

Summary

Week 50/2019 (9–15 December 2019)

- Influenza activity continued to increase across the Region: more countries or territories reported increases for intensity and geographic spread compared to the previous week.
- The majority of reported influenza virus detections across the Region were type A, although 5 countries reported type B virus dominance and 3 other countries reported co-dominance of types A and B viruses.
- 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.
- ECDC and WHO Europe published a joint [Regional Situation Assessment](#) of the 2019/20 influenza season as at 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 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.
- Type A viruses 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.

Primary care data

Syndromic surveillance data

For week 50/2019, of the 34 Member States with influenza-like illness (ILI) thresholds, 8 (24%) reported ILI activity above baseline levels; 3 countries (Ireland, Latvia and United Kingdom (England)) were in northern areas, 3 countries (Croatia, Israel and Italy) in southern areas and 2 countries (Austria and Portugal) in western areas of the European Region. Of the 17 Member States reporting acute respiratory infection (ARI) thresholds, 1 (6%) (Armenia) reported ARI above baseline level.

Influenza activity

Of 46 Member States and areas reporting on the intensity indicator, 30 reported activity at baseline levels, 13 reported low and 3 reported medium (Georgia, Latvia and United Kingdom (Scotland)) intensity for week 50/2019 (See Fig. 1).

Of 46 Member States and areas reporting on geographic spread, 8 reported no activity (in eastern, southern and western areas), 19 reported sporadic spread (across the region), 6

reported local spread (in northern and western areas), 5 reported regional spread (Austria, Israel, Italy, Sweden and Ukraine) and 8 reported widespread geographic activity (See Fig. 2).

Fig. 1. Intensity in the European Region, week 50/2019

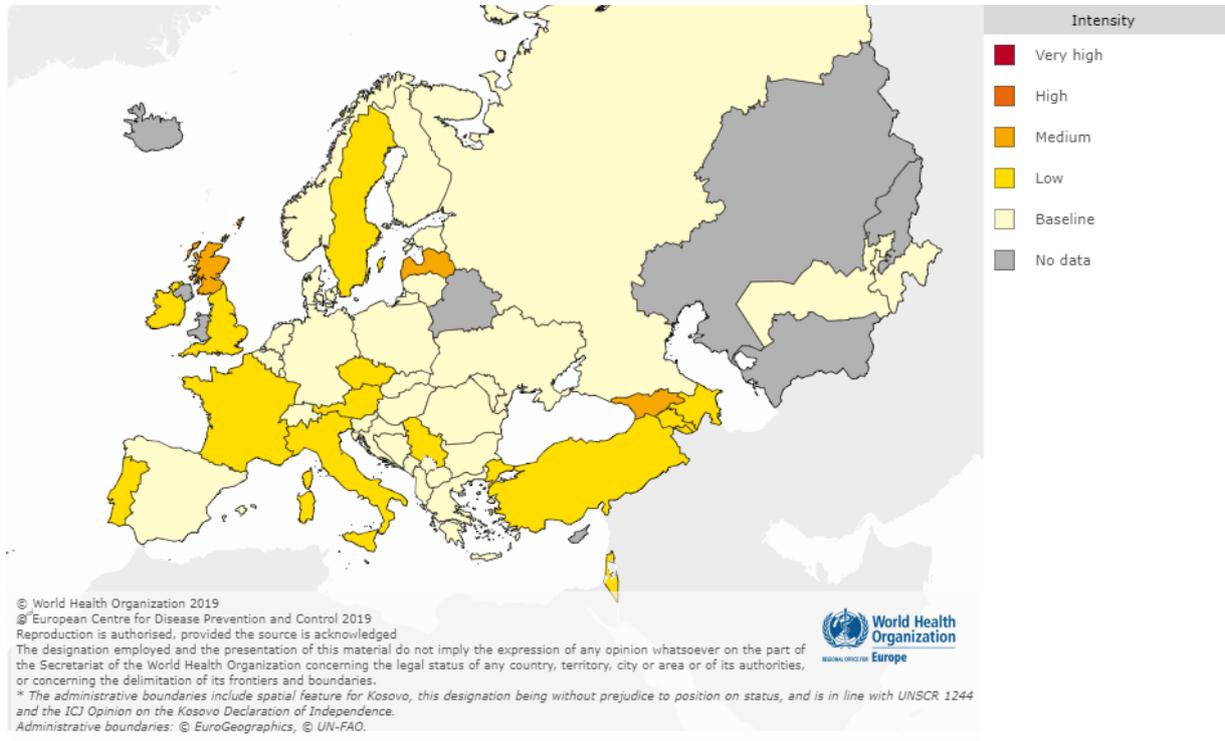
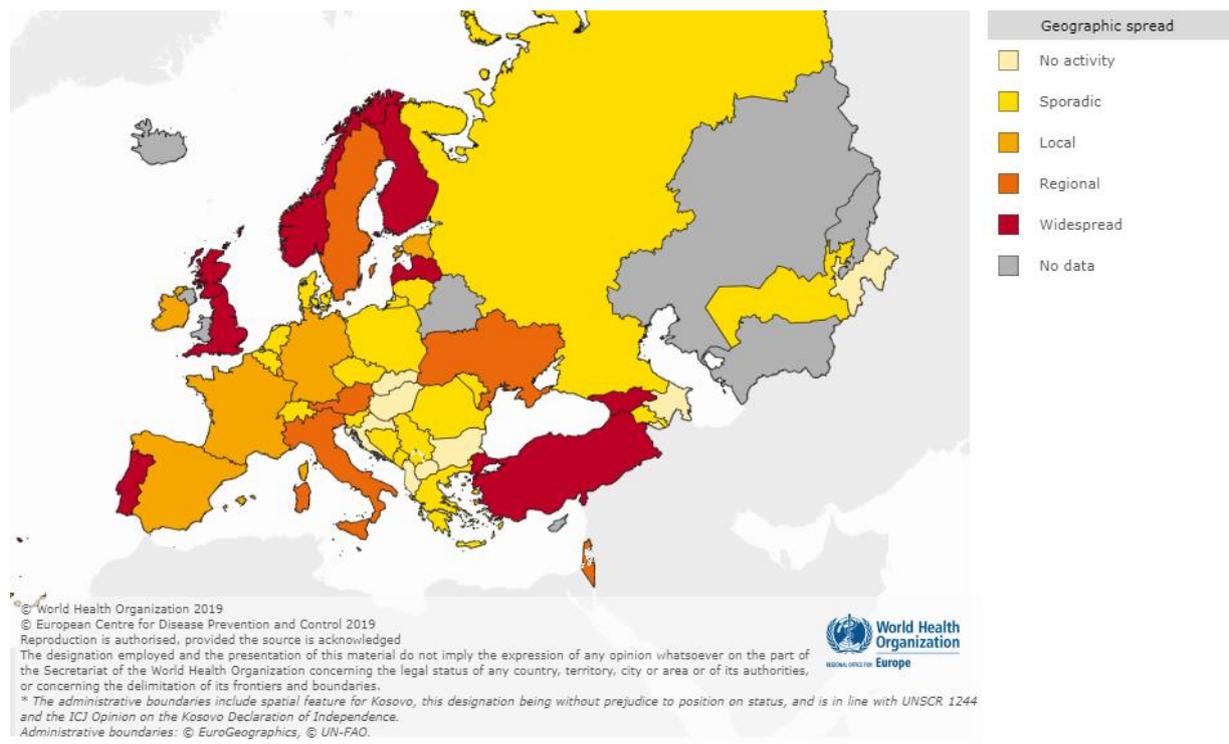


