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

Summary

Week 51/2017 (18–24 December 2017)

- Influenza activity was increasing in countries in western, northern and southern Europe.
- Both influenza type A and B viruses were co-circulating and mixed patterns were observed across the Region.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 32% tested positive for influenza viruses, an increase over 28% 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. A higher proportion of A(H1N1)pdm09 than 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, 60% 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, 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 2017–2018 in Norway. See full report here.
- 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

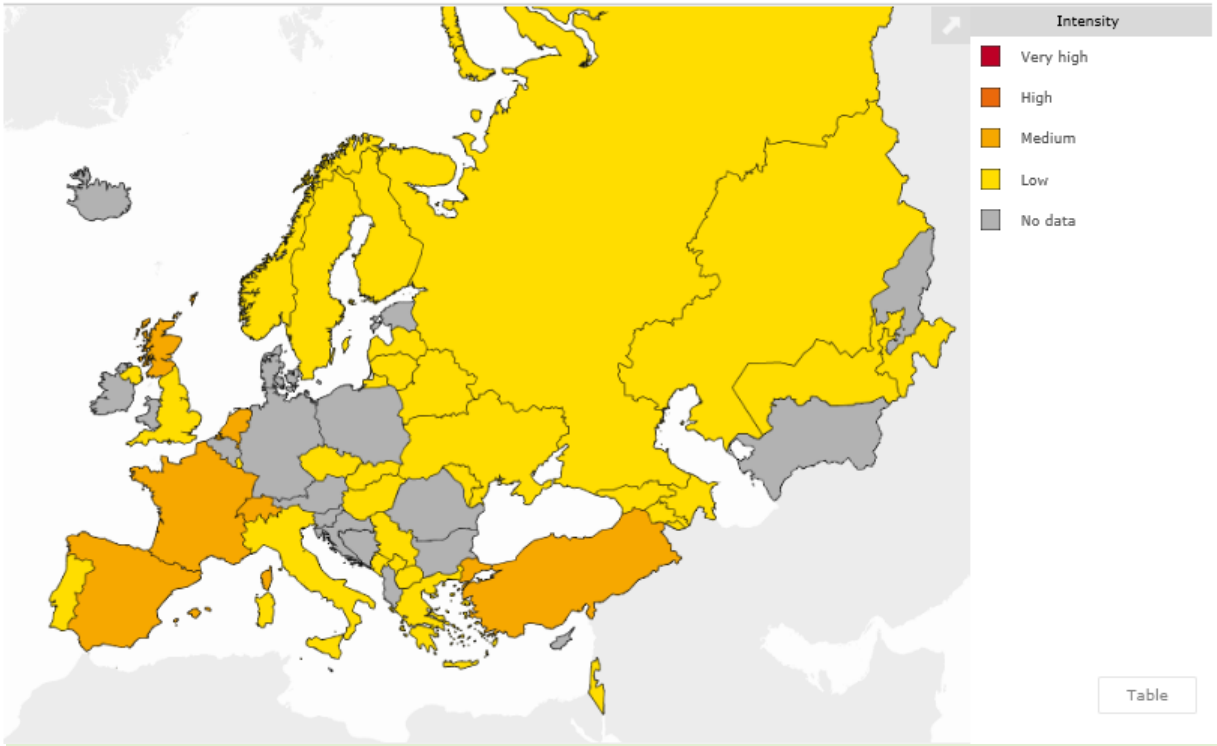
Overall, countries reported low activity of respiratory infections, based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI). 8 countries have passed the epidemic threshold indicating influenza activity based on ILI or ARI rates: Armenia, Israel, Italy, Luxembourg, the Netherlands, Spain, Switzerland and the United Kingdom (England and Scotland).

Influenza activity

For week 51/2017, due to the holiday period, fewer countries reported data compared to previous weeks. While low intensity of influenza activity was reported by 28 of the 33 countries reporting on this indicator, medium intensity of influenza activity was reported by 5 countries (France, the Netherlands, Spain, Switzerland and Turkey) and one region (the United Kingdom – Scotland) (Fig. 1). No geographic spread of influenza was reported by 6 of the 33 countries reporting on this indicator; 15 countries reported sporadic cases, 2 reported local geographic spread, 3 countries reported regional spread, and 7 countries (France, 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 51/2017



