

Weekly influenza overview

Week 46/2020 (9–15 November 2020)

- Influenza activity remained at interseasonal levels.
- No influenza viruses were detected in specimens from persons with respiratory illness presenting to primary medical care sentinel sites.
- Influenza viruses were detected sporadically from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, or nursing homes and other institutions). Both influenza type A and type B viruses were detected.
- There were no hospitalized laboratory-confirmed influenza cases reported for week 46/2020.
- The novel coronavirus disease 2019 (COVID-19) pandemic has affected healthcare presentations and testing capacities of countries and areas in the Region, which negatively impacted reporting of influenza epidemiologic and virologic data during the 2019-2020 season. It is not unusual for influenza activity to be low at this time of year. However, as the COVID-19 pandemic continues, the influenza data presented for the 2020-2021 season needs to be interpreted with caution, notably in terms of seasonal patterns.

Other news

The World Health Organization categorized COVID-19 as a pandemic on 11 March 2020. For more information about the situation in the WHO European Region visit:

- WHO website: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>
- ECDC website: <https://www.ecdc.europa.eu/en/novel-coronavirus-china>

Qualitative indicators

Of 33 countries and areas that reported on the intensity indicator, 29 reported activity at baseline levels, 1 country reported medium intensity (Georgia) and 3 reported low intensity (Azerbaijan, Serbia and Slovakia) for week 46/2020 (Fig. 1).

Of 34 countries and areas that reported on geographic spread, 29 reported no activity and 5 reported sporadic spread (in eastern, northern and western areas) for week 46/2020 (Fig. 2).

Please note: as all sentinel specimens tested for influenza viruses in this period were negative, the qualitative indicators based on intensity and geographic spread should be interpreted as indicating that increased intensity and spread were not caused by influenza infections.

