

## Summary

### Week 4/2019 (21–27 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 51.3%.
- Influenza type A virus detections dominated with A(H1N1)pdm09 viruses and A(H3N2) viruses co-circulating. Very few influenza B viruses were detected.
- Pooled data from 23 Member States and areas reporting to the [EuroMOMO](#) project indicated excess mortality in adults and elderly populations overall. However, this result was driven by data from only a few countries.

### 2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018 and has increased continuously into week 4/2019. Both subtypes of influenza A viruses are circulating widely, with either A(H1N1)pdm09 or A(H3N2) dominating in some countries, and co-circulation of the two viruses in other countries. Countries should continue to promote vaccination. In addition, countries are encouraged to use antivirals in accordance with national guidelines.
- In general, current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. [Preliminary results](#) from Canada where the predominate circulating viruses are influenza A(H1N1)pdm09 viruses, indicate good vaccine effectiveness. These results are supported by recent preliminary vaccine effectiveness [results](#) from Hong Kong, where the vaccine was very effective at preventing A(H1N1)pdm09 related hospitalizations in children.

## Primary care data

### Syndromic surveillance data

For week 4/2019, 22 (69%) of the 32 Member States that calculated influenza-like illness (ILI) thresholds and 9 (50%) of the 18 Member States that calculated acute respiratory infection (ARI) thresholds reported activity above their baseline level.

Of those Member States in which thresholds for ILI activity are defined, the following countries in eastern (n=2; Republic of Moldova, Russian Federation), northern (n=7; Denmark, Estonia, Ireland, Latvia, Lithuania, Norway, United Kingdom (England)), southern (n=6; Greece, Israel, Italy, Montenegro, Romania, Serbia) and western (n=7; Belgium, Czech Republic, Luxembourg, Netherlands, Portugal, Spain, Switzerland) areas of the European Region reported activity above baseline levels.

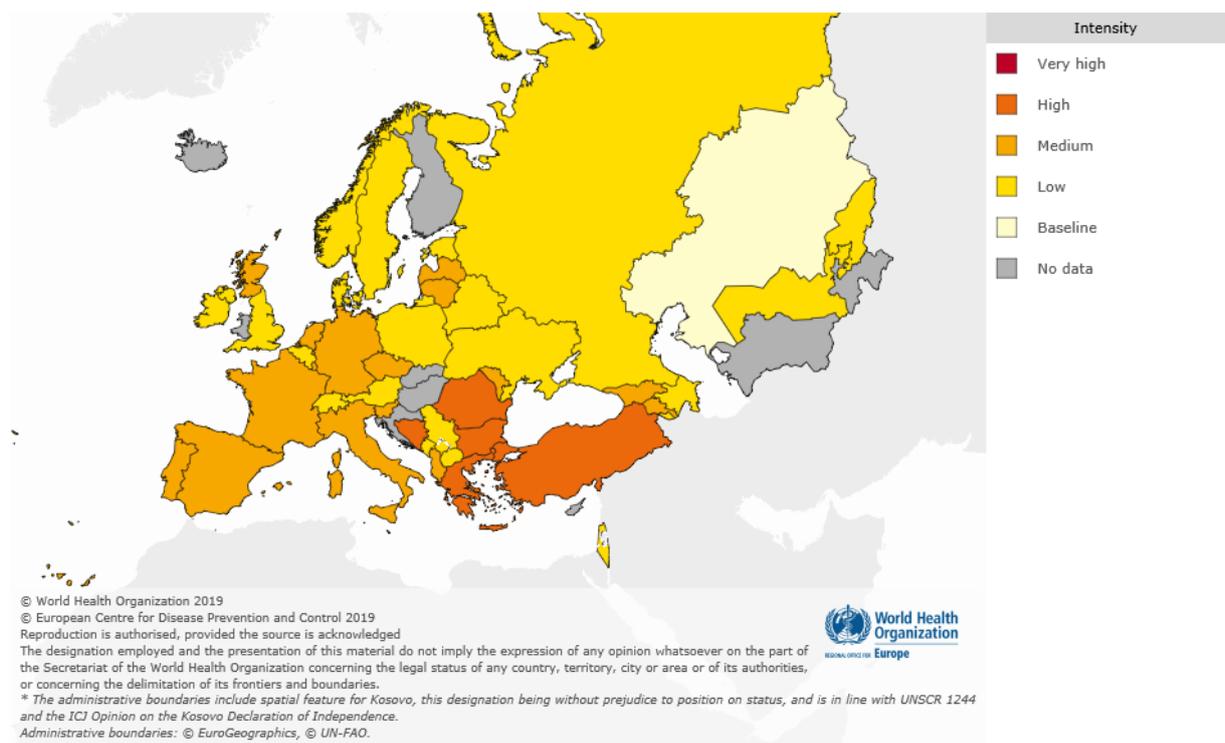
Of those Member States and areas in which thresholds for ARI activity are defined, the following countries in eastern (n=4; Armenia, Kyrgyzstan, Republic of Moldova, Russian Federation), northern (n=2; Estonia, Lithuania), southern (n=2; Albania, Bulgaria) and western (n=1; Czech Republic) areas of the European Region reported activity above baseline levels.

