

Weekly influenza overview

Week 48/2020 (23–29 November 2020)

- Influenza activity remained at interseasonal levels.
- Four 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.
- During week 48/2020, there were three hospitalized laboratory-confirmed influenza cases from ICUs and a further three cases in wards outside of ICUs.
- 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 38 countries and areas that reported on the intensity of activity indicator, 32 reported activity at baseline levels, 1 (Ukraine) and 5 (Armenia, Azerbaijan, Serbia, Slovakia and the United Kingdom (England)) reported medium and low intensity, respectively, for week 48/2020 (Fig. 1).

Of 39 countries and areas that reported on geographic spread, 31 reported no activity and 8 reported sporadic spread (in eastern, northern and western areas) for week 48/2020 (Fig. 2).

Please note:

1. Assessment of the intensity of activity indicator includes consideration of ILI or ARI rates. These ILI or ARI rates might be driven by respiratory infections other than influenza, including SARS-CoV-2, leading to observed increases in the absence of influenza detections.
2. Assessment of intensity and geographic spread indicators includes consideration of sentinel and non-sentinel influenza virus detection data. Non-sentinel influenza virus detections, often higher, might translate into reporting of elevated geographic spread even in the absence of sentinel detections.

Fig. 1. Intensity in the European Region, week 48/2020

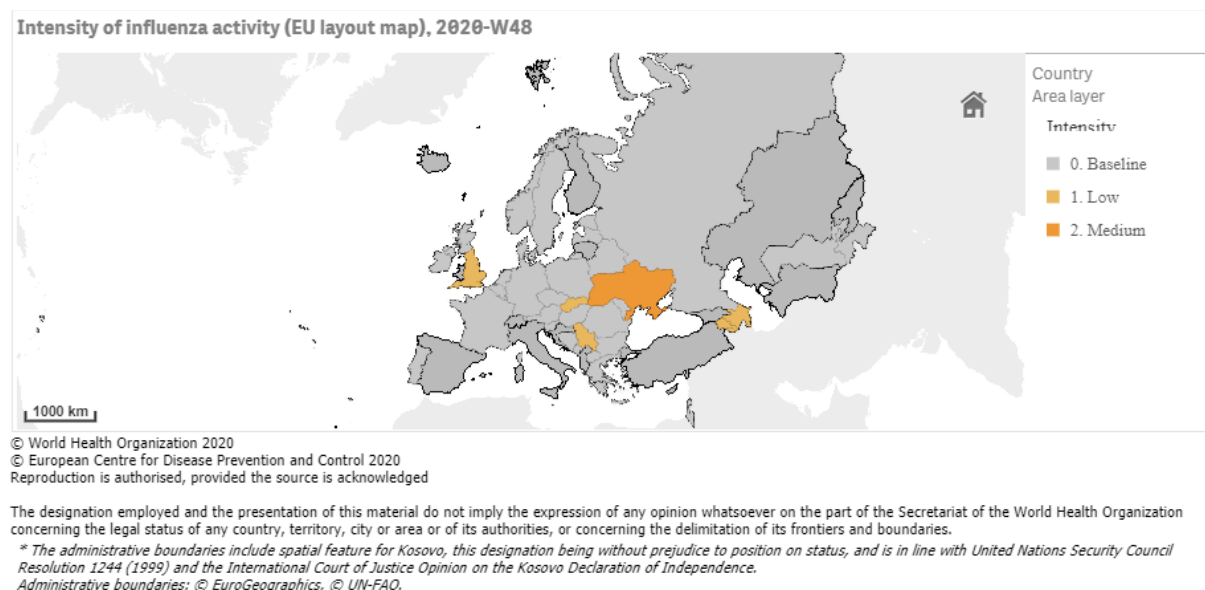
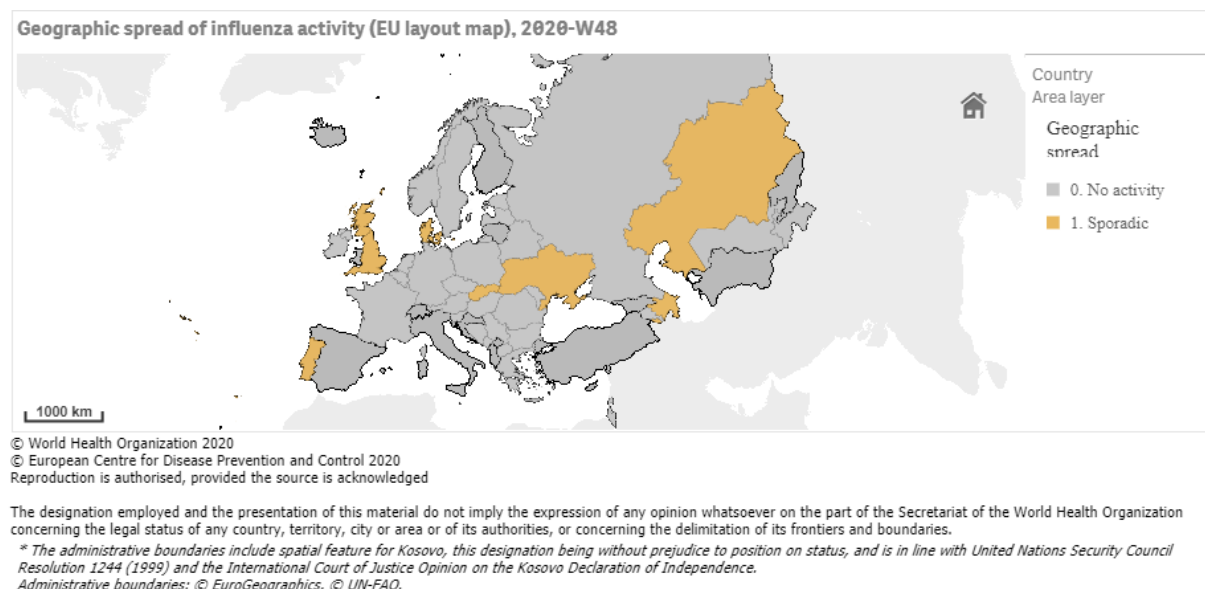