Fig. 1. Intensity in the European Region, week 46/2020

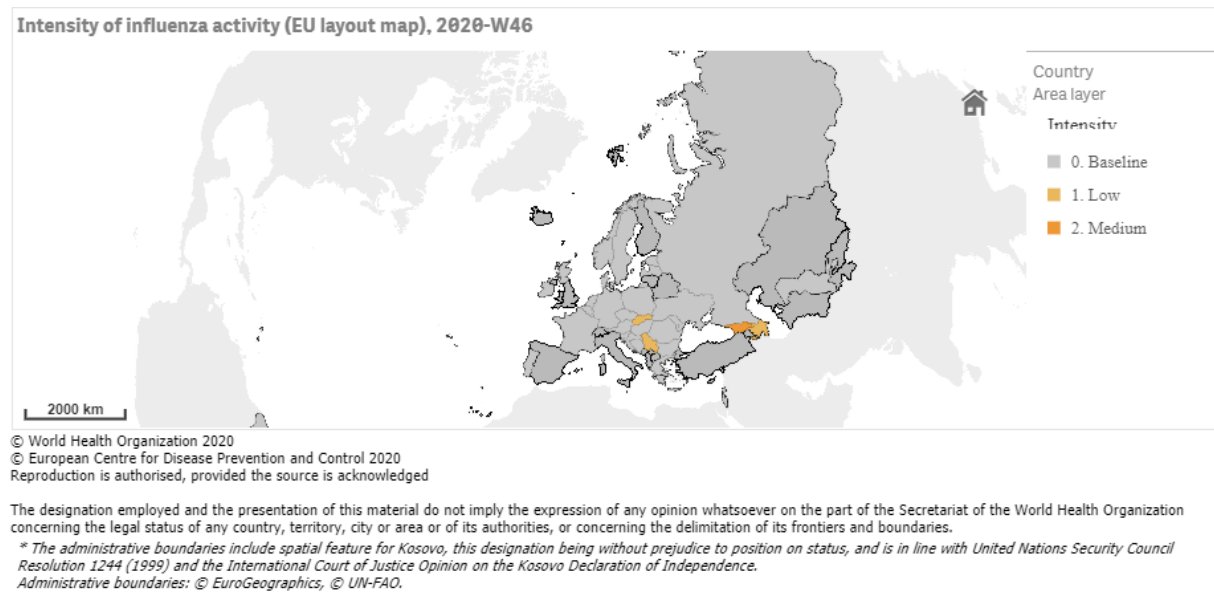
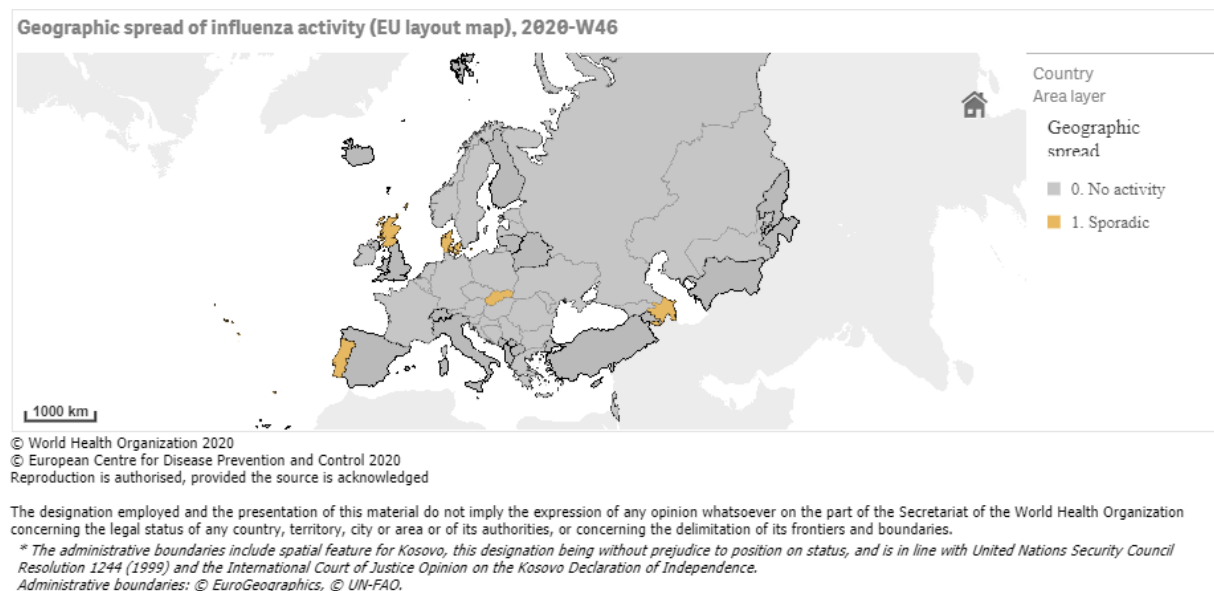


