

Weekly influenza overview

Week 44/2020 (26 October–1 November 2020)

- Influenza activity remained at interseasonal levels.
- Influenza viruses were detected sporadically in specimens from persons with respiratory illness presenting to primary medical care
- Both influenza type A and type B viruses were detected in sentinel and non-sentinel source specimens
- There were no hospitalized laboratory-confirmed influenza cases reported for week 44/2020.
- 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 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>

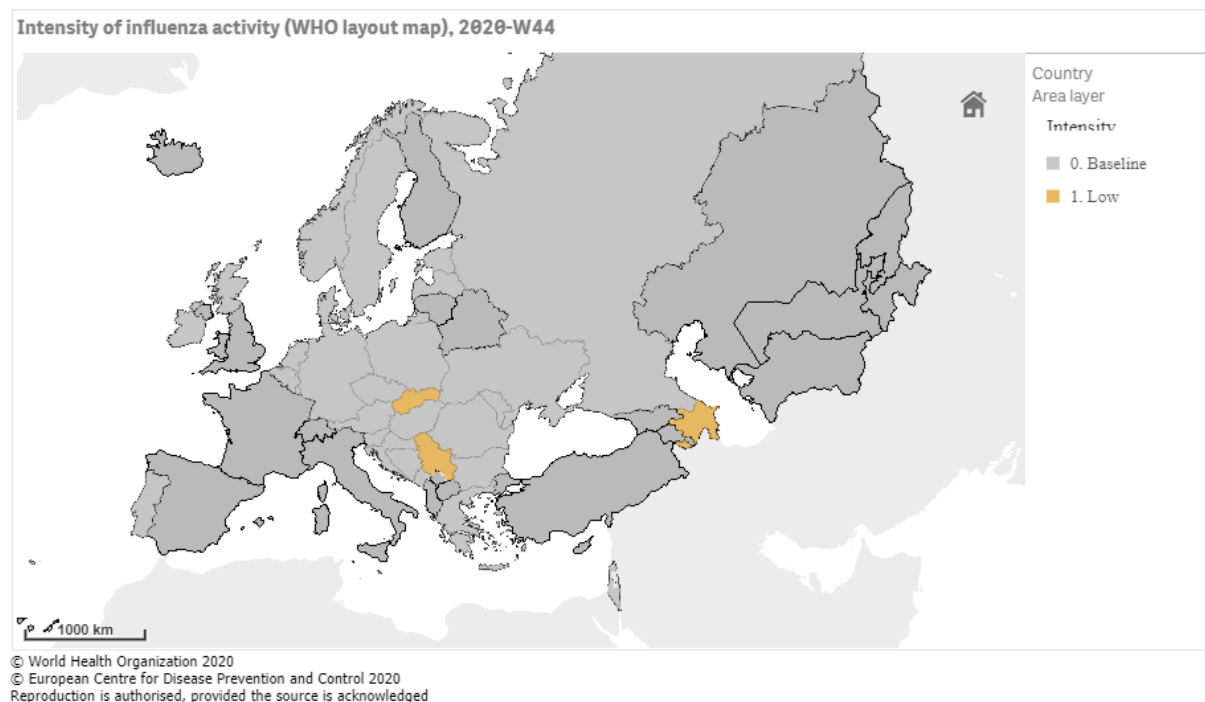
Qualitative indicators

Of 31 countries and areas that reported on the intensity indicator, 28 reported activity at baseline levels, and 3 reported low intensity (Azerbaijan, Serbia and Slovakia) for week 44/2020 (Fig. 1).

Of 32 countries and areas that reported on geographic spread, 27 reported no activity and 5 reported sporadic spread (Azerbaijan, Denmark, Portugal, Slovakia and United Kingdom (Scotland)) for week 44/2020 (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 44/2020

