

Summary

Week 02/2020 (6-12 January 2020)

- Activity increased compared to week 01/2020, particularly in the southern part of the Region, with two Member States reporting high intensity and six reporting medium intensity. The remainder reported baseline or low intensity levels.
- The percentage of samples from sentinel ILI surveillance patients that tested positive for influenza virus increased from 27% in the previous week to 40% this week.
- The majority of reported influenza virus detections from sentinel ILI surveillance across the Region for week 02/2020 were type A (67%): this percentage has decreased from a high of 78% in week 49. The distribution of viruses detected varied between Member States and areas and within sub-regions.
- Data from the 22 countries or regions reporting to the [EuroMOMO](#) project indicated that all-cause mortality was at expected levels for this time of the year.
- ECDC published an [Influenza virus characterization](#) report, summarizing surveillance data in Europe through December 2019

2019–2020 season overview

- For the Region as a whole, influenza activity commenced earlier than previous years.
- Influenza activity in the European Region, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019 and has remained over 10% for 8 weeks. There has been an overall increasing trend in the weekly positivity rate for influenza virus detections among sentinel ILI surveillance patients, following a dip in week 52.
- Type A viruses have dominated across the European Region, though several Member States and areas have reported influenza type B virus dominance or co-dominance of types A and B viruses.
- In sentinel sources, both influenza A subtypes, A(H3N2) and A(H1N1)pdm09, are co-circulating and of the influenza B viruses, the vast majority (98%) have been B/Victoria lineage.
- [Influenzanet](#), which uses self-reported symptoms for ILI surveillance in the general population of European countries, is included in the bulletin as a pilot for the 2019/2020 season.
- ECDC and WHO Regional Office published a joint [Regional Situation Assessment](#) for the 2019–2020 influenza season up to week 49/2019, which focused on disease severity and impact on healthcare systems to assist forward planning in Member States.

Primary care data

Syndromic surveillance data

For week 02/2020, of the 35 Member States and areas that have calculated ILI thresholds, 16 (52%) of 31 reported ILI activity above baseline levels. Of the 17 Member States and areas that have calculated acute respiratory infection (ARI) thresholds, 13 reported levels, none of which were above baselines.

Influenza activity

Of 45 Member States and areas that reported on the intensity indicator, 16 reported activity at baseline levels (across the Region), 21 reported low (across the Region), 6 reported medium (eastern, northern and southern areas), and 2 reported high (Israel and Turkey) intensity for week 02/2020 (See Fig. 1).

Of 45 Member States and areas that reported on geographic spread, 2 reported no activity, 10 reported sporadic spread, 8 reported local spread, 7 reported regional spread and 18 reported widespread geographic activity (See Fig. 2).

