Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 49/2017 (4–10 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, 11% tested positive for influenza viruses, which is similar to that in the previous week (13%).
- Data from 20 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 has 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, 61% of the genetically characterized A(H3N2) viruses 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, the viruses of which are antigenically similar to those of clade 3C.2a.

Other news

- The Norwegian Institute of Public Health has published an early risk assessment for the influenza season 2017/18 in Norway. See full report here.
- Influenza activity in the United States has been increasing since the beginning of November. Influenza A viruses have been the most commonly identified, with influenza A(H3N2) viruses predominating. The 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

Overall, 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 49/2017, medium intensity of influenza activity was reported by France, while low intensity was inferred by the remaining 42 of the 43 countries reporting on this indicator (Fig. 1).

No geographic spread of influenza was reported by 12 of the 43 countries reporting on this indicator; 26 countries reported sporadic cases, 2 reported local geographic spread, 1 country (France) reported regional spread, and 2 countries (Sweden and Turkey) reported widespread activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 49/2017

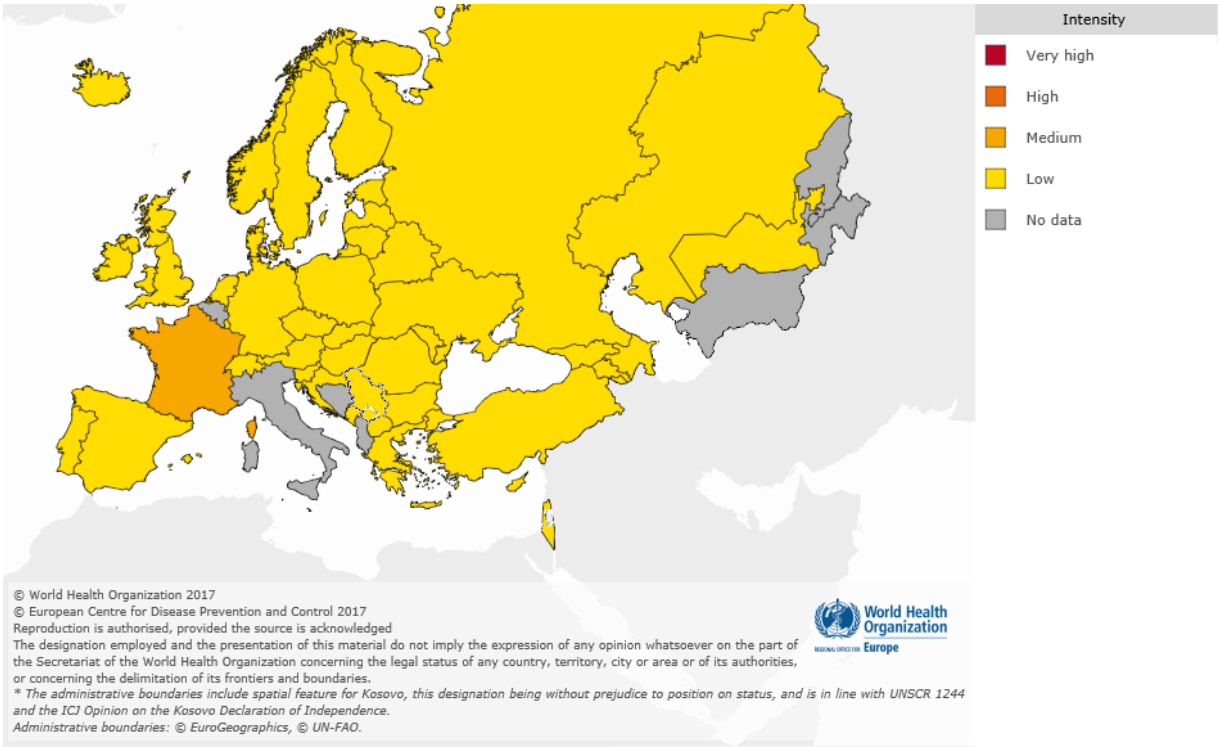
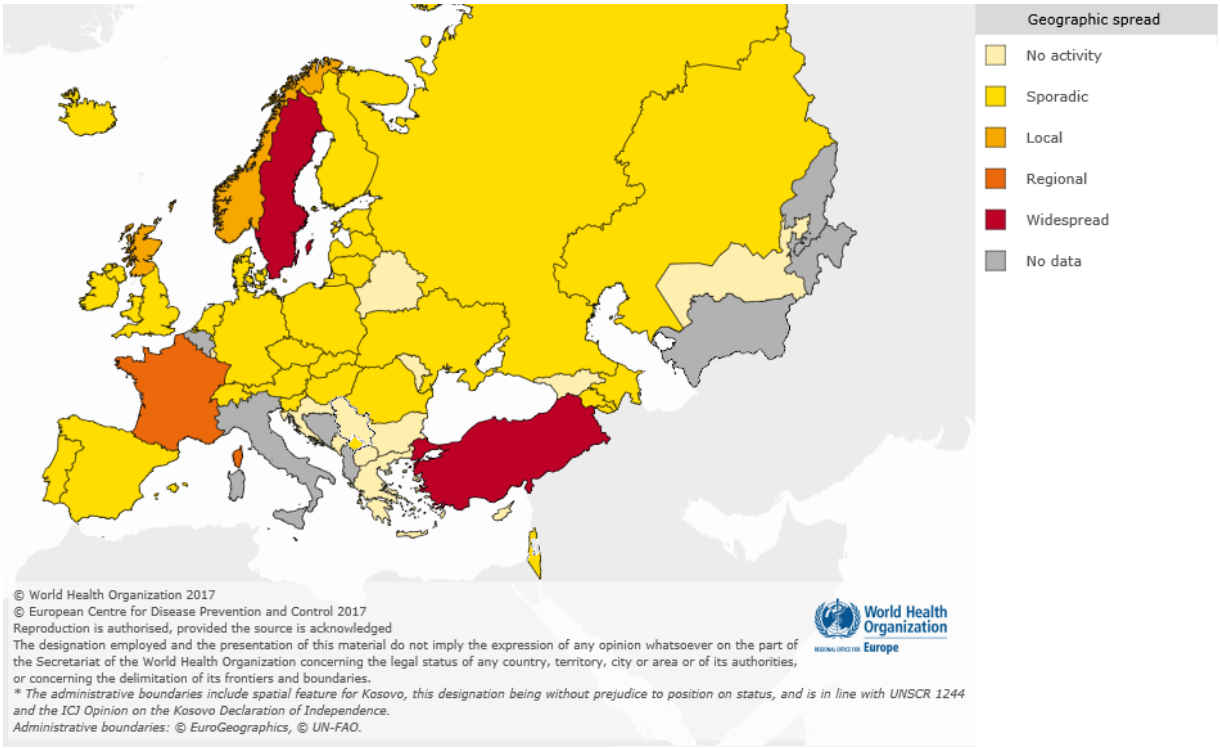


