Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 52/2017 (25–31 December 2017)

- Influenza activity was increasing in countries in northern, southern and western Europe.
- Both influenza type A and B viruses were co-circulating and mixed patterns of circulation were observed across the Region.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 44% tested positive for influenza viruses, an increase from 38% in the previous week.

2017–2018 season overview

- An early risk assessment based on data from EU/EEA countries was published by ECDC on 20 December 2017. First detections indicated circulation of A(H3N2) and B/Yamagata viruses in the highest proportions. As the A(H3N2) subtype dominated last season, a high proportion of the population should be protected.
- From sentinel sources, a higher proportion of type B viruses compared to type A viruses has been detected. Of the type A detections, A(H1N1)pdm09 viruses have outnumbered A(H3N2) viruses.
- 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, 59% 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 40% to clade 3C.2a1, with viruses in both clades being antigenically similar.

Other news

- The US CDC published a Health Alert Network (HAN) notice, regarding increased A(H3N2) activity that affects mostly people aged over 65 and younger children, leading to more hospitalizations and deaths. Based on the moderate vaccine effectiveness, detailed information on recommended antiviral treatment is provided. 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) and/or acute respiratory infection (ARI). Epidemic thresholds have been passed in 8 reporting countries, indicating influenza activity based on ILI or ARI rates: Ireland, Israel, Italy, the Netherlands, Norway, Spain, Switzerland and the United Kingdom (England, Scotland and Wales).

Influenza activity

For week 52/2017, while low intensity of influenza activity was reported by 28 of the 38 countries reporting on this indicator, medium intensity of influenza activity was reported by 10 countries (France, Ireland, Italy, Montenegro, the Netherlands, Norway, Spain, Switzerland, Turkey and the United Kingdom (England)) (Fig. 1). No geographic spread of influenza was reported by 7 of the 38 countries reporting on this indicator; 14 countries reported sporadic cases, 1 reported local geographic spread, 7 countries reported regional spread, and 9 countries (Croatia, France, Ireland, Norway, Portugal, Spain, Sweden, Switzerland and Turkey) reported widespread activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 52/2017