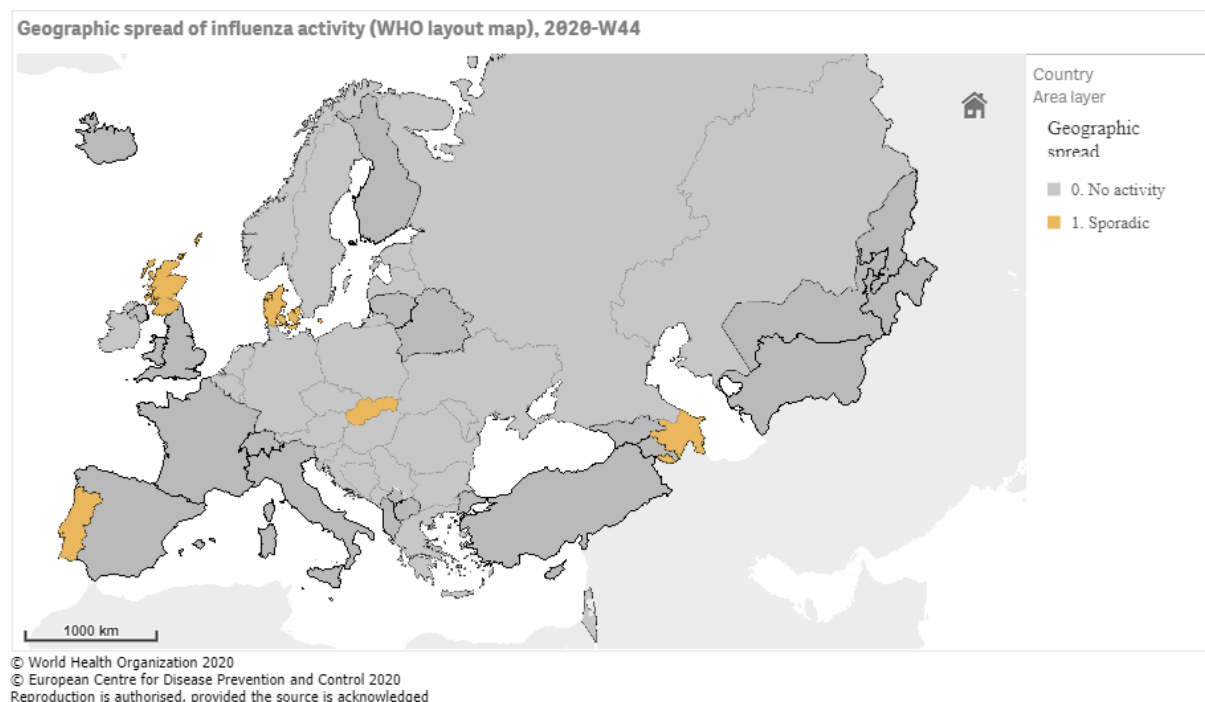


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* The administrative boundaries include spatial feature for Kosovo, this designation being without prejudice to position on status, and is in line with United Nations Security Council Resolution 1244 (1999) and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

Administrative boundaries: © EuroGeographics, © UN-FAO.

Fig. 2. Geographic spread in the European Region, week 44/2020



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

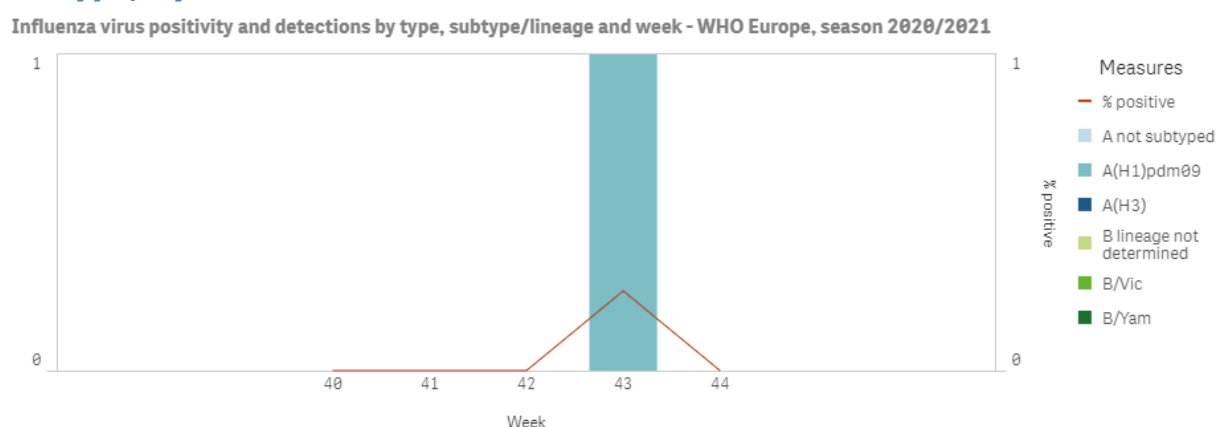
2020-2021 season overview

- For the Region as a whole, influenza activity has been at baseline level since the start of the season
- In total 39 specimens have tested positive for influenza viruses, 1 from sentinel sources and 38 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 44/2020, for the European Region, influenza virus positivity in sentinel specimens remained below the start of the epidemic threshold of 10% (Fig. 3).

Fig. 3. Influenza virus detections in sentinel-source specimens by type and subtype, by week for weeks 40-44/2020



External data sources

Mortality monitoring: Overall pooled estimates of all-cause mortality for 26 countries and areas participating in the [EuroMOMO](#) project showed an increase in excess mortality that was limited to some countries. The excess was primarily driven by mortality in those aged 45 years and older.

