

Summary

Week 3/2019 (14–20 January 2019)

- Influenza activity continued to increase in the European Region. Samples collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza positivity rate of 48.8%.
- Influenza type A virus detections dominated with A(H1N1)pdm09 viruses being more prevalent than A(H3N2). Very few influenza B viruses were detected.
- Data from the 23 Member States and areas reporting to the [EuroMOMO](#) project indicated that generally all-cause mortality was at expected levels for this time of year, but a few countries observed some excess mortality in elderly populations.
- In Sweden, a seasonal reassortant A(H1N2) influenza virus was detected in a specimen collected at the end of December from an adult. Preliminary whole genome sequence analysis suggests that the virus is a seasonal reassortant containing HA and NS, NP, PA, PB1 and PB2 genes of human seasonal A(H1N1)pdm09 influenza virus and NA genes of human seasonal A(H3N2) influenza virus. No increase in virulence is expected compared to seasonal influenza strains. Further analysis is being conducted by the WHO Collaborating Center on influenza. More information can be found [here](#).

2018–2019 season overview

- Influenza activity in Europe continued to increase, with both subtypes of influenza A viruses circulating widely. Countries should continue to promote vaccination. In addition, countries are encouraged to use antivirals in accordance with national guidelines.
- In general, current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. [Preliminary results](#) from Canada where the predominate circulating viruses are influenza A(H1N1)pdm09 viruses, indicate good vaccine effectiveness.

Primary care data

Syndromic surveillance data

For week 3/2019, 16 (50%) of the 32 Member States that calculated influenza-like illness (ILI) thresholds and 6 (33%) of the 18 Member States that calculated acute respiratory infection (ARI) thresholds reported activity above their baseline level.

Of those Member States in which thresholds for ILI activity are defined, countries in eastern (n=2; Republic of Moldova, Russian Federation), northern (n=6; Estonia, Ireland, Latvia, Lithuania, United Kingdom (England and Wales)), southern (n=4; Greece, Israel, Italy,

Montenegro) and western (n=4; Hungary, Netherlands, Portugal, Spain) areas of the European Region reported activity above baseline levels.

Of those Member States and areas in which thresholds for ARI activity are defined, countries in eastern (n=1; Republic of Moldova), northern (n=3; Estonia, Latvia, Lithuania) and southern (n=2; Albania, Bulgaria) areas of the European Region reported activity above baseline levels.

Influenza activity

Of 46 Member States and areas reporting on intensity, 7 reported baseline (eastern, northern, western areas), 22 reported low (across the region), 15 reported medium (across the region), and 2 reported high (Malta, Romania) intensity for week 3/2019 (Fig. 1).

Of 46 Member States and areas reporting on geographic spread, 2 reported no activity (The Former Yugoslav Republic of Macedonia, Uzbekistan), 9 reported sporadic spread (in eastern, northern, western areas), 4 reported local spread (Czech Republic, Ireland, Russian Federation, and Kosovo (in accordance with UNSCR 1244 (1999))), 8 reported regional spread (in eastern, southern, western areas) and 23 reported widespread (across the region) (Fig. 2).