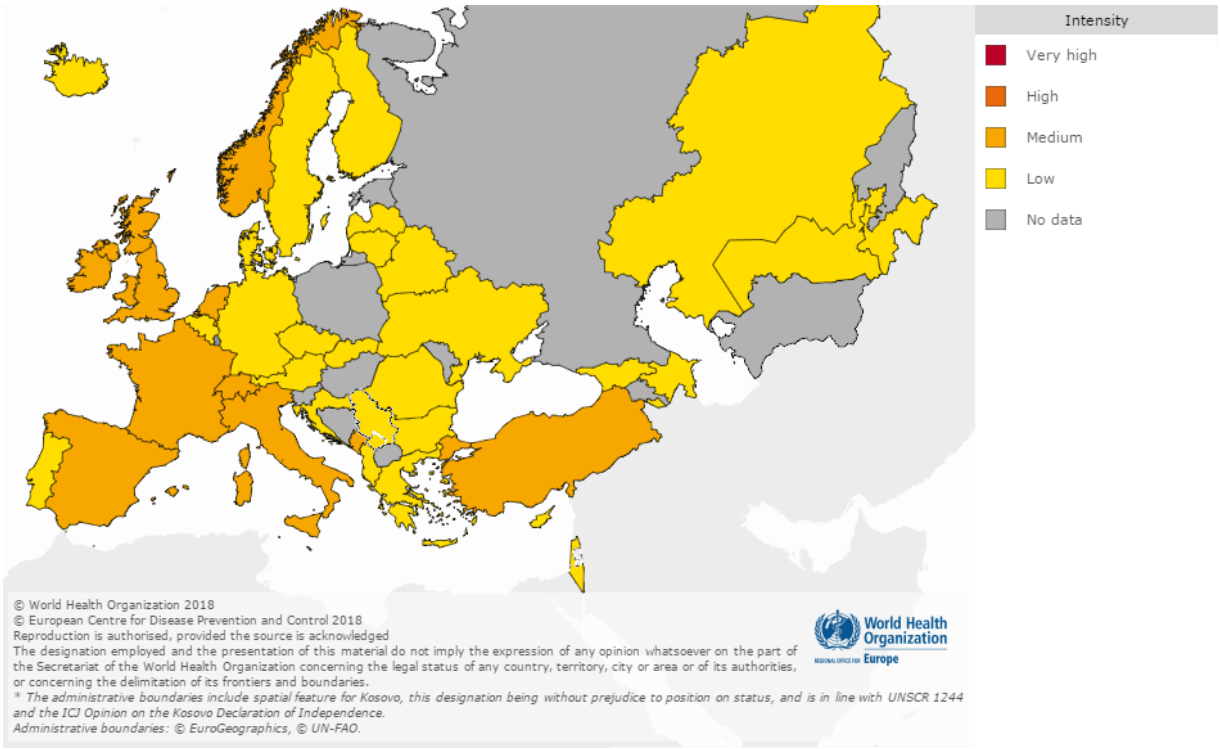
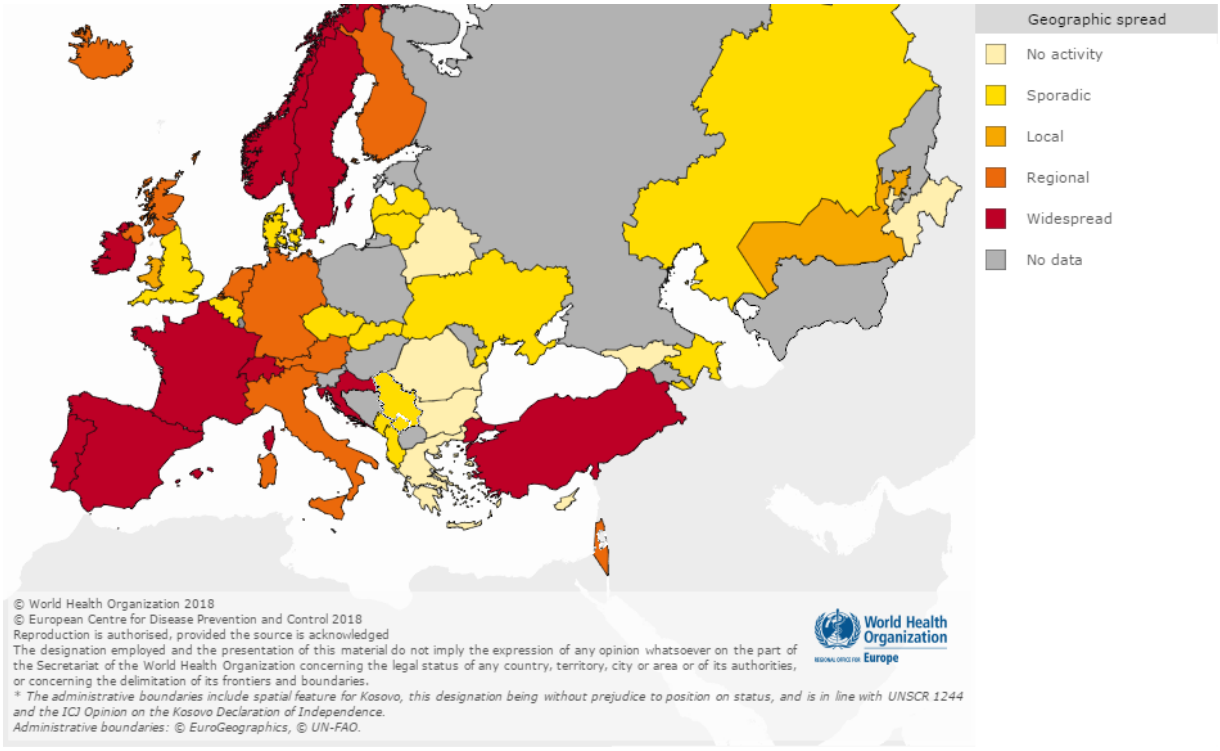


