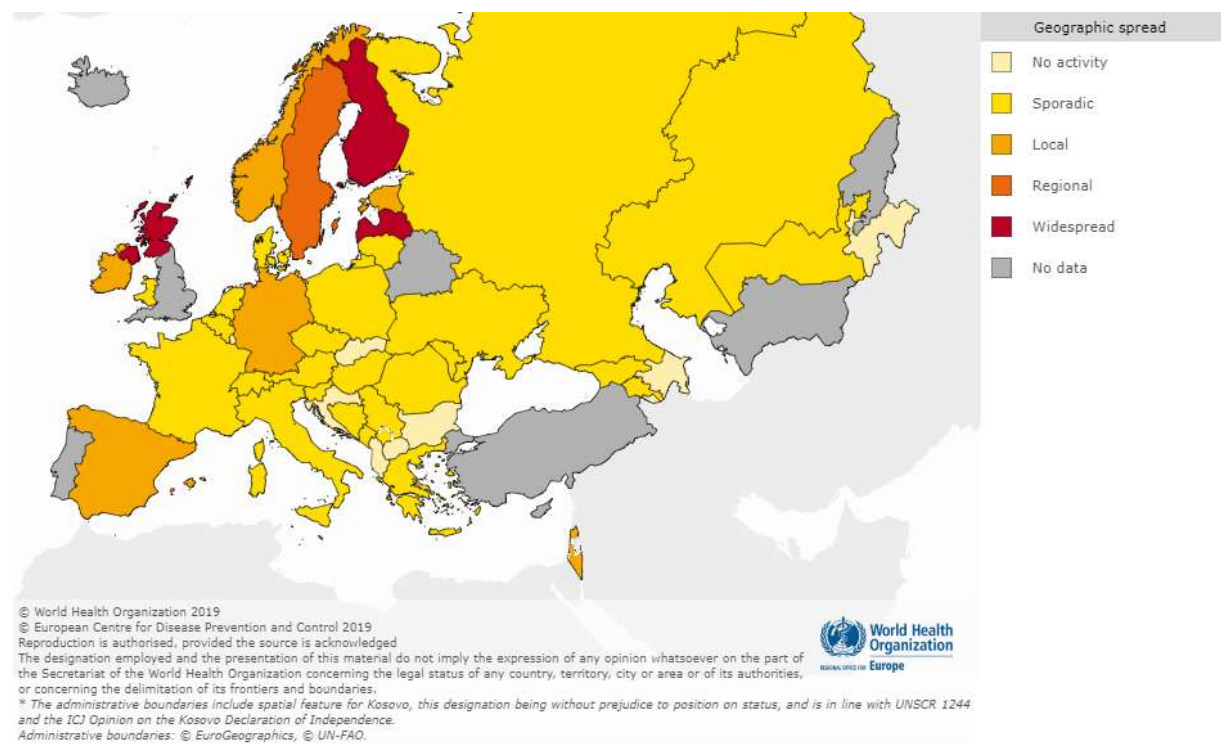
Of 46 Member States and areas reporting on intensity, 34 reported baseline levels, 10 reported low and 2 reported medium (Georgia and United Kingdom (Northern Ireland)) intensity for week 49/2019 (See Fig. 1).

Of 46 Member States and areas reporting on geographic spread, 8 reported no activity (in eastern, southern and western areas), 27 reported sporadic spread (across the region), 6 reported local spread (in northern, southern and western areas), 1 reported regional spread (Sweden) and 4 reported widespread geographic activity (Finland, Latvia and United Kingdom (Northern Ireland and Scotland)) (See Fig.2).

