

Summary

Week 13/2019 (25–31 March 2019)

- Of 45 countries reporting on geographic spread, 11, located in northern, southern, and western areas of the European Region, reported widespread activity. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 32%, a decrease for the third week in a row.
- Of 45 countries reporting on influenza activity, 42 reported baseline or low intensity levels and none reported high intensity.
- Influenza type A virus detections dominated with more A(H3N2) than A(H1N1)pdm09 viruses among sentinel and non-sentinel source specimens. Very few influenza B viruses were detected.
- Of the specimens from patients with severe acute respiratory infection (SARI) collected in week 13/2019 that were tested for influenza viruses, 33% were positive and all viruses were type A.
- Pooled data from 22 Member States and areas reporting to the [EuroMOMO](#) project indicated that the all-cause excess mortality observed in previous weeks has returned to normal levels.

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 have circulated, with co-circulation in some countries while others reported dominance of either A(H1N1)pdm09 or A(H3N2) viruses.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 99% were infected with type A viruses, and of those subtyped, 69% were A(H1N1)pdm09. Among influenza virus-infected patients admitted to other wards, 99% were infected with type A viruses, with 58% of those subtyped being A(H1N1)pdm09.
- Of the patient specimens from SARI surveillance that tested positive for influenza, 99% were infected with influenza type A virus, with 80% of those subtyped being A(H1N1)pdm09.
- A recent summary of regional activity from October 2018 to February 2019 was published in Eurosurveillance and can be found [here](#).

- Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. For more detail, see the [Vaccine effectiveness](#) section.
- WHO has published [recommendations](#) for the composition of influenza vaccines to be used in the 2019–2020 northern hemisphere season. The recommendation was that type B lineage viruses remain unchanged, while the A(H1N1)pdm09 and A(H3N2) viruses were updated.
- Circulating viruses in the European Region remained susceptible to neuraminidase inhibitors supporting use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

For week 13/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, 3 countries (9%) reported ILI activity above baseline levels, 1 in the eastern area of the European Region (Republic of Moldova) and 2 in the northern area (Estonia and Norway).

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, only Armenia reported ARI activity above its baseline level.

Influenza activity

For week 13/2019, of 45 Member States and areas reporting on intensity, 16 countries across the region reported baseline, 26 countries low and 3 reported medium (Bosnia and Herzegovina, Luxembourg and Slovakia) intensity (Fig. 1).

Of 45 Member States and areas reporting on geographic spread, 6 reported no activity (in eastern and southern areas), 16 reported sporadic cases (across the region), 6 reported local spread (in southern and western areas), 6 reported regional spread (in eastern, northern and southern areas) and 11 reported widespread activity (in northern, southern and western areas) (Fig. 2).

