Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 48/2017 (27 November–3 December 2017)

- Influenza activity across Europe remained at low levels.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 8.8% tested positive for influenza viruses, a higher proportion than the previous week (7%).
- Data from 16 countries or regions reporting to the EuroMOMO project indicated that all-cause excess mortality was within normal ranges for this time of year.

2017–2018 season overview

- Since week 40/2017, a relatively low number of influenza viruses have been detected in sentinel and non-sentinel specimens.
- From sentinel sources, a slightly higher proportion of type B viruses compared to type A viruses has been detected. Approximately equal proportions of A(H1N1)pdm09 and A(H3N2) viruses have been detected.
- For type B viruses from both sentinel and non-sentinel sources, B/Yamagata lineage viruses have greatly outnumbered those of the B/Victoria lineage.
- While low in number, of the A(H3N2) viruses genetically characterized 61% belonged to clade 3C.2a, the vaccine virus clade as described in the WHO recommendations for vaccine composition for the northern hemisphere 2017–18, and 39% to clade 3C.2a1 of which the viruses are antigenically similar to those of clade 3C.2a.

Other news

- The US CDC reports that several influenza activity indicators are higher in the United States than typically seen for this time of the year with A(H3N2) viruses dominating. A(H3N2) viruses are similar to the 2017–2018 Northern Hemisphere A(H3N2) vaccine component. See full report here.
- Additional information on global influenza activity is available from WHO's biweekly global updates.

Primary care data

All countries reported low activity of respiratory infections, based on syndromic surveillance data for influenza-like illness (ILI) or acute respiratory infection (ARI).

Influenza activity

For week 48/2017, low intensity of influenza activity was inferred by all of the 42 countries reporting on this indicator (Fig. 1).

No geographic spread of influenza was reported by 16 of the 42 countries reporting on this indicator; 23 countries reported sporadic cases, 2 reported local geographic spread and 1 country (Turkey) reported regional spread (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 48/2017

