

Summary

Week 41/2019 (7–13 October 2019)

- Influenza activity was low throughout the European Region.
- Influenza viruses were detected sporadically in specimens from persons with respiratory illness presenting to medical care.
- Both influenza A and B type viruses were detected.
- Data from the 20 countries or regions reporting to the [EuroMOMO](#) project indicated all-cause mortality to be at expected levels for this time of the year.

2019–2020 season overview

- As is usual for this time of year, influenza activity is low in the European Region.
- The report of the [Vaccine Composition Meeting for the southern hemisphere](#) 2020 season can be found [here](#).

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 activity within their baseline levels.

Influenza activity

Of 42 Member States and areas reporting on intensity, 30 reported baseline and 12 reported low (across the Region) intensity for week 41/2019 (Fig. 1). Of 42 Member States and areas reporting on geographic spread, 31 reported no activity and 11 reported sporadic cases (across the Region) (Fig. 2).

Fig. 1. Intensity in the European Region, week 41/2019

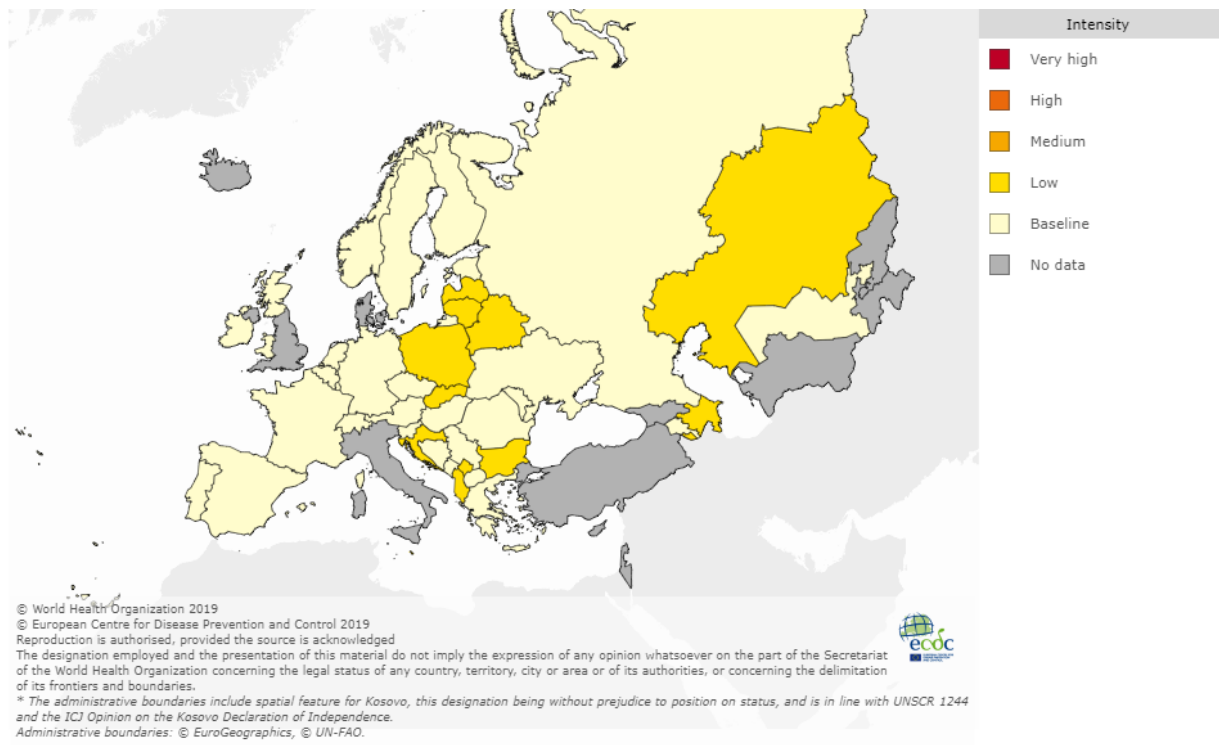
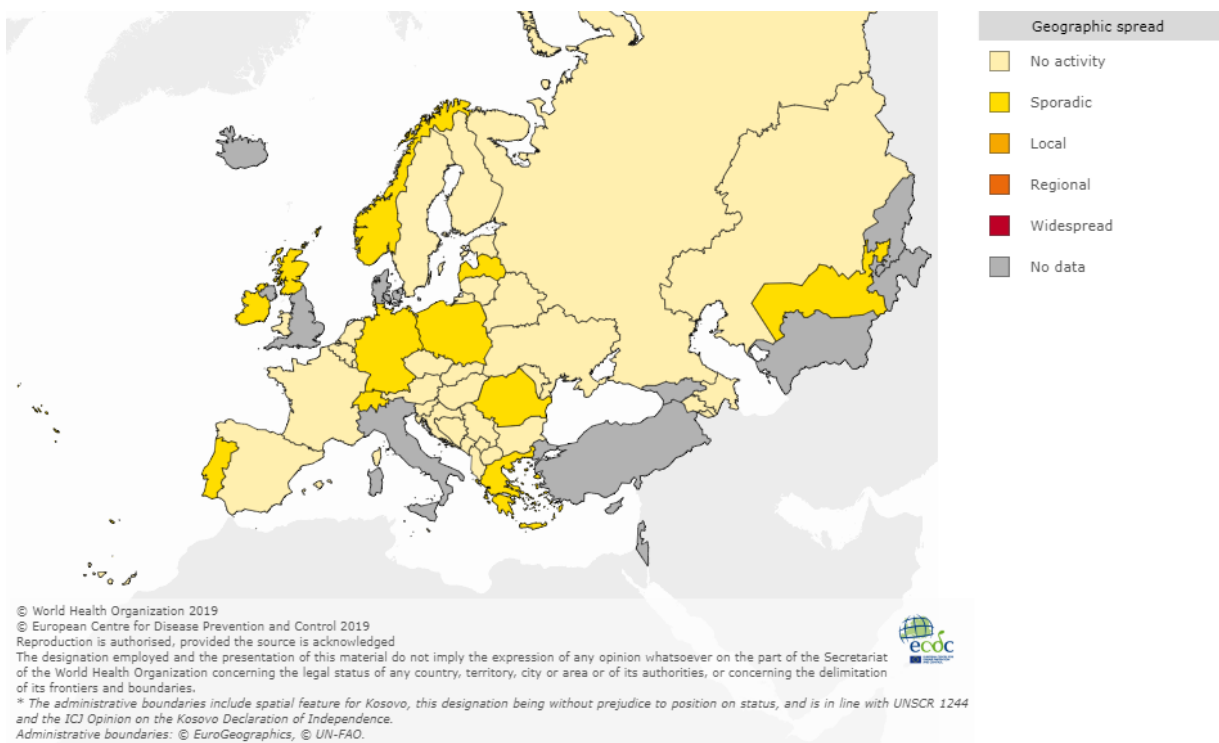