Fig. 2. Geographic spread in the European Region, week 50/2019



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

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

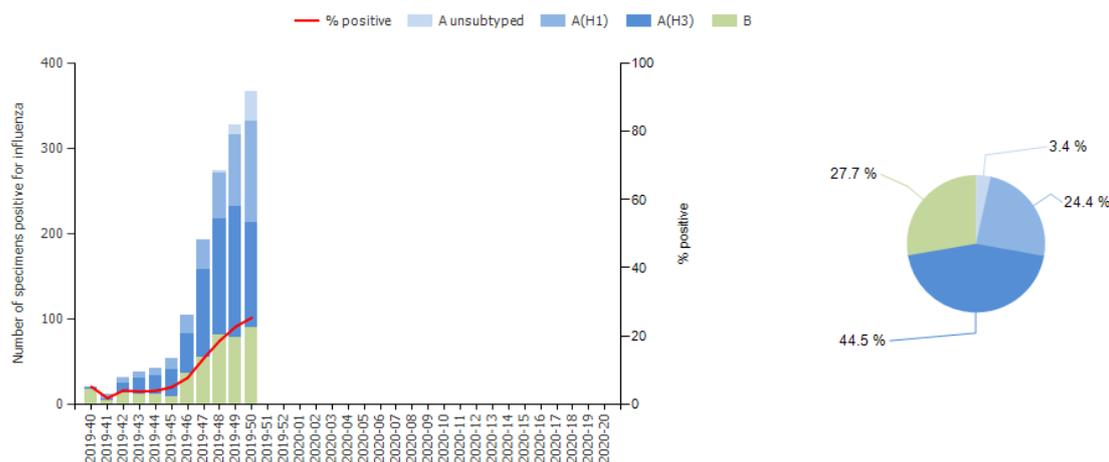
For week 50/2019, 366 (26%) of 1 413 sentinel specimens tested positive for an influenza virus; 75% were type A and 25% were type B (Fig. 3 and Table 1). Of 241 subtyped A viruses, 51% were A(H3N2) and 49% were A(H1N1)pdm09 (Fig. 3 and Table 1). Of 27 type B viruses ascribed to a lineage, all were B/Victoria (Table 1).

Of 30 Member States or areas across the Region that each tested at least 10 sentinel specimens in week 50/2019, 10 reported rates of influenza virus detections above 30% (median 40%; range 31% - 74%).

