Flu News Europe
Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 47/2017 (20–26 November 2017)

- Influenza activity across Europe remained at low levels.
- Of the individuals sampled on presenting with ILI or ARI to sentinel primary healthcare sites, 6.3% tested positive for influenza viruses, which is higher than the previous week (3.7%).
- Data from 21 countries or regions reporting to the EuroMOMO project indicated that all-cause excess mortality was within normal ranges for this time of year.
- Additional information on global influenza activity is available from WHO's biweekly global updates.

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, the proportion of B virus is slightly more important compared to A viruses.
- For type B viruses from both sources, B/Yamagata lineage viruses have greatly outnumbered those of the B/Victoria lineage.
- While low in number (n=35), over 59% of the A(H3N2) viruses genetically characterized belonged to clade 3C.2a, the vaccine virus clade, as described in the WHO recommendations for vaccine composition for the northern hemisphere 2017–18.

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

As a consequence of the low ILI and ARI rates for week 47/2017, low intensity of influenza activity was inferred by all of the 42 countries reporting on this indicator (Fig. 1).

Based on influenza virus detections in sentinel specimens taken from ILI and ARI cases, no geographic spread of influenza was reported by 19 of the 42 countries reporting on this indicator, 19 countries reported sporadic cases, 3 reported local geographic spread while 1 country (Finland) reported regional spread (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 47/2017

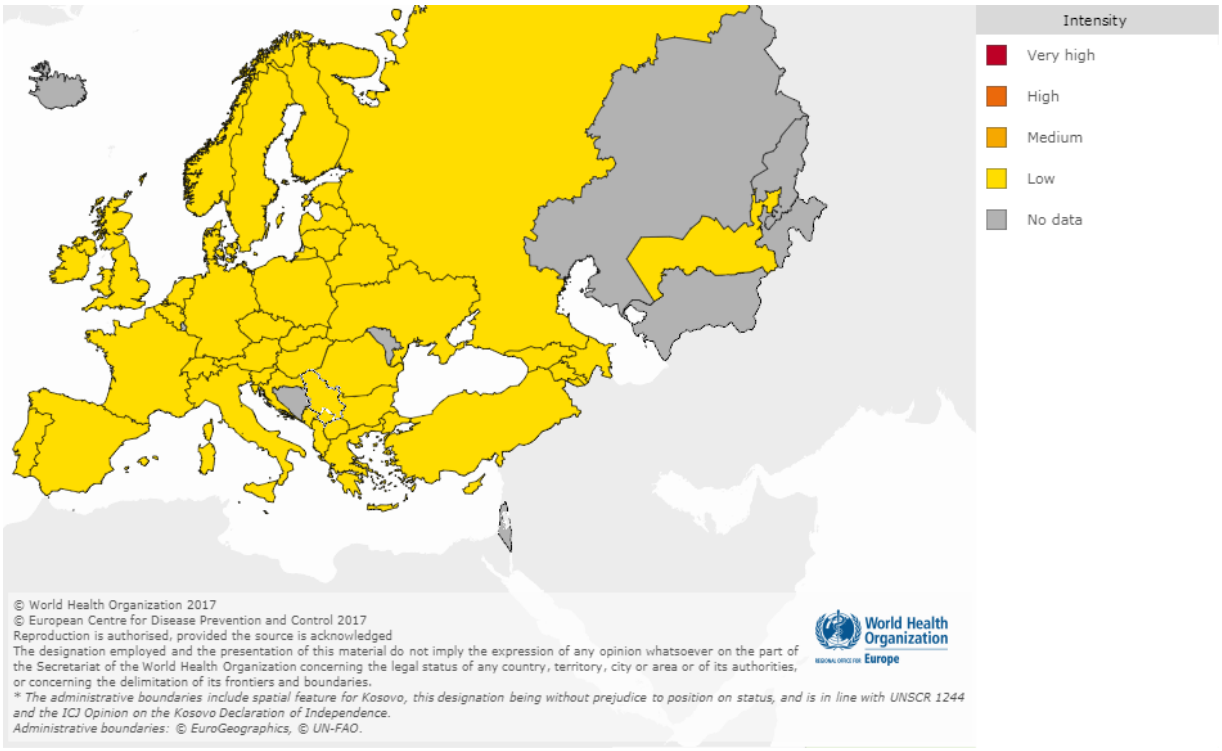
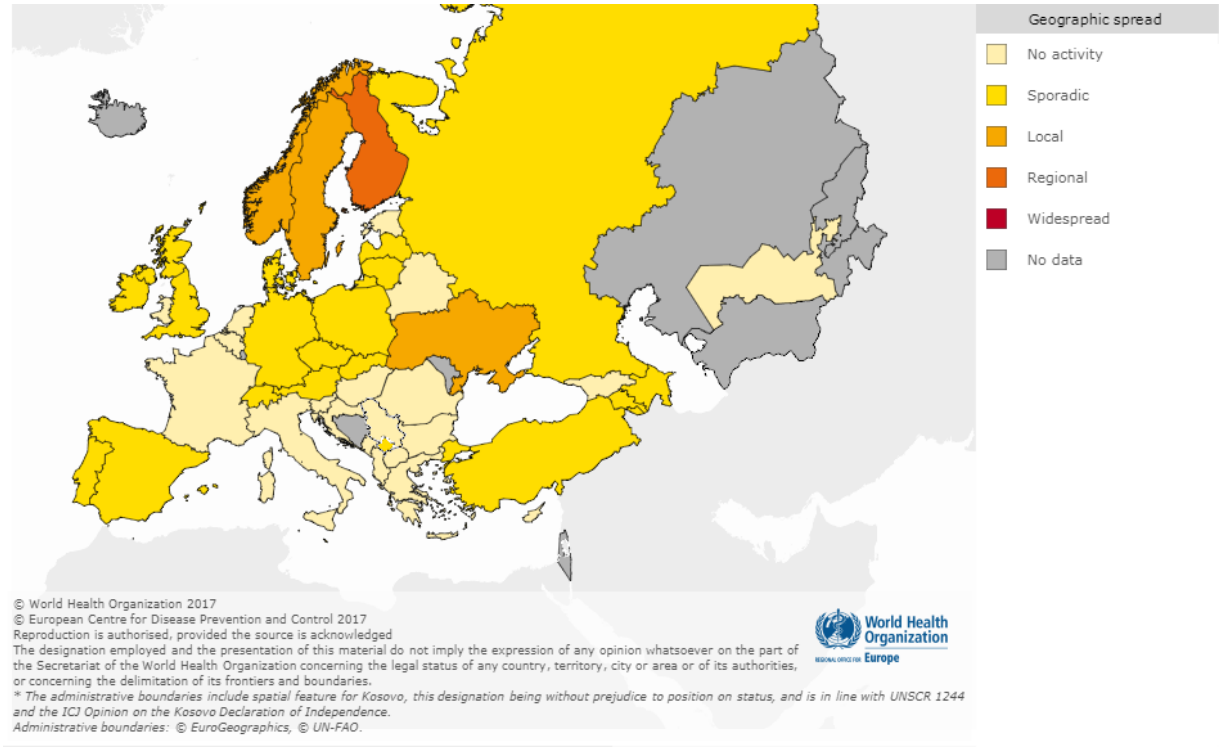


