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

Summary

Week 48/2019 (25 November–1 December 2019)

- Influenza activity continued to increase in parts of the region, as indicated by more countries reporting regional or widespread influenza activity. Influenza virus detections in sentinel specimens exceeded 10% for the second consecutive week, which indicates the start of the influenza season at European level.
- A majority of reported influenza virus detections across the region were type A, although 4 countries reported type B virus dominance.
- Data from the 21 countries or regions reporting to the EuroMOMO project indicated that all-cause mortality was at expected levels for this time of the year.

2019–2020 season overview

- Influenza activity is increasing in the European region, although most countries still reported influenza activity rates at baseline or low levels.
- Influenza activity in the European Region, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019.
- Some countries across the European Region have reported influenza type B virus dominance.

Primary care data

Syndromic surveillance data

Of those Member States for which thresholds for influenza-like illness (ILI) activity are defined, only the United Kingdom (Northern Ireland) reported intensity above their baseline level.

Of those Member States for which thresholds for acute-respiratory infection (ARI) activity are defined, only Armenia reported intensity above their baseline level.

Influenza activity

Of 47 Member States and areas reporting on intensity, 41 reported baseline, 5 (Armenia, Azerbaijan, Estonia, Georgia and Lithuania) reported low intensity, and 1 (the United Kingdom (Northern Ireland)) reported medium intensity for week 48/2019 (Fig. 1). Of 46 Member States and areas reporting on geographic spread, 12 reported no activity, 22 reported sporadic cases, 9 reported local spread (across the Region), 1 (the United Kingdom (England)) reported regional spread and 2 (Finland and Portugal) reported widespread activity (Fig. 1).