For the season to date, more influenza type A (72%) than type B (28%) viruses have been detected (Fig. 3 and Table 1). Of 1 007 subtyped A viruses, 65% were A(H3N2) and 35% were A(H1N1)pdm09. Of 122 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



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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 50/2019 and cumulatively for the season

| Virus type and subtype | Current Week | | Season 2019–2020 | |
|--|--------------------|----------------|-----------------------|----------------|
| | Number | % ^a | Number | % ^a |
| Influenza A | 276 | 75.4 | 1 057 | 72.3 |
| A(H1N1)pdm09 | 118 | 49 | 357 | 35.5 |
| A(H3N2) | 123 | 51 | 650 | 64.5 |
| A not subtyped | 35 | - | 50 | - |
| Influenza B | 90 | 24.6 | 405 | 27.7 |
| B/Victoria lineage | 27 | 100 | 117 | 95.9 |
| B/Yamagata lineage | 0 | 0 | 5 | 4.1 |
| Unknown lineage | 63 | - | 283 | - |
| Total detections (total tested) | 366 (1 413) | 25.9 | 1 462 (11 952) | 12.2 |

^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 or other wards (5 Member States or areas, two 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 50/2019 (n=193), influenza type A viruses (n=185, 96%) were detected more frequently than influenza type B viruses (n=8, 4%).

Since week 40/2019, more influenza type A (n=576, 94%) than type B (n=34, 6%) viruses were detected. Of 177 subtyped influenza A viruses, 28% were A(H1N1)pdm09 and 72% were A(H3N2). None of the influenza B viruses have been ascribed to a lineage. Of 70 cases with known age, 44% were 15–64 years old and 40% 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 50/2019 (n=143), influenza type A viruses (92%) were detected more frequently than influenza type B viruses (8%).

Since week 40/2019, more influenza type A (n=625, 94%) than type B (n=40, 6%) viruses have been detected. Of 224 subtyped influenza A viruses, 86% were A(H3N2) and 14% were A(H1N1)pdm09. None of the influenza B viruses have been ascribed to a lineage. Of 348 cases with known age, 35% were 65 years and older and 29% were 15–64 years old.

2. SARI surveillance

For week 50/2019, 471 SARI cases were reported by 12 Member States or areas. In total, specimens from 183 SARI cases were tested for influenza viruses and 29 (16%) were positive for influenza virus: 11 A(H1N1)pdm09, 3 A(H3N2) and 15 type B.

Of 8 834 SARI cases reported since week 40/2019, 8 756 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=152), type B viruses were the most common (n=119, 78%). Of the 31 influenza type A virus infected cases for which subtyping was performed, 18 were A(H1N1)pdm09 and 13 were A(H3N2) viruses. Of 16 influenza type B viruses ascribed to a lineage, all were B/Victoria.

Mortality monitoring

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 50/2019, 4 390 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; 86% were type A and 14% were type B. Of 611 subtyped A viruses, 61% were A(H3N2) and 39% were A(H1N1)pdm09. Of 21 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=15 418, 87%) than type B (n=2 221, 13%) viruses have been detected. Of 4 152 subtyped A viruses, 78% were A(H3N2) and 22% were A(H1N1)pdm09. Of 193 influenza type B viruses ascribed to a lineage, 82% were B/Victoria and 18% B/Yamagata (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 50/2019 and cumulatively for the season

| Virus type and subtype | Current Week | | Season 2019–2020 | |
|--|-----------------------|----------------|-------------------------|----------------|
| | Number | % ^a | Number | % ^a |
| Influenza A | 3 776 | 86 | 15 418 | 87.4 |
| A(H1N1)pdm09 | 236 | 38.6 | 921 | 22.2 |
| A(H3N2) | 375 | 61.4 | 3 231 | 77.8 |
| A not subtyped | 3 165 | - | 11 266 | - |
| Influenza B | 614 | 14 | 2 221 | 12.6 |
| B/Victoria lineage | 18 | 85.7 | 159 | 82.4 |
| B/Yamagata lineage | 3 | 14.3 | 34 | 17.6 |
| Unknown lineage | 593 | - | 2 028 | - |
| Total detections (total tested) | 4 390 (22 339) | - | 17 639 (174 313) | - |

^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 305 influenza viruses from weeks 40–50/2019 have been characterized genetically, 255 (84%) type A [188 A(H3N2) and 67 A(H1N1)pdm09] and 50 (16%) 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 62% clade 3C.2a and 38% clade 3C.3a, with the great majority falling 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 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 40/2019–50/2019

| Phylogenetic group | Number of viruses |
|---|-------------------|
| A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018 | 50 |
| 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 | 71 |
| 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 | 72 |
| 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 | 39 |
| 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 characterised 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 were characterised antigenically since the last report (for October, published in November). Two viruses from EU/EEA countries characterised genetically fell in the 6B.1A5A subgroup.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Two A(H3N2) viruses were characterised 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 characterised 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 characterised in the November reporting period. The two viruses from EU/EEA countries characterised genetically since the start of the 2019-20 season were 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, 118 viruses have been tested for susceptibility to neuraminidase inhibitors: 58 A(H3N2), 43 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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 50/2019.

Tables and figures should be referenced:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 50/2019.

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