

Summary

Week 52/2019 (23–29 December 2019)

- Although only 25 Member States and areas reported data for week 52, sentinel surveillance data indicated influenza activity was still increasing across the region.
- The majority of reported influenza virus detections from sentinel ILI surveillance across the Region were type A (62%).
- The proportion of influenza A viruses decreased from 75% in week 50 to 62% in week 52; the distribution of A and B viruses varied considerably between Member States and areas.

2019–2020 season overview

- Influenza activity, particularly in sentinel surveillance for ambulatory patients, is still increasing in the European Region, but most countries still reported influenza activity rates that did not exceed baseline levels or were at low levels.
- 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 6 weeks.
- Type A viruses have dominated across the European Region, although a number of countries 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 (97%) is B/Victoria lineage.
- ECDC and WHO Regional Office published a joint [Regional Situation Assessment](#) of the 2019–2020 influenza season up to week 49/2019, which focuses on disease severity and impact on healthcare systems to assist forward planning in Member States.

Primary care data

Syndromic surveillance data

For week 52/2019, of the 34 Member States and areas that have reported influenza-like illness (ILI) thresholds, 3 reported ILI activity above baseline levels; one country each in eastern (Republic of Moldova), southern (Israel) and western (Portugal) areas of the European Region. Of the 17 Member States and areas that have reported acute respiratory infection (ARI) thresholds, none reported ARI above baselines.

Influenza activity

Of 25 Member States and areas that reported on the intensity indicator, 16 reported activity at baseline levels (across the region), 9 reported low (across the region) and 3 reported

medium (France, Israel and United Kingdom (Scotland)) intensity for week 52/2019 (See Fig. 1).

Of 25 Member States and areas that reported on geographic spread, 3 reported no activity (Bulgaria, Tajikistan and Uzbekistan), 12 reported sporadic spread (in eastern, southern and western areas), 3 reported local spread (Luxembourg, Republic of Moldova and Slovakia), 3 reported regional spread (France, Slovenia and Sweden) and 4 reported widespread geographic activity (Finland, Israel, Portugal and United Kingdom (Scotland)) (See Fig. 2).

