

## Summary

### Week 2/2019 (7–13 January 2019)

- Influenza activity continued to increase in the European Region. Samples collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza-positivity rate of 42.2%.
- Influenza type A virus detections dominated with A(H1N1)pdm09 viruses being slightly more prevalent than A(H3N2). Very few influenza B viruses were detected.
- Data from the 23 Member States and areas reporting to the [EuroMOMO](#) project indicated that all-cause mortality was at expected levels for this time of year, but with a few countries starting to observe some excess mortality in elderly populations.

### 2018–2019 season overview

- Influenza activity in Europe is increasing, with both subtypes of influenza A viruses circulating widely. Countries should continue to encourage vaccination. In addition, countries are encouraged to use antivirals in accordance with national guidelines.
- The influenza A(H1N1)pdm09 viruses that have been characterized are antigenically similar to the 2018–2019 northern hemisphere influenza vaccine virus. Fewer influenza A(H3N2) viruses have been antigenically characterized. The effectiveness of vaccines in the population will be evaluated by vaccine effectiveness studies when data becomes available later in the season.

## Primary care data

### Syndromic surveillance data

For week 2/2019, of those Member States in which thresholds for influenza-like illness (ILI) consultation rates are defined, countries in eastern (n=1; Republic of Moldova), northern (n=6; Estonia, Ireland, Latvia, Lithuania, Norway and United Kingdom (England and Northern Ireland)), southern (n=4; Greece, Israel, Italy and Montenegro) and western (n=6; Hungary, Luxembourg, Netherlands, Portugal, Spain and Switzerland) areas of the European region reported activity above baseline levels.

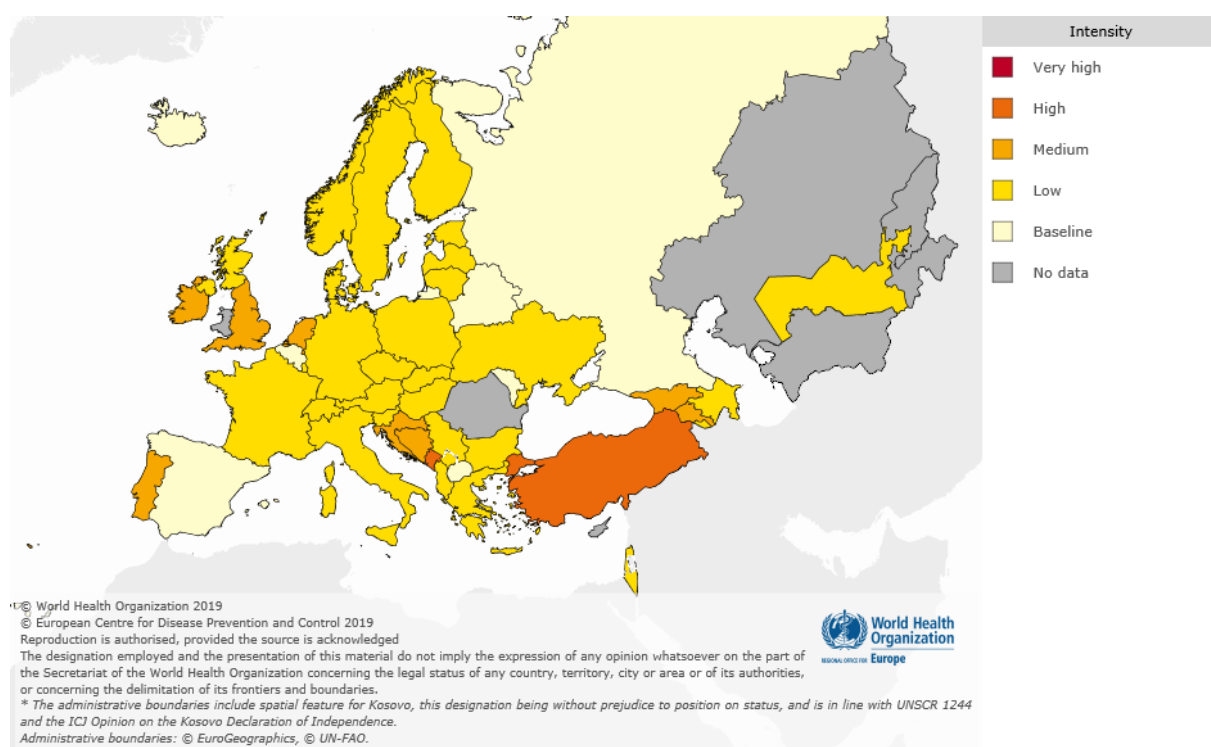
Of those Member States and areas in which thresholds for acute respiratory infection (ARI) consultation rates are defined, countries in eastern (n=1; Armenia), northern (n=1; Lithuania) and southern (n=1; Bulgaria) sectors of the European region reported activity above baseline levels.