Fig. 2. Geographic spread in the European Region, week 41/2019



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

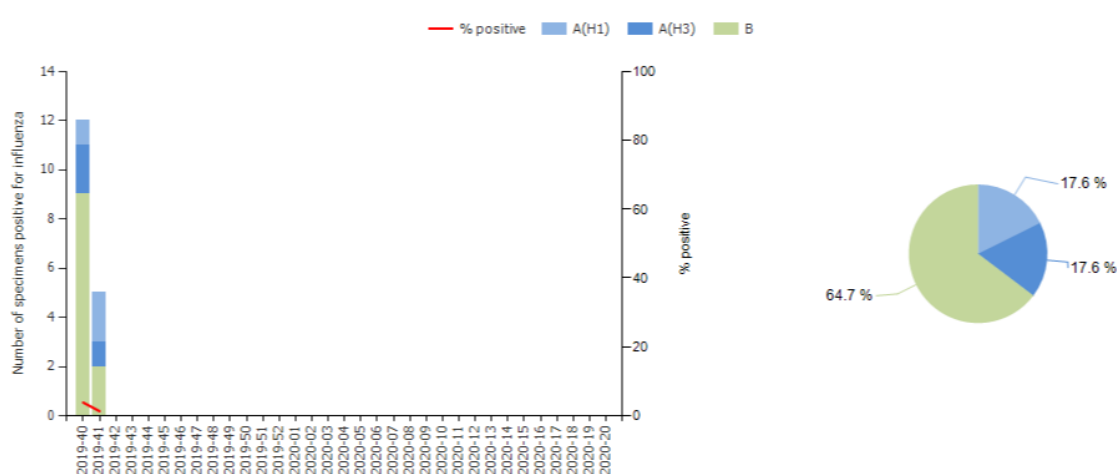
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 41/2019, 5 (1%) of 379 sentinel specimens tested positive for an influenza virus; 3 were influenza type A [2 A(H1N1)pdm09 and 1 A(H3N2)], and 2 were influenza type B (Fig. 3 and Table 1).

For the season overall, 17 influenza viruses have been detected: 3 A(H1N1)pdm09, 3 A(H3N2) and 11 type B viruses (7 ascribed to the B/Victoria 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 for the season^a



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 41/2019 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	3	60	6	35.3
A(H1N1)pdm09	2	66.7	3	50.0
A(H3N2)	1	33.3	3	50.0
A not subtyped	0	-	0	-
Influenza B	2	40	11	64.7
B/Victoria lineage	0	0.0	7	100.0
B/Yamagata lineage	0	0.0	0	0.0
Unknown lineage	2	-	4	-
Total detections (total tested)	5 (379)	1.3	17 (691)	2.5

^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, or other wards, or 2) severe acute respiratory infection (SARI; 18 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Only the UK reported cases from ICU since week 40/2019. All 9 laboratory-confirmed influenza cases reported in ICUs were reported as influenza type A, with 1 subtyped as A(H3N2).