Fig. 1. Intensity in the European Region, week 02/2020

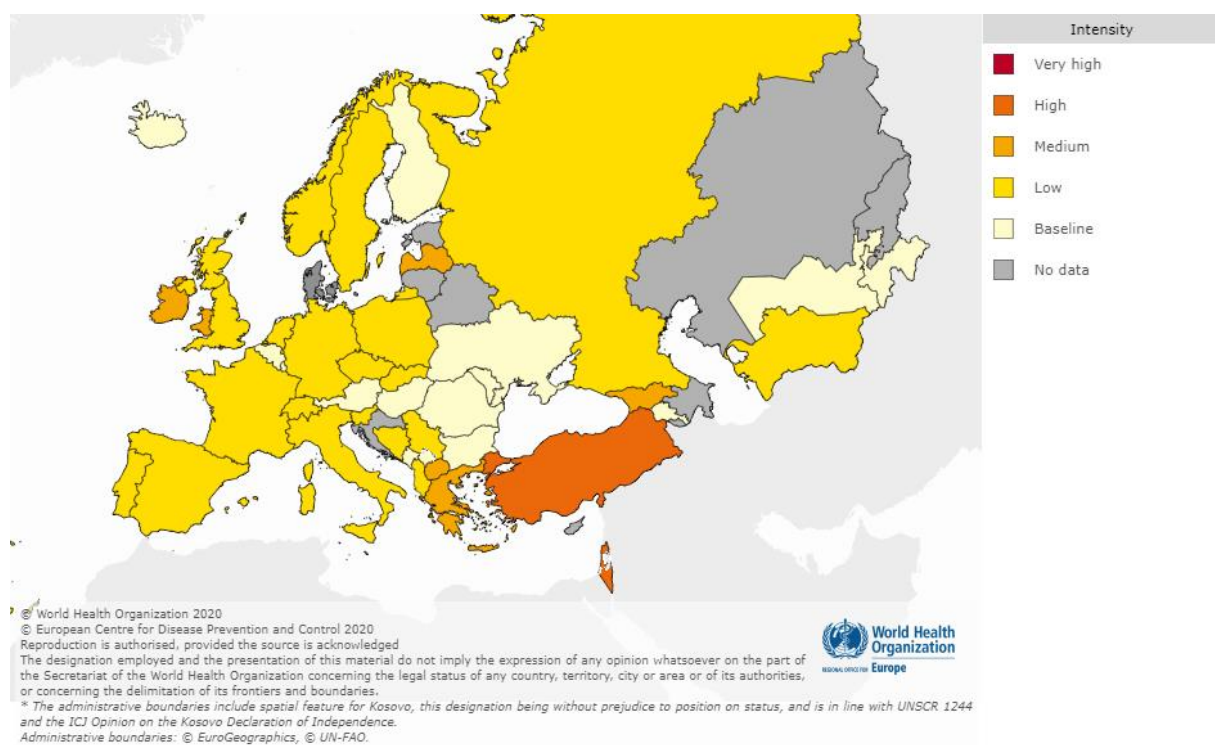
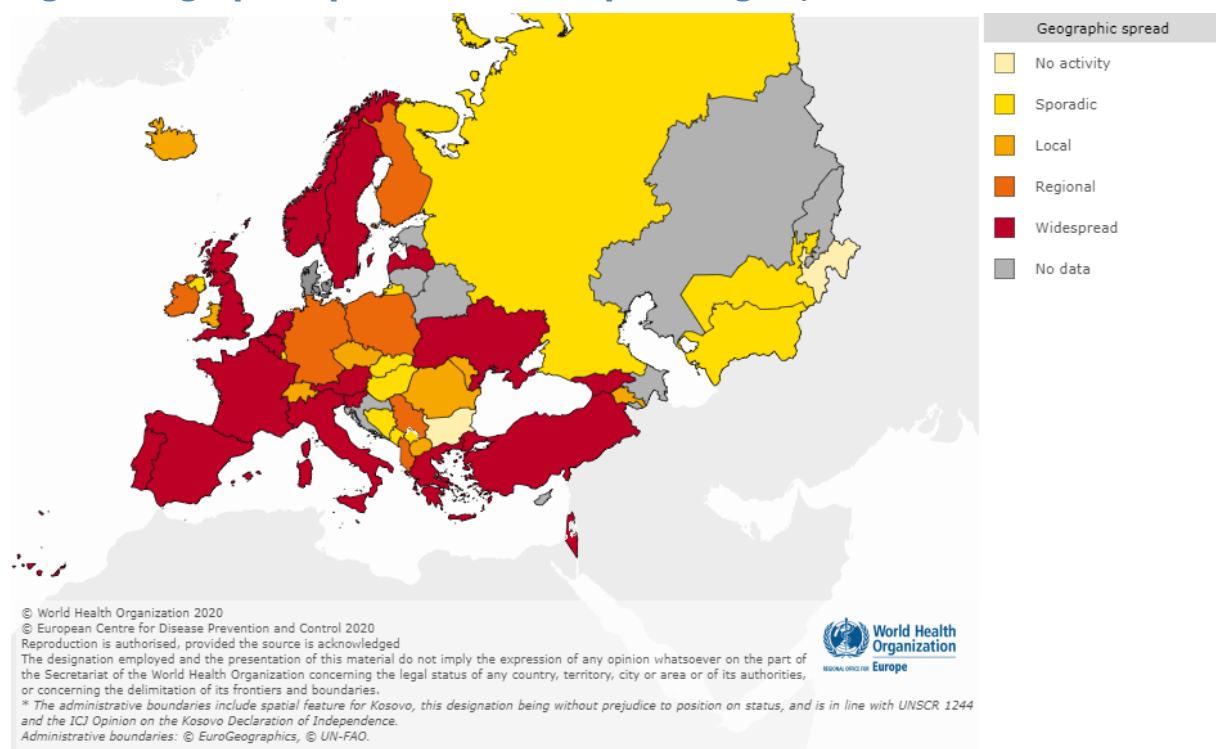


