

Summary

Weeks 33–39/2019 (12 August–29 September 2019)

- Influenza activity was low, at interseasonal levels.
- Of 1 584 sentinel specimens tested for influenza virus, 11 tested positive (<1%). A similar proportion (<1%) was observed for the SARI specimens tested for influenza virus.
- This is the last summer report for the 2018–2019 influenza season. Weekly reporting will resume on 11 October 2019 for the 2019–2020 season.

2018–2019 season overview

- Influenza activity in the European Region, based on sentinel sampling, reached 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, with 66% of those subtyped being A(H1N1)pdm09. Among influenza virus-infected patients admitted to other wards, 99% were infected with type A viruses, with 54% of those subtyped being A(H1N1)pdm09.
- Of the clinical specimens from SARI surveillance that tested positive for an influenza virus, 99% were type A viruses, with 79% of those subtyped being A(H1N1)pdm09.
- A 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 details, 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. While recommendations for both type B lineages were unchanged, updated recommendations were made for both A(H1N1)pdm09 and A(H3N2) viruses.
- The vast majority of circulating viruses in the European Region were susceptible to neuraminidase inhibitors, which supports use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

Based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI), all countries reported baseline or low activity of respiratory infections.

Influenza activity

For week 39/2019, of 23 Member States and areas reporting on intensity, all reported baseline or low intensity (Fig. 1). Of 24 Member States and areas reporting on geographic spread, 19 reported no activity and 5 reported sporadic cases (Greece, Norway, Poland, Sweden and the United Kingdom (Northern Ireland and Scotland); Fig. 2).