Fig. 1. Intensity in the European Region, week 52/2019

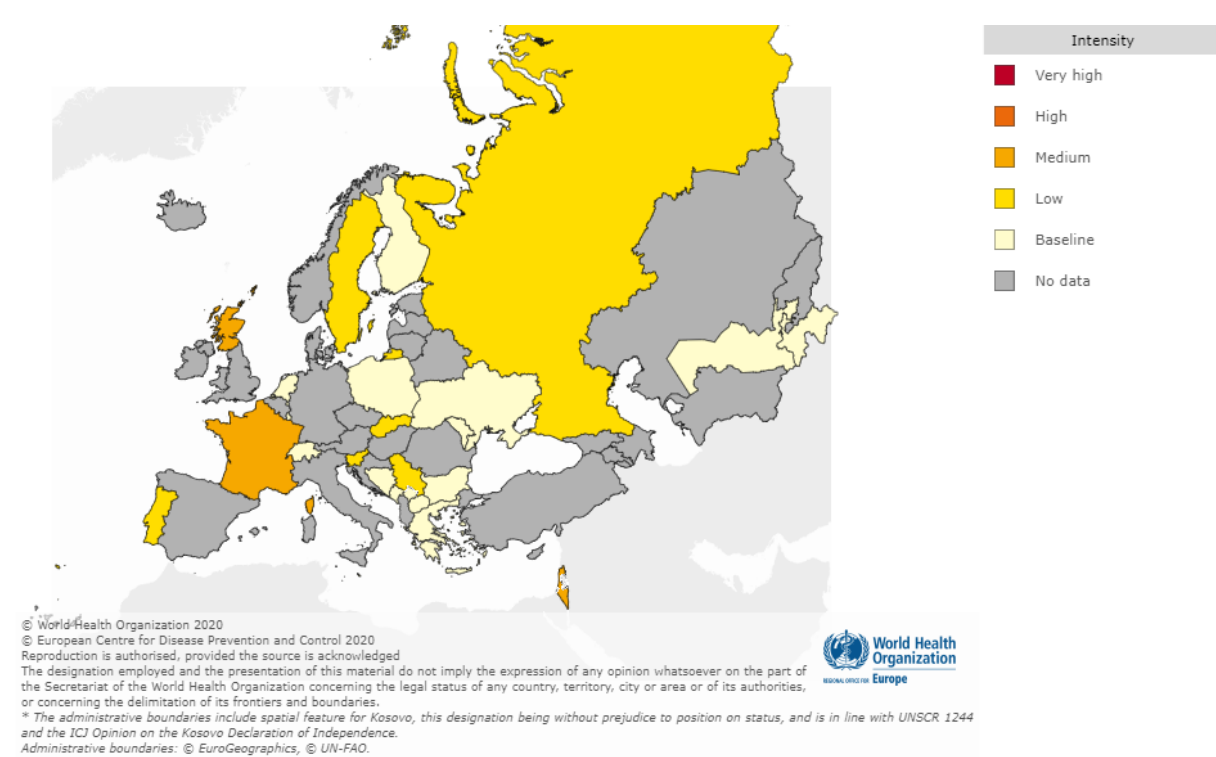
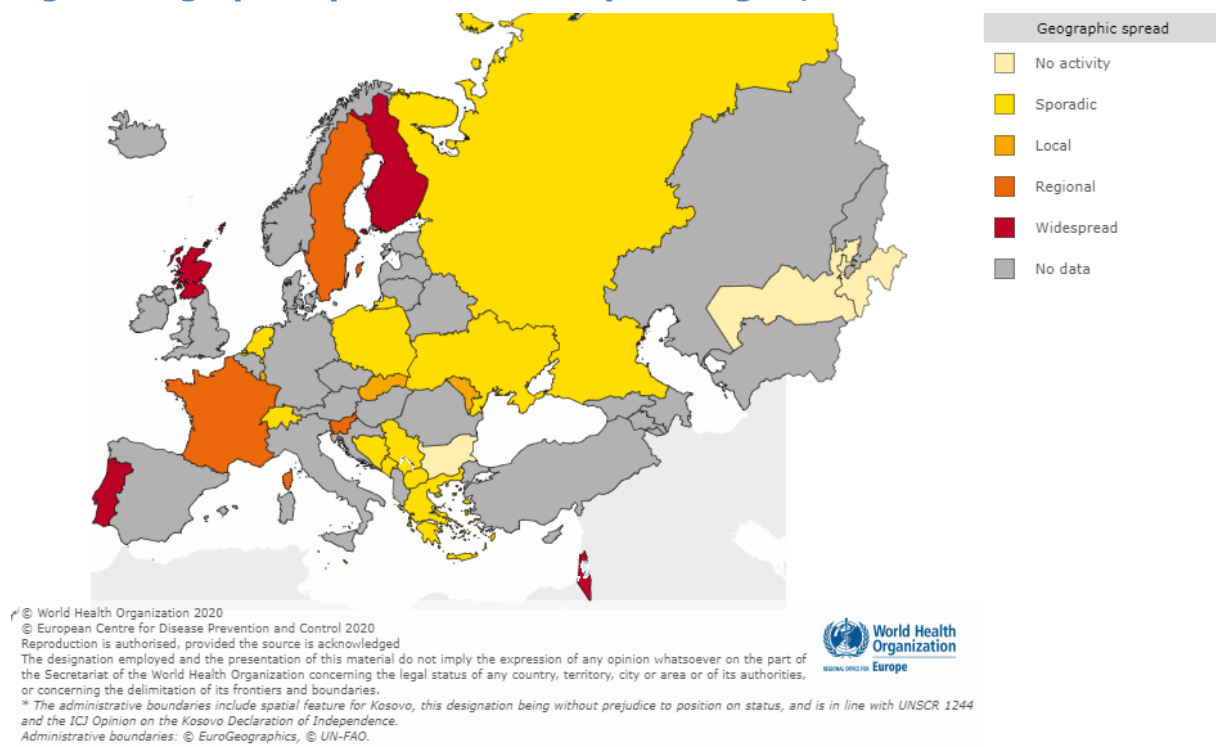


