

Summary

Week 52/2018 (24–30 December 2018)

- Influenza activity continued to increase in the European Region. Of the individuals sampled after presenting with ILI or ARI to sentinel primary healthcare sites, 37% tested positive for influenza viruses.
- The majority of influenza virus detections were type A in both inpatients and outpatients.
- From sentinel samples, influenza A(H3N2) and A(H1N1)pdm09 viruses were detected in similar proportions.
- From non-sentinel samples, about two third of the A viruses were A(H1N1)pdm09.
- Most of the hospitalized laboratory confirmed influenza infections were associated with A(H1N1)pdm09 virus and were in persons aged 15–64 years.
- The predominant A(H1N1)pdm09 and A(H3N2) viruses that are circulating match the vaccine components, although fewer than 50 A(H3N2) viruses have been genetically characterized and only 13 have been antigenically characterized so far.
- Data from the 13 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 A viruses circulating widely. Countries should continue to encourage vaccination.
- 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 52/2018, of those Member States in which thresholds for influenza-like illness (ILI) activity are defined, only Israel reported activity above its baseline level.

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 35 Member States and areas reporting on influenza activity, 11 reported baseline (across the region), 22 low (across the region) and 2 medium (Netherlands and Turkey) intensity for week 52/2018 (Fig. 1).

Of 34 Member States and areas reporting on geographic spread, 5 reported no activity (Albania, Azerbaijan, Bulgaria, The Former Yugoslav Republic of Macedonia and Tajikistan), 12 sporadic spread (across the region), 4 local spread (Greece, Latvia, Slovakia and Uzbekistan), 8 regional spread (across the region) and 5 widespread (Iceland, Norway, Portugal, Sweden and Turkey) activity for week 52/2018 (Fig. 2).