Fig. 1. Intensity in the European Region, week 3/2019

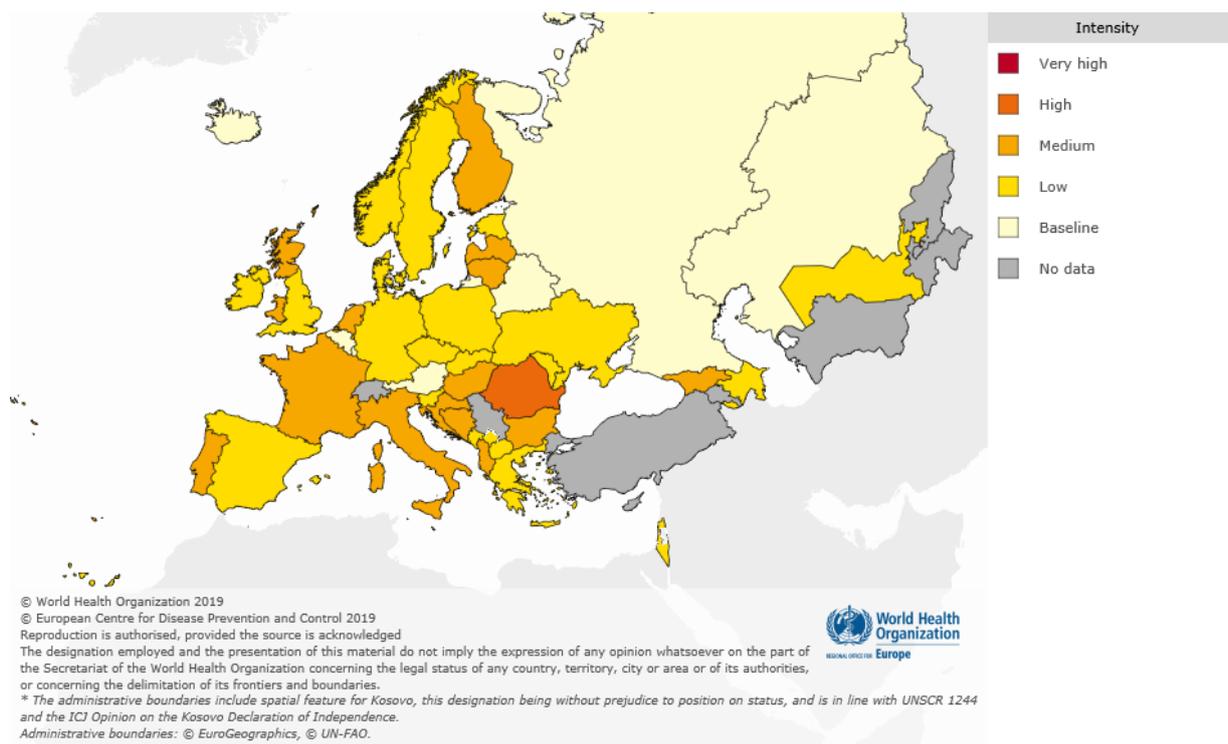
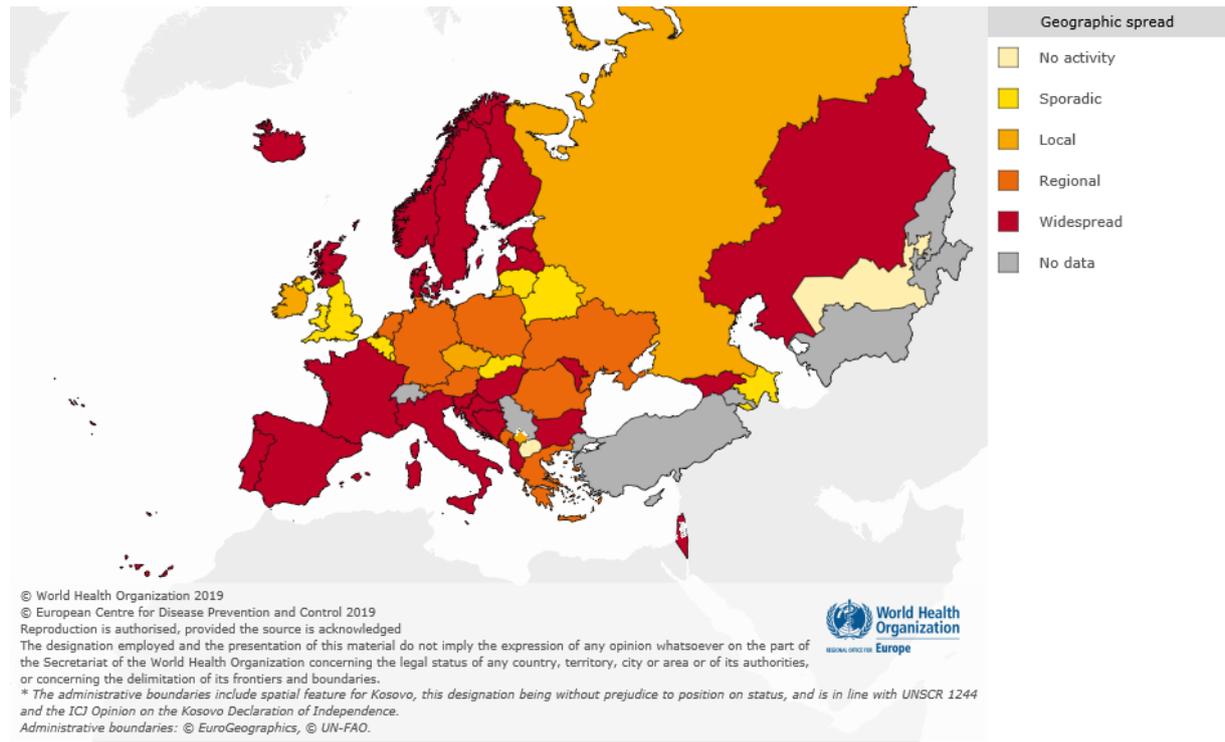