Fig. 2 Geographic spread in the European Region, week 47/2017



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)

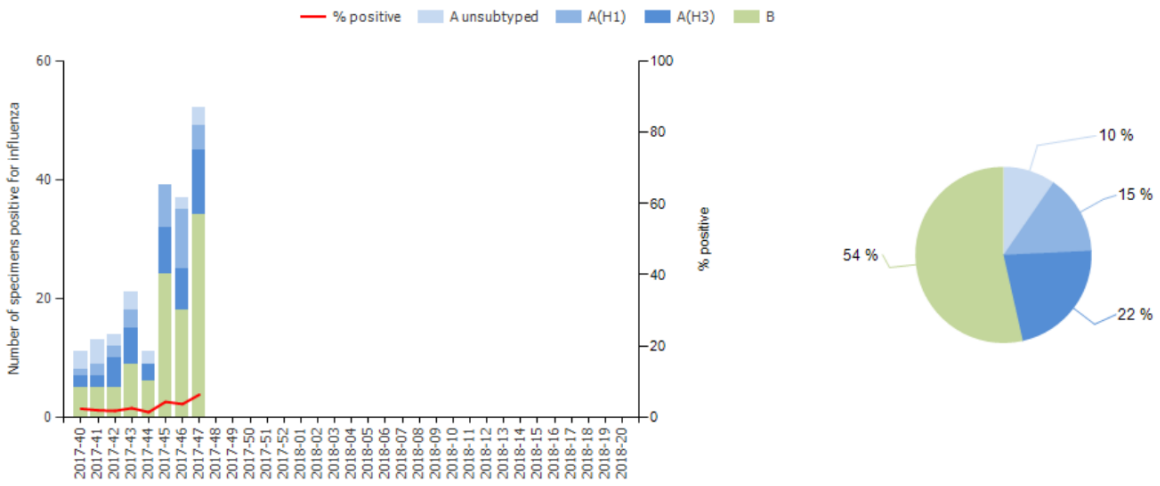
For week 47/2017, 52 (6.3%) of 820 sentinel specimens tested positive for influenza viruses: 4 A(H1N1)pdm09, 11 A(H3N2), 3 un-subtyped A viruses, 11 B/Yamagata lineage and 23 B viruses not ascribed to a lineage (Fig. 3 and Table 1).

Since week 40/2017, approximately equal proportions of influenza types A and B viruses have been detected.

Of 73 subtyped A viruses, 60% were A(H3N2). Of 33 influenza B viruses ascribed to a lineage, 32 (97%) were B/Yamagata (Table 1).

