

Summary

Week 10/2019 (4–10 March 2019)

- Influenza activity was widespread in the European Region. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 42.8%.
- Influenza type A virus detections dominated with slightly more A(H1N1)pdm09 than A(H3N2) viruses. Very few influenza B viruses were detected.
- 28.3% of specimens from patients with severe acute respiratory infection (SARI) collected in week 10/2019 tested positive for influenza virus, and almost all were type A.
- Pooled data from 22 Member States and areas reporting to the [EuroMOMO](#) project indicated that the excess mortality observed in previous weeks continued to decline. Excess mortality was seen in persons aged 65 years and above and, to a lesser extent, in persons 15–64 years.

2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018, exceeded 50% between weeks 3/2019 and 7/2019, and peaked in week 5/2019.
- Both influenza A virus subtypes are circulating widely, with co-circulation in some countries while others report dominance of either A(H1N1)pdm09 or A(H3N2) viruses.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 41% of influenza A viruses were subtyped; of these 72% were A(H1N1)pdm09 viruses. Among influenza virus-infected patients admitted to other wards, 35% of influenza A viruses were subtyped and 63% were A(H1N1)pdm09 viruses.
- Over 90% of influenza A viruses detected from SARI surveillance since week 40/2018 were subtyped and 81% were A(H1N1)pdm09 viruses.
- 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 vaccine effectiveness estimates continue to support the use of vaccines. Early data suggest the vaccines are effective, but estimates vary depending on the population studied and the proportions of circulating influenza A virus subtypes. See data from [a European study \(6 countries\)](#), [Canada](#), [Finland](#), [Hong Kong](#), [Sweden](#), and the [United States](#).

- On 21 February 2019, WHO published the recommendations for the influenza vaccine composition to be used in the 2019–2020 northern hemisphere season. The recommendation for type B lineages was unchanged, for A(H1N1)pdm09 it was updated, and for A(H3N2) the decision was postponed until 21 March 2019.
- A recent summary of regional activity from October 2018 to February 2019 was published in Eurosurveillance and can be found [here](#).
- Circulating viruses remain susceptible to neuraminidase inhibitors supporting use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

For week 10/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, 15 (47%) reported ILI activity above baseline levels.

These include countries in eastern areas of the European Region (n=2; Republic of Moldova, Russian Federation), northern areas (n=3; Iceland, Latvia, Norway), southern areas (n=3; Cyprus, Greece, Montenegro) and western areas (n=7; Belgium, Czech Republic, Luxembourg, Netherlands, Portugal, Slovakia, Switzerland).

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, 2 (11%) reported ARI above baseline levels. These were countries in the east (n=1; Armenia) and west (n=1; Slovakia) areas of the European Region.

Influenza activity

For week 10/2019, of 46 Member States and areas reporting on intensity, 1 reported high intensity (Kosovo*), 13 reported medium (northern, southern and western areas), 24 reported low intensity (across the region), and 8 reported baseline (eastern, northern, western areas) (Fig. 1).

Of 46 Member States and areas reporting on geographic spread, 20 reported widespread (in northern, southern, western areas), 13 reported regional spread (across the region), 5 reported local spread (Azerbaijan, Belarus, Russian Federation, Slovakia, Switzerland), 5 reported sporadic cases (Armenia, Hungary, Ireland, Israel, United Kingdom (Northern Ireland)), and 3 reported no activity (Bulgaria, Cyprus, Uzbekistan) (Fig. 2).