Fig. 2. Geographic spread in the European Region, week 48/2020



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

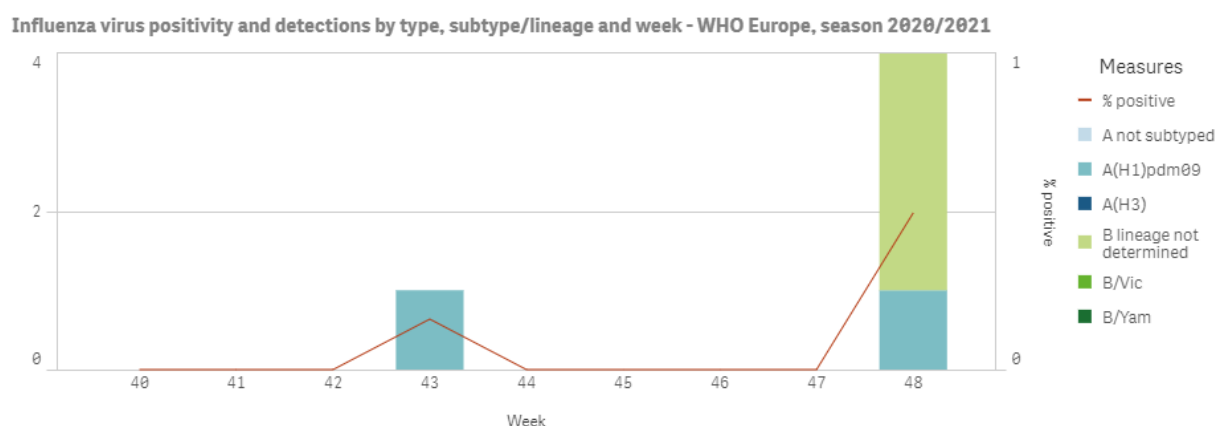
2020-2021 season overview

- For the Region as a whole, influenza activity has been at baseline level since the start of the season.
- In total, 288 specimens have tested positive for influenza viruses, 5 from sentinel sources and 283 from non-sentinel sources, with A(H1)pdm09, A(H3) and type B viruses detected.
- Since the start of the season, there have been 10 hospitalized laboratory-confirmed influenza cases reported from ICUs (9 infected with type A viruses and 1 with type B). A further three cases (all type B viruses) in wards outside ICUs have been reported with 1 fatality.
- 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 48/2020, 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 40-48/2020



External data sources

Mortality monitoring: Overall pooled estimates of all-cause mortality for 25 countries and areas participating in the [EuroMOMO](#) project showed substantially increased excess mortality, coinciding with a reported increase in COVID-19 cases in several countries.

