

Summary

Week 1/2019 (31 December 2018–6 January 2019)

- Influenza activity continued to increase in the European Region. Of the individuals sampled after presenting with ILI or ARI to sentinel primary health care sites, 44.6% tested positive for influenza viruses.
- The majority of influenza virus detections were type A in both inpatients and outpatients.
- Both influenza A(H3N2) and A(H1N1)pdm09 viruses were detected.
- Data from the 21 Member States and areas reporting to the [EuroMOMO](#) project indicated all-cause mortality was at expected levels for this time of year.

2018–2019 season overview

- Influenza activity in Europe is increasing, with both subtypes of type A viruses circulating widely. Countries should continue to encourage vaccination.
- Most of the hospitalized laboratory confirmed influenza infections were associated with A(H1N1)pdm09 viruses and were in persons aged 15–64 years.
- The predominant A(H1N1)pdm09 and A(H3N2) viruses circulating match the vaccine components, although relatively low numbers of influenza A(H3N2) viruses have been characterized and concerns related to egg-adaptation of the virus during production persist, as in previous years.
- The northern hemisphere Vaccine Composition Meeting for 2019–2020 has been planned for 18–20 February 2019 in Beijing, China. For more information see [here](#).

Primary care data

Syndromic surveillance data

For week 1/2019, of those Member States in which thresholds for influenza-like illness (ILI) activity are defined, countries in northern (n=55; Estonia, Ireland, Latvia, Lithuania and United Kingdom (England and Wales)), southern (n=3; Greece, Israel and Italy) and western (n=1; Portugal) sectors of the European region reported activity above baseline levels.

Of those Member States and areas in which thresholds for acute respiratory infection (ARI) activity are defined, all reported activity within baseline levels.

Influenza activity

Of 43 Member States and areas reporting on influenza activity, 12 reported baseline (across the region), 28 low (across the region), 2 medium (Portugal and United Kingdom (England)) and 1 high (Malta) intensity for week 1/2019 (Fig. 1).

Of 42 Member States and areas reporting on geographic spread, 5 reported no activity (Azerbaijan, Bulgaria, Luxembourg, The Former Yugoslav Republic of Macedonia and Kosovo), 15 sporadic spread (across the region), 8 local spread (in northern, southern and western areas), 5 regional spread (Israel, the Netherlands, Republic of Moldova, Spain and Ukraine) and 9 widespread (in northern, southern and western areas) activity for week 1/2019 (Fig. 2).