Fig. 1. Intensity in the European Region, week 39/2019

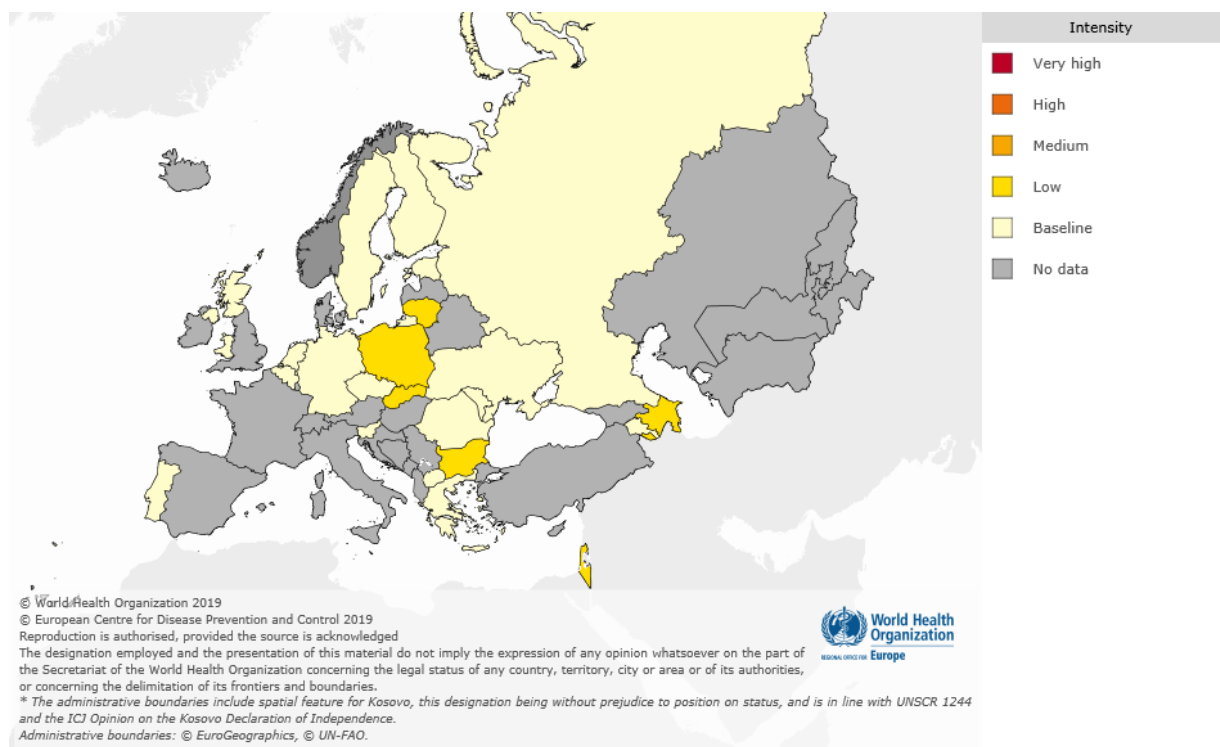
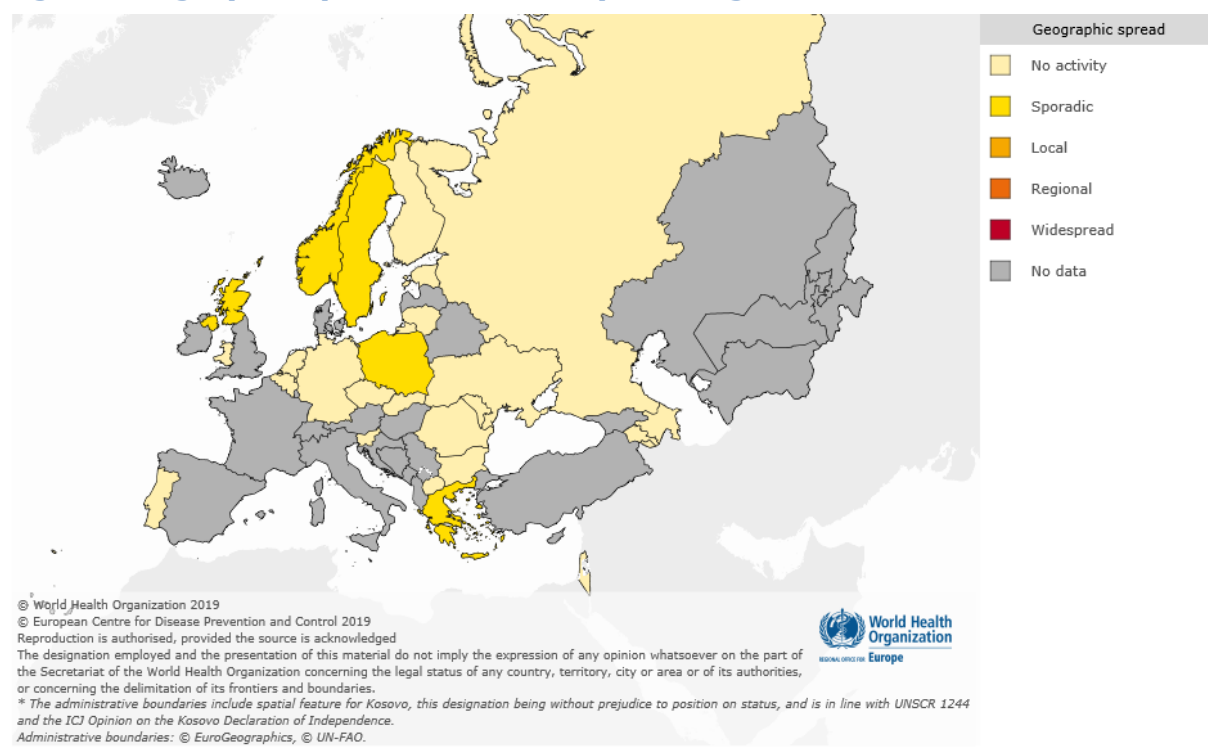