**Fig. 1. Intensity in the European Region, week 49/2019**



**Fig. 2. Geographic spread in the European Region, week 49/2019**



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

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

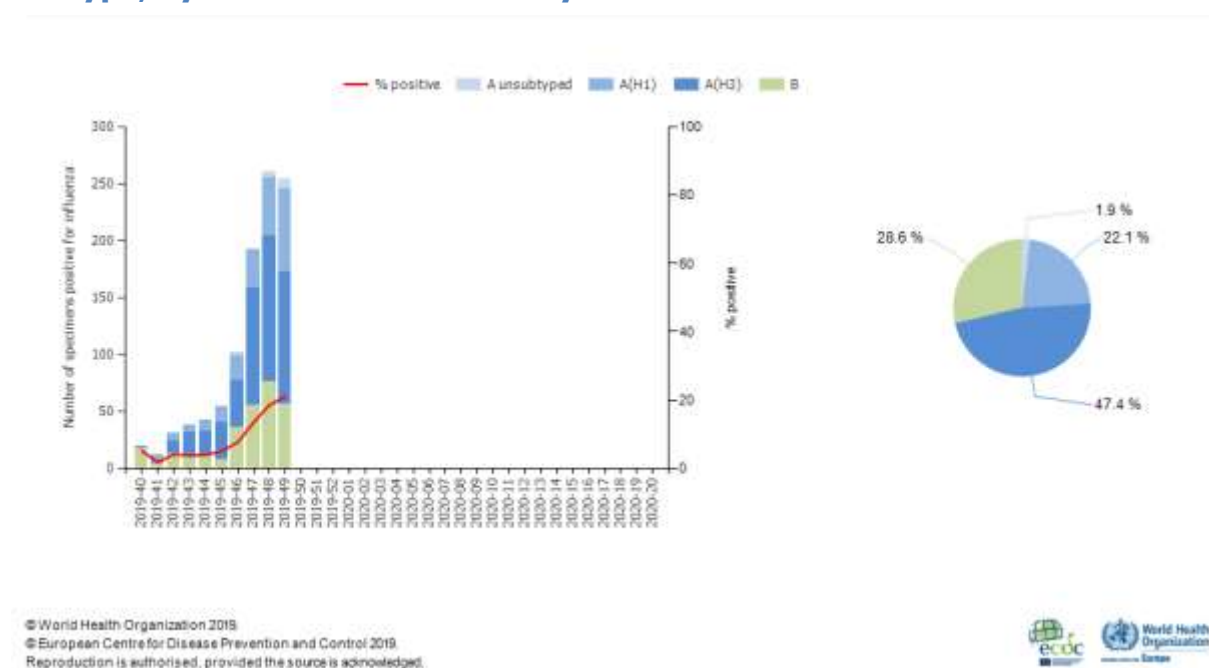
For week 49/2019, 254 (21.2%) of 1 196 sentinel specimens tested positive for an influenza virus; 78% were type A and 22% were type B (Fig. 3 and Table 1). Of 189 subtyped A viruses, 62% were A(H3N2) and 38% were A(H1N1)pdm09 (Fig. 3 and Table 1). Of 11 type B viruses ascribed to a lineage, all were B/Victoria (Table 1).

Of 25 Member States or areas across the Region that each tested at least 10 sentinel specimens in week 49/2019, 7 reported a rate of influenza virus detections above 30% (median 34%; range 31% - 44%).

For the season to date, more influenza type A (71.4%) than type B (28.6%) viruses have been detected (Fig. 3 and Table 1). Of 700 subtyped A viruses, 68% were A(H3N2) and 32% were A(H1N1)pdm09. Of 84 influenza type B viruses ascribed to a lineage, 95% were B/Victoria and 5% were 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 49/2019 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>198</b>	<b>78</b>	<b>719</b>	<b>71.4</b>
A(H1N1)pdm09	72	38.1	223	31.9
A(H3N2)	117	61.9	477	68.1
A not subtyped	9	-	19	-
<b>Influenza B</b>	<b>56</b>	<b>22</b>	<b>288</b>	<b>28.6</b>
B/Victoria lineage	11	100	80	95.2
B/Yamagata lineage	0	0	4	4.8
Unknown lineage	45	-	204	-
<b>Total detections (total tested)</b>	<b>254 (1 196)</b>	<b>21.2</b>	<b>1007 (10 231)</b>	<b>9.8</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 (5 Member States or areas, two of which have both), or 2) severe acute respiratory infection (SARI; 17 Member States and areas).

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

Among laboratory-confirmed influenza cases reported in ICUs for week 49/2019 (n=132), influenza type A viruses (n=125, 95%) were detected more frequently than influenza type B viruses (n=7, 5%).

Since week 40/2019, more influenza type A (n=360, 94%) than type B (n=23, 6%) viruses were detected. Of 103 subtyped influenza A viruses, 29% were A(H1N1)pdm09 and 71% were A(H3N2). None of the influenza B viruses have been ascribed to a lineage. Of 37 cases with known age, 46% were 15–64 years old and 43% 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 for week 49/2019 (n=66), influenza type A viruses (92%) were detected more frequently than influenza type B viruses (8%).

Since week 40/2019, more influenza type A (n=325, 93%) than type B (n=23, 7%) viruses have been detected. Of 156 subtyped influenza A viruses, 13% were A(H1N1)pdm09 and 87% were A(H3N2). None of the influenza B viruses have been ascribed to a lineage. Of 348 cases with known age, 32% were 15–64 years old and 35% were 65 years and older.