Fig. 2. Geographic spread in the European Region, week 02/2020



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

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

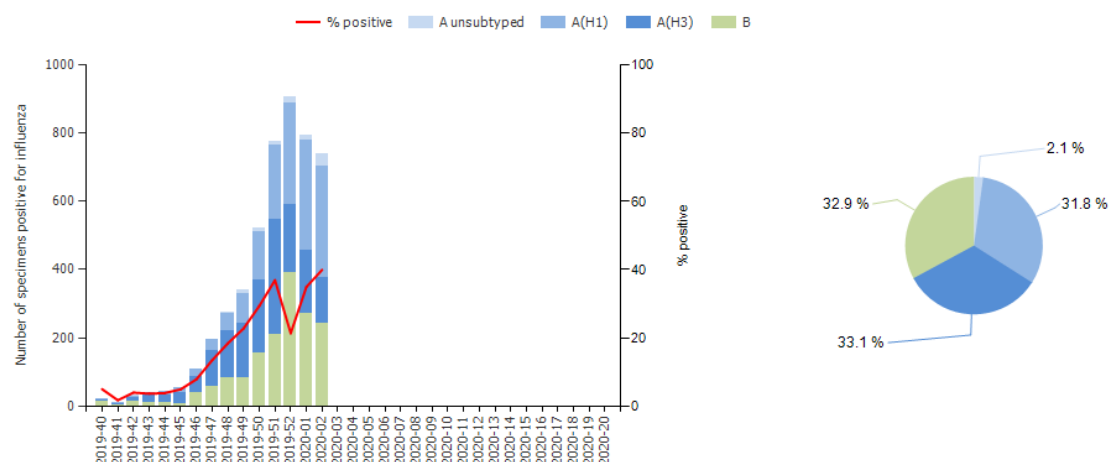
For week 02/2020, 737 (40%) of 1 856 sentinel specimens tested positive for an influenza virus; 67% were type A and 33% were type B (Fig. 3 and Table 1). Of 460 subtyped A viruses, 70% were A(H1N1)pdm09 and 30% were A(H3N2) (Fig. 3 and Table 1). Of 44 type B viruses ascribed to a lineage, all but two were B/Victoria (Table 1).

Of 31 Member States or areas across the Region that each tested at least 10 sentinel specimens from week 02/2020, 17 reported rates of influenza virus detections above 30% (median 46%; range 33% - 80%).

For the season to date, more influenza type A (n=3 253, 67%) than type B (n=1 593, 33%) viruses have been detected (Fig. 3 and Table 1). Of 3 149 subtyped A viruses, 1 606 (51%) were A(H3N2) and 1 543 (49%) were A(H1N1)pdm09. Of 406 influenza type B viruses ascribed to a lineage, 98% were B/Victoria and 2% were B/Yamagata (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



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^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 02/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	496	67.3	3 253	67.1
A(H1N1)pdm09	324	70.4	1 543	49
A(H3N2)	136	29.6	1 606	51
A not subtyped	36	-	104	-
Influenza B	241	32.7	1 593	32.9
B/Victoria lineage	42	95.5	397	97.8
B/Yamagata lineage	2	4.5	9	2.2
Unknown lineage	197	-	1 187	-
Total detections (total tested)	737 (1 856)	39.7	4 846 (22 776)	21.3

^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.

Influenzanet

[Influenzanet](#) is a European wide initiative providing surveillance of influenza-like illness (ILI) in the general population using citizens self-reported symptoms. This week, all 8 participating countries reported less than 20 ILI cases per 1 000 active participants, except for Ireland which reported approximately 30 cases per 1 000 active participants. Based on this system, activity was low in all reporting countries: it is below the first quantile of influenza incidence for this time in previous years.

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 (9 Member States and areas) or other wards (7 Member States and areas), with 6 Member States and areas reporting both 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

Among laboratory-confirmed influenza cases reported in ICUs for week 02/2020 (n=166), influenza type A viruses (n=158, 95%) were detected more frequently than influenza type B viruses (n=8, 5%).

Since week 40/2019, more influenza type A (n=1 619, 95%) than type B (n=87, 5%) viruses were detected. Of 507 subtyped influenza A viruses, 68% were A(H3N2) and 32% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 326 cases with known age, 52% were 15-64 years old and 39% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Among laboratory-confirmed influenza cases reported in wards other than ICUs for week 02/2020 (n=239), influenza type A viruses (91%) were detected more frequently than influenza type B viruses (9%).

Since week 40/2019, more influenza type A (n=2 743, 94%) than type B (n=166, 6%) viruses were detected. Of 549 subtyped influenza A viruses, 78% were A(H3N2) and 21% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 2 909 cases with known age, 47% were 65 years and older and 27% were 15-64 years old.

2. SARI surveillance

For week 02/2020, 593 SARI cases were reported by 11 Member States or areas. In total, specimens from 225 SARI cases were tested for influenza viruses and 95 (42%) were positive for influenza virus: 57 type B and 38 type A.

Of 14 042 SARI cases reported since week 40/2019, 13 869 had a recorded age and, of these, 58% were 0–4 years old and 22% were 15–64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=532), type B viruses were the most common (n=362, 68%). Of the 161 influenza type A virus infected cases for which subtyping was performed, 119 were A(H1N1)pdm09 and 42 were A(H3N2) viruses. Of the 126 influenza type B viruses ascribed to a lineage, 119 were B/Victoria and 7 were B/Yamagata.

