Flu News Europe
Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 51/2019 (16–23 December 2019)

- The majority of reported influenza virus detections across the Region were type A, although 5 countries reported type B virus dominance and 2 reported co-dominance of type A and B viruses.
- Data from the 21 countries or regions that reported to the EuroMOMO project up to week 50/2019 indicated that all-cause mortality was at expected levels for this time of the year.
- 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.

2019–2020 season overview

- Influenza activity has increased in the European Region, although most countries still reported influenza activity rates below/at baseline levels or low levels.
- Influenza activity in the European Region, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019.
- 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%) are B/Victoria lineage.

Primary care data

Syndromic surveillance data

For week 51/2019, of the 33 Member States that reported influenza-like illness (ILI) thresholds, 4 (12%) reported ILI activity above baseline levels; one country each in eastern (Republic of Moldova), northern (United Kingdom (Wales)), southern (Israel) and western (Portugal) areas of the European Region. Of the 16 Member States that reported acute respiratory infection (ARI) thresholds, 1 (6%) (Armenia) reported ARI above baseline level.

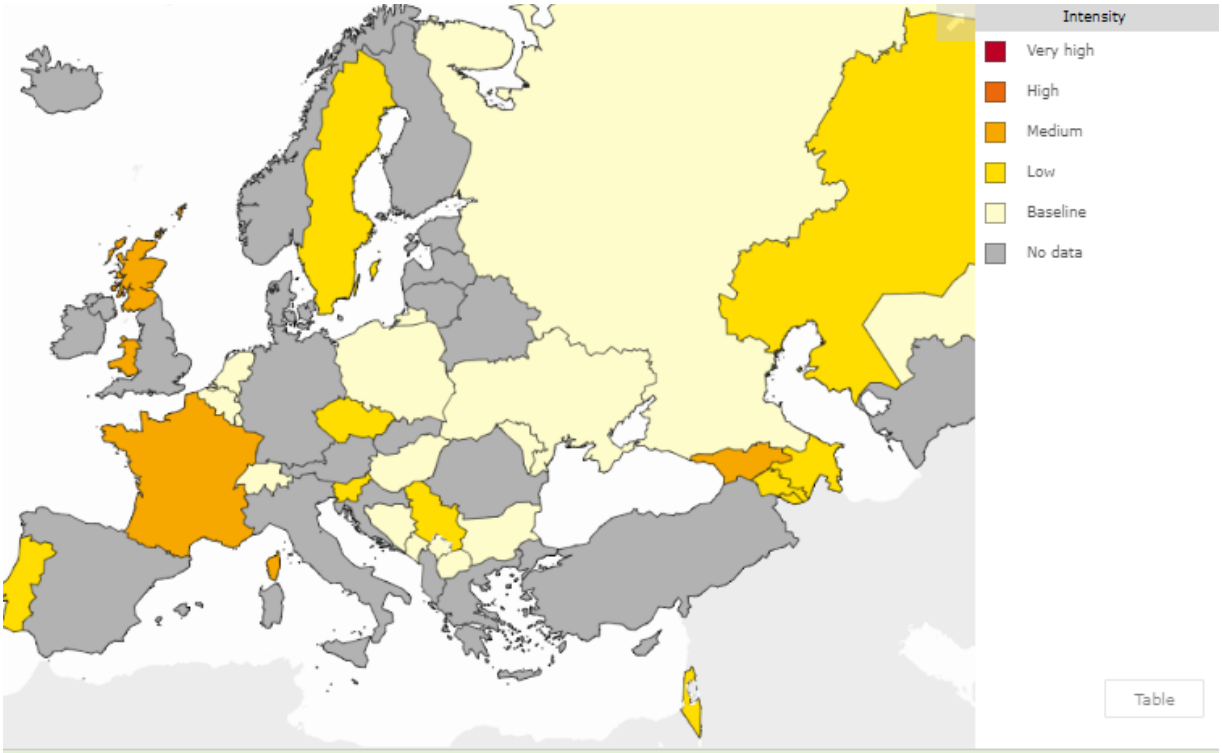
Influenza activity

Of 28 Member States and areas that reported on the intensity indicator, 15 reported activity below/at baseline levels (in eastern, southern, western areas), 9 reported low (across the

region) and 4 reported medium (France, Georgia, United Kingdom (Scotland and Wales)) intensity for week 51/2019 (See Fig. 1).

Of 28 Member States and areas that reported on geographic spread, 4 reported no activity (Azerbaijan, Bulgaria, Hungary, North Macedonia), 14 reported sporadic spread (in eastern, southern, western areas), 4 reported local spread (Czech Republic, Luxembourg, Republic of Moldova, United Kingdom (Wales)), 3 reported regional spread (France, Slovenia, Sweden) and 3 reported widespread geographic activity (Israel, Portugal, United Kingdom (Scotland)) (See Fig. 2).

