

Summary

Weeks 26–30/2020 (22 June – 26 July 2020)

- Influenza activity is at inter-seasonal levels.
- Of 506 sentinel specimens tested for influenza virus in weeks 26-30, none tested positive for influenza.
- The novel coronavirus disease 2019 (COVID-19) pandemic is affecting healthcare presentations and testing capacities of Member States in the Region, which has a negative impact on reporting of influenza epidemiologic and virologic data. Therefore, the data we present, notably in terms of seasonal patterns, must be interpreted with caution.
- The next inter-seasonal update will be published on 29 August 2020.

2019–2020 season overview

- For the Region as a whole, influenza activity commenced earlier than in recent years and, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019.
- The influenza season for the Region as a whole peaked in week 05/2020, reaching a maximum positivity rate of 55%. The peak phase with positivity levels above 50% lasted for just two weeks, 05/2020 and 06/2020, but reporting in subsequent weeks has been adversely affected by Member State responses to the COVID-19 pandemic. In the previous influenza season, the influenza positivity rate exceeded 50% for six weeks.
- Both influenza types A and B co-circulated in the Region. Of the influenza A viruses, both influenza A(H1N1)pdm09 and A(H3N2) co-circulated. Of the circulating B viruses, the vast majority belonged to the B/Victoria lineage.
- The percentage of specimens testing positive for an influenza virus from patients who presented with ILI or ARI to sentinel primary healthcare sites dropped below 10% in week 13/2020, where it has since remained. In the 2018/2019 season, the positivity rate first dropped below 10% in week 17/2019.
- The great majority of analysed viruses were susceptible to neuraminidase inhibitors supporting early treatment or prophylactic use according to national guidelines.
- Interim estimates of 2019–2020 seasonal influenza vaccine effectiveness in the northern hemisphere are [available](#). Vaccination remains the best possible method for prevention of influenza and/or reducing the risk of serious complications.
- 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 for the 2020–2021 influenza vaccine.

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>

Primary care data

Syndromic surveillance data

For week 30/2020, 13 Member States or areas with defined thresholds for ILI activity and 7 Member States with defined thresholds for ARI all reported baseline activity levels.

Influenza activity

Of 19 Member States and areas that reported on the intensity indicator, 17 reported activity at baseline levels and 2 reported low intensity (Azerbaijan and Slovakia) for week 30/2020 (Fig. 1).

Of 18 Member States and areas that reported on geographic spread, 16 reported no activity, 2 reported sporadic spread (Ireland and United Kingdom (Northern Ireland)) for week 30/2020 (Fig. 2).