Fig. 2. Geographic spread in the European Region, week 39/2019



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

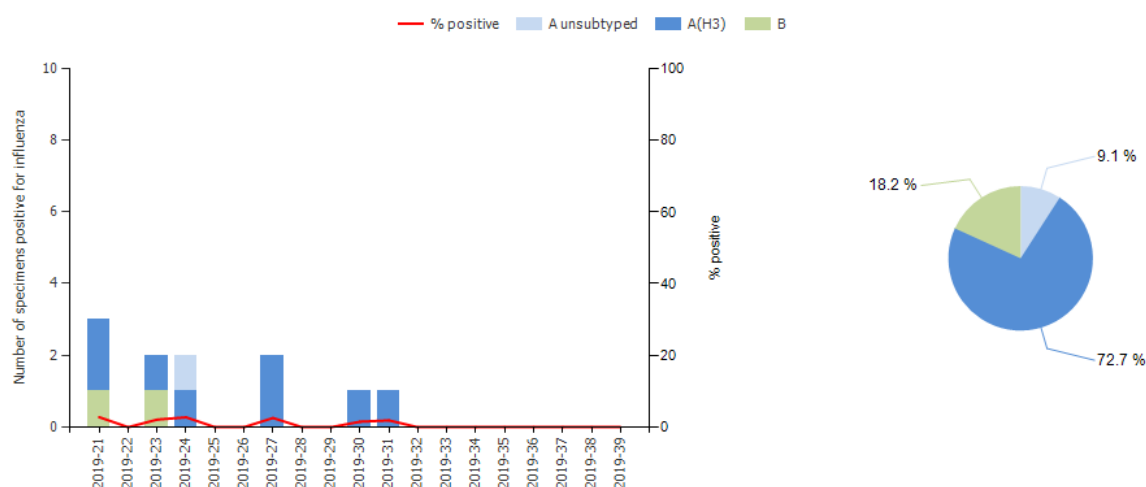
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 39/2019, no specimens from sentinel sources were reported.

For weeks 21–39/2019, 11 of 1 584 (<1%) sentinel specimens tested positive for an influenza virus; 9 were influenza type A and 2 were influenza type B (Fig. 3 and Table 1). The 8 influenza A viruses subtyped were A(H3N2) (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 for weeks 21/2019 to 39/2019^a



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, for the current week and cumulatively for weeks 21/2019 to 39/2019

	Current Week	Season 2018–2019, week 21-39
Virus type and subtype	Number	Number
Influenza A	0	9
A(H1N1)pdm09	0	0
A(H3N2)	0	8
A not subtyped	0	1
Influenza B	0	2
B/Victoria lineage	0	0
B/Yamagata lineage	0	0
Unknown lineage	0	2
Total detections (total tested)	0 (54)	11 (1584)

^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 monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (13 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

From week 21/2019 through week 39/2019, five countries (Czech Republic, Ireland, Spain, Sweden and Turkey) reported 14 laboratory-confirmed influenza cases in ICUs; 12 were infected with influenza A and 2 with influenza B viruses. Of 6 viruses subtyped, 2 were influenza A(H3N2) and 4 were influenza A(H1N1)pdm09.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 21/2019 through week 39/2019, five countries (Armenia, Czech Republic, Ireland, Spain and Turkey) reported 88 laboratory-confirmed influenza cases from other wards, of which 84 were infected with influenza A and 4 with influenza B viruses. Of 35 influenza A viruses subtyped, 28 were A(H3N2) and 7 were A(H1N1)pdm09.

2. SARI surveillance

For weeks 21–39/2019, 13 004 SARI cases were reported by 9 Member States or areas. Of these cases, 1 032 specimens were tested for influenza viruses and 9 (<1%) tested positive; 6 were infected with type B and 3 with type A viruses. All influenza A viruses were subtype A(H3N2).

Mortality monitoring

For week 39/2019, the [EuroMOMO](#) project received data from 22 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality showed mortality levels within normal expected ranges for the participating countries.