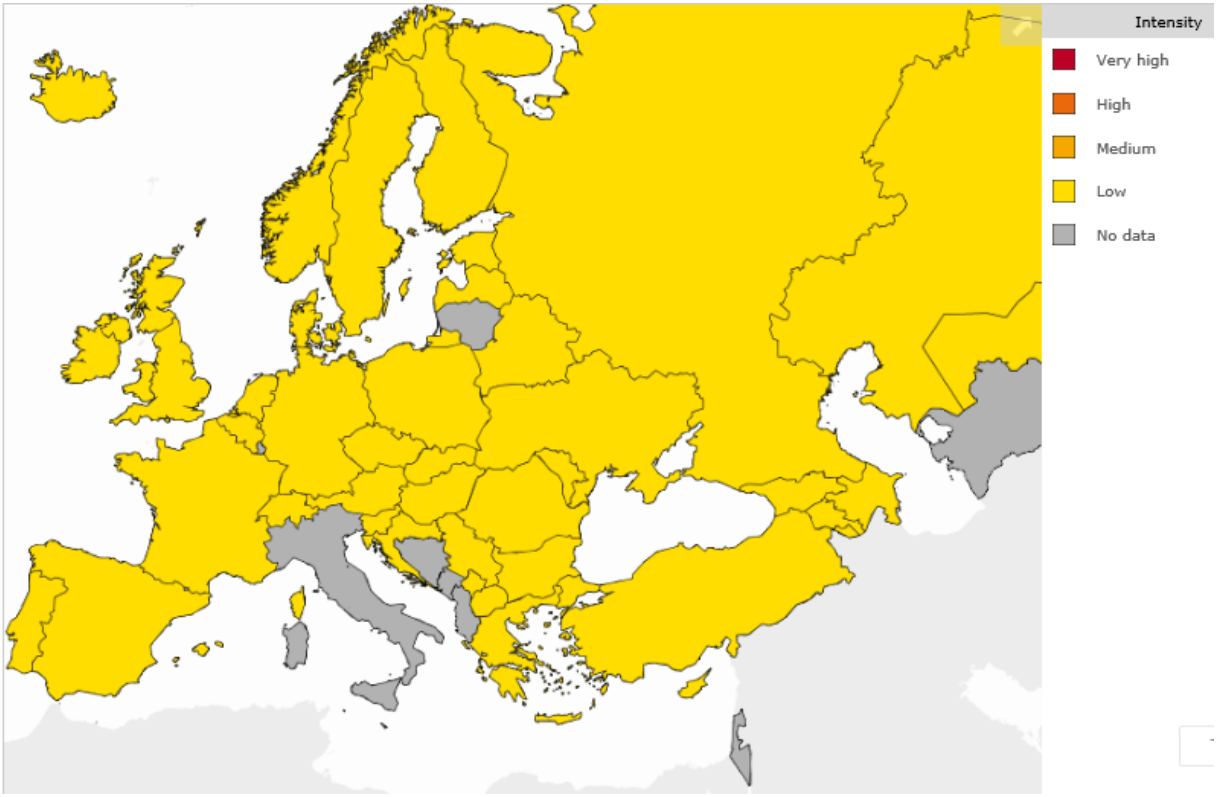
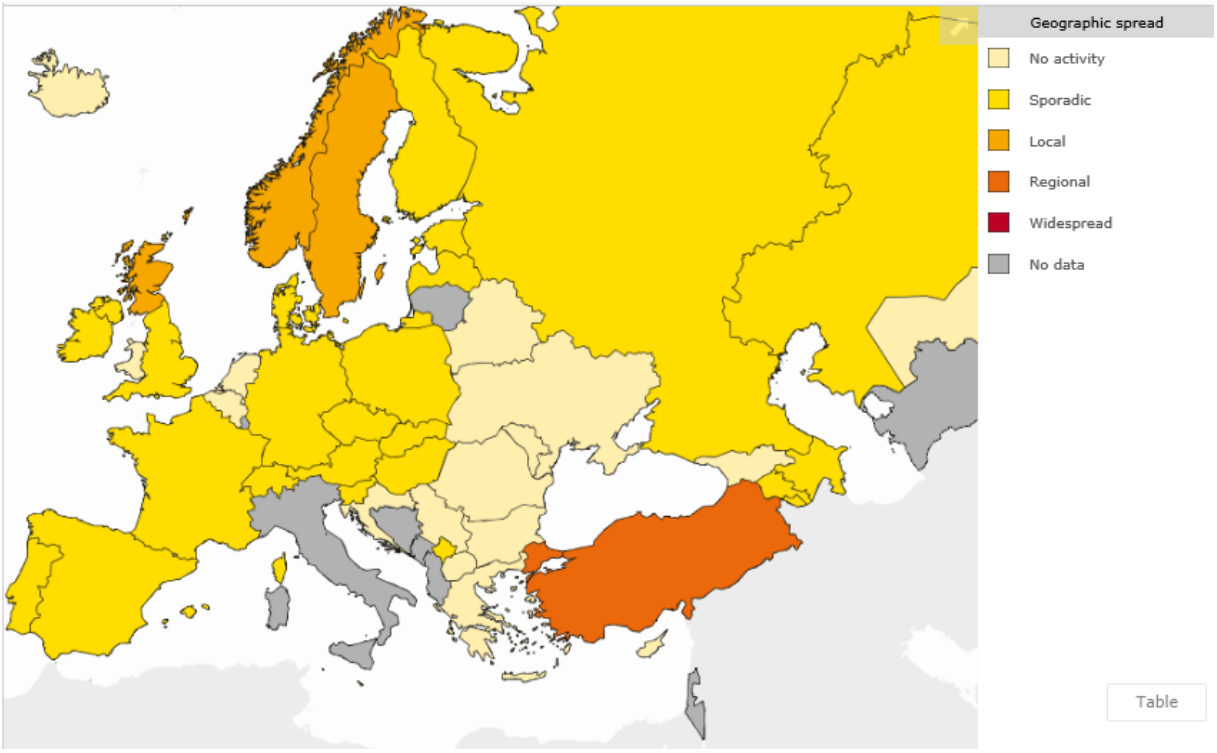