Fig. 1. Intensity in the European Region, week 30/2020

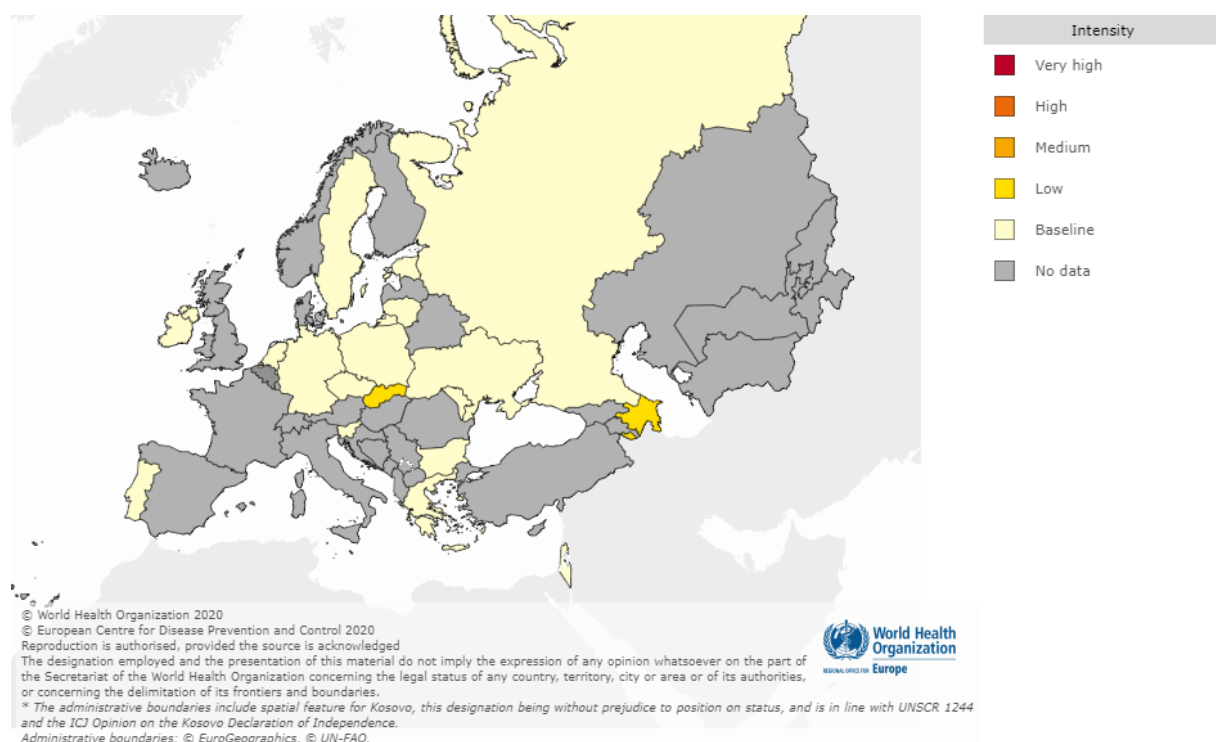
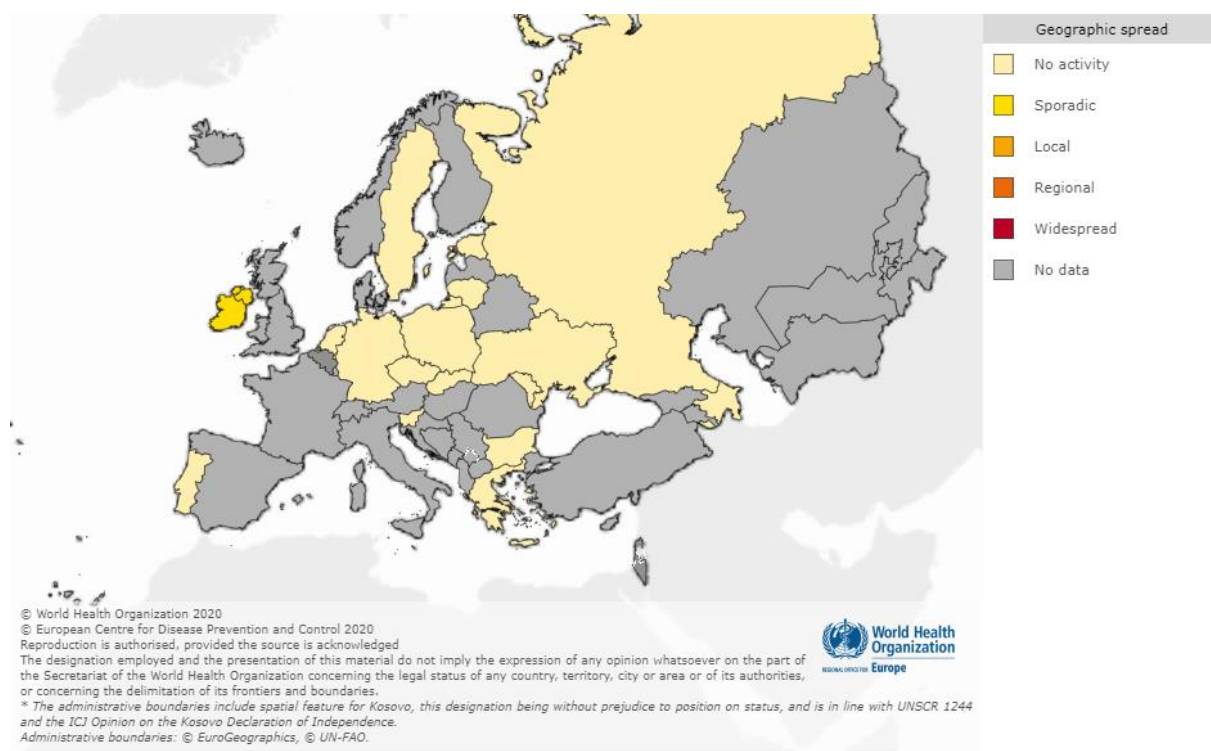


Fig. 2. Geographic spread in the European Region, week 30/2020



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

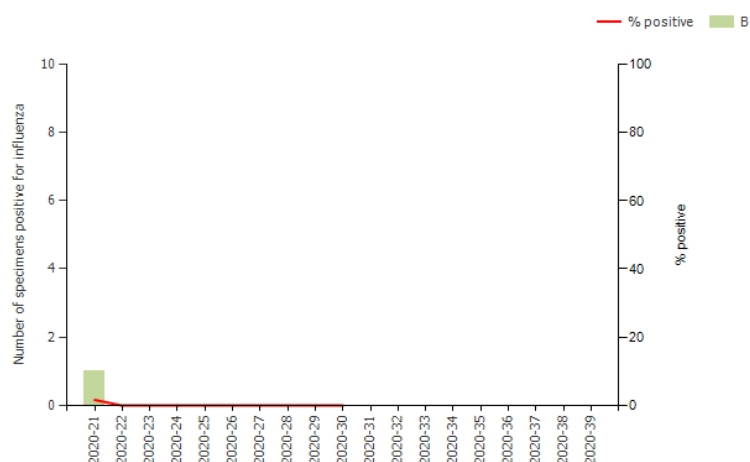
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 30/2020, of 55 sentinel specimens tested for influenza virus, none were positive (Fig. 3 and Table 1).