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Only Ireland reported cases from other wards since week 40/2019. 5 laboratory-confirmed influenza cases from other wards were reported; 4 influenza A viruses, with 3 subtyped as A(H3N2), and with 1 type B virus.

2. SARI surveillance

Since week 40/2019, 1 195 SARI cases (645 for week 41/2019), were reported by 10 Member States or areas. Of 200 specimens tested for influenza viruses, one was positive for influenza B virus.

Mortality monitoring

For week 41/2019, the [EuroMOMO](#) project received data from 20 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality show mortality levels within normal expected ranges for the time of year.

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 41/2019, 67 of 9 120 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 influenza viruses; 90% were type A and 10% were type B. Of 34 subtyped A viruses, 12% were A(H1N1)pdm09 and 88% were A(H3N2) (Table 2).

For the season to date, more influenza type A (84%) than type B (16%) viruses have been detected. Of 69 subtyped A viruses, 10 (14%) were A(H1N1)pdm09 and 59 (86%) were A(H3N2). Of 2 influenza type B viruses ascribed to a lineage, both were B/Victoria lineage (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 41/2019 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	60	89.6	166	83.8
A(H1N1)pdm09	4	11.8	10	14.5
A(H3N2)	30	88.2	59	85.5
A not subtyped	26	-	97	-
Influenza B	7	10.4	32	16.2
B/Victoria lineage	0	0.0	2	100.0
B/Yamagata lineage	0	0.0	0	0.0
Unknown lineage	7	-	30	-
Total detections (total tested)	67 (9 120)	-	198 (18 648)	-

^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

Since the beginning of the season there have been no reports of influenza virus genetic characterization.

ECDC published a [report](#) in October on detailed influenza virus characterizations conducted in September 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 85 test viruses characterized antigenically since the July 2019 characterization report were antigenically similar to the vaccine viruses used in the 2018–2019 (A/Michigan/45/2015, clade 6B.1) and 2019–2020 (A/Brisbane/02/2018, clade 6B.1A1) northern hemisphere seasons. All 613 viruses with collection dates from week 40/2018 that were genetically characterized at the WHO Collaborating Centre, including two A(H1N2) reassortants, fell in a 6B.1 subclade, designated as 6B.1A, defined by HA1 amino acid substitutions of S74R, S164T and I295V. Within this subclade there has been increasing genetic diversity of the HA genes and, of these recently circulating viruses, 564 also have an HA1 S183P substitution, often with additional substitutions in HA1 and/or HA2, that define several emerging genetic subgroups.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the last characterization report, 37 A(H3N2) viruses had sufficient HA titre to allow antigenic characterization by HI assay in the presence of oseltamivir. All these viruses were poorly recognized by antisera raised against the currently used clade 3C.2a1 vaccine virus, egg-propagated A/Singapore/INFIMH-16-0019/2016. Of the 505 viruses with collection dates from week 40/2018 that were genetically characterized at the WHO Collaborating Centre, 399

were in clade 3C.2a with many falling in subclades (43 in 3C.2a2, 17 in 3C.2a3, 8 in 3C.2a4 and 331 in 3C.2a1b) and 106 were clade 3C.3a.

B/Victoria viruses

Ten B/Victoria lineage viruses had been tested by HI since the last characterization report. All recent viruses carry HA genes that fall in clade 1A but encode HA1 amino acid substitutions of I117V, N129D and V146I when compared to 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 [1A(Δ 3A)] and African [1A(Δ 3B)] origin. HI analyses with panels of post-infection ferret antisera have shown these 4 virus groups to be antigenically distinguishable. Of a total of 20 viruses genetically characterized from EU/EEA countries this season, 1 has been 1A(Δ 2) and 17 1A(Δ 3) [16 1A(Δ 3B) and 1 1A(Δ 3A) subgroup].

B/Yamagata viruses

Nine B/Yamagata lineage viruses had been characterized antigenically since the last characterization report and a total of 23 had been characterized from the 2018–2019 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 2018-2019 and 2019-2020 northern hemisphere influenza seasons, B/Phuket/3073/2013. However, all 23 viruses remained antigenically similar to the vaccine virus.

Vaccine composition

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 (Clade 6B.1A1);
- an A/Kansas/14/2017 (H3N2)-like virus (Clade 3C.3a);
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage) (Clade 1A_Δ2); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage) (Clade 3).

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](#).

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has not been reported for viruses with collection dates since week 40/2019.

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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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 41/2019.

Tables and figures should be referenced:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 41/2019.

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