Map disclaimer

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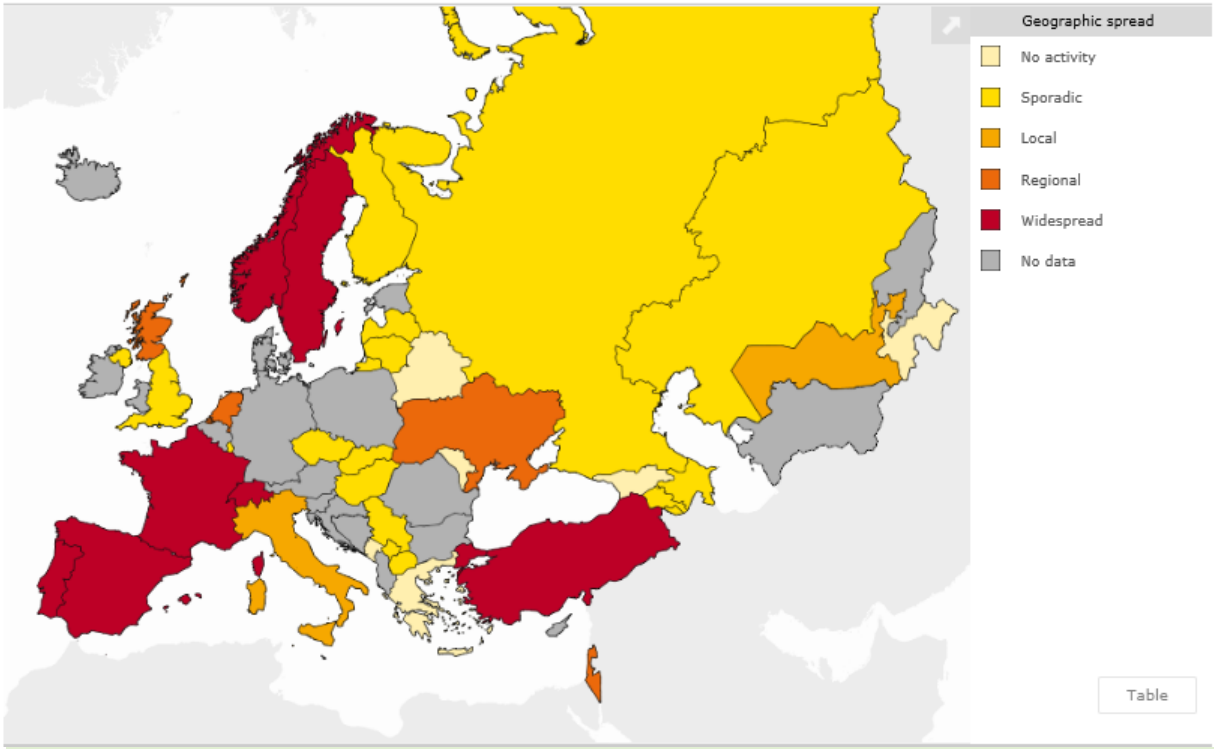
Fig. 2 Geographic spread in the European Region, week 51/2017



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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)

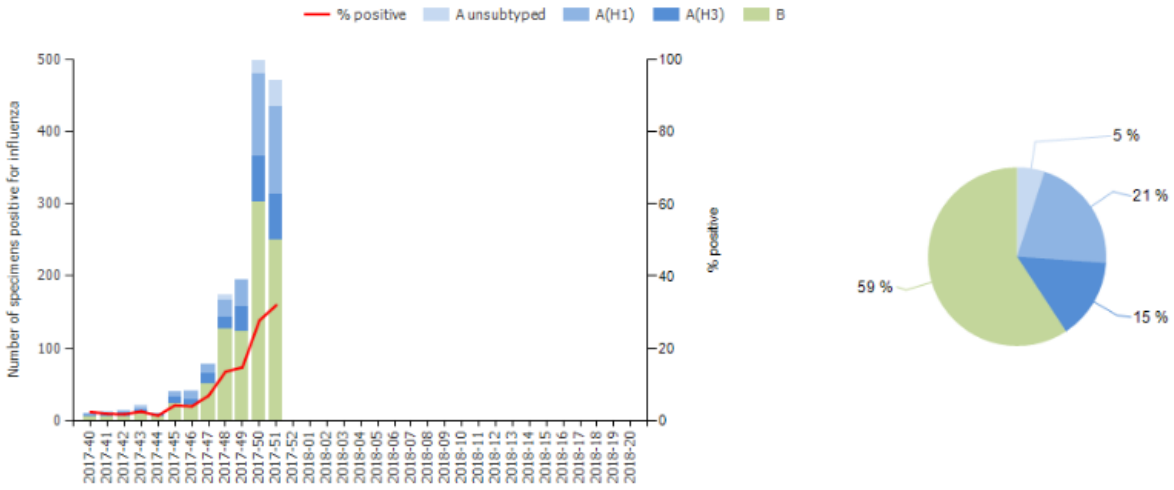
For week 51/2017, 471 (31.8%) of 1 483 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 47% were type A and 53% were type B. Out of 184 subtyped A viruses, 66% were influenza A(H1N1)pdm09 and 34% A(H3N2). Of 94 B viruses ascribed to a lineage, 98% were B/Yamagata and 2% B/Victoria (Fig. 3 and Table 1).