Cumulatively, for weeks 21-30/2020, 1 of 688 (0.1%) sentinel specimens tested positive for influenza virus. It was influenza type B and not ascribed to a lineage (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 for weeks 21-30/2020



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Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 30/2020 and cumulatively for weeks 21-30/2020

Virus type and subtype	Current Week		Season 2019–2020 Weeks 21-30	
	Number	% ^a	Number	% ^a
Influenza A	0	-	0	0
A(H1N1)pdm09	0	-	0	-
A(H3N2)	0	-	0	-
A not subtyped	0	-	0	-
Influenza B	0	-	1	100
B/Victoria lineage	0	-	0	-
B/Yamagata lineage	0	-	0	-
Unknown lineage	0	-	1	-
Total detections (total tested)	0 (55)	-	1 (688)	0.1

^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.

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 (11 Member States and areas) or other wards (7 Member States and areas), or 2) severe acute

respiratory infection (SARI; 17 Member States and areas, mostly located in the eastern part of the Region).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

There were no reports of hospitalized laboratory-confirmed influenza in ICUs for weeks 26-30/2020.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

There were no reports of laboratory-confirmed influenza in wards other than ICUs for weeks 26-30/2020.

2. SARI surveillance

For week 30/2020, 62 SARI cases were reported by 3 Member States. None of the 58 specimens tested for influenza virus were positive.

Of the SARI cases tested for influenza viruses in weeks 21-30/2020, 1 tested positive. It was influenza type B.

Of 2 966 SARI cases reported in weeks 21-30/2020, 2 965 had a recorded age and, of these, 45% were 15–64 years old and 31% were 0-4 years old.

Mortality monitoring

Pooled estimates of all-cause mortality for the countries participating in the [EuroMOMO](#) network have reached normal levels, following a period of substantial excess mortality observed in some countries, coinciding with the COVID-19 pandemic. However, in some countries there might be a tendency towards an increase in mortality, possibly due to heat waves.

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 30/2020, no 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 (Table 2).

Cumulatively, for weeks 21-30/2020, 10 influenza type A and 8 influenza type B viruses were detected. The 2 subtyped A viruses were A(H3N2) (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 30/2020 and cumulatively for weeks 21-30/2020

Virus type and subtype	Current Week		Season 2019–2020 Weeks 21-30	
	Number	% ^a	Number	% ^a
Influenza A	0	-	10	55.6
A(H1N1)pdm09	0	-	0	0
A(H3N2)	0	-	2	100
A not subtyped	0	-	8	-
Influenza B	0	-	8	44.4
B/Victoria lineage	0	-	0	-
B/Yamagata lineage	0	-	0	-
Unknown lineage	0	-	8	-
Total detections (total tested)	0 (1 781)	-	18 (30 466)	-

^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

From weeks 21-30/2020, no influenza viruses were characterised genetically. Genetic data for the 2019-2020 season can be found in the FNE report for week 20/2020.

The great majority of A(H1N1)pdm09 viruses have fallen within subgroups of subclade 6B.1A5 and subclade 6B.1A7, with those of 6B.1A5A becoming dominant as the season progressed. While these viruses have 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 has been significant genetic diversity among circulating A(H3N2) viruses in the European region for the 2019–2020 influenza season to date, with 53% clade 3C.3a and 47% subclade 3C.2a. All subclade 3C.2a1 viruses have fallen 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 may be less well covered by human immune responses to the vaccine.

For the B/Victoria-lineage, viruses in the B/Colorado/06/2017 vaccine virus double deletion clade (1A (del 162-163)) have been in the great minority. However, there is 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 have been detected in low numbers worldwide and, despite some genetic drift with associated HA amino acid substitutions, retain good reactivity with post-infection ferret antisera raised against the B/Phuket/3073/2013 vaccine virus.

ECDC published a [report](#) in July relating to viruses circulating globally, with collection dates after 31 August, but focusing on those from European Union/European Economic Area

(EU/EEA) countries. Since the May 2020 characterization report, 9 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, 1 608 virus specimens had been received, with collection dates after 31 August. A summary of viruses from EU/EEA countries characterized in June is given below. Previously published [influenza virus characterization reports](#) are also available on the ECDC website.