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

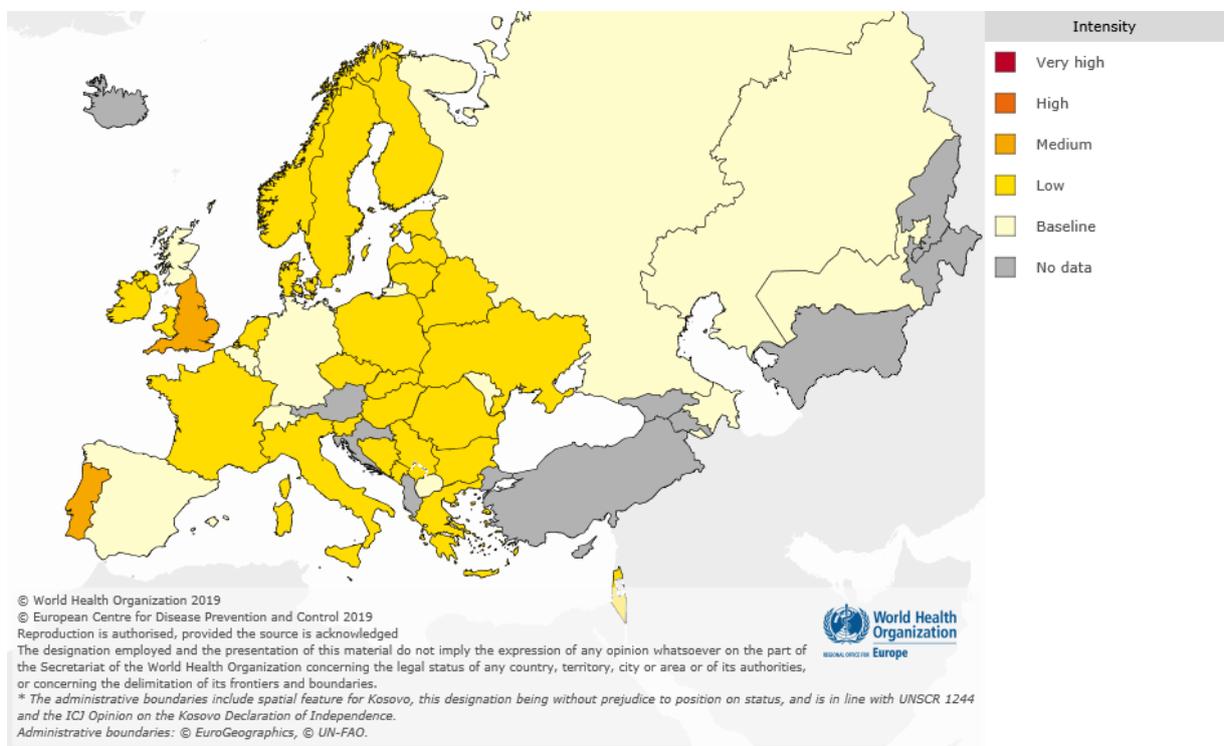
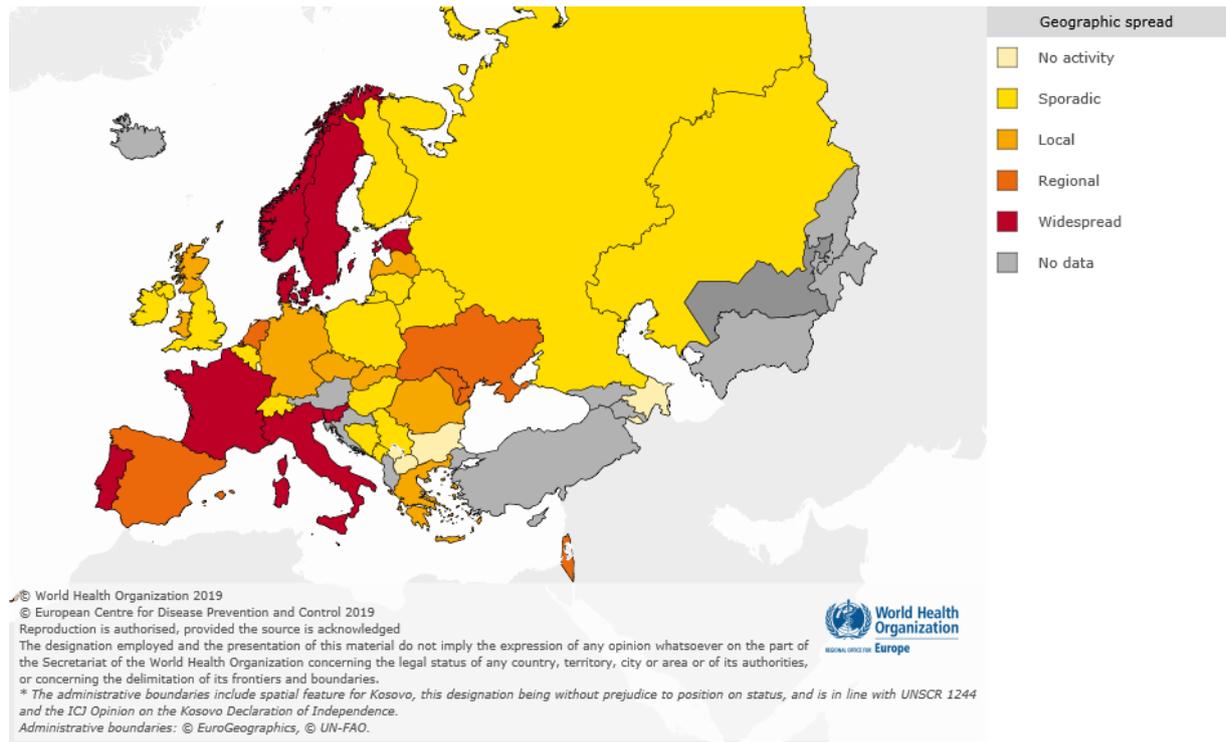