## 2. SARI surveillance

For week 49/2019, 1 001 SARI cases were reported by 13 Member States or areas. In total, specimens from 173 SARI cases were tested for influenza viruses and 16 (9%) were positive for influenza virus: 6 A(H1N1)pdm09, 1 A(H3N2) and 9 type B.

Of 8 363 SARI cases reported since week 40/2019, 8 290 had a recorded age and, of these, 58% were 0–4 years old and 21% were 15–64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=105), type B viruses were the most common (n=86, 82%). Of the 17 influenza type A virus infected cases for which subtyping was performed, 10 were A(H3N2) and 7 were A(H1N1)pdm09 viruses. Of 10 influenza type B viruses ascribed to a lineage, all were B/Victoria.

## **Mortality monitoring**

For week 49/2019, 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 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 49/2019, 3 225 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; 87% were type A and 13% were type B. Of 858 subtyped A viruses, 81% were A(H3N2) and 19% were A(H1N1)pdm09. Of 42 influenza type B viruses ascribed to a lineage, all were B/Victoria (Table 2).

For the season to date, more influenza type A (n=11 077, 87.5%) than type B (n=1 579, 13%) viruses have been detected. Of 3 020 subtyped A viruses, 19% were A(H1N1)pdm09 and 81% were A(H3N2). Of 141 influenza type B viruses ascribed to a lineage, 83% were B/Victoria and 17% B/Yamagata (Table 2).

**Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 49/2019 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>2 798</b>	<b>86.8</b>	<b>11 077</b>	<b>87.5</b>
A(H1N1)pdm09	162	18.9	585	19.4
A(H3N2)	696	81.1	2 435	80.6
A not subtyped	1 940	-	8 057	-
<b>Influenza B</b>	<b>427</b>	<b>13.2</b>	<b>1 579</b>	<b>12.5</b>
B/Victoria lineage	42	100	117	83
B/Yamagata lineage	0	0	24	17
Unknown lineage	385	-	1 438	-
<b>Total detections (total tested)</b>	<b>3 225 (19 473)</b>	<b>-</b>	<b>12 656 (146 533)</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

A total of 247 influenza viruses from weeks 40–49/2019 have been characterized genetically, 209 (85%) type A [46 A(H1N1)pdm09 and 163 A(H3N2)] and 38 (15%) type B viruses (Table 3).

While the A(H1N1)pdm09 viruses fall within subgroups of subclade 6B.1A5 that are different to that of the vaccine virus, A/Brisbane/02/2018 (6B.1A1), it is anticipated that the vaccine virus will be effective based on HI assays conducted with post-infection ferret antisera raised against the vaccine virus.

As seen elsewhere in the world, there is significant genetic diversity among circulating A(H3N2) viruses in the European region for the 2019–2020 influenza season to date, with 40% clade 3C.3a and 60% clade and subgroup 3C.2a1b (with the latter splitting between 3 designated genetic clusters), being observed. The vaccine virus, A/Kansas/14/2017, falls within clade 3C.3a and viruses within this clade induce clade-specific antibodies in ferrets, so viruses falling in other clades/subclades may be less well covered by the vaccine.

For the B/Victoria-lineage, viruses in the B/Colorado/06/2017 vaccine virus clade (1A (double del 162-163)) have been in the minority. However, there is evidence of some cross-reactivity with viruses in the 1A (triple del 162-164) clades by post-infection ferret antisera raised against the egg-propagated vaccine virus.

B/Yamagata lineage viruses have been detected in low numbers worldwide and, despite some genetic drift with associated HA amino acid substitutions, retain good reactivity with post-infection ferret antisera raised against the B/Phuket/3073/2013 vaccine virus.



**Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2019–49/2019**

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	31
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	1
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	14
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	27
A(H3) clade 3C.3a representative A/Kansas/14/2017 <sup>a</sup>	65
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	5
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	66
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017 <sup>a</sup>	2
B(Vic)-lineage clade 1A (del162-164) representative B/Hong Kong/269/2017	3
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	28
B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>b</sup>	5

<sup>a</sup> Vaccine component for 2019–2020 northern hemisphere.

<sup>b</sup> Vaccine component of quadrivalent vaccines for use in 2019–2020 northern hemisphere season.

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 with collection dates from 31 August to 31 October 2019, that have been 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 characterized 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 characterization is pending, the profiles of both viruses indicate that 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**

Since the beginning of the season, 91 viruses have been tested for susceptibility to neuraminidase inhibitors: 52 A(H3N2), 27 A(H1N1)pdm09 and 12 type B viruses. All showed normal inhibition (NI) by both 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.

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