Fig. 2 Geographic spread in the European Region, week 48/2017



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

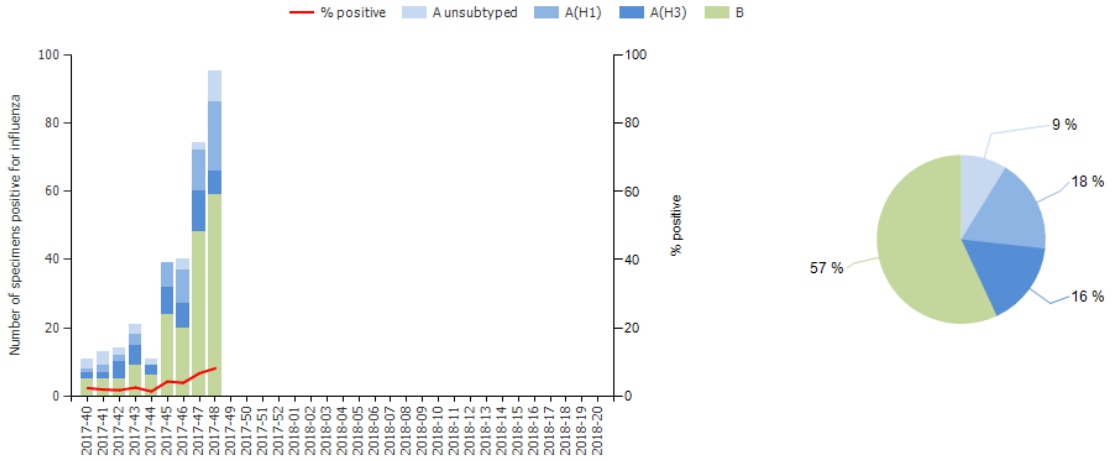
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 48/2017, 95 (8.8%) of 1 079 sentinel specimens tested positive for influenza viruses: 20 A(H1N1)pdm09, 7 A(H3N2), 9 un-subtyped A viruses, 11 B/Yamagata, 1 B/Victoria lineage and 47 B viruses not ascribed to a lineage (Fig. 3 and Table 1). 28% of all influenza B virus detections are reported from Spain. This is the second consecutive week with more type B virus detections than type A viruses. While the majority of B viruses were not ascribed to a lineage, of those that were, 92% were B/Yamagata and of the type A viruses subtyped, 74% were influenza A(H1N1)pdm09 viruses.

Of 21 countries across the region that each tested at least 10 sentinel specimens in week 48, 9 countries reported detection proportions of at least 10%: Armenia (15%), France (25%), Hungary (13%), Israel (19%), Italy (10%), Poland (10%), Spain (13%), Switzerland (13%) and the United Kingdom (Scotland) (41%).

Since week 40/2017, more influenza type B than A viruses have been detected. Of 109 subtyped A viruses, 52% were A(H1N1)pdm09. The majority of B viruses were reported without lineage and of 53 influenza B viruses ascribed to a lineage, 51 (96%) were B/Yamagata (Table 1).

Fig. 3 Influenza virus detections in sentinel-source specimens by type and subtype, by week and cumulatively[a]



[a]Pie chart shows cumulative data.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 48/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**36**	**37.9**	**137**	**43.1**
A(H1N1)pdm09	20	74.1	57	52.3
A(H3N2)	7	25.9	52	47.7
A not subtyped	9	-	28	-
Influenza B	**59**	**62.1**	**181**	**56.9**
B/Victoria lineage	1	8.3	2	3.8
B/Yamagata lineage	11	91.7	51	96.2
Unknown lineage	47	-	128	-
Total detections (total tested)	**95 (1 079)**	**8.8**	**318 (7 505)**	**4.2**

[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

Severe disease related to influenza virus infection is monitored by surveillance of hospitalized laboratory-confirmed influenza cases or severe acute respiratory infections (SARI) in some

countries. For week 48/2017, relatively low numbers of severe cases were reported by countries operating these surveillance systems.

For week 48/2017, few laboratory-confirmed influenza-infected cases from intensive care units (ICU) or other wards were reported by Denmark (n=3), France (n=7), Spain (n=9), and Sweden (n=1).

Since week 40/2017, 7 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 81 cases in ICU (37 in the United Kingdom, 19 in France, 18 in Spain, 5 in Sweden and 1 each in the Czech Republic and Denmark), and 78 in other wards (27 in Ireland, 25 in Spain, 24 in Denmark, and 2 in the Czech Republic).

Of 81 cases in ICU, 63 (78%) were infected with type A viruses (14 A(H1N1)pdm09, 16 A(H3N2), 33 A un-subtyped) and 18 (22%) with type B viruses. More patients with influenza type B virus infection were observed in other wards: of 78 patients, 45 (58%) were infected with influenza type A (10 A(H1N1)pdm09, 11 A(H3N2), 24 A un-subtyped) and 33 (42%) with influenza B viruses.

For week 48/2017, 1 085 SARI cases were reported by 11 countries from which 263 specimens were tested with 11 (Armenia 7, Ukraine 3, Kazakhstan 1) testing positive for influenza virus. Since week 40/2017, 6 985 SARI cases have been reported from 14 countries; of 1 835 specimens tested for influenza viruses, 27 were positive for influenza virus: 10 from Armenia (type B), 7 from Kazakhstan (2 A(H3N2) and 5 type B), 7 from Ukraine (1 A(H1N1)pdm09 and 6 type B), and 3 from Tajikistan (1 type A and 2 type B).