## Influenza activity

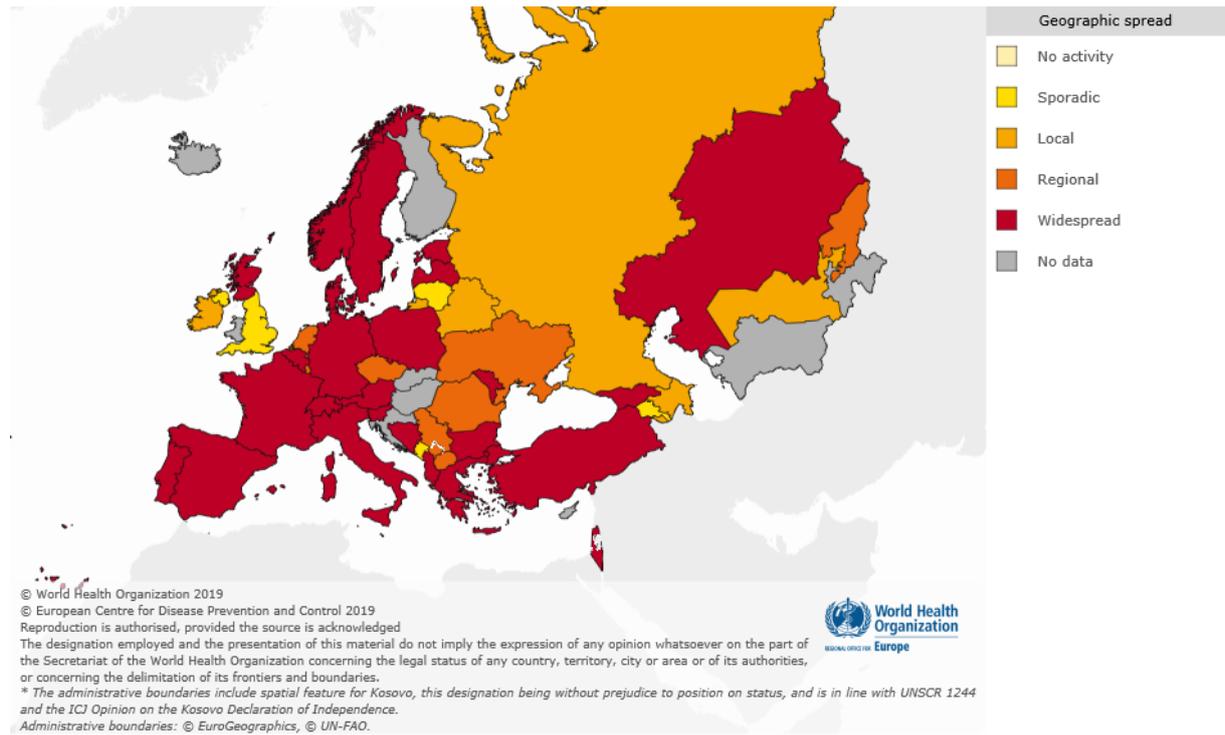
Of 45 Member States and areas reporting on intensity, 1 reported baseline (Kazakhstan), 22 reported low (across the region), 16 reported medium (across the region), and 6 reported high (southern areas) intensity for week 4/2019 (Fig. 1).

Of 45 Member States and areas reporting on geographic spread, 5 reported sporadic spread (Armenia, Lithuania, Montenegro, United Kingdom (England and Northern Ireland)), 5 reported local spread (Azerbaijan, Belarus, Ireland, Russian Federation, Uzbekistan), 9 reported regional spread (in eastern, southern, western areas) and 26 reported widespread (across the region) (Fig. 2).