Fig. 1. Intensity in the European Region, week 51/2019



Map disclaimer

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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 UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.*
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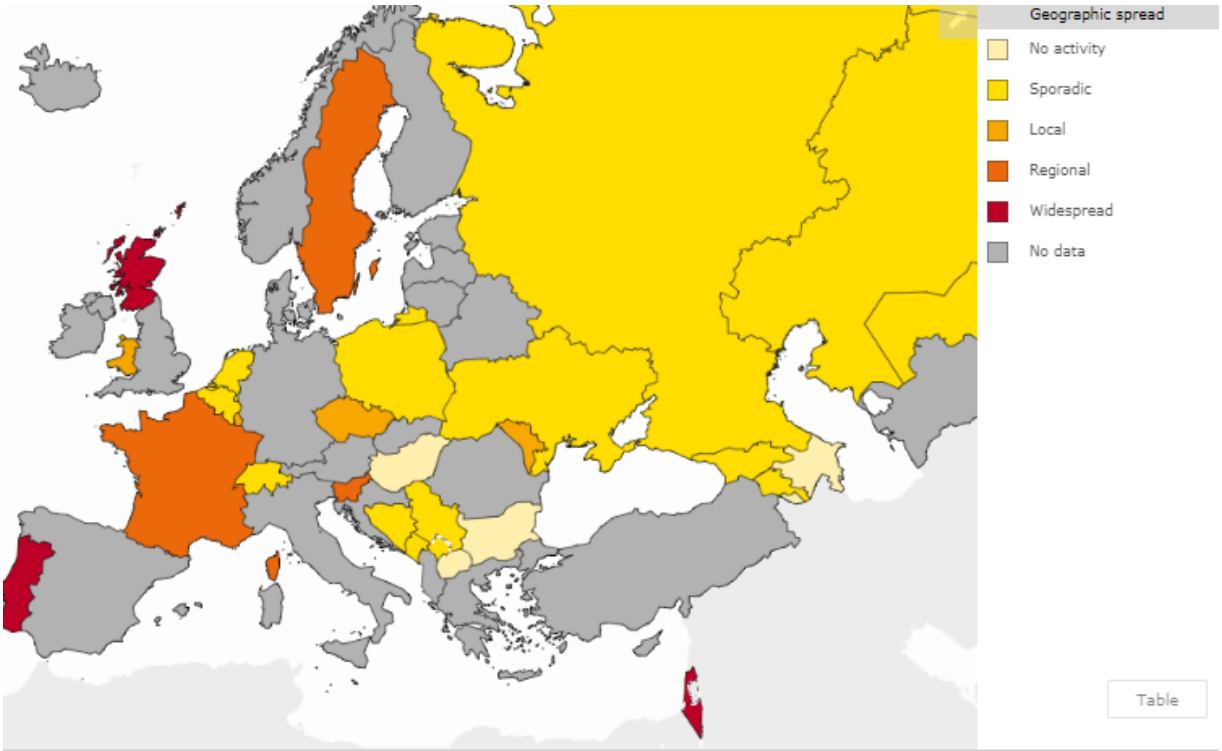
Fig. 2. Geographic spread in the European Region, week 51/2019



For interactive maps of influenza intensity and geographic spread, see the Flu News Europe website.

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

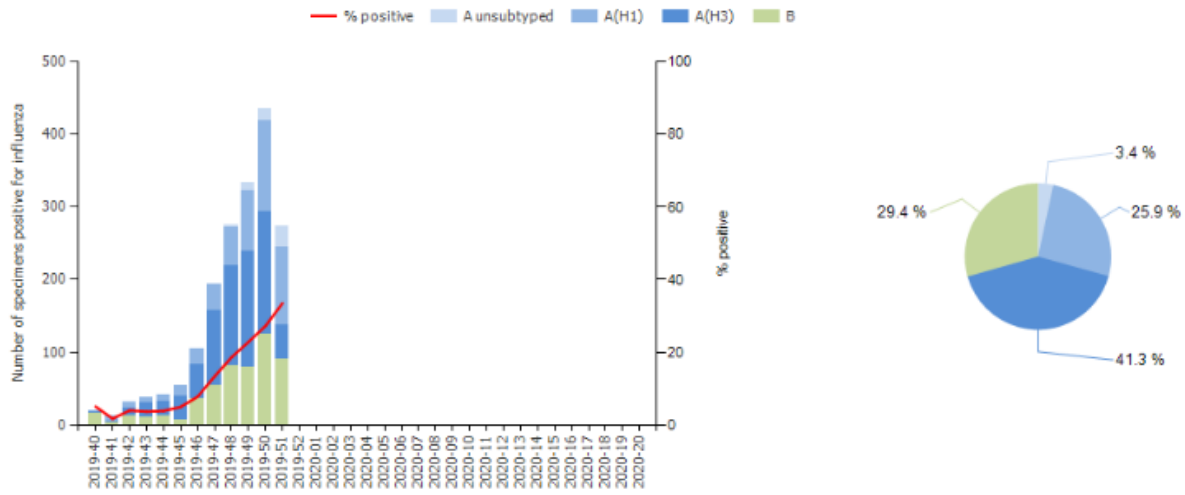
For week 51/2019, 273 (34%) of 799 sentinel specimens tested positive for an influenza virus; 67% were type A and 33% were type B (Fig. 3 and Table 1). Of 154 subtyped A viruses, 69% were A(H1N1)pdm09 and 31% were A(H3N2) (Fig. 3 and Table 1). Of 20 type B viruses ascribed to a lineage, all were B/Victoria (Table 1).