Fig. 1. Intensity in the European Region, week 13/2019

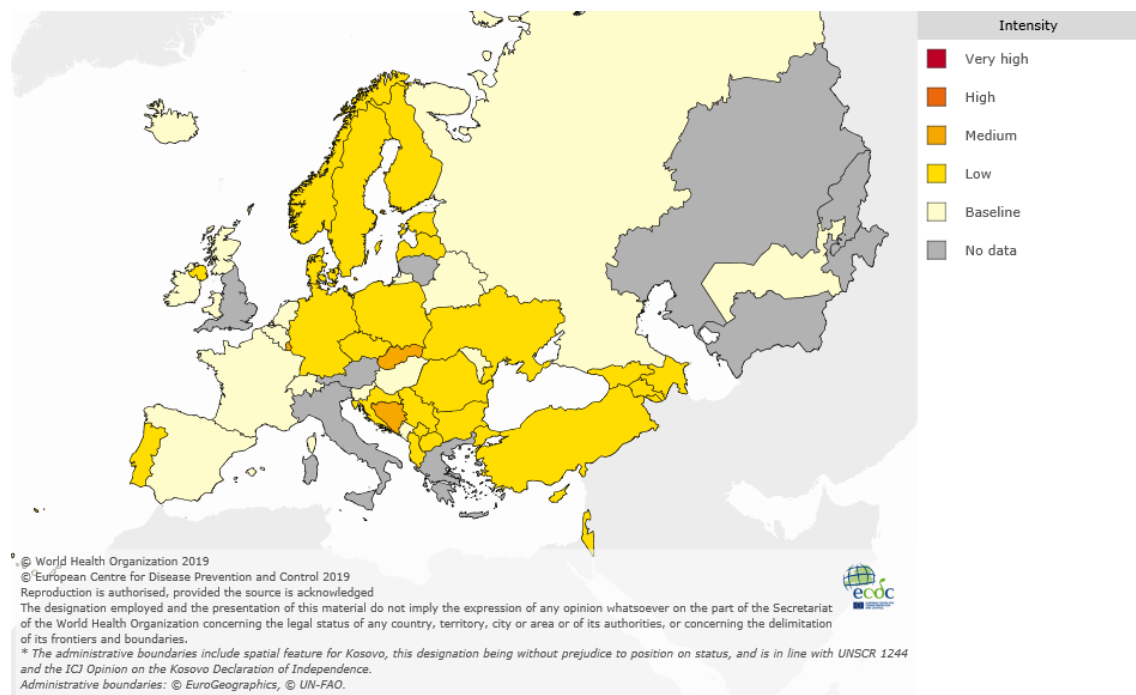
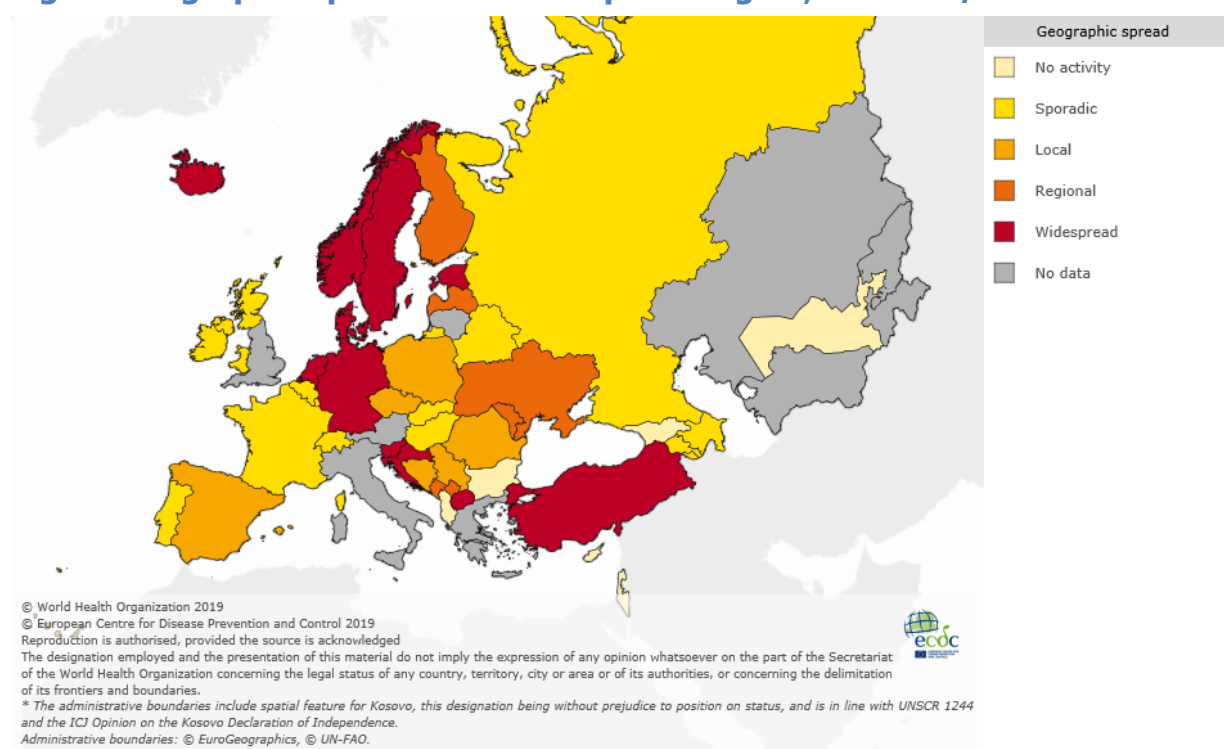