Fig. 1. Intensity in the European Region, week 52/2018

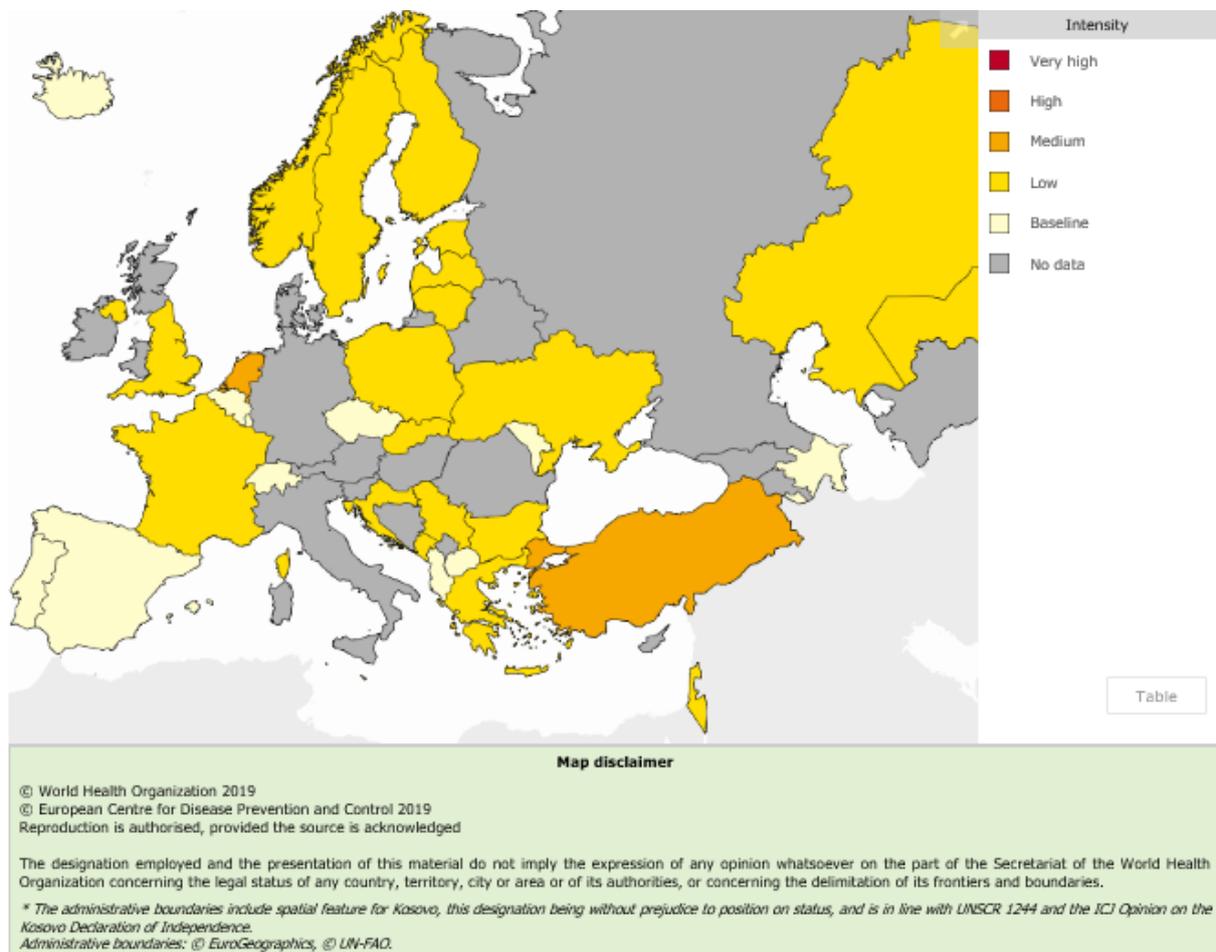
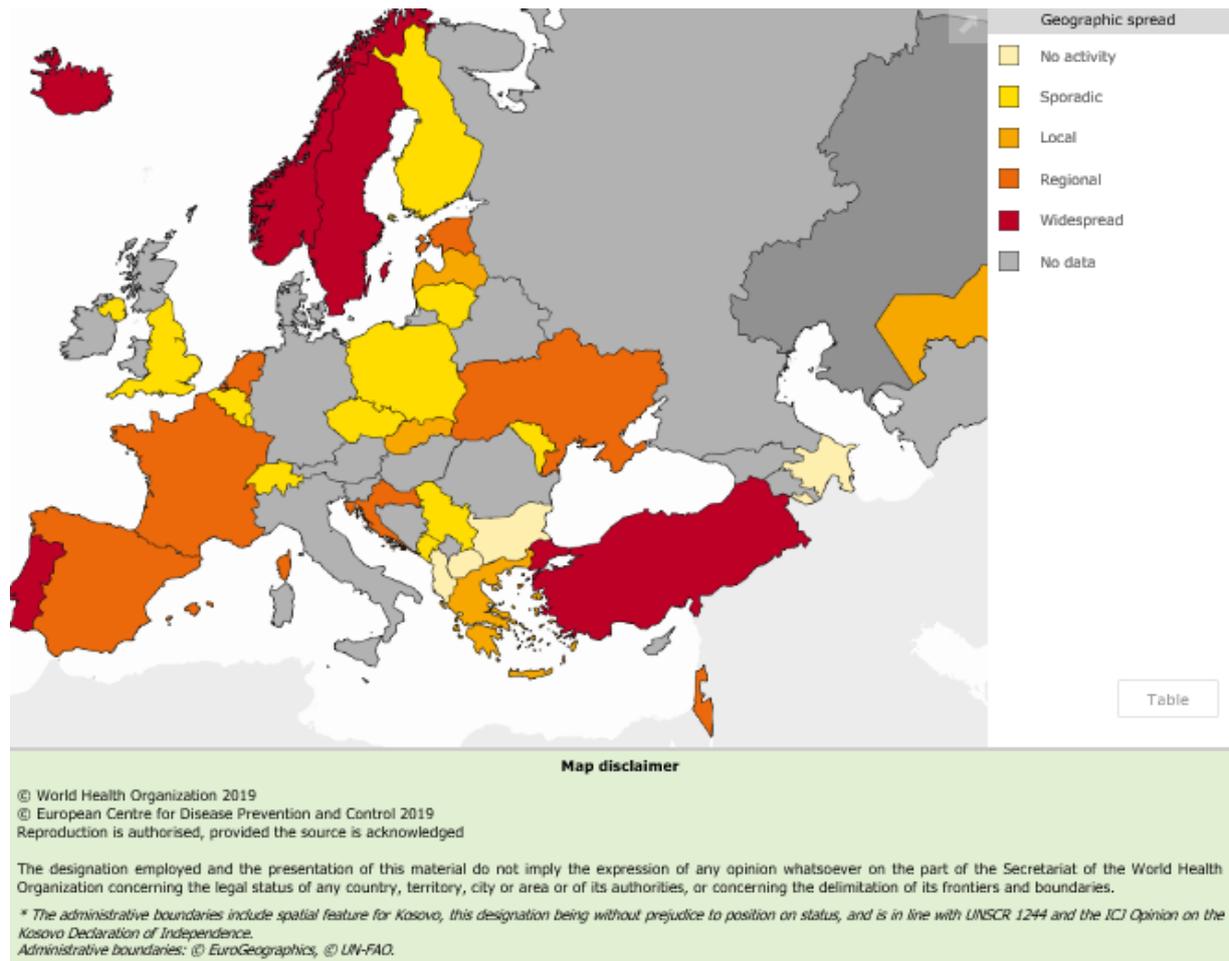