The excess all-cause mortality was seen primarily in the 45 years and above age groups.

Primary care data

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

For week 48/2020, of 804 sentinel specimens tested for influenza viruses, four were positive. Since the start of the season, of 6 832 sentinel-source specimens that have been tested for influenza viruses, five were positive: 2 type A and 3 type B viruses (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 48/2020 and cumulatively for the influenza season 2020-2021

Virus type and subtype	Current Week (48)		Influenza Season 2020-2021	
	Number	% ^a	Number	% ^a
Influenza A	1	25.0	2	40.0
A(H1)pdm09	1	100	2	100
A(H3)	0	-	0	-
A not subtyped	0	-	0	-
Influenza B	3	75.0	3	60.0
B/Victoria lineage	0	-	0	-
B/Yamagata lineage	0	-	0	-
Unknown lineage	3	-	3	-
Total detections (total tested)	4 (804)	<1	5 (6 832)	<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.

External data sources

[Influenzanet](#) collects weekly data on symptoms in the general community from different participating countries across the EU/EEA. For week 48/2020, data reported from 8 countries representing between 62 and 7 958 active participants were included, for a total of 25 906 participants.

ILI activity: France, Germany, Italy, Portugal, Spain, Switzerland and the UK have reported between 0 and 5 cases per 1 000 active participants. Denmark has reported between 5 and 10 cases per 1 000 active participants. Activity is low (below the first quartile of historical data for this week).

COVID-19 activity: France has reported between 20 and 30 possible cases per 1 000 weekly participants, Italy, Spain, Switzerland and the UK have reported between 25 and 30 possible cases per 1 000 weekly participants. Portugal has reported between 30 and 35 possible cases per 1 000 weekly participants.

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

Laboratory-confirmed hospitalized cases

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

There were three hospitalized laboratory-confirmed influenza cases in ICUs reported for week 48/2020.

Since the start of the season, there have been 10 hospitalized laboratory-confirmed influenza cases in ICUs (9 infected with A viruses and 1 with type B) reported by Ukraine (n = 2) and the UK (n = 8). At the time of the latest reports all cases were non-fatal.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

There were three laboratory-confirmed influenza cases (all type B viruses) in wards outside ICUs reported for week 48/2020: two cases were in patients aged 15-64 years and 1 case, which was fatal, in a patient over 65 years old.

Severe acute respiratory infection (SARI)-based hospital surveillance

For week 48/2020, specimens from 157 SARI cases were tested for influenza viruses. Four of 28 (14%) specimens from Ukraine were positive (1 type A and 3 type B viruses were detected).

For the season to date, 11 countries and areas have reported 6 414 SARI cases and 907 were tested for influenza viruses. Just the four specimens from Ukraine, in week 48/2020, were positive to date.

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 48/2020, 40 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: 21 type A and 19 type B viruses (Table 2).

Influenza virus detections in non-sentinel source specimens by type and subtype, week 48/2020 and cumulatively for the influenza season 2020-2021). The vast majority of virus detections (85%; 34/40) were reported from the UK (England 25, Northern Ireland 2 and Scotland 7).

Since the beginning of the season, 283 of 94 011 non-sentinel specimens tested positive for influenza viruses; 147 (51.9%) were type A and 136 (48.1%) type B. Thirty-one of the type A viruses were subtyped: 23 (74.2%) as A(H3) and 8 (25.8%) as A(H1)pdm09. Of 283 type B viruses, only 2 were ascribed to a lineage both B/Victoria.

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 48/2020 and cumulatively for the influenza season 2020-2021

Virus type and subtype	Current Week (48)		Influenza Season 2020-2021	
	Number	% ^a	Number	% ^a
Influenza A	21	52.5	147	51.9
A(H1)pdm09	3	50.0	8	25.8
A(H3)	3	50.0	23	74.2
A not subtyped	15	-	116	-
Influenza B	19	47.5	136	48.1
B/Victoria lineage	0	-	2	100.0
B/Yamagata lineage	0	-	0	-
Unknown lineage	19	-	134	-
Total detections (total tested)	40 (10 960)		283 (94 011)	

^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 40-48/2020 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 and 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 48/2020 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(Δ3)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(Δ3)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](#).

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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 48/2020.

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 48/2020.

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