Fig. 2. Geographic spread in the European Region, week 13/2019



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

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

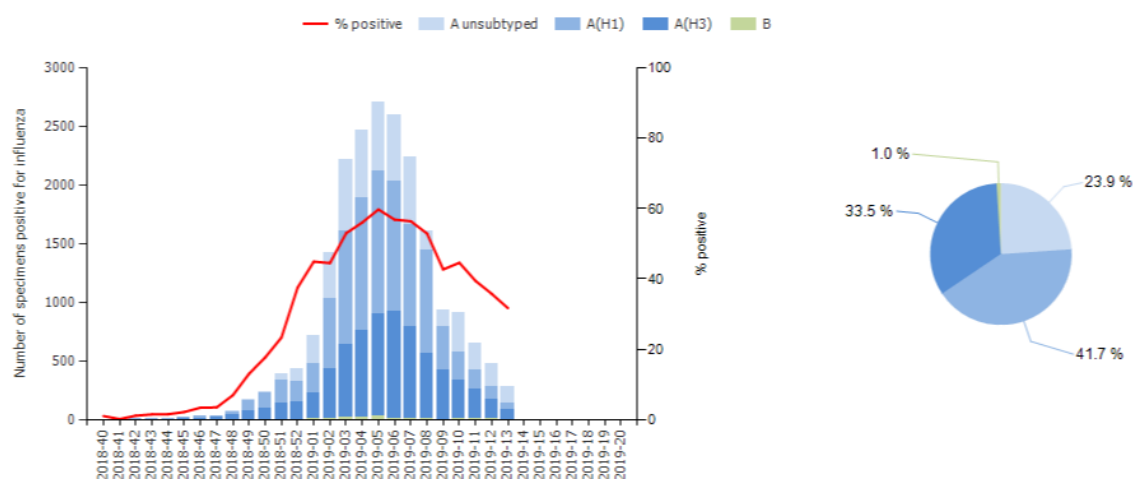
For week 13/2019, 287 (32%) of 911 sentinel specimens tested positive for an influenza virus; 283 were type A and 4 were type B. Of 138 subtyped A viruses, 38% were A(H1N1)pdm09 and 62% were A(H3N2). Only 1 type B virus was ascribed to a lineage and it was B/Yamagata (Fig. 3 and Table 1).

Of 20 countries or areas across the region that each tested at least 10 sentinel specimens in week 13/2019, 8 reported a proportion of influenza virus detections above 30% (median 44%; range 31%–60%).

For the season to date, almost all viruses detected were influenza type A (99%) with type B accounting for only 1% of detections. Of subtyped A viruses, 56% were A(H1N1)pdm09 and 44% were A(H3N2). Of influenza type B viruses ascribed to a lineage, 86% were B/Yamagata (71% 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 13/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	283	98.6	20 468	99
A(H1N1)pdm09	52	37.7	8 613	55.5
A(H3N2)	86	62.3	6 915	44.5
A not subtyped	145	-	4 940	-
Influenza B	4	1.4	200	1
B/Victoria lineage	0	0	8	13.8
B/Yamagata lineage	1	100	50	86.2
Unknown lineage	3	-	142	-
Total detections (total tested)	287 (911)	31.5	20 668 (49 920)	41.4

^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 infection (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs for week 13/2019 (n=36), all were influenza type A viruses.

Since week 40/2018 substantially more influenza type A (n=6 837, 99%) than type B viruses (n=55, 1%) were detected. Of 2 935 subtyped influenza A viruses, 69% were A(H1N1)pdm09 and 31% were A(H3N2). No influenza type B viruses were ascribed to a lineage. Of 3 842 cases with known age, 47% were 15–64 years old and 45% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

All laboratory-confirmed influenza cases reported in wards other than ICUs in week 13/2019 (n=51) were influenza type A viruses.

Since week 40/2018, substantially more influenza type A (n=9 175, 99%) than type B viruses (n=59, 1%) were detected. Of 3 559 subtyped influenza A viruses, 58% were A(H1N1)pdm09 and 42% were A(H3N2). Of 2 influenza type B virus ascribed to a lineage, 1 was B/Yamagata and 1 B/Victoria. Of 9 234 cases with known age, 46% were 65 years and older and 33% were 15–64 years old.

2. SARI surveillance

For week 13/2019, 439 SARI cases were reported by 13 Member States or areas. Of these cases, 126 specimens were tested for influenza viruses with 33% of them being positive. All detected viruses were influenza type A.

Of 35 147 SARI cases reported since week 40/2018, 35 091 had a recorded age and, of these, 58% were 0–4 years old and 24% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 752), almost all were type A viruses (99.6%). Of the 2 473 influenza type A virus-infected cases for which subtyping was performed, 80% were infected by A(H1N1)pdm09 viruses and 20% by A(H3N2) viruses. The 1 influenza type B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 13/2019, the [EuroMOMO](#) project received data from 22 countries or areas that were included in pooled analyses. The pooled estimates indicated that the all-cause excess mortality observed in previous weeks has returned to normal levels.