Fig. 1. Intensity in the European Region, week 48/2019

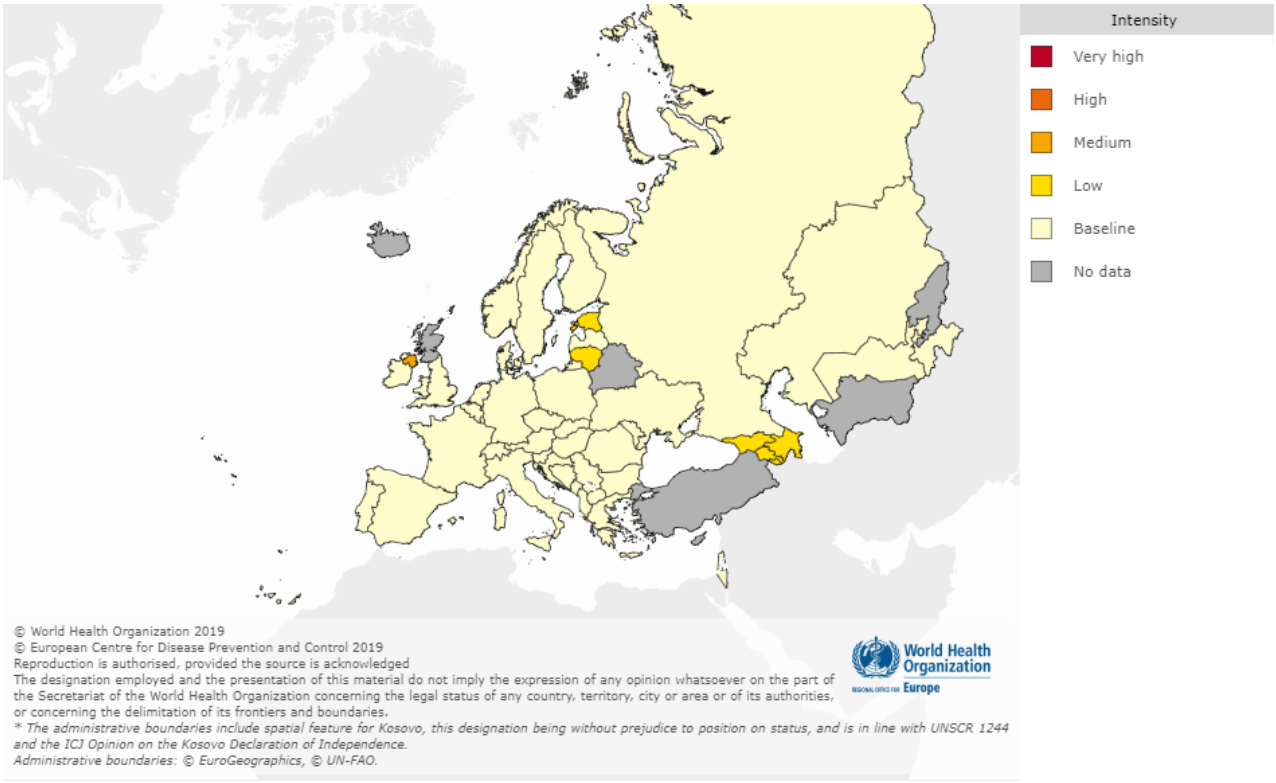
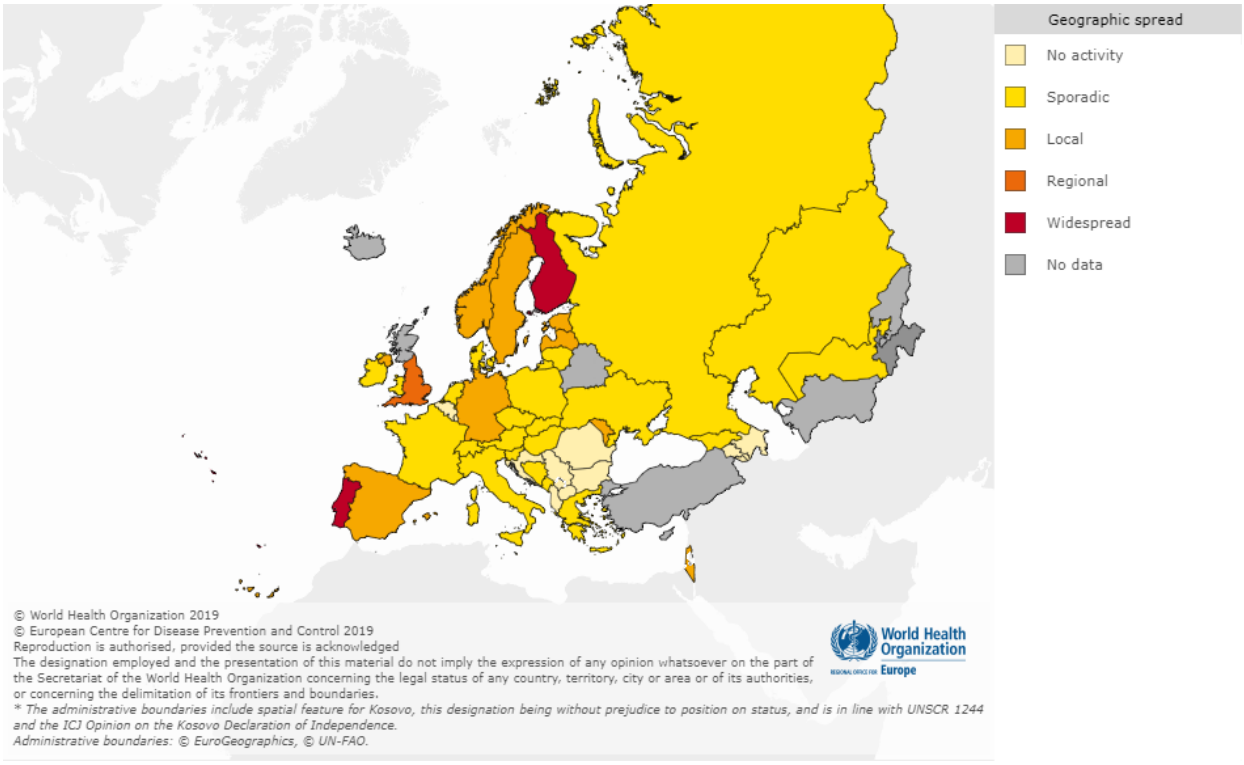