Fig. 2. Geographic spread in the European Region, week 1/2019



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

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

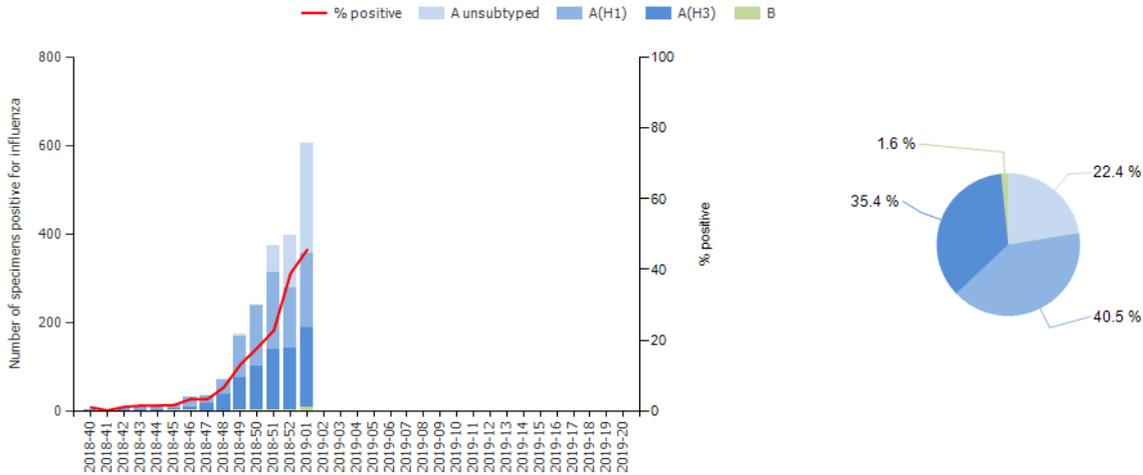
For week 1/2019, 605 (44.6%) of 1 356 sentinel specimens tested positive for an influenza virus; 98.5% were type A and 9 were type B. Of 346 subtyped A viruses, 52% were A(H3N2) and 48% were A(H1N1)pdm09 (Fig. 3 and Table 1). Of 5 type B viruses ascribed to a lineage, 1 was Victoria lineage and 4 were Yamagata lineage (Fig. 3 and Table 1).

Of 26 Member States or areas across the region that each tested at least 10 sentinel specimens in week 01/2019, 16 reported rates of influenza virus detections in the range of 30% to 75.0% (median 49.7%).

For the season to date, more influenza type A (n=1 941, 98.4%) than type B (n=32, 1.6%) viruses have been detected. Of 1 499 subtyped A viruses, 800 (53.4%) were A(H1N1)pdm09 and 699 (46.6%) were A(H3N2). Of 12 influenza type B viruses ascribed to a lineage, 9 were B/Yamagata and 3 were B/Victoria; 20 (62.5%) type B viruses were reported without a lineage (Fig. 3 and 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 ^a



^a Pie chart shows cumulative data for this period.

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

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	596	98.5	1941	98.4
A(H1N1)pdm09	166	48.0	800	53.4
A(H3N2)	180	52.0	699	46.6
A not subtyped	250	-	442	-
Influenza B	9	1.5	32	1.6
B/Victoria lineage	1	20.0	3	25.0
B/Yamagata lineage	4	80.0	9	75.0
Unknown lineage	4	-	20	-
Total detections (total tested)	605 (1356)	44.6	1973 (13 201)	14.9

^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 monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (12 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infections (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs in week 1/2019 (n=252), influenza type A viruses (n=250, 99.2%) were detected more frequently than influenza type B viruses (n=2, 0.8%).

Since week 40/2018, more influenza type A (n=889, 97.3%) than type B (n=25, 2.7%) viruses were detected. Of 366 subtyped influenza A viruses, 318 (86.9%) were A(H1N1)pdm09 and 48 (13.1%) A(H3N2). No influenza B viruses were ascribed to a lineage. Of 248 cases with known age, 45.2% were 15–64 years old and 44.8% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Laboratory-confirmed influenza cases reported in wards other than ICUs in week 1/2019 (n=156) were all infected with influenza type A viruses.

Since week 40/2018, more influenza type A (n=885, 97.7%) than type B (n=21, 2.3%) viruses were detected. Of 171 subtyped influenza A viruses, 122 (71.3%) were A(H1N1)pdm09 and 49 (28.7%) A(H3N2). No influenza B viruses were ascribed to a lineage. Of 906 cases with known age, 43.6% were 15–64 years old and 33.7% were 65 years and older.