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 weeks 21–39/2019, 1 324 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; 84% were type A and 16% were type B. Of 697 A viruses subtyped, 81% were A(H3N2) (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for the current week and cumulative for weeks 21–39/2019

Virus type and subtype	Current Week		Season 2018–2019, week 21–39	
	Number	% ^a	Number	% ^a
Influenza A	38	84.4	1149	86.8
A(H1N1)pdm09	5	23.8	133	19.1
A(H3N2)	16	76.2	564	80.9
A not subtyped	17	-	452	-
Influenza B	7	15.6	175	13.2
B/Victoria lineage			23	88.5
B/Yamagata lineage			3	11.5
Unknown lineage	7	-	149	-
Total detections (total tested)	45	-	1324	-

^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

A total of 78 influenza viruses from weeks 21–39/2019 have been characterized genetically, 64 influenza type A and 14 influenza type B viruses (Table 3).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 21/2018–39/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	25
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	36
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	0
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	1
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	2
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup ^d	0
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	0
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	1
B(Vic)-lineage clade 1A representative B/Colorado/06/2017 ^a	2
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	8
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	3

^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.

Genetic data from the 2018–2019 season can be found in the FNE report from week 20/2019 (see Archives page).

ECDC published a [report](#) in September detailing influenza virus characterizations conducted in July 2019 by the WHO Collaborating Centre, London (the Francis Crick Institute), on influenza-positive specimens received from European Union/European Economic Area countries. A summary is given below.

A(H1N1)pdm09 viruses

All 103 test viruses characterized antigenically since the May 2019 characterization report were similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1) and all fell in subclade 6B.1A. Within this subclade, there has been increasing genetic diversity of the HA genes with several emerging genetic subgroups. The 539 test viruses with collection dates from week 40/2018 genetically characterized at the WHO Collaborating Centre, including an A(H1N2) reassortant, all fell in a 6B.1 subclade, designated 6B.1A, defined by HA1 amino acid substitutions of S74R, S164T and I295V. Of these recently circulating viruses, 493 also have an HA1 S183P substitution, often with additional substitutions in HA1 and/or HA2.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the May 2019 characterization report, 21 A(H3N2) viruses had sufficient HA titre to allow antigenic characterization by HI assay in the presence of oseltamivir. This virus was poorly recognized by antisera raised against the currently used clade 3C.2a1 vaccine virus, egg-propagated A/Singapore/INFIMH-16-0019/2016, in HI assays. Of the 446 viruses with collection dates from week 40/2018 genetically characterized at the WHO Collaborating Centre, 363 were clade 3C.2a (including 32 3C.2a2, 13 3C.2a3, 6 3C.2a4 and 216 3C.2a1b) and 83 were clade 3C.3a.

B/Victoria viruses

Four B/Victoria lineage virus had been tested by HI since the May 2019 characterization report. All recent viruses carry HA genes that fall in clade 1A but encode HA1 amino acid substitutions of I117V, N129D and V146I compared to a previous vaccine virus, B/Brisbane/60/2008. Groups of viruses defined by deletions of 2 (Δ 162-163, 1A(Δ 2)) or 3 (Δ 162-164, 1A(Δ 3)) amino acids in HA1 have emerged, with the triple deletion group having subgroups of Asian and African origin. HI analyses with panels of post-infection ferret antisera have shown these virus groups to be antigenically distinguishable. Of a total of 12 viruses characterized from EU/EEA countries this season, 1 has been Δ 162-163 and 11 Δ 162-164 (3 African and 1 Asian subgroup).

B/Yamagata viruses

Two B/Yamagata lineage viruses had been characterized antigenically since the May characterization report, a total of 15 had been characterized from the 2018–19 season. All had HA genes that fell into clade 3 and encoded 2 HA amino acid substitutions not present in the virus recommended for inclusion in quadrivalent vaccines for the current and subsequent northern hemisphere influenza seasons, B/Phuket/3073/2013. However, all remained

antigenically similar to the vaccine virus recommended for use in quadrivalent vaccines for the current and subsequent northern hemisphere influenza seasons.

Vaccine composition

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](#).

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;
- 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 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 WHO meeting on the composition of influenza vaccines for the 2020 southern hemisphere influenza season was held in [Geneva on 23–26 September](#).

Vaccine effectiveness

Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. 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 has not been assessed on viruses with collection dates from week 21/2019 through week 39/2019.

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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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