Fig. 2. Geographic spread in the European Region, week 48/2019



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

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

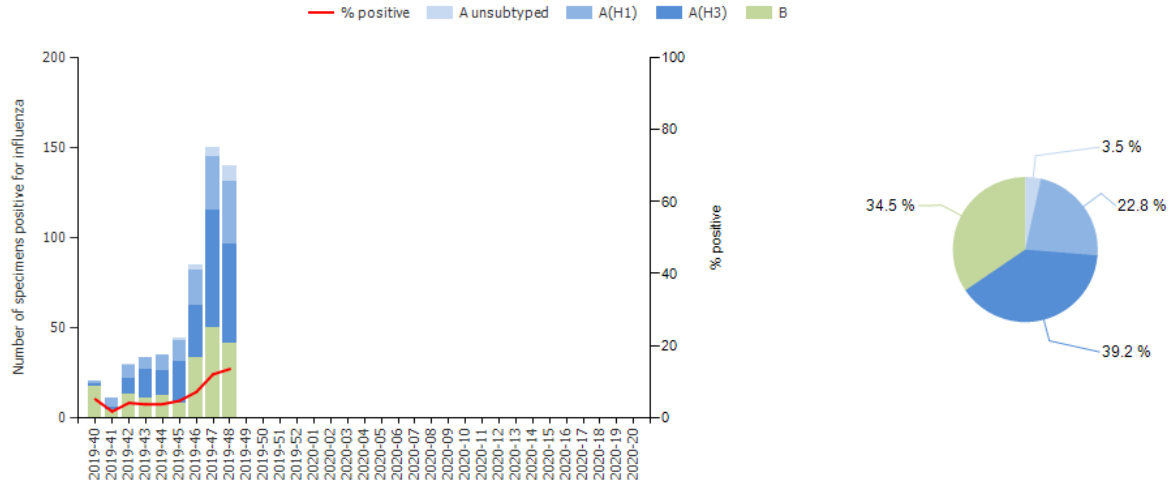
For week 48/2019, 140 (13.8%) of 1 016 sentinel specimens tested positive for influenza viruses; 71% were type A and 29% were type B (Fig. 3 and Table 1). Of 90 subtyped A viruses, 39% were A(H1N1)pdm09 and 61% were A(H3N2) (Fig. 3 and Table 1). Of 13 type B viruses ascribed to a lineage, 12 were B/Victoria and 1 was B/Yamagata (Table 1).

Of 23 Member States and areas across the Region that each tested at least 10 sentinel specimens in week 48/2019, 12 reported a positivity rate above 10%.

For the season overall, more influenza type A (66%) than type B (34%) viruses have been detected (Fig. 3 and Table 1). Of 340 subtyped A viruses, 37% were A(H1N1)pdm09 and 63% were A(H3N2) (Fig. 3 and Table 1). Of 56 influenza type B viruses ascribed to a lineage, 96% were B/Victoria and 4% 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]



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

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 48/2019 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**99**	**70.7**	**359**	**65.5**
A(H1N1)pdm09	35	38.9	125	36.8
A(H3N2)	55	61.1	215	63.2
A not subtyped	9	-	19	-
Influenza B	**41**	**29.3**	**189**	**34.5**
B/Victoria lineage	12	92.3	54	96.4
B/Yamagata lineage	1	7.7	2	3.6
Unknown lineage	28	-	133	-
Total detections (total tested)	**140 (1 016)**	**13.8**	**548 (7 833)**	**7.0**

[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, 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 48/2019 (n=87), influenza type A viruses (n=83, 95%) were detected more frequently than influenza type B viruses (n=4, 5%).

Since week 40/2019, more influenza type A (n=218, 94%) than type B (n=15, 6%) viruses have been detected. Of 57 subtyped influenza A viruses, 32% were A(H1N1)pdm09 and 68% were A(H3N2). None of the influenza B viruses have been ascribed to a lineage. Of 21 cases with known age, 48% were 15–64 years old and 43% 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 48/2019 (n=38), influenza type A viruses (n=28) were detected more frequently than influenza type B viruses (n=7).

Since week 40/2019, more influenza type A (n=180, 92%) than type B (n=16, 8%) viruses have been detected. Of 104 subtyped influenza A viruses, 7% were A(H1N1)pdm09 and 93% were A(H3N2). No influenza B viruses have been ascribed to a lineage. Of 196 cases with known age, 34% were 15–64 years old and 30% were 65 years and older.

2. SARI surveillance

For week 48/2019, 994 SARI cases were reported by 12 Member States or areas. In total, 176 specimens were tested for influenza viruses and 13 (7%) were positive for influenza: 1 A(H1N1)pdm09, 2 A(H3N2) and 10 type B.

Of 7 350 SARI cases reported since week 40/2019, 7 286 had a recorded age and, of these, 59% were 0-4 years old and 20% were 15-64 years old. Of the SARI cases testing positive for an influenza virus since week 40/2019 (n=64), type B viruses were the most common (n=53, 83%). Of the 10 influenza type A infected cases for which subtyping was performed, 1 was A(H1N1)pdm09 and 9 were A(H3N2) viruses. Of 5 influenza type B viruses ascribed to a lineage, all were B/Victoria lineage.