Mortality monitoring

For week 02/2020, the [EuroMOMO](#) project received data from 22 countries or areas that were included in pooled analyses. Pooled estimates of all-cause mortality were within the expected range 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 02/2020, 6 770 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; 80% were type A and 20% were type B. Of 1 269 subtyped A viruses, 61% were A(H1N1)pdm09 and 39% were A(H3N2). Of 36 influenza type B viruses ascribed to a lineage, all were B/Victoria (Table 2).

For the season to date, more influenza type A (n=41 005, 86%) than type B (n=6 629, 14%) viruses have been detected. Of 11 553 subtyped A viruses, 69% were A(H3N2) and 31% were A(H1N1)pdm09. Of 466 influenza type B viruses ascribed to a lineage, 91% were B/Victoria and 9% B/Yamagata (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 02/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	5 445	80.4	41 005	86.1
A(H1N1)pdm09	778	61.3	3 566	30.9
A(H3N2)	491	38.7	7 987	69.1
A not subtyped	4 176	-	29 452	-
Influenza B	1 325	19.6	6 629	13.9
B/Victoria lineage	36	100	424	91
B/Yamagata lineage	0	0	42	9
Unknown lineage	1 289	-	6 163	-
Total detections (total tested)	6 770 (28 642)		47 634 (283 551)	

^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

538 influenza viruses from weeks 40/2019-02/2020 have been characterized genetically (Table 3):

- 424 (79%) type A: 289 A(H3N2) and 135 A(H1N1)pdm09
- 114 (21%) type B: 99 B/Victoria and 15 B/Yamagata

While the A(H1N1)pdm09 viruses fall within subgroups of subclade 6B.1A5 and subclade 6B.1A7 that are different to that of the vaccine virus A/Brisbane/02/2018 (6B.1A1), it is anticipated that the vaccine virus will be effective based on HI assays conducted with post-infection ferret antisera raised against the vaccine virus.

As seen elsewhere in the world, there is significant genetic diversity among circulating A(H3N2) viruses in the European region for the 2019–2020 influenza season to date, with 56% subclade 3C.2a. and 44% clade 3C.3a. All subclade 3C.2a1 viruses fall 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 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.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2019–02/2020

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	113
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	6
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	16
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	45
A(H3) clade 3C.3a representative A/Kansas/14/2017 ^a	128
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	12
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	104
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017 ^a	4
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	95
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^b	15

^a Vaccine component for 2019–2020 northern hemisphere.

^b Vaccine component of quadrivalent vaccines for use in 2019–2020 northern hemisphere season.

ECDC published a [report](#) in January that largely focused on viruses from across the world, with collection dates after 31 August, that had full length HA gene sequence data deposited in GISAID by 2 January 2020. Since the November 2019 characterisation report, 12 shipments of influenza-positive specimens from European Union/European Economic Area (EU/EEA) countries were received by the WHO Collaborating Centre, London (the Francis Crick Institute). A total of 397 virus specimens have been received, with collection dates after 31 August. A summary of viruses from EU/EEA countries characterized in December is given below. Previously published [influenza virus characterisation reports](#) are also available on the ECDC website.

A(H1N1)pdm09 viruses

17 A(H1N1)pdm09 viruses from EU/EEA countries were characterized antigenically since the last report (for November, published in December), with 16 showing good reactivity with antiserum raised against the 2019–20 vaccine virus, A/Brisbane/02/2018. The 21 viruses

from EU/EEA countries characterized genetically fell within subclades of clade 6B.1A: 15 6B.1A5A, 3 6B.1A5B, 1 6B.1A6 and 2 6B.1A7.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. 17 A(H3N2) viruses were characterized antigenically since the last characterization report. Of the 17, 12 were clade 3C.3a viruses that were antigenically similar to the vaccine virus, A/Kansas/14/2017. The remaining five were subgroup 3C.2a1b+T135K viruses that were poorly recognised by the vaccine virus. Of the 57 viruses characterized genetically, 38 were clade 3C.3a, 11 were subgroup 3C.2a1b+T131K, 3 were subgroup 3C.2a1b+T135K-A and 5 were subgroup 3C.2a1b+T135K-B.

B/Victoria viruses

14 B/Victoria-lineage viruses were characterised in December. All gave antigenic profiles characteristic of the triple deletion subgroup 1A(Δ 3)B, represented by B/Washington/02/2019, the vaccine virus for the 2020 southern hemisphere season. The subgroup has been confirmed for nine of the viruses.

B/Yamagata viruses

1 B/Yamagata-lineage virus was characterised antigenically in December. It reacted poorly with antiserum raised against the vaccine virus B/Phuket/3073/2013 (clade 3) and only reacted well with an antiserum raised against a B/Yamagata-lineage virus carrying multiple unusual substitutions in HA1.

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](#).

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

Antiviral susceptibility testing

Since the beginning of the season, 234 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 128 A(H1N1)pdm09, 84 A(H3N2) and 22 type B viruses. All showed normal inhibition (NI) by both oseltamivir and zanamivir.

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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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