Mortality monitoring

Data from 16 countries or regions reporting to the EuroMOMO project were received for week 48/2017 and included in the pooled analyses of all-cause excess mortality. All-cause excess mortality has been within normal ranges over the past few weeks.

Virus characteristics

For reports based on sentinel surveillance systems, most influenza viruses detected were type B viruses with those assigned to a lineage being mainly B/Yamagata viruses, while of the type A viruses subtyped A(H1N1)pdm09 have been in the majority. Details can be found in Table 1.

Conversely, most detections from non-sentinel systems have been influenza type A viruses, with A(H3N2) being the majority, while the B/Yamagata lineage has also predominated among type B viruses. Details below.

Viruses detected in non-sentinel-source specimens

For week 48/2017, 679 specimens from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, nursing homes and other institutions) tested positive for influenza viruses. Of these, 57% were type A and 43% type B viruses (Table 2). The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage.

While relatively few of the viruses detected in non-sentinel samples since week 40/2017 have been ascribed to a subtype or lineage, of all subtyped A viruses 82% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage (n=76), 92% were B/Yamagata lineage and 8% were B/Victoria lineage.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 48/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**390**	**57.4**	**1 659**	**65.2**
A(H1N1)pdm09	22	17.9	124	18.0
A(H3N2)	101	82.1	563	82.0
A not subtyped	267	-	972	-
Influenza B	**289**	**42.6**	**884**	**34.8**
B/Victoria lineage	1	28.6	6	7.9
B/Yamagata lineage	6	71.4	70	92.1
Unknown lineage	282	-	808	-
Total detections (total tested)	**679 (13 949)**	**-**	**2 543 (105478)**	**-**

[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; as not all countries have a true non-sentinel testing denominator, no percentage calculations for total tested are shown.

Genetic characterization

For specimens collected since week 40/2017, genetic characterization of 122 viruses has been reported (Table 3). Among 74 influenza A(H3N2) viruses, 45 (61%) fell in the vaccine virus component clade (3C.2a), and 29 (39%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin. Viruses in these 2 groups are antigenically similar, but both clade and subclade are evolving rapidly with the emergence of several virus clusters defined by additional amino acid substitutions in the haemagglutinin, thereby requiring continued monitoring of antigenic characteristics. 3 B/Yamagata viruses were not attributed to any clade.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–48/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	16
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	45
A(H3N2) A/Singapore/INFIMH-16-0019/2014 (clade 3C.2a1) [c]	29
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b,d]	3
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, e]	26
B/Yamagata lineage not attributed to any clade	3

[a] Vaccine component of vaccines for both northern (2017–2018 season) and southern (2018 season) hemispheres
[b] Vaccine component for northern hemisphere 2017–2018 season
[c] Vaccine component for southern hemisphere 2018 season
[d] Vaccine component of quadrivalent vaccines for use in southern hemisphere 2018 season
[e] Vaccine component of quadrivalent vaccines for use in northern hemisphere 2017–2018 season

The recommended composition of trivalent influenza vaccines for the 2017–2018 season in the northern hemisphere includes an A/Michigan/45/2015 (H1N1)pdm09-like virus; an A/Hong Kong/4801/2014 (H3N2)-like virus; and a B/Brisbane/60/2008-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended.

On 28 September 2017, WHO recommended two changes, compared to the current trivalent vaccine recommended for the 2017–2018 northern hemisphere influenza season, in trivalent vaccine composition for the 2018 season in the southern hemisphere. The recommendations matched the A(H1N1)pdm09 component for the 2017–2018 northern hemisphere season, but the A(H3N2) component was changed to an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and the B component was switched to a B/Yamagata-lineage virus. These changes were made due to the emergence of numerous genetic subclades of A(H3N2) viruses – none of which showed significant antigenic drift compared to the vaccine component – while for type B viruses the B/Yamagata lineage predominated by a large margin in the course of the 2017 southern hemisphere season. See also the ECDC commentary.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 55 viruses (33 A(H3N2), 11 A(H1N1)pdm09 and 11 type B) with collection dates since week 40/2017. One A(H3N2) virus showed evidence of reduced inhibition by neuraminidase inhibitors oseltamivir and zanamivir.

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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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Tables and figures should be referenced:

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