Fig. 2. Geographic spread in the European Region, week 3/2019



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

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

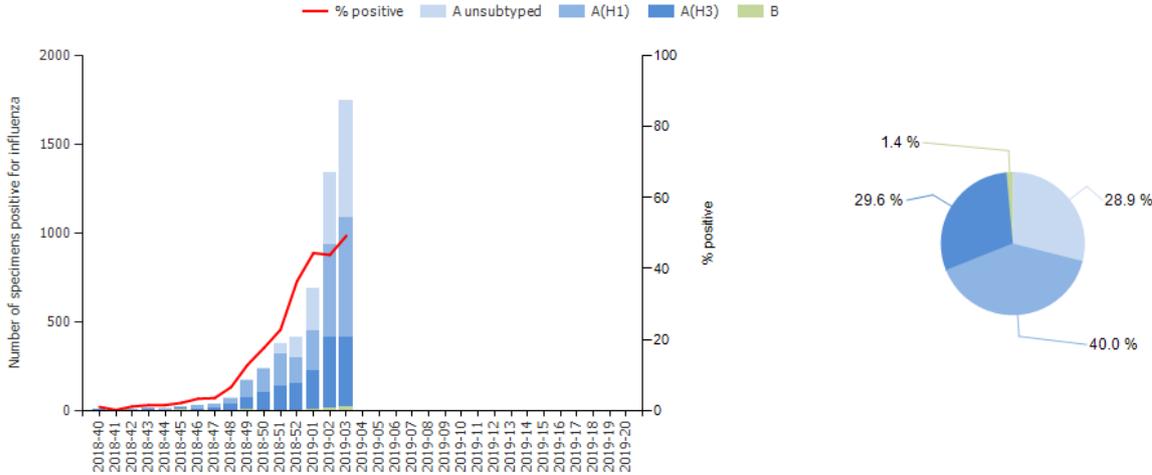
For week 3/2019, 1 742 (48.8%) of 3 569 sentinel specimens tested positive for an influenza virus; 98.6% were type A and 1.4% were type B. Of 1 057 subtyped A viruses, 63.7% were A(H1N1)pdm09 and 36.3% A(H3N2). All 10 type B viruses ascribed to a lineage were B/Yamagata.

Of 37 Member States or areas across the region that each tested at least 10 sentinel specimens in week 3/2019, 31 reported a rate of influenza virus detections above 30% (median 52.6%; range 32.1% – 68.8%).

For the season to date, more influenza type A (n=5 092, 98.6%) than type B (n=73, 1.4%) viruses have been detected. Of 3 598 subtyped A viruses, 2 067 (57.4%) were A(H1N1)pdm09 and 1 531 (42.6%) were A(H3N2). Of 73 influenza type B viruses 27 (37.0%) were ascribed to a lineage and 24 (88.9%) were B/Yamagata (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 3/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	1 717	98.6	5 092	98.6
A(H1N1)pdm09	673	63.7	2 067	57.4
A(H3N2)	384	36.3	1 531	42.6
A not subtyped	660	-	1 494	-
Influenza B	25	1.4	73	1.4
B/Victoria lineage	0	0.0	3	11.1
B/Yamagata lineage	10	100.0	24	88.9
Unknown lineage	15	-	46	-
Total detections (total tested)	1 742 (3 569)	48.8	5 165 (20 311)	25.4

^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 3/2019 (n=340), influenza type A viruses (n=338, 99.4%) were detected more frequently than influenza type B viruses (n=2, 0.6%).

Since week 40/2018, more influenza type A (n=1 814, 98.3%) than type B (n=31, 1.7%) viruses were detected. Of 715 subtyped influenza A viruses, 602 (84.2%) were A(H1N1)pdm09 and 113 (15.8%) were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 591 cases with known age, 50.3% were 15–64 years old and 41.6% 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 3/2019 (n = 227), influenza type A viruses (n=225, 99.1%) were detected more frequently than influenza type B viruses (n=2, 0.9%).

Since week 40/2018, more influenza type A (n=1 836, 98.5%) than type B (n=28, 1.5%) viruses were detected. Of 492 subtyped influenza A viruses, 345 (70.1%) were A(H1N1)pdm09 and 147 (29.9%) were A(H3N2). The only influenza B virus ascribed to a lineage was B/Yamagata. Of 1 864 cases with known age, 38.9% were 15–64 years old and 37.9% were 65 years and older.