## Influenza activity

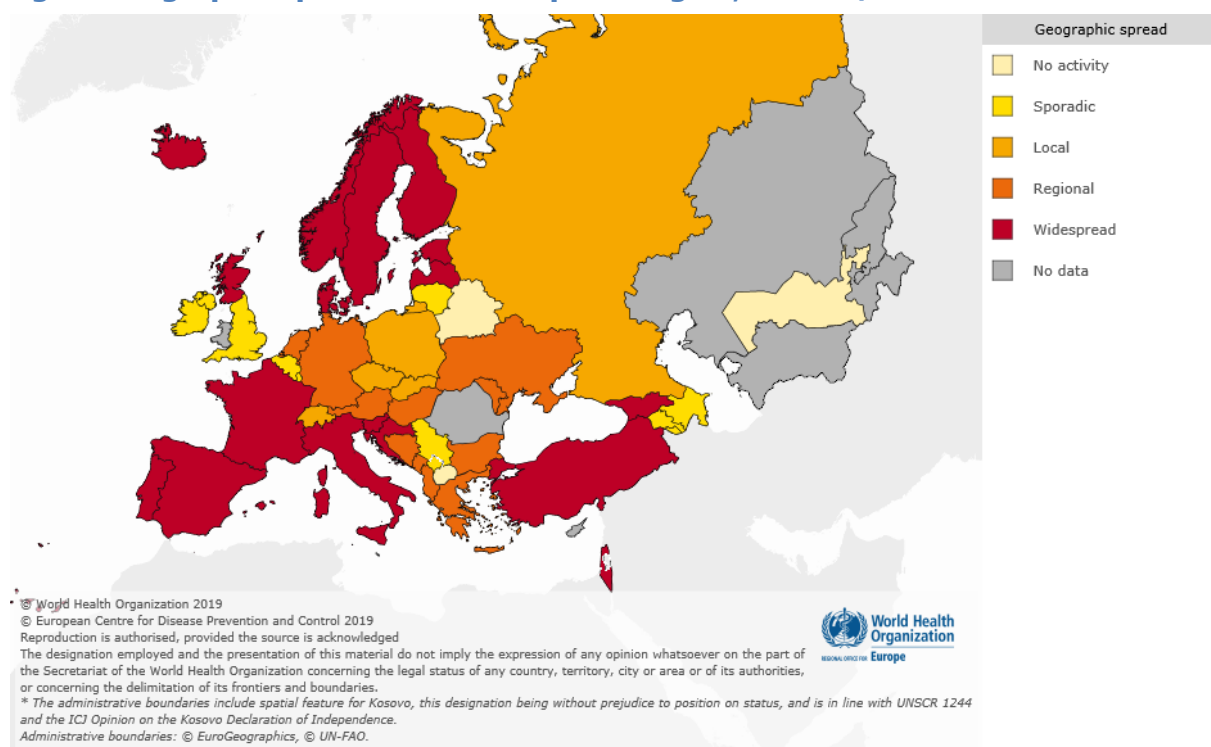
Of 46 Member States and areas reporting on the intensity of influenza activity, 7 reported baseline (across the region), 29 low (across the region), 8 medium (across the region) and 2 high (Montenegro and Turkey) intensity for week 2/2019 (Fig. 1).

Of 46 Member States and areas reporting on geographic spread, 3 reported no activity (Belarus, The Former Yugoslav Republic of Macedonia and Uzbekistan), 10 sporadic (across the region), 5 local (Czech Republic, Poland, Russian Federation, Slovakia and Switzerland), 11 regional (in eastern, southern and western areas) and 17 widespread (across the region) geographical distribution of influenza activity for week 2/2019 (Fig. 2).