* This designation is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

Fig. 1. Intensity in the European Region, week 10/2019

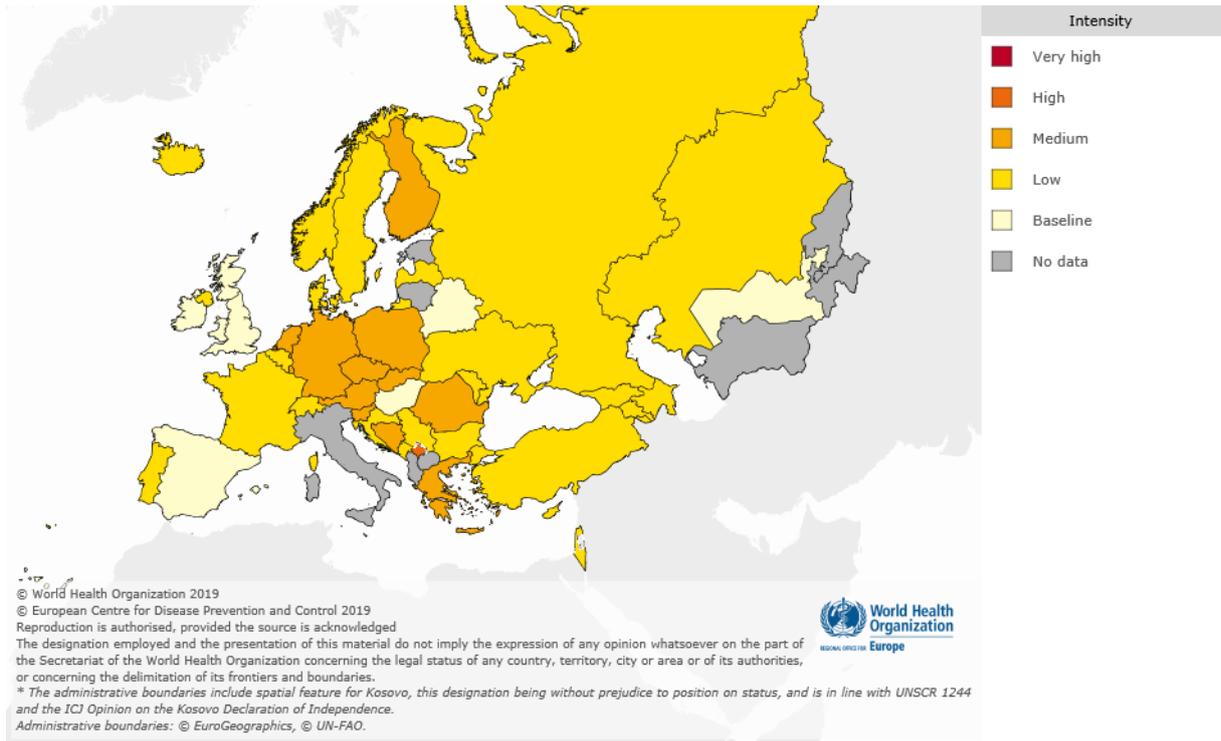
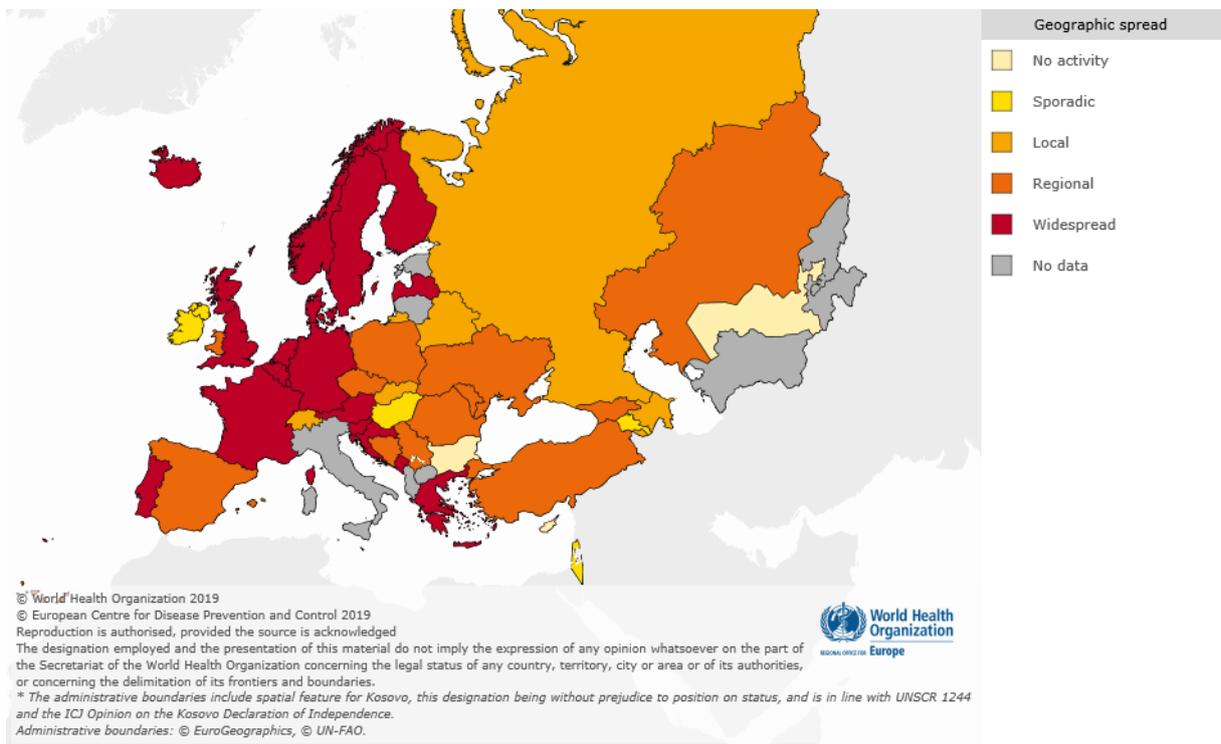