**Fig. 1. Intensity in the European Region, week 4/2019**



**Fig. 2. Geographic spread in the European Region, week 4/2019**



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

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

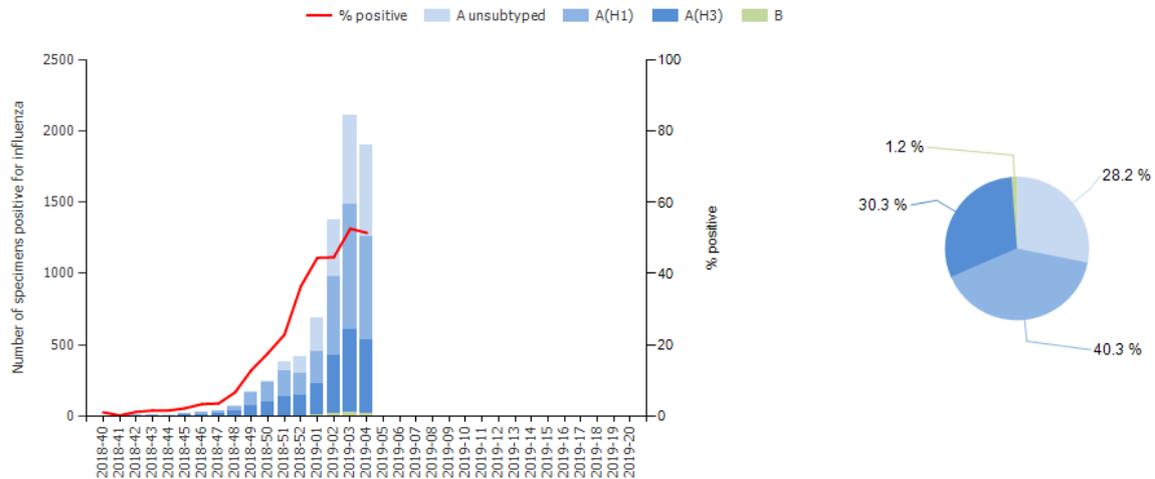
For week 4/2019, 1 899 (51.3%) of 3 704 sentinel specimens tested positive for an influenza virus; 99% were type A and 1% were type B. Of 1 235 subtyped A viruses, 58% were A(H1N1)pdm09 and 42% A(H3N2). All 5 type B viruses ascribed to a lineage were B/Yamagata (Fig. 3 and Table 1).

Of 38 Member States or areas across the region that each tested at least 10 sentinel specimens in week 4/2019, 31 reported rates of influenza virus detections above 30% (median 52.8%; range 33.0% to 73.2%).

For the season to date, more influenza type A (n=7 377, 98.8%) than type B (n=92, 1.2%) viruses have been detected. Of 5 274 subtyped A viruses, 3 013 (57.1%) were A(H1N1)pdm09 and 2 261 (42.9%) were A(H3N2). Of 92 influenza type B viruses detected, 32 (35.0%) were ascribed to a lineage and 29 (90.6%) 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 4/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>1 880</b>	<b>99.0</b>	<b>7 377</b>	<b>98.8</b>
A(H1N1)pdm09	716	58.0	3 013	57.1
A(H3N2)	519	42.0	2 261	42.9
A not subtyped	645	-	2 103	-
<b>Influenza B</b>	<b>19</b>	<b>1.0</b>	<b>92</b>	<b>1.2</b>
B/Victoria lineage	0	0.0	3	9.4
B/Yamagata lineage	5	100.0	29	90.6
Unknown lineage	14	-	60	-
<b>Total detections (total tested)</b>	<b>1 899 (3 704)</b>	<b>51.3</b>	<b>7 469 (24 534)</b>	<b>30.4</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 (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

All laboratory-confirmed influenza cases in ICUs reported for week 4/2019 (n=439) were infected with influenza type A viruses.

Since week 40/2018, more influenza type A (n=2 578, 98.8%) than type B (n=32, 1.2%) viruses were detected. Of 1 010 subtyped influenza A viruses, 811 (80.3%) were A(H1N1)pdm09 and 199 (19.7%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 062 cases with known age, 48.8% were 15–64 years old and 42.3% 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 in week 4/2019 (n=481), influenza type A viruses (n=478, 99.4%) were detected more frequently than influenza type B viruses (n=3, 0.6%).

Cumulatively since week 40/2018, more influenza type A (n=3 203, 98.9%) than type B (n=37, 1.1%) viruses were detected. Of 807 subtyped influenza A viruses, 573 (71.0%) were A(H1N1)pdm09 and 234 (29.0%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 3 240 cases with known age, 39% were 15–64 years old and 37.4% were 65 years and older.

## 2. SARI surveillance

For week 4/2019, 2 413 SARI cases were reported by 16 Member States or areas. Of 623 specimens tested for influenza viruses, 284 (45.6%) were positive. Of these, 283 were influenza type A and only one was type B.