**Fig. 1. Intensity in the European Region, week 2/2019**



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



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

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

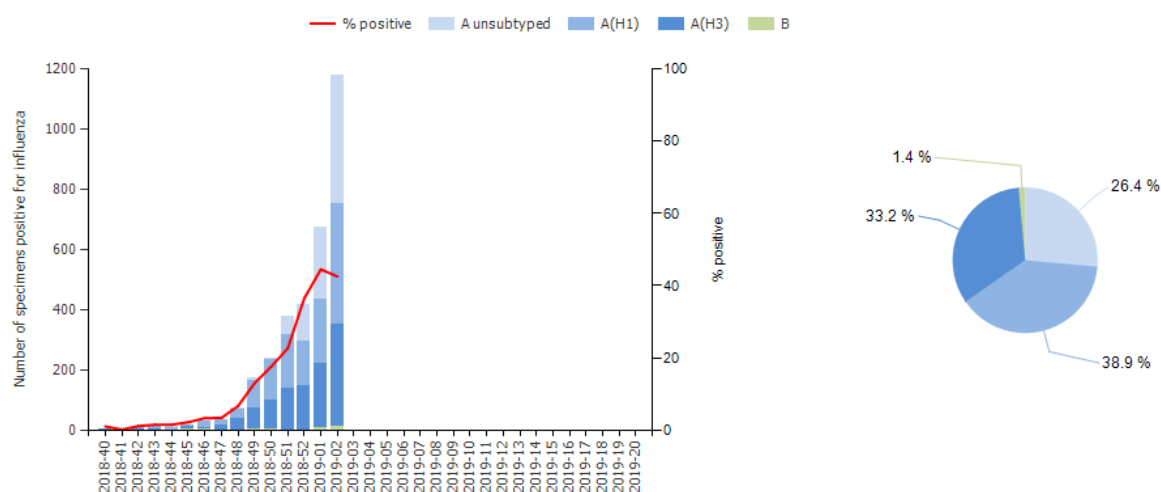
For week 2/2019, 1 177 (42.2%) of 2 788 sentinel specimens tested positive for an influenza virus; 98.8% were type A and 1.2% were type B. Of 737 subtyped A viruses, 54% were A(H1N1)pdm09 and 46% A(H3N2). All 5 type B viruses ascribed to a lineage were B/Yamagata (Fig. 3 and Table 1).

Of 38 Member States or areas across the region that each tested at least 10 sentinel specimens in week 02/2019, 22 reported a rate of influenza virus detections at or above 30% (median 51.2%; range 30.0% – 66.7%).

For the season to date, more influenza type A (n=3 196, 98.6%) than type B (n=47, 1.4%) viruses have been detected. Of 2 339 subtyped A viruses, 1 261 (53.9%) were A(H1N1)pdm09 and 1 078 (46.1%) were A(H3N2). Of 47 influenza type B viruses 17 (36.2%) were ascribed to a lineage and 14 (82.4%) were B/Yamagata (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 2/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>1 163</b>	<b>98.8</b>	<b>3 196</b>	<b>98.6</b>
A(H1N1)pdm09	398	54.0	1 261	53.9
A(H3N2)	339	46.0	1 078	46.1
A not subtyped	426	-	857	-
<b>Influenza B</b>	<b>14</b>	<b>1.2</b>	<b>47</b>	<b>1.4</b>
B/Victoria lineage	0	0.0	3	17.6
B/Yamagata lineage	5	100.0	14	82.4
Unknown lineage	9	-	30	-
<b>Total detections (total tested)</b>	<b>1 177 (2 788)</b>	<b>42.2</b>	<b>3 243 (16 371)</b>	<b>19.8</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 (12 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infections (SARI; 17 Member States or areas).

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

Among laboratory-confirmed influenza cases (n=321) reported in ICUs in week 2/2019, influenza type A viruses (n=319, 99.4%) were detected more frequently than influenza type B viruses (n=2, 0.6%).

Since week 40/2018, more influenza type A (n=1 338, 98.0%) than type B (n=27, 2.0%) viruses were detected. Of 531 subtyped influenza A viruses, 448 (84.4%) were A(H1N1)pdm09 and 83 (15.6%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 433 cases with known age, 48.0% were 15–64 years old and 42.7% were 65 years and older.

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

Laboratory-confirmed influenza cases reported in wards other than ICUs (n=172) in week 2/2019 were all infected with influenza type A viruses.

Since week 40/2018, more influenza type A (n=1 309, 98.1%) than type B (n=25, 1.9%) viruses were detected. Of 314 subtyped influenza A viruses, 226 (72.0%) were A(H1N1)pdm09 and 88 (28.0%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 334 cases with known age, 41.0% were 15–64 years old and 35.7% were 65 years and older.