Fig. 2. Geographic spread in the European Region, week 46/2020



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

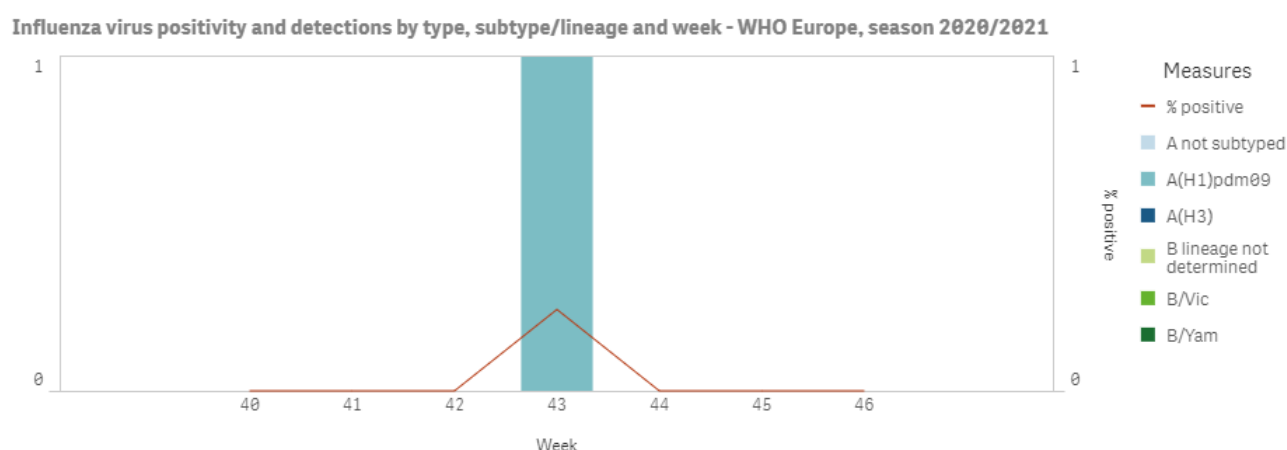
2020-2021 season overview

- For the Region as a whole, influenza activity has been at baseline level since the start of the season
- In total, 61 specimens have tested positive for influenza viruses, 1 from sentinel sources and 60 from non-sentinel sources, with A(H1)pdm09, A(H3) and type B viruses detected.
- No cases of hospitalization due to influenza virus infection have been reported.
- WHO has published [recommendations](#) for the composition of influenza vaccines to be used in the 2020–2021 northern hemisphere season. Based on these recommendations, the influenza A(H1N1)pdm09, A(H3N2) and B/Victoria-lineage virus components should be updated compared to the 2019–2020 influenza vaccine.

Influenza positivity

As of week 46/2020, for the European Region, influenza virus positivity in sentinel specimens remained below the epidemic threshold, which is set at 10% (Fig. 3.).

Fig. 3. Influenza virus detections in sentinel-source specimens by type and subtype, and week for weeks 40-46/2020



External data sources

Mortality monitoring: Overall pooled estimates of all-cause mortality for 26 countries and areas participating in the [EuroMOMO](#) project showed a substantial excess mortality, coinciding with a reported increase in COVID-19 cases in several countries.

The excess all-cause mortality was seen primarily in the 65 years and above age group, but was also raised in the age groups of 15-44 and 45-64 years.

Primary care data

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

For week 46/2020, of 979 sentinel specimens tested for influenza viruses, none were positive. Since the start of the season, of 3 376 sentinel-source specimens that have been tested for influenza viruses, one was positive (Table 1).

Details of the distribution of viruses detected in non-sentinel-source specimens are presented in the [Virus characteristics](#) section.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype for week 46/2020 and cumulatively for the influenza season 2020-2021

Virus type and subtype	Current Week (46)		Influenza Season 2020-2021	
	Number	% ^a	Number	% ^a
Influenza A	0	-	1	100
A(H1)pdm09	0	-	1	100
A(H3)	0	-	0	0
A not subtyped	0	-	0	-
Influenza B	0	-	0	0
B/Victoria lineage	0	-	0	-
B/Yamagata lineage	0	-	0	-
Unknown lineage	0	-	0	-
Total detections (total tested)	0 (979)	-	1 (3 376)	<1

^a 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.

Hospital surveillance

A subset of countries 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; mostly located in the eastern part of the Region).

Laboratory-confirmed hospitalized cases

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

There were no hospitalized laboratory-confirmed influenza cases in ICUs reported for week 46/2020 and since the start of the season.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

There were no laboratory-confirmed influenza cases in wards outside ICUs reported for week 46/2020 and since the start of the season.

Severe acute respiratory infection (SARI)-based hospital surveillance

For week 46/2020, specimens from 78 SARI cases were tested for influenza viruses. All were negative.

For the season to date, 10 countries and areas have reported 3 299 SARI cases and 460 were tested for influenza viruses. All were negative.

Virus characteristics

Details of the distribution of viruses detected in sentinel-source specimens can be found in the [Primary care data](#) section.

Non-sentinel virologic data

For week 46/2020, 7 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: 3 type A and 4 type B viruses (Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 46/2020 and cumulatively for the influenza season 2020-2021).

Since the beginning of the season, 60 of 63 997 non-sentinel specimens tested positive for influenza viruses, 32 (53.3%) were type A and 28 (46.7%) type B. Nineteen of the type A viruses were subtyped: 14 (73.7%) as A(H3) and 5 (26.3%) as A(H1)pdm09. Two (7%) of the 28 type B viruses were B/Victoria lineage, the remainder were not ascribed to a lineage.