Of 21 938 SARI cases reported since week 40/2018, 21 514 had a recorded age and, of these, 62.7% were 0–4 years old and 20.3% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=1 242), type A viruses were the most common (99.7%). Of the 1 186 influenza type A infected cases for which subtyping was performed, 935 (78.8%) were infected by A(H1N1)pdm09 viruses and 251 (21.2%) were infected by A(H3N2) viruses.

## **Mortality monitoring**

For week 4/2019, 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 elevated levels for this time of year in adults and elderly populations. However, these trends appeared to be driven by a few of the Member States.

## **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 4/2019, 13 151 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; 13 074 (99.4%) were type A and 77 (0.6%) type B. Of 4 010 subtyped A viruses, 2 707 (67.5%) were A(H1N1)pdm09 and 1 304 (32.5%) were A(H3N2). The 1 influenza B virus ascribed to a lineage was B/Victoria (Table 2).

For the season so far, a substantially greater number of influenza type A (n=49 314, 98.7%) than type B viruses (n=660, 1.3%) has been detected. Of 16 561 subtyped A viruses, 11 238 (67.9%) were A(H1N1)pdm09 and 5 232 (32.1%) were A(H3N2). Of 23 influenza type B viruses ascribed to a lineage, 14 (60.9%) were B/Yamagata and 9 (39.1%) were B/Victoria; 637 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 4/2019 and cumulatively**

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>13 074</b>	<b>99.4</b>	<b>49 314</b>	<b>98.7</b>
A(H1N1)pdm09	2 707	67.5	11 238	67.9
A(H3N2)	1 303	32.5	5 323	32.1
A not subtyped	9 064	-	32 753	-
<b>Influenza B</b>	<b>77</b>	<b>0.6</b>	<b>660</b>	<b>1.3</b>
B/Victoria lineage	1	100	9	39.1
B/Yamagata lineage	0	0	14	60.9
Unknown lineage	76	-	637	-
<b>Total detections (total tested)</b>	<b>13 151 (36 825)</b>	<b>35.7</b>	<b>49 974 (336 862)</b>	<b>14.8</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 1 158 viruses have been reported by the network laboratories.

Of the genetically characterized viruses 684 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 457 were A(H3) viruses, with 283 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 31 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 14 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 62 to the A/England/538/2018 (3C.3a) clade, 37 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 1 to the A/Hong Kong/4801/2014 (3C.2a) clade, 3 attributed to a subgroup not listed, and 26

not attributed to a clade. Of the 17 genetically characterized influenza B viruses, 9 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 8 B/Victoria viruses characterized, 1 was not attributed to a clade. All others belonged to the B/Brisbane/60/2008 clade (clade 1A), but 2 fell in a subclade with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 3 fell in a subclade with a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

**Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–4/2019**

Phylogenetic group	Number of viruses
A(H1N1)pdm09 group 6B.1 representative A/Michigan/45/2015 <sup>a</sup>	684
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	283
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup <sup>b</sup>	31
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	14
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	62
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup	37
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	1
A(H3) attributed to recognized group in current guidance but not listed here	3
A(H3) not attributed to a clade	26
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	2
B(Vic)-lineage clade 1A representative B/Colorado/06/2017	2
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	3
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>c</sup>	9

<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.

A summary of recent antigenic characterization data for type A influenza viruses from the WHO collaborating centres in the WHO Global Influenza Surveillance and Response System (GISRS) is given below. A summary for influenza type B viruses is not included as very low numbers have been detected globally.

### **A(H1N1)pdm09 Viruses**

The great majority of A(H1N1)pdm09 viruses characterized so far were antigenically similar to the vaccine virus for use in the 2018-2019 northern hemisphere and 2019 southern hemisphere influenza seasons, A/Michigan/45/2015 (clade 6B.1), as assessed in HI assays using post-infection ferret antisera.

### **A(H3N2) Viruses**

Antigenic characterization of A(H3N2) viruses remains technically difficult, requiring the use of modified HI and/or virus neutralization assays for analysis. In virus neutralization assays or HI assays using post-infection ferret antisera, the majority of recent A(H3N2) viruses have shown similarity to cell culture-propagated A/Singapore/INFIMH-16-0019/2016 (subclade 3C.2a1) vaccine virus.

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](#). The majority of influenza vaccines used in Europe are egg-based.

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

454 A(H1N1)pdm09, 260 A(H3N2), and 12 type B viruses with collection dates since week 40/2018 have been tested for susceptibility to neuraminidase inhibitors. 7 A(H1N1)pdm09, 1 A(H3N2) and 3 type B viruses 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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