Fig. 2 Geographic spread in the European Region, week 49/2017



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

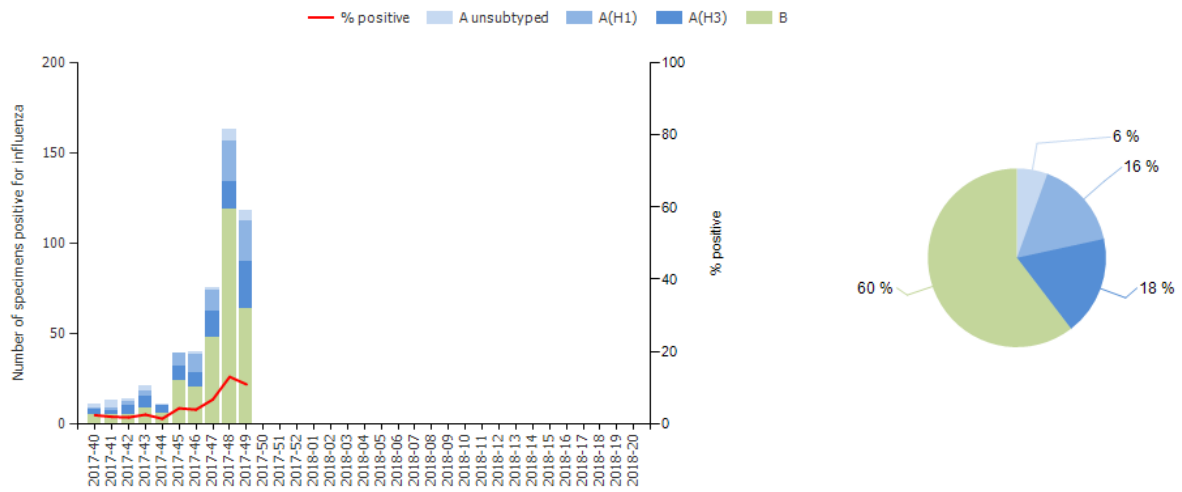
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 49/2017, 118 (11%) of 1 070 sentinel specimens tested positive for influenza viruses: 22 A(H1N1)pdm09, 26 A(H3N2), 6 un-subtyped A viruses, 19 B/Yamagata, and 45 B viruses not ascribed to a lineage (Fig. 3 and Table 1). 42% of all influenza B virus detections were reported from Spain. This is the third consecutive week with more type B than type A virus detections. While the majority of type B viruses were not ascribed to a lineage, of those that were, 100% were B/Yamagata and of the type A viruses subtyped, 45.8% were influenza A(H1N1)pdm09 viruses.