## 2. SARI surveillance

For week 2/2019, 848 SARI cases were reported by 13 Member States or areas. Of 423 specimens tested for influenza viruses, 133 (31.4%) were positive and all were type A.

Of 15 577 SARI cases reported since week 40/2018, 15 564 had a recorded age and, of these, 65.5% were 0–4 years old, 18.5% were 15–64 years old and 16.0% were 65 years and older. For SARI cases testing positive for influenza viruses since week 40/2018 (n=596), type A viruses were the most common (99.8%). Of the 587 influenza type A infected cases for which subtyping was performed, 486 (82.8%) were infected by A(H1N1)pdm09 viruses and 101 (17.2%) by A(H3N2) viruses. The 1 influenza type B virus was not ascribed to a lineage.

## **Mortality monitoring**

For week 2/2019, the [EuroMOMO](#) project received data from 23 Member States or areas that were included in pooled analyses. The pooled estimates of all-cause mortality showed expected levels for this time of year in the participating countries. However, a few countries were starting to observe some excess mortality in elderly populations.

## **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 2/2019, 6 981 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; 6 901 (98.9%) were type A and 80 (1.1%) type B. Of 1 997 subtyped A viruses, 1 379 (69.1%) were A(H1N1)pdm09 and 618 (30.9%) were A(H3N2). Of 2 type B viruses ascribed to a lineage, 1 was Victoria lineage and 1 was Yamagata lineage (Fig. 3 and Table 1).

For the season so far, a substantially greater number of influenza type A (n=23 597, 98.0%) than type B viruses (n=472, 2.0%) has been detected. Of 7 761 subtyped A viruses, 5 406 (69.7%) were A(H1N1)pdm09 and 2 355 (30.3%) were A(H3N2). Of 17 influenza type B viruses ascribed to a lineage, 10 (58.8%) were B/Yamagata and 7 (41.2%) were B/Victoria; 455 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 2/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>6 901</b>	<b>98.9</b>	<b>23 597</b>	<b>98</b>
A(H1N1)pdm09	1 379	69.1	5 406	69.7
A(H3N2)	618	30.9	2 355	30.3
A not subtyped	4 904	-	15 836	-
<b>Influenza B</b>	<b>80</b>	<b>1.1</b>	<b>472</b>	<b>2</b>
B/Victoria lineage	1	50.0	7	41.2
B/Yamagata lineage	1	50.0	10	58.8
Unknown lineage	78	-	455	-
<b>Total detections (total tested)</b>	<b>6 981 (29 524)</b>		<b>24 069 (257 576)</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 and antigenic 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 339 viruses have been reported.

Of the genetically characterized viruses 220 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 117 were A(H3) viruses, with 78 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 6 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 7 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 23 to the A/England/538/2018 (3C.3a) clade and 3 attributed to a subgroup not listed. 1 B/Yamagata lineage virus was characterized as belonging to the B/Phuket/3073/2013 clade (clade 3) and

1 B/Victoria lineage virus was characterized as belonging to the B/Brisbane/60/2008 clade (clade 1A) (Table 3).

**Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–2/2019**

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 <sup>a</sup>	220
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	78
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup <sup>b</sup>	6
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	7
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	23
A(H3) attributed to recognized group in current guidance but not listed here	3
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>c</sup>	1

<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.

Very few influenza viruses have been antigenically characterized to date. The latest characterization data that includes antigenic characterization data by the WHO Collaborating Centre (CC) in London are summarized in the [ECDC summary report for November](#).

For more information on virus characterizations for EU/EEA countries, see earlier [WHO CC London Influenza virus characterisation reports](#).

The recommended composition of the trivalent influenza vaccine for the 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](#). A comment by ECDC can be seen [here](#).

On 27 September 2018, WHO announced the recommended vaccine composition for the southern hemisphere 2019 season. The recommendations matched the A(H1N1)pdm09 and B components for the 2018–2019 northern hemisphere season, but the A(H3N2) component was changed for egg-based vaccines. The full report can be found [here](#).

The northern hemisphere Vaccine Composition Meeting for 2019–2020 has been planned for 18–20 February 2019 in Beijing, China. More information can be found [here](#).

## Antiviral susceptibility testing

176 A(H1N1)pdm09, 427 A(H3N2), and 3 type B viruses since week 40/2018 have been tested for susceptibility to neuraminidase inhibitors. 1 A(H1N1)pdm09 and 1 B virus showed evidence of reduced inhibition by neuraminidase inhibitors.

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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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