Fig. 2. Geographic spread in the European Region, week 52/2018



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

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

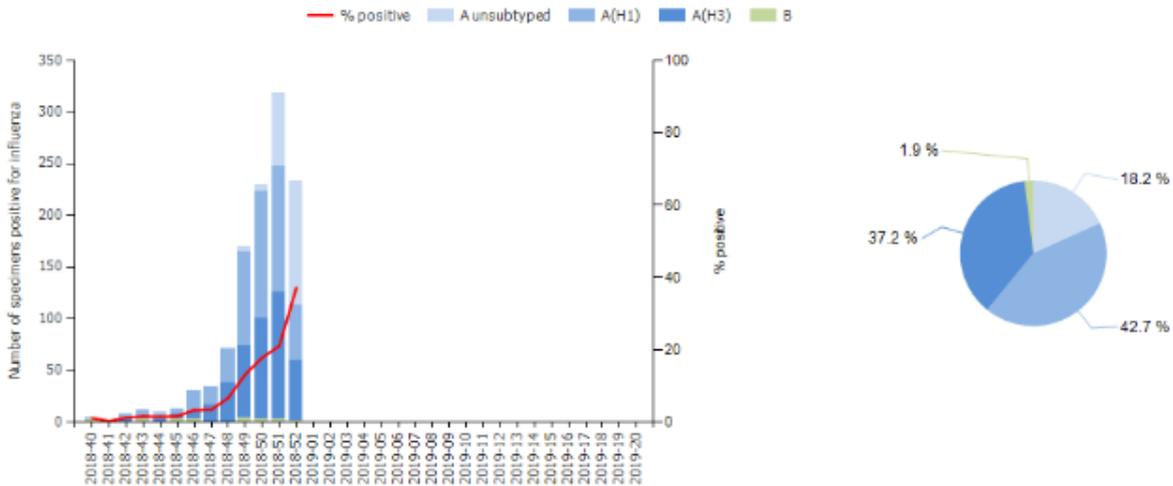
For week 52/2018, 233 (37%) of 629 sentinel specimens tested positive for an influenza virus; 99.6% were type A and 1 was type B. Of 112 subtyped A viruses, 47.3% were A(H1N1)pdm09 and 52.7% A(H3N2) (Fig. 3 and Table 1).

Of 9 Member States or areas across the region that each tested at least 10 sentinel specimens in week 52/2018, 7 reported a rate of influenza virus detections above 10% (median 39.5%; range 12.5% –50.0%).

For the season to date, more influenza type A (n=1110, 98.1%) than type B (n=22, 1.9%) viruses have been detected. Of 904 subtyped A viruses, 483 (53.4%) were A(H1N1)pdm09 and 421 (46.6%) were A(H3N2). Of 6 influenza type B viruses ascribed to a lineage, 5 were B/Yamagata; 16 (72.7%) 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 52/2018 and cumulatively.