Of 18 countries across the region that each tested at least 10 sentinel specimens in week 51, 8 countries reported proportions of influenza virus detections proportions of 30% or more: France (72%), Israel (42%), Italy (58%), Lithuania (38%), Serbia (58%), Spain (38%), Switzerland (64%) and the United Kingdom (Northern Ireland 52% and Scotland 73%).

Since week 40/2017, more influenza type B (59%) than type A (41%) viruses have been detected. Of 560 subtyped A viruses, 59% were A(H1N1)pdm09. The majority of B viruses were reported without lineage and of 313 influenza B viruses ascribed to a lineage, 97% 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 51/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**221**	**46.9**	**638**	**40.7**
A(H1N1)pdm09	121	65.8	331	59.1
A(H3N2)	63	34.2	229	40.9
A not subtyped	37	-	78	-
Influenza B	**250**	**53.1**	**928**	**59.3**
B/Victoria lineage	2	2.1	8	2.6
B/Yamagata lineage	92	97.9	305	97.4
Unknown lineage	156	-	615	-
Total detections (total tested)	**471 (1 483)**	**31.8**	**1 566 (12 315)**	**12.7**

[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 51/2017, increased numbers of severe cases were reported by countries operating these surveillance systems compared to the previous week, particularly from the United Kingdom.

For week 51/2017, 104 laboratory-confirmed influenza-infected cases from intensive care units (ICU) or other wards were reported by Romania (n=1), Spain (n=39), Sweden (n=3), and the United Kingdom (n=61).

Since week 40/2017, 9 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 336 cases in ICU (206 in the United Kingdom, 76 in Spain, 37 in France, 13 in Sweden, 2 in Denmark and 1 each in the Czech Republic and Ireland), and 310 in other wards (171 in Spain, 81 in Ireland, 52 in Denmark, 2 each in the Czech Republic, Romania and Slovakia).

Of 336 cases in ICU, 211 (63%) were infected with type A viruses (32 A(H1N1)pdm09, 46 A(H3N2), 133 A un-subtyped) and 125 (37%) with type B viruses. A higher proportion of patients with influenza type B virus infection was observed in other wards: of 310 patients, 133 (43%) were infected with influenza type A (18 A(H1N1)pdm09, 29 A(H3N2), 86 A un-subtyped) and 177 (57%) with influenza B viruses.

For week 51/2017, 1 099 SARI cases were reported by 10 countries from which 307 specimens were tested with 15 (12 in Armenia, 1 Kazakhstan, 1 Serbia, and 1 in Uzbekistan) testing positive for influenza viruses. Since week 40/2017, 11 374 SARI cases have been reported from 15 countries; of 2 751 specimens tested for influenza viruses, 70 were positive for influenza virus: 33 from Armenia (30 type B and 3 A(H1N1)pdm09), 20 from Ukraine (1 A(H1N1)pdm09, 1 un-subtyped and 18 type B), 10 from Kazakhstan (5 A(H3N2) and 5 type B), 3 from Tajikistan (1 type A and 2 type B), 2 from Belarus (2 A(H3N2)), 1 from Serbia (type B), and 1 from Uzbekistan (1 A(H1N1)).

Mortality monitoring

No data was available from the EuroMOMO project for week 51/2017. Data from week 50/2017 showed that all-cause excess mortality has been within normal ranges over the past few weeks for the 19 reporting countries and regions.

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, most detections from non-sentinel systems have been influenza type A viruses, with A(H3N2) being the majority. The B/Yamagata lineage has predominated among type B viruses, as seen in sentinel systems. Details are given below.

Viruses detected in non-sentinel-source specimens

For week 51/2017, 3 258 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% were type A and 41% 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 75% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage, 97% were B/Yamagata lineage and 3% were B/Victoria lineage.

The higher proportion of influenza A, and subtype A(H3N2), since the start of the season detected in non-sentinel specimens compared to sentinel source specimens may be expected. Influenza A is more common in specimens from non-sentinel sources as a higher proportion is derived from hospital-based settings, with type B virus infections being generally milder and leading to less hospitalization than type A virus infections. 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.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 51/2017 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**1 911**	**58.7**	**6 287**	**59.5**
A(H1N1)pdm09	160	29.5	615	25.0
A(H3N2)	382	70.5	1 840	75.0
A not subtyped	1 369	-	3 832	-
Influenza B	**1 347**	**41.3**	**4 281**	**40.5**
B/Victoria lineage	0	0.0	7	3.3
B/Yamagata lineage	25	100.0	261	96.7
Unknown lineage	1 322	-	4 013	-
Total detections (total tested)	**3 258 (12 945)**	**-**	**10 568 (160 241)**	**-**

[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 218 viruses has been reported (Table 3). Among 105 influenza A(H3N2) viruses, 62 (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 40–51/2017

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]	62
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1) [c]	42
A(H3N2) not attributable to any clade	1
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	7
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	5
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	67
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.

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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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