Fig. 2. Geographic spread in the European Region, week 10/2019



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

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

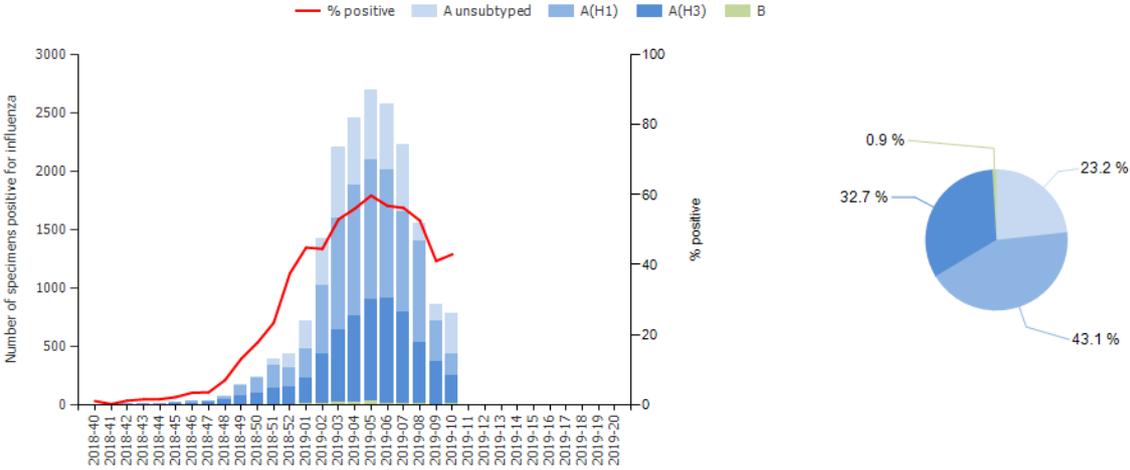
For week 10/2019, 786 (42.8%) of 1 836 sentinel specimens tested positive for an influenza virus; 774 were type A and 12 were type B. Of 425 subtyped A viruses, 44.5% were A(H1N1)pdm09 and 55.5% were A(H3N2). Of 3 type B viruses ascribed to a lineage, all were Yamagata lineage (Fig. 3 and Table 1).

Of 33 countries or areas across the region that each tested at least 10 sentinel specimens in week 10/2019, 22 reported a proportion of influenza virus detections above 30% (median 40.9%; range 30.3% – 73.1%).

For the season to date, almost all viruses detected were influenza type A (n=18 753, 99.1%) with type B accounting for only 0.9% of detections (n=171). Of 14 358 subtyped A viruses, 8 163 (56.9%) were A(H1N1)pdm09 and 6 195 (43.1%) were A(H3N2). Of 55 influenza type B viruses ascribed to a lineage, 85.5% were B/Yamagata (67.8% of type B viruses were reported without a lineage) (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 ^a



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 10/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	774	98.5	18 753	99.1
A(H1N1)pdm09	189	44.5	8 163	56.9
A(H3N2)	236	55.5	6 195	43.1
A not subtyped	349	-	4 395	-
Influenza B	12	1.5	171	0.9
B/Victoria lineage	0	0	8	14.5
B/Yamagata lineage	3	100	47	85.5
Unknown lineage	9	-	116	-
Total detections (total tested)	786 (1 836)	42.8	18 924 (45 491)	41.6

^aFor 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 reported in ICUs in week 10/2019 (n=181), influenza type A viruses (n=178, 98.3%) were detected almost exclusively.

Since week 40/2018 substantially more influenza type A (n=6 373, 99.2%) than type B viruses (n=53, 0.8%) were detected. Of 2 582 subtyped influenza A viruses, 71.9% were A(H1N1)pdm09 and 28.1% were A(H3N2). No influenza type B viruses were ascribed to a lineage. Of 3 480 cases with known age, 46.3% were 15–64 years old and 45.3% 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 10/2019 (n=138), all were influenza type A viruses.