Fig. 2 Geographic spread in the European Region, week 52/2017



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)

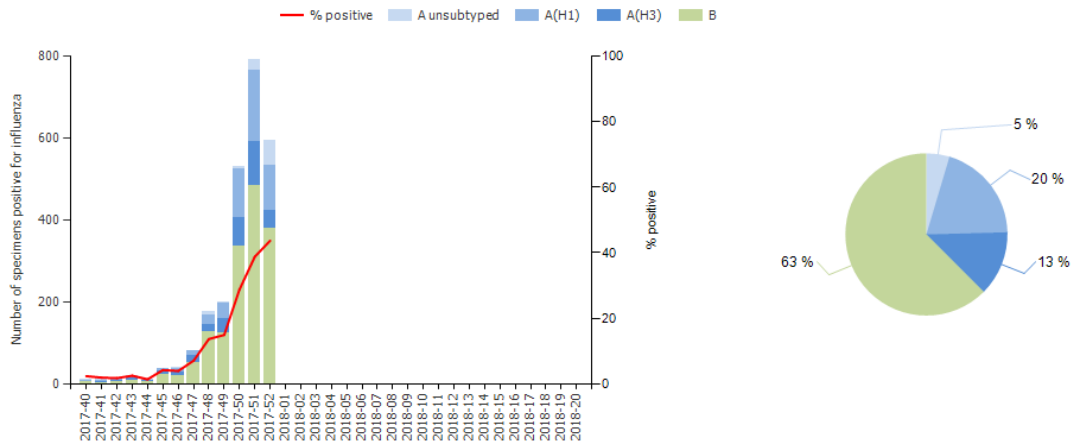
For week 52/2017, 594 (43.6%) of 1 364 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 36% were type A and 64% were type B. Out of 154 subtyped A viruses, 71% were influenza A(H1N1)pdm09 and 29% A(H3N2). Of 94 B viruses ascribed to a lineage, 98% were B/Yamagata and 2% B/Victoria (Fig. 3 and Table 1).

Of 18 countries across the region that each tested at least 10 sentinel specimens in week 52, 14 in northern, western and southern European areas reported proportions of influenza virus detections of at least 30% or more (median of 60%, range of 34% to 88%).

Since week 40/2017, more influenza type B (62.5%) than type A (37.5%) viruses have been detected. Of 830 subtyped A viruses, 61% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 505 ascribed to a lineage, 96% were B/Yamagata (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.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 52/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**214**	**36.0**	**946**	**37.5**
A(H1N1)pdm09	110	71.4	504	60.7
A(H3N2)	44	28.6	326	39.3
A not subtyped	60	-	116	-
Influenza B	**380**	**64.0**	**1577**	**62.5**
B/Victoria lineage	2	2.1	20	4.0
B/Yamagata lineage	92	97.9	485	96.0
Unknown lineage	286	-	1 072	-
Total detections (total tested)	**594 (1 364)**	**43.5**	**2 523 (14 330)**	**17.6**

[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 52/2017, increasing numbers of severe cases were reported by countries operating these surveillance systems.

For week 52/2017, 318 laboratory-confirmed influenza-infected cases from intensive care units (ICU) were reported by the Czech Republic (n=1), France (n=166), Spain (n=28), Sweden (n=9), and the United Kingdom (n=114) and 127 cases were reported from other wards by Ireland (n=43) and Spain (n=84).

Since week 40/2017, 9 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 960 cases in ICU (434 in France, 355 in the United Kingdom, 138 in Spain, 24 in Sweden, 4 in the Czech Republic, 3 in Ireland and 2 in Denmark), and 631 in other wards (364 in Spain, 208 in Ireland, 52 in Denmark, 3 in the Czech Republic, and 2 each in Romania and Slovakia).

Of 960 cases in ICU, 648 (67.5%) were infected with type A viruses (133 A(H1N1)pdm09, 90 A(H3N2), 425 A un-subtyped) and 312 (32.5%) with type B viruses. A higher proportion of patients with influenza type B virus infection was observed in other wards: of 631 patients, 258 (41%) were infected with influenza type A (32 A(H1N1)pdm09, 50 A(H3N2), 176 A un-subtyped) and 373 (59%) with influenza B viruses.