Of 16 countries across the region that have each tested at least 10 sentinel specimens in week 47, 6 countries reported detection proportions of at least 10%: the Czech Republic (12%), France (16%), Spain (17%) and the United Kingdom (Scotland) (12%).

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 47/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**18**	**34.6**	**92**	**46.5**
A(H1N1)pdm09	4	26.7	29	39.7
A(H3N2)	11	73.3	44	60.3
A not subtyped	3	-	19	-
Influenza B	**34**	**65.4**	**106**	**53.5**
B/Victoria lineage	0	0.0	1	3.0
B/Yamagata lineage	11	100.0	32	97.0
Unknown lineage	23	-	73	-
Total detections (total tested)	**52 (820)**	**6.3**	**198 (6 120)**	**3.2**

[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 47/2017, relatively low numbers of severe cases were reported by countries operating these surveillance systems.

For week 47/2017, few laboratory-confirmed influenza-infected cases from intensive care units (ICU) or other wards were reported by France (n=2), Ireland (n=2), Spain (n=7), and the United Kingdom (n=7).

Since week 40/2017, 7 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 89 cases in ICU (37 in the United Kingdom, 36 in France, 11 in Spain, 3 in Sweden and 1 each in the Czech Republic and Denmark), and 61 in other wards (27 in Ireland, 18 in Denmark, 14 in Spain and 2 in the Czech Republic).

Of 89 cases in ICU, 63 (71%) were infected with type A viruses (26 A(H1N1)pdm09, 14 A(H3N2), 23 A un-subtyped) and 26 (29%) with type B viruses. A similar distribution was observed in other wards: of 61 patients, 41 (67%) were infected with influenza A (10 A(H1N1)pdm09, 11 A(H3N2), 20 A un-subtyped) and 20 (33%) with influenza B viruses.

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 47/2017, 417 SARI cases were reported by 11 countries from which 197 specimens were tested with 3 (from Armenia) testing positive for influenza virus. Since week 40/2017, 5 420 SARI cases have been reported from 14 countries; of 1 560 specimens tested for influenza viruses, 13 were positive for influenza virus: 3 from Armenia (type B), 6 from Kazakhstan (1 A(H3N2) and 5 type B), 3 from Tajikistan (1 type A and 2 type B) and 1 from Ukraine (type A).

Mortality monitoring

Data from 21 countries or regions reporting to the EuroMOMO project were received for week 47/2017 and included in the pooled analyses of all-cause excess mortality. All-cause excess mortality was within normal ranges over the past few weeks.

Virus characteristics

For detections from both sentinel and non-sentinel surveillance systems, most influenza viruses subtyped or assigned to a lineage this season were identified as A(H3N2) and B/Yamagata viruses, respectively.

Viruses detected in non-sentinel-source specimens

For week 47/2017, 481 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, 62% were type A and 38% type B viruses (Table 2). The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage.

While 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 80% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage (n=42), 95% were B/Yamagata lineage and 5% were B/Victoria lineage.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 47/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**299**	**62.2**	**1 206**	**68.1**
A(H1N1)pdm09	18	29.5	93	20.2
A(H3N2)	43	70.5	367	79.8
A not subtyped	238	-	746	-
Influenza B	**182**	**37.8**	**565**	**31.9**
B/Victoria lineage	0	0.0	2	4.8
B/Yamagata lineage	2	100.0	40	95.2
Unknown lineage	180	-	523	-
Total detections (total tested)	**481 (13 799)**	**-**	**1 771 (90 308)**	**-**

[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 94 viruses has been reported (Table 3). Among 59 influenza A(H3N2) viruses, 35 (59%) fell in the vaccine virus component clade (3C.2a), and 24 (41%) 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. 2 B/Yamagata viruses were not attributed to any clade.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–47/2017

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]	35
A(H3N2) A/Singapore/INFIMH-16-0019/2014 (clade 3C.2a1) [c]	24
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b,d]	2
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, e]	14
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 28 viruses (14 A(H3N2), 10 A(H1N1)pdm09 and 4 type B) with collection dates since week 40/2017. 1 A(H3N2) virus showed evidence of reduced inhibition by neuraminidase inhibitors oseltamivir and zanamivir.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Cornelia Adlhoch, René Snacken, Pasi Penttinen) and the WHO Regional Office for Europe (Caroline Brown, Piers Mook, Dmitriy Pereyaslov and Tamara Meerhoff, Temporary Advisor to WHO). It was reviewed by country experts (Raquel Guiomar, Instituto Nacional de Saúde Doutor Ricardo Jorge, Portugal; Vladimir Mikic, Institute of Public Health, The former Yugoslav Republic of Macedonia) and by experts from the network (Adam Meijer, National Institute for Public Health and the Environment (RIVM), the Netherlands; Rod Daniels and John McCauley, WHO Collaborating Centre for Reference and Research on Influenza, Francis Crick Institute, United Kingdom; Tyra Grove Krause, Statens Serum Institut and EuroMOMO network, Denmark).

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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