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 46/2020 and cumulatively for the influenza season 2020-2021

Virus type and subtype	Current Week (46)		Influenza Season 2020-2021	
	Number	% ^a	Number	% ^a
Influenza A	3	42.9	32	53.3
A(H1)pdm09	1	100	5	26.3
A(H3)	0	0	14	73.7
A not subtyped	2	-	13	-
Influenza B	4	57.1	28	46.7
B/Victoria lineage	0	-	2	7
B/Yamagata lineage	0	-	0	0
Unknown lineage	4	-	26	93
Total detections (total tested)	7 (10 182)		60 (63 997)	

^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

No virus characterization data for viruses detected in weeks 40-46/2020 have been reported.

Data from influenza season 2019-2020

The great majority of A(H1N1)pdm09 viruses fell within subgroups of subclade 6B.1A5 and subclade 6B.1A7, with those of 6B.1A5A becoming dominant as the season progressed. While these viruses had HA amino acid substitutions compared to the vaccine virus A/Brisbane/02/2018 (6B.1A1), it was anticipated that the vaccine virus would still be effective based on HI assays conducted with post-infection ferret antisera raised against the vaccine virus, until emergence of a group of viruses with HA1 N156K substitution.

As seen elsewhere in the world, there was significant genetic diversity among circulating A(H3N2) viruses in the European region for the 2019–2020 influenza season, with 53% being clade 3C.3a and 47% subclade 3C.2a1. All subclade 3C.2a1 viruses fell in subgroup 3C.2a1b (with the latter splitting between 3 designated genetic clusters). The vaccine virus, A/Kansas/14/2017, falls within clade 3C.3a and viruses within this clade induce clade-specific antibodies in ferrets, so viruses falling in other clades/subclades were expected to be less well covered by human immune responses to the vaccine virus.

For the B/Victoria-lineage, viruses in the B/Colorado/06/2017 vaccine virus double deletion clade (1A (del 162-163)) were in the great minority. However, there was evidence of some cross-reactivity with viruses in the triple deletion clade (1A (del 162-164)) by post-infection ferret antisera raised against the egg-propagated vaccine virus.

B/Yamagata lineage viruses were detected in low numbers worldwide and, despite some genetic drift with associated HA amino acid substitutions, retained good reactivity with post-infection ferret antisera raised against the B/Phuket/3073/2013 vaccine virus.

ECDC published a [report](#) in October relating to viruses circulating globally, with collection dates after 31 August 2019, but focusing on those from European Union/European Economic Area (EU/EEA) countries. This was the final report for the 2019-2020 season.

ECDC published the first [report](#) for the 2020-2021 season in November. No antigenic data relating to viruses detected in the course of the 2020-2021 influenza season had been generated and the report was based on an analysis of seasonal influenza HA sequenced most recently submitted to GISAID. The following text is repeated from the Summary text of this report with minor modification. Previously published influenza virus characterization reports are also available on the [ECDC website](#).

A(H1N1)pdm09 viruses

The vast majority of A(H1N1)pdm09 viruses had continued to fall in genetic subclade 6B.1A5, mostly in the 6B.1A5A group with few in the 6B.1A5B group. 6B.1A5A viruses have continued to evolve and two subgroups have emerged designated 6B.1A5A+187V/A, representatives of which are recommended for use in the northern hemisphere 2020-2021 season, and 6B.1A5A+156K, an antigenically distinct group representatives of which are recommended for use in the southern hemisphere 2021 season. Following a rise in the number of 6B.1A5A+156K viruses detected, the two subgroups appear to be circulating in approximately equal proportions currently.

A(H3N2) viruses

Recently circulating A(H3N2) viruses had continued to fall in clades 3C.2a and 3C.3a, with the vast majority of clade 3C.2a viruses being in the 3C.2a1b group which has now been divided into four subgroups designated 3C.2a1b+T131K-A, 3C.2a1b+T131K-B, 3C.2a1b+T135K-A and 3C.2a1b+T135K-B. Antisera raised in ferrets show high levels of clade/group specificity, though there is some subgroup cross-reactivity. Viruses representative of subgroup 3C.2a1b+T135K-B have been recommended for use in influenza vaccines for the northern hemisphere 2020-2021 and southern hemisphere 2021 seasons.