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 13/2019, 2 751 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; 99% were type A and 1% were type B. Of A viruses subtyped, 41% were A(H1N1)pdm09 and 59% were A(H3N2) (Table 2).

For the season to date, more influenza type A (99%) than type B viruses (1%) have been detected. Of A viruses subtyped, 60% were A(H1N1)pdm09 and 40% were A(H3N2). Of influenza type B viruses ascribed to a lineage, 42% were B/Yamagata (97% 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 13/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	2 725	99.1	171 272	99.2
A(H1N1)pdm09	413	41.5	34 192	59.8
A(H3N2)	583	58.5	22 959	40.2
A not subtyped	1 729	-	114 121	-
Influenza B	26	0.9	1 445	0.8
B/Victoria lineage	1	100	26	57.8
B/Yamagata lineage	0	0	19	42.2
Unknown lineage	25	-	1 400	-
Total detections (total tested)	2 751 (19 546)		172 717 (698 058)	

^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 and antigenic 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 2 960 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 481 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; 1 432 were A(H3) viruses, with 984 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 65 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 25 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 335 to the A/England/538/2018 (3C.3a) clade, 12 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 4 to the A/Hong Kong/4801/2014 (3C.2a) clade, and 7 attributed to a subgroup not listed.

Of the 44 genetically characterized influenza B viruses, 22 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). All 22 B/Victoria viruses characterized belonged to clade 1A (represented by B/Brisbane/60/2008); but of these, 5 fell in a subclade with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 12 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 40/2018–13/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	1 481
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	984
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	65
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	25
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	335
A(H3) clade 3c.2a1 representative A/Singapore/INFIMH-16-0019/2016 subgroup ^d	12
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	4
A(H3) attributed to recognized group in current guidance but not listed here	7
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	5
B(Vic)-lineage clade 1A representative B/Colorado/06/2017 ^a	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	12
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	22

^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

A [report](#) detailing influenza virus characterization data conducted in January and February 2019 by the WHO Collaborating Centre, London (the Francis Crick Institute), on influenza positive specimens received from EU/EEA countries, was published by the European Centre for Disease Prevention and Control. A summary is given below.

A(H1N1)pdm09 viruses

The great majority (203/204) of A(H1N1)pdm09 viruses characterized were antigenically similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1) and fell in subclade 6B.1A. Within this subclade, there has been increasing genetic diversity of the HA genes with several emerging genetic subgroups. Most viruses carried the HA1 amino acid substitution of S183P.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the previous report published in December 2018, only 33 A(H3N2) viruses have had a sufficient HA titre to allow antigenic characterization by haemagglutination inhibition (HI) assay. By HI assay, all viruses belonging to subgroups within clades 3C.2a and 3C.3a were poorly recognized by antisera raised against egg-propagated A/Singapore/INFIMH-16-0019/2016, the current vaccine virus.

B/Victoria viruses

Only 5 B/Victoria lineage viruses were characterized antigenically. Of these, 2 were antigenically similar to the current vaccine virus, B/Colorado/06/2017, which belongs to a subclade with a two amino acid deletion in HA (Δ 162-163, 1A. Δ 2). The other 3 were antigenically similar to a virus of African origin with a three amino acid deletion in HA1 (Δ 162-164, 1A. Δ 3).

B/Yamagata viruses

Only 7 B/Yamagata lineage viruses were characterized antigenically. HI analyses with post-infection ferret antisera raised against B/Phuket/3072/2013, the virus recommended for inclusion in quadrivalent vaccines for the current and subsequent northern hemisphere influenza seasons, indicated that all 7 viruses were antigenically similar to the vaccine virus.

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](#) and [here](#).

On 21 February 2019, WHO published recommendations for the components of influenza vaccines for use in the 2019–2020 northern hemisphere influenza season, and on 21 March it was updated. Vaccines should contain the following

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;
- an A/Kansas/14/2017 (H3N2)-like virus;
- 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).

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 “Frequently Asked Questions” are available for the 21 February decision and the 21 March addendum on the [WHO website](#).

Vaccine effectiveness

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 that vaccines are moderately effective, with estimates varying 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 \(China\)](#), [Sweden](#), and the [United States of America](#).

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 2 048 viruses with collection dates since week 40/2018 [1 248 A(H1N1)pdm09, 771 A(H3N2), and 29 type B]. 8 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 3 of them were confirmed by phenotypic testing. 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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