Of 19 Member States or areas across the Region that each tested at least 10 sentinel specimens from week 51/2019, 8 reported rates of influenza virus detections above 30% (median 45.3%; range 31.0% - 78.9%).

For the season to date, more influenza type A (n=1 279, 71%) than type B (n=533, 29%) viruses have been detected (Fig. 3 and Table 1). Of 1 218 subtyped A viruses, 470 (39%) were A(H1N1)pdm09 and 748 (61%) were A(H3N2). Of 149 influenza type B viruses ascribed to a lineage, 97% were B/Victoria (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]



[a] Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 51/2019 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**183**	**67**	**1 279**	**70.6**
A(H1N1)pdm09	106	68.8	470	38.6
A(H3N2)	48	31.2	748	61.4
A not subtyped	29	-	61	-
Influenza B	**90**	**33**	**533**	**29.4**
B/Victoria lineage	20	100	144	96.6
B/Yamagata lineage	0	0	5	3.4
Unknown lineage	70	-	384	-
Total detections (total tested)	**273 (799)**	**34.2**	**1 812 (12 926)**	**14**

[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 monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs or other wards (9 Member States or areas, four of which report 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 51/2019 (n=191), influenza type A viruses (n=187, 98%) were detected more frequently than influenza type B viruses (n=4, 2%).

Since week 40/2019, more influenza type A (n=775, 95%) than type B (n=38, 5%) viruses were detected. Of 233 subtyped influenza A viruses, 25% were A(H1N1)pdm09 and 75% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 81 cases with known age, 44% 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 51/2019 (n=166), influenza type A viruses (93%) were detected more frequently than influenza type B viruses (7%).

Since week 40/2019, more influenza type A (n=971, 94%) than type B (n=60, 6%) viruses were detected. Of 302 subtyped influenza A viruses, 13% were A(H1N1)pdm09 and 87% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 031 cases with known age, 35% were 65 years and older and 27% were 15-64 years old.

2. SARI surveillance

For week 51/2019, 1 268 SARI cases were reported by 12 Member States or areas. In total, specimens from 216 SARI cases were tested for influenza viruses and 51 (24%) were positive for influenza virus: 15 A(H1N1)pdm09, 4 A(H3N2) and 32 type B.

Of 10 106 SARI cases reported since week 40/2019, 10 028 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=227), type B viruses were the most common (n=171, 75%). Of the 52 influenza type A virus infected cases for which subtyping was performed, 35 were A(H1N1)pdm09 and 17 were A(H3N2) viruses. All of 34 influenza type B viruses ascribed to a lineage were B/Victoria.

Mortality monitoring

No data for week 51/2019 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 51/2019, 1 918 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; 78% were type A and 22% were type B. Of

723 subtyped A viruses, 66% were A(H3N2) and 34% were A(H1N1)pdm09. Of 16 influenza type B viruses ascribed to a lineage, 86% were B/Victoria and 14% were B/Yamagata (Table 2).

For the season to date, more influenza type A (n=17 445, 87%) than type B (n=2 687, 13%) viruses have been detected. Of 5 410 subtyped A viruses, 78% were A(H3N2) and 22% were A(H1N1)pdm09. Of 232 influenza type B viruses ascribed to a lineage, 84% were B/Victoria and 16% B/Yamagata (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 51/2019 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**1 501**	**78.3**	**17 445**	**86.7**
A(H1N1)pdm09	243	33.6	1 205	22.3
A(H3N2)	480	66.4	4 205	77.7
A not subtyped	778	-	12 035	-
Influenza B	**417**	**21.7**	**2 687**	**13.3**
B/Victoria lineage	16	100	196	84.5
B/Yamagata lineage	0	0	36	15.5
Unknown lineage	401	-	2 455	-
Total detections (total tested)	**1 918 (13 626)**	**14.1**	**20 132 (191 132)**	**10.5**

[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

348 influenza viruses from weeks 40–51/2019 have been characterized genetically:

- 278 (80%) type A – 210 A(H3N2) and 68 A(H1N1)pdm09
- 70 (20%) type B

See Table 3.

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 40/2019–51/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	51
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]	89
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	5
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	76
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. 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(Δ3)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_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, 126 viruses have been tested for susceptibility to neuraminidase inhibitors: 60 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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