B/Victoria viruses

Of four antigenically distinct groups of viruses in the B/Victoria-lineage, only two had circulated recently, small numbers of that designated subclade 1A (Δ 2) with a two amino acid deletion in HA1 and that designated subclade 1A(Δ 3)B with a three amino acid deletion in HA1 being hugely dominant. Viruses representative of subclade 1A(Δ 3)B have been recommended for use in influenza vaccines for the northern hemisphere 2020-2021 and southern hemisphere 2021 seasons.

B/Yamagata viruses

When the report published in November was written, genetic information for only 70 B/Yamagata-lineage viruses with collection dates in 2020 was available in GISAID. All 67 viruses for which full-length HA sequences were available belonged to genetic clade 3 and contained at least two HA amino acid substitutions (HA1 L172Q and M251V) compared to B/Phuket/3073/2013-like viruses which have been recommended for use in quadrivalent influenza vaccines for the northern hemisphere 2020-2021 and southern hemisphere 2021 seasons. The antigenic effects of these amino acid substitutions have been minimal as assessed in earlier reports.

Antiviral susceptibility of seasonal influenza viruses

For week 46/2020 and since the beginning of the season, no influenza viruses were tested for susceptibility to neuraminidase inhibitors.

Vaccine

Available vaccines in Europe

<https://www.ecdc.europa.eu/en/seasonal-influenza/prevention-and-control/vaccines/types-of-seasonal-influenza-vaccine>

Vaccine composition

On 28 February 2020, WHO published recommendations for the components of influenza vaccines for use in the **2020–2021 northern hemisphere influenza season**.

Egg-based vaccines should contain the following:

- an A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus (Clade 6B.1A5A);

- an A/Hong Kong/2671/2019 (H3N2)-like virus (Clade 3C.2a1b+T135K-B);
- a B/Washington/02/2019 (B/Victoria lineage)-like virus (Clade 1A(Δ 3)B); and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus (Clade 3).

Cell- or recombinant-based vaccines should contain the following:

- an A/Hawaii/70/2019 (H1N1)pdm09-like virus (Clade 6B.1A5A);
- an A/Hong Kong/45/2019 (H3N2)-like virus (Clade 3C.2a1b+T135K-B);
- a B/Washington/02/2019 (B/Victoria lineage)-like virus (Clade 1A(Δ 3)B); and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus (Clade 3).

It is recommended that the influenza B virus component of **both trivalent vaccine types** for use in the 2020–2021 northern hemisphere influenza season should be a B/Washington/02/2019-like virus of the B/Victoria-lineage.

The [full report](#) and [Frequently Asked Questions](#) for the 28 February 2020 decision are available on the [WHO website](#).

Based on WHO published recommendations on 25 September 2020, the composition of influenza vaccines for use in the **2021 southern hemisphere influenza season** will contain the following:

Egg-based Vaccines

- an A/Victoria/2570/2019 (H1N1)pdm09-like virus;
- an A/Hong Kong/2671/2019 (H3N2)-like virus;
- a B/Washington/02/2019 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Cell- or recombinant-based Vaccines

- an A/Wisconsin/588/2019 (H1N1)pdm09-like virus;
- an A/Hong Kong/45/2019 (H3N2)-like virus;
- a B/Washington/02/2019 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

It is recommended that the influenza B virus component of **both trivalent vaccine types** for use in the 2021 southern hemisphere influenza season should be a B/Washington/02/2019-like virus of the B/Victoria-lineage.

The full report is published [here](#).

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, Lisa Ferland, Favelle Lamb, Andrew Amato-Gauci, and Angeliki Melidou) and the WHO Regional Office for Europe (Piers Mook, Richard Pebody and Miriam Sneiderman). It was reviewed by experts from the network (Adam Meijer, National Institute for Public Health and the Environment (RIVM), the Netherlands); Rod Daniels and John McCauley, WHO Collaborating Centre for Reference and Research on Influenza, Francis Crick Institute, United Kingdom.

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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