2. SARI surveillance

For week 3/2019, 1 673 SARI cases were reported by 11 Member States or areas. Of 278 specimens tested for influenza viruses, 120 (43.2%) were positive and all were type A.

Of 18 304 SARI cases reported since week 40/2018, 18 272 had a recorded age and, of these, 64.7% were 0–4 years old and 19.3% were 15–64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=723), type A viruses have been the most common (99.9%). Of the 711 influenza type A infected cases for which subtyping was performed, 590 (83%) were infected by A(H1N1)pdm09 viruses and 121 (17%) were infected by A(H3N2) viruses.

Mortality monitoring

For week 3/2019, the [EuroMOMO](#) project received data from 23 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. However, a few countries observed some excess mortality in elderly populations.

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 3/2019, 9 484 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; 9 401 (99.1%) were type A and 83 (0.9%) type B. Of 3 125 subtyped A viruses, 1 950 (62.4%) were A(H1N1)pdm09 and 1 175 (37.6%) were A(H3N2). No influenza B viruses were ascribed to a lineage (Table 2).

For the season so far, a substantially greater number of influenza type A (n=34 890, 98.4%) than type B viruses (n=571, 1.6%) has been detected. Of 11 674 subtyped A viruses, 7 961 (68.2%) were A(H1N1)pdm09 and 3 713 (31.8%) were A(H3N2). Of 19 influenza type B viruses ascribed to a lineage, 12 (63.2%) were B/Yamagata and 7 (36.8%) were B/Victoria; 552 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 3/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	9 401	99.1	34 890	98.4
A(H1N1)pdm09	1 950	62.4	7 961	68.2
A(H3N2)	1 175	37.6	3 713	31.8
A not subtyped	6 276	-	23 216	-
Influenza B	83	0.9	571	1.6
B/Victoria lineage	0	-	7	36.8
B/Yamagata lineage	0	-	12	63.2
Unknown lineage	83	-	552	-
Total detections (total tested)	9 484 (32 454)		35 461 (295 641)	

^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

Genetic and antigenic characterization of influenza viruses is routinely performed to understand how similar currently circulating influenza viruses are to the viruses used in influenza vaccines for an ongoing season.

Since week 40/2018, genetic characterizations of 528 viruses have been reported by the network laboratories.

Of the genetically characterized viruses 332 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 188 were A(H3) viruses, with 121 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 10 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 7 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 47 to the A/England/538/2018 (3C.3a) clade and 3 attributed to a subgroup not listed. Of the 8 genetically characterized influenza B viruses, 5 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 3 B/Victoria viruses characterized all belonged

to the B/Brisbane/60/2008 clade (clade 1A), but one each fell in subclades with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) or a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

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

Phylogenetic group	Number of viruses
A(H1N1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	332
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	121
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	10
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	7
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	47
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(Vic)-lineage clade 1A representative B/Colorado/06/2017	1
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	5

^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.

A summary of recent antigenic characterization data for type A influenza viruses from the WHO collaborating centres in the WHO Global Influenza Surveillance and Response System (GISRS) is given below. We are not including the summary for influenza type B viruses this week as very low numbers have been detected globally.

A(H1N1)pdm09 Viruses

The great majority of A(H1N1)pdm09 viruses characterized so far were antigenically similar to the vaccine virus for use in the 2018-2019 northern hemisphere and 2019 southern hemisphere influenza seasons, A/Michigan/45/2015 (clade 6B.1), as assessed in HI assays using post-infection ferret antisera.

A(H3N2) Viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult, requiring the use of modified HI and/or virus neutralization assays for analysis. In virus neutralization assays or HI assays using post-infection ferret antisera, the majority of recent A(H3N2) viruses have shown similarity to cell culture-propagated A/Singapore/INFIMH-16-0019/2016 (subclade 3C.2a1) vaccine virus.

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](#). The majority of influenza vaccines used in Europe are egg-based.

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](#).

The northern hemisphere Vaccine Composition Meeting for 2019–2020 has been planned for 18–20 February 2019 in Beijing, China. More information can be found [here](#).

Antiviral susceptibility testing

254 A(H1N1)pdm09, 78 A(H3N2), and 6 type B viruses with collection dates since week 40/2018 have been tested for susceptibility to neuraminidase inhibitors. 1 A(H1N1)pdm09 and 3 type B viruses 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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