Fig. 2. Geographic spread in the European Region, week 52/2019



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

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

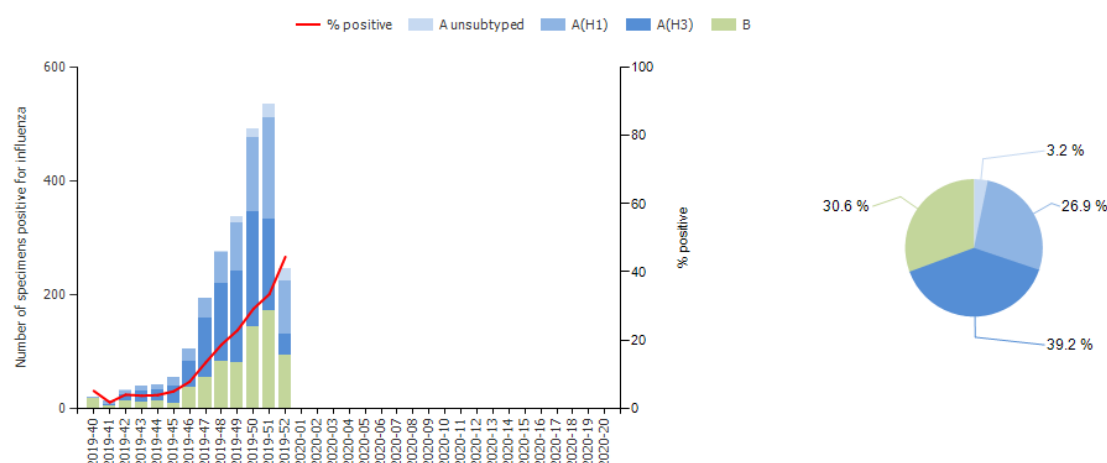
For week 52/2019, 246 (45%) of 552 sentinel specimens tested positive for an influenza virus; 62% were type A and 38% were type B (Fig. 3 and Table 1). Of 130 subtyped A viruses, 72% were A(H1N1)pdm09 and 28% were A(H3N2) (Fig. 3 and Table 1). Of 24 type B viruses ascribed to a lineage, all were B/Victoria (Table 1).

Of 13 Member States or areas across the Region that each tested at least 10 sentinel specimens from week 52/2019, 6 reported rates of influenza virus detections above 30% (median 58%; range 43% - 74%).

For the season to date, more influenza type A (n=1 650, 69%) than type B (n=729, 31%) viruses have been detected (Fig. 3 and Table 1). Of 1 573 subtyped A viruses, 932 (59%) were A(H3N2) and 641 (41%) were A(H1N1)pdm09. Of 200 influenza type B viruses ascribed to a lineage, 97% were B/Victoria and 3% 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 52/2019 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	153	62.2	1 650	69.4
A(H1N1)pdm09	93	71.5	641	40.8
A(H3N2)	37	28.5	932	59.2
A not subtyped	23	-	77	-
Influenza B	93	37.8	729	30.6
B/Victoria lineage	24	100	194	97.0
B/Yamagata lineage	0	0	6	3.0
Unknown lineage	69	-	529	-
Total detections (total tested)	246 (552)	44.6	2 379 (14 369)	16.6

^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.

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).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs for week 52/2019 (n=182), influenza type A viruses (n=175, 96%) were detected more frequently than influenza type B viruses (n=7, 4%).

Since week 40/2019, more influenza type A (n=1 013, 96%) than type B (n=47, 4%) viruses were detected. Of 300 subtyped influenza A viruses, 71% were A(H3N2) and 29% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 108 cases with known age, 47% were 15-64 years old and 42% 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 52/2019 (n=111), influenza type A viruses (95%) were detected more frequently than influenza type B viruses (5%).

Since week 40/2019, more influenza type A (n=1 329, 95%) than type B (n=74, 5%) viruses were detected. Of 307 subtyped influenza A viruses, 86% were A(H3N2) and 14% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 1 403 cases with known age, 40% were 65 years and older and 27% were 15-64 years old.