Primary care data

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

For week 44/2020, of 260 sentinel specimens tested for influenza viruses, none were positive. Since the start of the season, of 1 457 sentinel-source specimens that have been tested for influenza viruses, one specimen was positive (Table 1).

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

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype for week 44/2020 and cumulatively for the influenza season 2020-2021

Virus type and subtype	Current Week (44)		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 (260)	-	1 (1 457)	<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 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 for week 44/2020 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 for week 44/2020 and since the start of the season.

Severe acute respiratory infection (SARI)-based hospital surveillance

For week 44/2020, specimens from 53 SARI cases were tested for influenza viruses. All were negative.

For the season to date, 10 countries and areas have reported 2 044 SARI cases and 257 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 44/2020, 3 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: 1 type A and 2 type B viruses. The type A virus was not subtyped and neither of the type B viruses were assigned to a lineage (

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 44/2020 and cumulatively for influenza season 2020-2021).

Since the beginning of the season, 38 of 42 963 non-sentinel specimens tested positive for influenza viruses, 22 (57.9%) type A and 16 (42.1%) type B with no lineage determination. Eleven of the type A viruses were subtyped: 9 as A(H3) and 2 as A(H1)pdm09.

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 44/2020 and cumulatively for influenza season 2020-2021

Virus type and subtype	Current Week (44)		Influenza Season 2020-2021	
	Number	% ^a	Number	% ^a
Influenza A	1	33.3	22	57.9
A(H1)pdm09	0	-	2	18.2
A(H3)	0	-	9	81.8
A not subtyped	1	-	11	-
Influenza B	2	66.7	16	42.1
B/Victoria lineage	0	-	0	-
B/Yamagata lineage	0	-	0	-
Unknown lineage	2	-	16	-
Total detections (total tested)	3 (8 723)		38 (42 963)	

^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 40-44/2020 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. Since the July 2020 characterization report, 2 shipments of influenza positive specimens from EU/EEA countries had been received by the WHO Collaborating Centre, London (the Francis Crick Institute, Worldwide Influenza Centre (WIC)). In total, 1 719 virus specimens had been received, with collection dates after 31 August 2019.

A summary of viruses from EU/EEA countries characterized since July is given below. Previously published influenza virus characterization reports are also available on the [ECDC website](#).

A(H1N1)pdm09 viruses

Of the 33 A(H1N1)pdm09 viruses from EU/EEA countries characterised antigenically since the July report, 23 were well recognised by antisera raised against the 2019–20 vaccine virus, A/Brisbane/02/2018. The 10 viruses that showed poor reactivity generally carried amino acid substitutions (notably N156K) in the HA1 150-loop region. The 498 EU/EEA test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 455 6B.1A5A, 30 6B.1A5B, 1 6B.1A6 and 12 6B.1A7.

A(H3N2) viruses

The majority (7) of the 10 A(H3N2) viruses from EU/EEA countries characterised antigenically since the July report were clade 3C.3a and were well recognised by antiserum raised against egg-propagated A/Kansas/14/2017, the current vaccine virus. Globally, approximately equal proportions of viruses in clade 3C.3a and subclade 3C.2a1b subgroups have been detected, but for viruses detected since 1 February 2020, subclade 3C.2a1b subgroup viruses have prevailed in many countries worldwide while those of clade 3C.3a and subgroup 3C.2a1b+T131K have dominated in Europe. In total, 512 viruses from EU/EEA countries have been characterised genetically at the WIC: 288 clade 3C.3a, 139 3C.2a1b+T131K, 64 3C.2a1b+T135K-A and 21 3C.2a1b+T135K-B.

B/Victoria viruses

Thirty-two B/Victoria-lineage viruses from EU/EEA countries were antigenically characterised since the July report. All but one were subclade 1A(Δ 3)B and four of these viruses were not recognised well by antiserum raised against the vaccine virus for the 2020–2021 northern hemisphere influenza season, B/Washington/02/2019. Poor recognition was associated with HA1 amino acid substitutions of either N126K (n = 3) or N150K (n = 1). In total, 333 EU/EEA viruses have been characterised genetically at the WIC: 316 subclade 1A(Δ 3)B and 17 subclade 1A(Δ 2).

B/Yamagata viruses

A single B/Yamagata-lineage virus from Norway, with a collection date in February 2020, was antigenically characterised in August. All nine EU/EEA viruses characterised genetically at the WIC since week 40/2019, as for all recently circulating B/Yamagata-lineage viruses, belong to genetic clade 3 and contain at least two HA amino acid substitutions (HA1 L172Q and M251V) compared to B/Phuket/3073/2013, the antigenic effects of which have been minimal as assessed in earlier reports.

Antiviral susceptibility of seasonal influenza viruses

For week 44/2020 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 can be found [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.

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