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	232	99.6	1 110	98.1
A(H1N1)pdm09	53	47.3	483	53.4
A(H3N2)	59	52.7	421	46.6
A not subtyped	120	-	206	-
Influenza B	1	0.4	22	1.9
B/Victoria lineage	0	0	1	16.7
B/Yamagata lineage	0	0	5	83.3
Unknown lineage	1	-	16	-
Total detections (total tested)	233 (629)	37.0	1 132 (11 221)	-

^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 52/2018 (n=178), influenza type A viruses (176, 98.9%) were detected more frequently than influenza type B viruses (2, 1.1%).

Since week 40/2018, more influenza type A (n=542, 96.1%) than type B (n=22, 3.9%) viruses were detected. Of 245 subtyped influenza A viruses, 86.9% were A(H1N1)pdm09 and 13.1% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 140 cases with known age, 45% were 15–64 years old and 44.3% 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 in week 52/2018 (n=20), all were influenza type A viruses.

Since week 40/2018, more influenza type A (n=352, 94.6%) than type B (n=20, 5.4%) viruses were detected. Of 82 subtyped influenza A viruses, 72% were A(H1N1)pdm09 and 28% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 372 cases with known age, 46.8% were 15–64 years old and 29.3% were 65 years and older.

2. SARI surveillance

For week 52/2018, 918 SARI cases were reported by 8 Member States or areas. Of 56 specimens tested for influenza viruses, 9 (16.1%) were positive and all were type A.

Of 12 562 SARI cases reported since week 40/2018, 12 551 had a recorded age and, of these, 67.8% were 0–4 years old and 16.3% were 15–64 years old. For SARI cases testing positive for influenza viruses since week 40/2018 (n=260), 259 (99.6%) were type A viruses. Of the 252 influenza type A infected cases for which subtyping was performed, 179 (71%) were infected by A(H1N1)pdm09 viruses and 73 (29%) were infected by A(H3N2) viruses. The influenza B virus was ascribed to the B/Victoria lineage.

Mortality monitoring

For week 52/2018, the EuroMOMO project received data from 13 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 52/2018, 1 714 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; 1 695 (98.9%) were type A and 19 (1.1%) type B. Of 261 subtyped A viruses, 63.6% were A(H1N1)pdm09 and 36.4% were A(H3N2).

For the season so far, a substantially greater number of influenza type A (n=8 474, 96.3%) than type B viruses (n=327, 3.7%) has been detected. Of 2 507 subtyped A viruses, 65.7% were A(H1N1)pdm09 and 34.3% A(H3N2). Of 8 influenza type B viruses ascribed to a lineage, 6 were B/Yamagata and 2 were B/Victoria; 319 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 52/2018 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	1 695	98.9	8 474	96.3
A(H1N1)pdm09	166	63.6	1 647	65.7
A(H3N2)	95	36.4	860	34.3
A not subtyped	1 434	-	5 967	-
Influenza B	19	1.1	327	3.7
B/Victoria lineage	0	0	2	25.0
B/Yamagata lineage	0	0	6	75.0
Unknown lineage	19	-	319	-
Total detections (total tested)	1 714 (8 826)	-	8 801 (186 387)	-

^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 176 viruses were reported: 124 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 49 were A(H3) viruses, with 39 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 3 to the A/Switzerland/8060/2017 (3C.2a2) subgroup, 3 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subgroup. Only 13 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](#)). 3 A(H3N2) viruses belonged to the A/England/538/2018 (3C.3a) clade and 1 attributed to a subgroup not listed. 2 B/Yamagata lineage viruses were 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).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–52/2018

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	124
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	39
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	3
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	3
A(H3) attributed to recognized group in current guidance but not listed here	1
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	2

^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

92 A(H1N1)pdm09, 27 A(H3N2), and 2 type B viruses with collection dates in weeks 40–52/2018 have been tested for susceptibility to neuraminidase inhibitors. One 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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