A(H1N1)pdm09 viruses

Of the 99 A(H1N1)pdm09 viruses from EU/EEA countries characterised antigenically since the May report, 77 were well recognised by antisera raised against the 2019–20 vaccine virus, A/Brisbane/02/2018. The 22 viruses that showed poor reactivity generally carried amino acid substitutions (notably N156K) in the HA1 150-loop region. The 397 EU/EEA test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 358 6B.1A5A, 29 6B.1A5B, 1 6B.1A6 and 9 6B.1A7.

A(H3N2) viruses

The majority (52) of the 68 A(H3N2) viruses from EU/EEA countries characterised antigenically in June 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 clade 3C.3a and subgroups 3C.2a1b+T131K and 3C.2a1b+T135K viruses have been detected, but for viruses detected since 1 February 2020, subgroups 3c.2a1b+T135KA/B have prevailed in the USA while those of clade 3C.3a and subgroup 3C.2a1b+T131K have dominated in Europe. In total, 438 viruses from EU/EEA countries have been characterised genetically at the WIC: 245 clade 3C.3a, 126 3C.2a1b+T131K, 48 3C.2a1b+T135K-A and 19 3C.2a1b+T135K-B.

B/Victoria viruses

Sixty-nine B/Victoria-lineage viruses from EU/EEA countries were antigenically characterised in June, 63 subclade 1A(Δ 3)B, one subclade 1A(Δ 2) and five not sequenced. Approximately 25% of the subclade 1A(Δ 3)B viruses were not recognised well by antiserum raised against B/Washington/02/2019, the vaccine virus for the 2020–2021 northern hemisphere influenza season. Poor recognition was generally associated with HA1 amino acid substitutions of either N126K or E128K. In total, 269 EU/EEA viruses have been characterised genetically at the WIC: 255 subclade 1A(Δ 3)B and 14 subclade 1A(Δ 2).

B/Yamagata viruses

No B/Yamagata-lineage viruses were characterised antigenically in June. All 8 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.

Vaccine composition

Based on WHO published recommendations on 21 February 2019, the composition of influenza vaccines for use in the **2019–2020 northern hemisphere influenza season** 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(Δ 2)); 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 2019 decision and the 21 March 2019 [addendum](#) are available on the [WHO website](#).

The report from the [Vaccine Composition Meeting for the southern hemisphere](#) 2020 season can be found [here](#).

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 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 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](#).

Vaccine effectiveness

Interim estimates of 2019-2020 seasonal influenza vaccine effectiveness (VE) for the northern hemisphere have been published based on [six European studies](#) (see below) and independent studies conducted in [Finland](#), [Canada](#) and [the United States of America](#). Influenza vaccine effectiveness estimates can vary depending on several factors, for example, study methods, health facility type, population, disease outcome, influenza vaccine types, influenza activity and type/subtype/lineage of circulating viruses. Vaccination against influenza remains the best method for prevention of influenza infection and/or development of severe disease during the ongoing 2019-2020 influenza season.

Interim 2019-2020 influenza VE estimates from the six European studies for all ages ranged from 29% to 61% against any influenza in the primary care setting and 35% to 60% in hospitalized older adults (aged 65 years and over). The VE point estimates against influenza A(H1N1)pdm09 (all ages, both settings) was 48% to 75%, and against influenza A(H3N2) ranged from –58% to 57% (primary care) and –16% to 60% (hospital). Against influenza type B, VE for all ages was 62% to 83% (primary care only).

Antiviral susceptibility testing

From week 40/2019 to week 30/2020, 1 789 influenza viruses, collected up to week 14, were tested for susceptibility to neuraminidase inhibitors: 758 A(H1N1)pdm09, 626 A(H3N2) and 405 type B viruses.

In total, 6 A(H1N1)pdm09 viruses showed highly reduced inhibition (HRI) or reduced inhibition (RI) to oseltamivir and/or zanamivir. Of these, 4 viruses carried amino acid substitution H275Y in NA, with one of them also having H295S substitution, both of which are indicative of HRI by oseltamivir. An additional 2 A(H1N1)pdm09 viruses showed RI by oseltamivir by phenotypic assay; 1 of these viruses also showed RI by zanamivir by phenotypic assay.

1 A(H3N2) virus carried amino acid substitution R292K in NA and showed evidence of HRI by oseltamivir and RI by zanamivir.

1 B/Victoria-lineage virus showed RI by zanamivir and highly reduced inhibition (HRI) by oseltamivir by phenotypic assay.

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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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