Mortality monitoring

For week 48/2019, 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 48/2019, 2 249 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; 87% were type A and 13% were type B. Of 516 subtyped A viruses, 24% were A(H1N1)pdm09 and 76% were A(H3N2). Of 12 influenza type B viruses ascribed to a lineage, 11 were B/Victoria and 1 was B/Yamagata (Table 2).

For the season to date, more influenza type A (n=5 389, 85%) than type B (n=950, 15%) viruses have been detected. Of 1 673 subtyped A viruses, 22% were A(H1N1)pdm09 and

78% were A(H3N2). Of 81 influenza type B viruses ascribed to a lineage, 85% were B/Victoria and 15% B/Yamagata (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 48/2019 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**1 961**	**87.2**	**5 389**	**85.0**
A(H1N1)pdm09	122	23.6	368	22.0
A(H3N2)	394	76.4	1 305	78.0
A not subtyped	1 445	-	3 716	-
Influenza B	**288**	**12.8**	**950**	**15.0**
B/Victoria lineage	11	91.7	69	85.2
B/Yamagata lineage	1	8.3	12	14.8
Unknown lineage	276	-	869	-
Total detections (total tested)	**2 249 (17 887)**	**-**	**6 339 (124 781)**	**-**

[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

A total of 131 influenza viruses from weeks 40–48/2019 have been characterized genetically, 107 (82%) type A [33 A(H1N1)pdm09 and 74 A(H3N2)] and 24 (18%) type B viruses (Table 3).

While the A(H1N1)pdm09 viruses fall within subgroups of subclade 6B.1A5 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 proportions of 35% clade 3C.3a and 65% subgroup 3C.2a1b (with the latter splitting between 3 designated genetic clusters), being observed. 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 the vaccine.

For the B/Victoria-lineage, viruses in the B/Colorado/06/2017 vaccine virus clade (1A (del 162-163)) have been in the minority. However, there is evidence of some cross-reactivity with viruses in the 1A (del 162-164) clades 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 40/2019–48/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	22
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	11
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	9
A(H3) clade 3C.3a representative A/Kansas/14/2017[a]	26
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	3
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	36
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017[a]	2
B(Vic)-lineage clade 1A (del162-164) representative B/Hong Kong/269/2017	3
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	17
B(Yam)-lineage clade representative B/Phuket/3073/2013[b]	2

[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 November on detailed influenza virus characterizations conducted since week 40/2019 by the WHO Collaborating Centre, London (the Francis Crick Institute), on influenza-positive specimens with collection dates after 31 August 2019, that have been received from European Union/European Economic Area countries. A summary is given below.

A(H1N1)pdm09 viruses

Three test viruses characterized antigenically since the last report were antigenically similar to the vaccine virus used in the 2019–2020 northern hemisphere season (A/Brisbane/02/2018, clade 6B.1A1). The single virus that was genetically characterized at the WHO Collaborating Centre carried the HA1 S183P substitution and fell in the 6B.1A5B subgroup.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the last characterization report, no A(H3N2) viruses have been characterized antigenically or genetically. However, viruses from EU/EEA countries with collection dates in January through August 2019 have HA genes that fall mainly in subclades 3C.2a1b+T131K and 3C.2a1b+T135K, and clade 3C.3a, with the most recently collected viruses (from Norway) falling in subclade 3C.2a1b+T131K.

B/Victoria viruses

Two B/Victoria lineage viruses have been tested by HI in this reporting period. While genetic characterization is pending, the profiles of both viruses indicate that they are of the HA triple deletion group that originated in Africa and are designated as the Δ162-164, 1A(Δ3)B subgroup, represented by B/Washington/02/2019, which was recently recommended for use in vaccines for the southern hemisphere 2020 influenza season. While relatively low numbers

of B/Victoria-lineage viruses have been detected in recent months, the large majority have fallen in this genetic subgroup.

B/Yamagata viruses

Two B/Yamagata lineage viruses have been characterized antigenically in this reporting period. They were similar to the vaccine virus B/Phuket/3073/2013 (clade 3) recommended for use in quadrivalent vaccines for the current northern hemisphere influenza season. While all recently circulating B/Yamagata-lineage viruses contain HA amino acid substitutions compared to B/Phuket/3073/2013, antigenic effects have been minimal based on this and earlier reports.

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, 46 viruses have been tested for susceptibility to neuraminidase inhibitors: 22 A(H3N2), 20 A(H1N1)pdm09 and 4 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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