Since week 40/2018, substantially more influenza type A (n=8 118, 99.3%) than type B viruses (n=56, 0.7%) were detected. Of 2 846 subtyped influenza A viruses, 62.9% were A(H1N1)pdm09 and 37.1% were A(H3N2). The 1 influenza type B virus ascribed to a lineage was B/Yamagata. Of 8 174 cases with known age, 44.5% were 65 years and older and 33.7% were 15–64 years old.

2. SARI surveillance

For week 10/2019, 1 185 SARI cases were reported by 13 Member States or areas. Of 276 specimens tested for influenza viruses, 28.3% were positive. Of these, influenza type A viruses (97.4%) were detected much more frequently than influenza type B viruses (2.6%).

Of 31 336 SARI cases reported since week 40/2018, 31 278 had a recorded age and, of these, 57.5% were 0–4 years old and 24.0% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 527), almost all were type A viruses (99.6%). Of the 2 283 influenza type A virus-infected cases for which subtyping was performed, 80.9% were infected by A(H1N1)pdm09 viruses and 19.1% by A(H3N2) viruses. The 1 influenza type B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 10/2019, the [EuroMOMO](#) project received data from 22 countries or areas that were included in pooled analyses. The pooled estimates indicated that the excess mortality among persons aged 15–64 years and 65 years and older observed in recent weeks has continued to decline.

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 10/2019, 7 574 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; 98.7% were type A and 1.3% were type B. Of 2 418 subtyped A viruses, 48.4% were A(H1N1)pdm09 and 51.6% were A(H3N2) (Table 2).

For the season to date, more influenza type A (n=155 132, 99.2%) than type B viruses (n=1 211, 0.8%) have been detected. Of 51 388 subtyped A viruses, 31 708 (61.7%) were A(H1N1)pdm09 and 19 680 (38.3%) were A(H3N2). Of 40 influenza type B viruses ascribed to a lineage, 47.5% were B/Yamagata (96.7% of 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 10/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	7 478	98.7	155 132	99.2
A(H1N1)pdm09	1 170	48.4	31 708	61.7
A(H3N2)	1 248	51.6	19 680	38.3
A not subtyped	5 060	-	103 744	-
Influenza B	96	1.3	1 211	0.8
B/Victoria lineage	0	-	21	52.5
B/Yamagata lineage	0	-	19	47.5
Unknown lineage	96	-	1 171	-
Total detections (total tested)	7 574 (30 910)		156 343 (620 150)	

^a 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 characterization

Genetic 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 2 098 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 159 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade with a further 3 attributed to a subgroup not listed; 897 were A(H3) viruses, with 595 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 45 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 17 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 157 to the A/England/538/2018 (3C.3a) clade, 46 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 4 to the A/Hong Kong/4801/2014 (3C.2a) clade, 7 attributed to a subgroup not listed, and 26 not attributed to a clade.

Of the 39 genetically characterized influenza B viruses, 21 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 18 B/Victoria viruses characterized, 1 was not attributed to a clade. The remaining 17 belonged to clade 1A (represented by B/Brisbane/60/2008), but 5 fell in a subclade with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 9 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 40/2018–10/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	1 159
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	3
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	595
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	45
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	17
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	157
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup ^d	46
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	4
A(H3) not attributed to clade	26
A(H3) attributed to recognized group in current guidance but not listed here	7
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	3
B(Vic)-lineage clade 1A representative B/Colorado/06/2017 ^a	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	9
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	21

^a Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^b Vaccine component for 2019 southern hemisphere season.

^c Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^d Vaccine component for 2018-2019 northern hemisphere season

Vaccine composition

The recommended composition of the trivalent influenza vaccine for the current 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](#).

On 21 February 2019, WHO published the recommendations for quadrivalent vaccines for use in the 2019–2020 northern hemisphere influenza season to contain the following:

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;
- an A(H3N2) virus to be announced on 21 March 2019*;
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).

* In light of recent changes in the proportions of genetically and antigenically diverse A(H3N2) viruses, the recommendation for the A(H3N2) component has been postponed.

It is 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 a "Frequently Asked Questions" document are available on the WHO website at:

http://www.who.int/influenza/vaccines/virus/recommendations/2019_20_north/en/

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 1 353 viruses with collection dates since week 40/2018 [899 A(H1N1)pdm09, 435 A(H3N2), and 19 type B]. 6 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 2 of them were confirmed by phenotypic testing. 1 A(H3N2) virus showed evidence of reduced inhibition (RI) by oseltamivir only. 1 type B virus showed evidence of RI by zanamivir only.

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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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