Of 22 countries across the region that each tested at least 10 sentinel specimens in week 49, 9 countries reported detection proportions of at least 10%: Spain (32%), France (31%), Italy (22%), Norway (20%), Armenia (17%), Ireland (13%), Switzerland (13%), Sweden (12%) and the United Kingdom (England and Scotland 11% and 18% respectively).

Since week 40/2017, more influenza type B than type A viruses have been detected. Of 172 subtyped A viruses, 53% were A(H3N2). The majority of B viruses were reported without lineage and of 115 influenza B viruses ascribed to a lineage, 111 (97%) 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 49/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**54**	**45.8**	**200**	**39.6**
A(H1N1)pdm09	22	45.8	81	47.1
A(H3N2)	26	54.2	91	52.9
A not subtyped	6	-	28	-
Influenza B	**64**	**54.2**	**305**	**60.4**
B/Victoria lineage			4	3.5
B/Yamagata lineage	19	100.0	111	96.5
Unknown lineage	45	-	190	-
Total detections (total tested)	**118 (1 070)**	**11.0**	**505 (8 726)**	**5.8**

[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 49/2017, relatively low numbers of severe cases were reported by countries operating these surveillance systems.

For week 49/2017, 56 laboratory-confirmed influenza-infected cases from intensive care units (ICU) or other wards were reported by Denmark (n=5), France (n=12), Ireland (n=8); Romania (n=1), Spain (n=7), and United Kingdom (n=23).

Since week 40/2017, 9 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 166 cases in ICU (97 in the United Kingdom, 37 in France, 22 in Spain, 7 in Sweden and 1 each in the Czech Republic, Denmark and Ireland), and 122 in other wards (50 in Ireland, 36 in Spain, 31 in Denmark, 2 each in the Czech Republic and Slovakia, and 1 in Romania).

Of 166 cases in ICU, 121 (73%) were infected with type A viruses (22 A(H1N1)pdm09, 23 A(H3N2), 76 A un-subtyped) and 45 (27%) with type B viruses. A higher proportion of patients with influenza type B virus infection was observed in other wards: of 122 patients, 66 (54%) were infected with influenza type A (13 A(H1N1)pdm09, 17 A(H3N2), 36 A un-subtyped) and 56 (46%) with influenza B viruses.

For week 49/2017, 1 082 SARI cases were reported by 9 countries from which 266 specimens were tested with 8 (6 in Armenia and 2 in Kazakhstan) testing positive for influenza virus. Since week 40/2017, 8 067 SARI cases have been reported from 14 countries; of 2 101 specimens tested for influenza viruses, 35 were positive for influenza virus: 16 from Armenia (15 type B and 1 A(H1N1)pdm09), 9 from Kazakhstan (4 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 20 countries or regions reporting to the EuroMOMO project were received for week 49/2017 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 this season, 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 similar distribution of influenza A(H1N1)pdm09 and A(H3N2) viruses has been observed.

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 49/2017, 1 322 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, 59.2% were type A and 40.8% 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 78% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage (n=136), 96% were B/Yamagata lineage and 4% were B/Victoria lineage.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 49/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**782**	**59.2**	**2538**	**63.3**
A(H1N1)pdm09	73	31.5	226	21.7
A(H3N2)	159	68.5	817	78.3
A not subtyped	550	-	1495	-
Influenza B	**540**	**40.8**	**1470**	**36.7**
B/Victoria lineage			6	4.4
B/Yamagata lineage	11	100.0	130	95.6
Unknown lineage	529	-	1334	-
Total detections (total tested)	**1322 (15 615)**	**-**	**4008 (123 557)**	**-**

[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 172 viruses has been reported (Table 3). Among 88 influenza A(H3N2) viruses, 57 (65%) fell in the vaccine virus component clade (3C.2a), and 31 (35%) 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. Three B/Yamagata viruses were not attributed to any clade. For more information on characterizations, see the WHO CC London November 2017 report.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–49/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	26
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	57
A(H3N2) A/Singapore/INFIMH-16-0019/2014 (clade 3C.2a1) [c]	31
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	6
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, e]	49
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 87 viruses (52 A(H3N2), 16 A(H1N1)pdm09 and 19 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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 49/2017.

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 49/2017.