For week 52/2017, 927 SARI cases were reported by 10 countries from which 199 specimens were tested for influenza viruses with 6 (2 in Albania, 3 in Kazakhstan and 1 in Uzbekistan) being positive. Since week 40/2017, 12 338 SARI cases have been reported from 15 countries; of 2 975 specimens tested for influenza viruses, 77 were positive for influenza virus: 33 from Armenia (30 type B and 3 A(H1N1)pdm09), 21 from Ukraine (1 A(H1N1)pdm09, 1 un-subtyped and 19 type B), 13 from Kazakhstan (6 A(H3N2) and 7 type B), 3 from Tajikistan (1 type A and 2 type B), 2 from Albania (1 A(H1N1)pdm09 and 1 type B) 2 from Belarus (2 A(H3N2)), 2 from Uzbekistan (1 A(H1N1)pdm09 and 1 type B) and 1 from Serbia (type B).

Mortality monitoring

Data from 11 countries or regions reporting to the EuroMOMO project were received for week 52/2017 and included in the pooled analyses of all-cause excess mortality. All-cause excess mortality has been within normal ranges over the past weeks.

Virus characteristics

For reports based on sentinel surveillance systems this season, most influenza viruses detected were type B with those assigned to a lineage being mainly B/Yamagata viruses, while of the type A viruses subtyped most were influenza A(H1N1)pdm09 viruses. Details of the distribution of viruses detected in sentinel-source specimens can be found in the Primary care data section.

Conversely, the majority of detections from non-sentinel systems have been influenza type A viruses, and of those typed most were A(H3N2). The B/Yamagata lineage has predominated among type B viruses, as seen in sentinel systems. Further details are given in the section below.

The higher proportion of influenza type A detections in non-sentinel specimens, compared to sentinel source specimens, may be related to the higher proportion of non-sentinel specimens being derived from hospital-based settings, with type B virus infections being generally milder and leading to less hospitalization than type A virus infections. Similarly, A(H3N2) viruses often cause more severe disease than A(H1N1)pdm09 viruses. In addition, the proportions of influenza virus subtypes may vary between countries, possibly related to the contributions of sentinel and non-sentinel surveillance, which may lead to differences in (sub)type proportions within the Region.

Viruses detected in non-sentinel-source specimens

For week 52/2017, 6 347 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, 51% were type A and 49% 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 72% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage, 97.5% were B/Yamagata lineage and 2.5% were B/Victoria lineage.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 52/2017 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**3 225**	**50.8**	**10 464**	**56.3**
A(H1N1)pdm09	361	45.6	1 094	28.4
A(H3N2)	430	54.4	2 760	71.6
A not subtyped	2 434	-	6 610	-
Influenza B	**3 122**	**49.2**	**8 121**	**43.7**
B/Victoria lineage	1	4.3	8	2.5
B/Yamagata lineage	22	95.7	313	97.5
Unknown lineage	3099	-	7 800	-
Total detections (total tested)	**6 347 (19 231)**	**-**	**18 585 (187 187)**	**-**

[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 235 viruses has been reported (Table 3). Among 107 influenza A(H3N2) viruses, 63 (59%) fell in the vaccine virus component clade (3C.2a), and 42 (40%) 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. 1 A(H1N1)pdm09, 1 A(H3N2) and 3 B/Yamagata viruses were not attributed to any clade. For more information on virus characterizations for EU/EEA countries, see the WHO CC London November 2017 report.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–52/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	30
A(H1N1)pdm09 not attributable to any clade	1
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	63
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1) [c]	43
A(H3N2) not attributable to any clade	1
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	8
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	6
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	80
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] Deletion of K162 and N163 in the HA1 subunit of the hemagglutinin and antigenically different from the vaccine component.
[f] 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 111 viruses (57 A(H3N2), 23 A(H1N1)pdm09 and 31 type B) with collection dates since week 40/2017. One 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).

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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