2. SARI surveillance

For week 1/2019, 960 SARI cases were reported by 11 Member States or areas. Of 118 specimens tested for influenza viruses, 17 (14.4%) were positive and all were type A.

Of 13 908 SARI cases reported since week 40/2018, 13 897 had a recorded age and, of these, 66.4% were 0–4 years old, 17.9% were 15–64 years old and 15.7% were 65 years and older. For SARI cases testing positive for influenza viruses since week 40/2018 (n=394), type A viruses have been the most common (99.7%). Of the 386 influenza type A infected cases for which subtyping was performed, 290 (75.1%) were infected by A(H1N1)pdm09 viruses and 96 (24.9%) were infected by A(H3N2) viruses. The influenza B virus was ascribed to the B/Victoria lineage.

Mortality monitoring

For week 1/2019, the [EuroMOMO](#) project received data from 21 Member States or areas that were included in pooled analyses. The pooled estimates of all-cause mortality showed expected levels for this time of year in the participating countries.

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 1/2019, 4 896 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 an influenza virus; 4 851 (99.1%) were type A and 45 (0.9%) type B. Of 1 068 subtyped A viruses, 70.7% were A(H1N1)pdm09 and 29.3% were A(H3N2).

For the season so far, a substantially greater number of influenza type A (n=15 690, 97.6%) than type B viruses (n=386, 2.4%) has been detected. Of 4 779 subtyped A viruses, 68.8% were A(H1N1)pdm09 and 31.2% A(H3N2). Of 13 influenza type B viruses ascribed to a lineage, 6 were B/Yamagata and 7 were B/Victoria; 373 type B viruses were reported without a lineage (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 1/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	4851	99.1	15690	97.6
A(H1N1)pdm09	755	70.7	3289	68.8
A(H3N2)	313	29.3	1490	31.2
A not subtyped	3783	-	10911	-
Influenza B	45	0.9	386	2.4
B/Victoria lineage	0		6	46.2
B/Yamagata lineage	0		7	53.8
Unknown lineage	45	-	373	-
Total detections (total tested)	4896 (21 898)	-	16076 (223 326)	-

^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 characterization

Since week 40/2018, genetic characterizations of 215 viruses have been reported: 151 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 62 were A(H3) viruses, with 44 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 3 to the A/Switzerland/8060/2017 (3C.2a2) subgroup, 4 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subgroup, 8 to the A/England/538/2018 (3C.3a) clade and 3 attributed to a subgroup not listed. 1 B/Yamagata lineage virus was characterized as belonging to the B/Phuket/3073/2013 clade (clade 3) and 1 B/Victoria lineage virus was characterized as belonging to the B/Brisbane/60/2008 clade (clade 1A) (Table 3).

Only 14 A(H3N2) viruses have been antigenically characterized, but recent A(H3N2) viruses were shown to be antigenically similar to the reference virus A/Singapore/INFIMH-16-0019/2016 that is the vaccine virus component included in the northern hemisphere vaccine for 2018-2019 (more information can be found [here](#)).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–1/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	151
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	44
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	3
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	4
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	8
A(H3) attributed to recognized group in current guidance but not listed here	3
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	1

^a Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^b Vaccine component for 2019 southern hemisphere season.

^c Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

The latest characterization data are summarized in the [ECDC summary report for November](#).

For more information on virus characterizations for EU/EEA countries, see earlier [WHO CC London Influenza virus characterisation reports](#).

The recommended composition of the trivalent influenza vaccine for the northern hemisphere 2018–2019 season included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and a B/Colorado/06/2017-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. The full report can be found [here](#). A comment by ECDC can be seen [here](#).

On 27 September 2018, WHO announced the recommended vaccine composition for the southern hemisphere 2019 season. The recommendations matched the A(H1N1)pdm09 and B components for the 2018–2019 northern hemisphere season, but the A(H3N2) component was changed for egg-based vaccines. The full report can be found [here](#).

Antiviral susceptibility testing

131 A(H1N1)pdm09, 27 A(H3N2), and 2 type B viruses with collection dates in weeks 40/2018–1/2019 have been tested for susceptibility to neuraminidase inhibitors. 1 A(H1N1)pdm09 and 1 B virus showed evidence of reduced inhibition by neuraminidase inhibitors.

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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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