2. SARI surveillance

For week 52/2019, 229 SARI cases were reported by 8 Member States or areas. In total, specimens from 86 SARI cases were tested for influenza viruses and 16 (19%) were positive for influenza virus: 8 type A and 8 type B.

Of 10 934 SARI cases reported since week 40/2019, 10 829 had a recorded age and, of these, 59% were 0–4 years old and 21% were 15–64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=269), type B viruses were the most common (n=190, 71%). Of the 72 influenza type A virus infected cases for which subtyping was performed, 41 were A(H1N1)pdm09 and 31 were A(H3N2) viruses. Of the 41 influenza type B viruses ascribed to a lineage, 34 were B/Victoria and 7 were B/Yamagata.

Mortality monitoring

No data for week 52/2019 were reported. For week 50/2019, the [EuroMOMO](#) project received data from 21 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 52/2019, 1 703 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; 85% were type A and 15% were type B. Of

309 subtyped A viruses, 53% were A(H1N1)pdm09 and 47% were A(H3N2). Of 4 influenza type B viruses ascribed to a lineage, all were B/Victoria (Table 2).

For the season to date, more influenza type A (n=20 796, 86%) than type B (n=3 350, 14%) viruses have been detected. Of 6 735 subtyped A viruses, 77% were A(H3N2) and 23% were A(H1N1)pdm09. Of 254 influenza type B viruses ascribed to a lineage, 86% were B/Victoria and 14% B/Yamagata (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 52/2019 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	1 447	85.0	20 796	86.1
A(H1N1)pdm09	164	53.1	1 547	23.0
A(H3N2)	145	46.9	5 188	77.0
A not subtyped	1138	-	14 061	-
Influenza B	256	15.0	3 350	13.9
B/Victoria lineage	4	100	218	85.8
B/Yamagata lineage	0	0	36	14.2
Unknown lineage	252	-	3 096	-
Total detections (total tested)	1 703 (9565)	-	24 146 (213 672)	-

^aFor 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

369 influenza viruses from weeks 40–52/2019 have been characterized genetically (Table 3):

- 299 (81%) type A: 215 A(H3N2) and 84 A(H1N1)pdm09
- 70 (19%) type B : 62 B/Victoria and 8 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 58% subclade 3C.2a. and 42% 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 40/2019–52/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	67
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	3
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	14
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	40
A(H3) clade 3C.3a representative A/Kansas/14/2017 ^a	90
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	6
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	79
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017 ^a	3
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	59
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^b	8

^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 December that largely focused on viruses from across the world, with collection dates after 31 August, that had been characterized genetically with data having been submitted to GISAID as of 4 December. Limited detailed influenza virus characterization for influenza-positive specimens from European Union/European Economic Area (EU/EEA) countries, with collection dates from 31 August, was presented as few had been received in a timely manner by the WHO Collaborating Centre, London (the Francis Crick Institute). A summary of viruses from EU/EEA countries characterized in November is given below. Previously published [influenza virus characterisation reports](#) are also available on the website.

A(H1N1)pdm09 viruses

No A(H1N1)pdm09 viruses from EU/EEA countries have been characterized antigenically since the last report (for October, published in November). 2 viruses from EU/EEA countries characterized genetically fell in the 6B.1A5A subgroup.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. 2 A(H3N2) viruses have been characterized antigenically since the last characterization report. Both were clade 3C.3a and antigenically similar to the vaccine virus, A/Kansas/14/2017. Of the 11 viruses characterized genetically, 7 were subgroup 3C.2a1b+T131K, 2 were subgroup 3C.2a1b+T135K-A and 2 were clade 3C.3a.

B/Victoria viruses

No B/Victoria-lineage viruses were characterized in the November reporting period. The 2 viruses from EU/EEA countries characterized genetically since the start of the 2019-20 season were of the triple deletion subgroup 1A(Δ 3)B, represented by B/Washington/02/2019.

B/Yamagata viruses

No B/Yamagata-lineage viruses from EU/EEA countries, or others that share influenza-positive samples with the Francis Crick Institute, have been assessed by HI assay since the October 2019 report.

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_ 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 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, 127 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 61 A(H3N2), 49 A(H1N1)pdm09 and 17 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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