Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 50/2017 (11–17 December 2017)

- Influenza activity was increasing in countries in Western Europe, Scandinavia and Turkey.
- Both influenza types A and B viruses were common and mixed patterns were observed across the Region.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 26% tested positive for influenza viruses, significantly higher compared to previous weeks.
- Data from 19 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

- An early risk assessment based on data from EU/EEA countries was published by ECDC on 20 Dec 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 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. 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 50/2017, while low intensity was reported by 40 of the 45 countries reporting on this indicator, medium intensity of influenza activity was reported by 4 countries (France, Ireland, the Netherlands and Spain) and high intensity of influenza activity was reported by Turkey (Fig. 1).

No geographic spread of influenza was reported by 8 of the 45 countries reporting on this indicator; 23 countries reported sporadic cases, 5 reported local geographic spread, 6 countries (Israel, the Netherlands, Norway, Portugal, Spain and Ukraine) reported regional spread, and 3 countries (France, Sweden and Turkey) reported widespread activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 50/2017

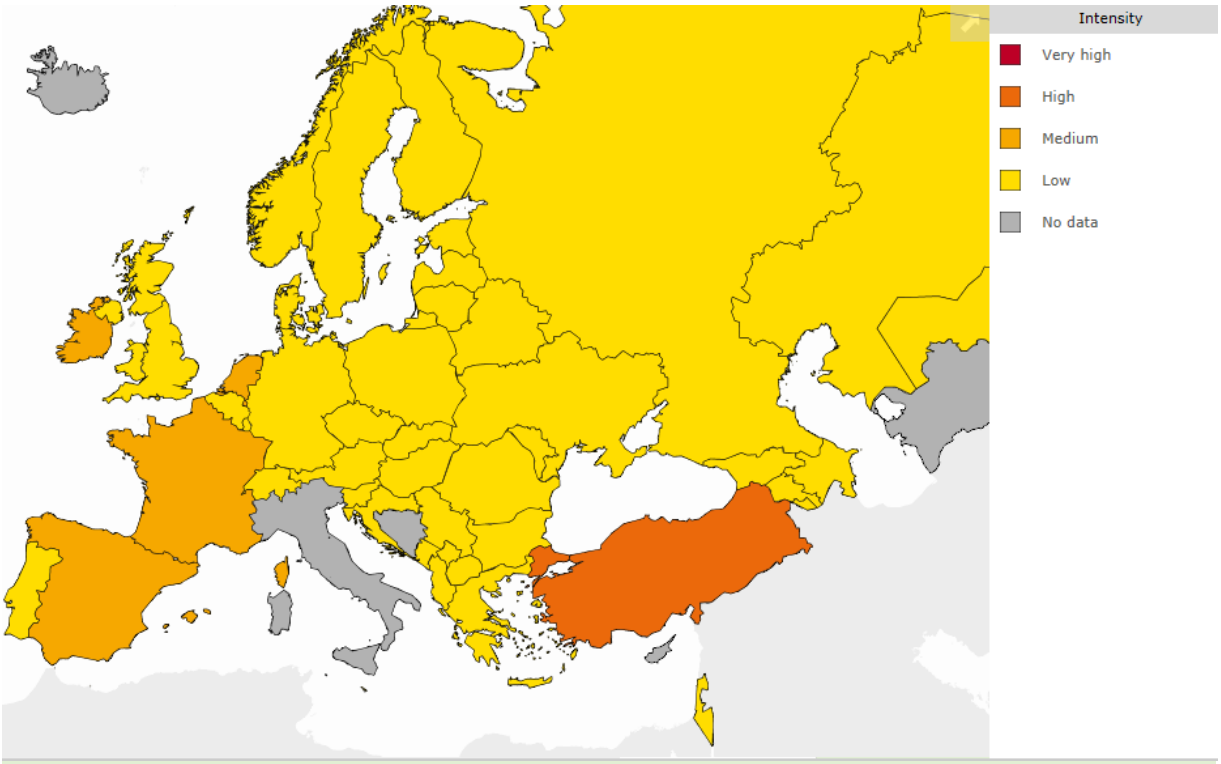
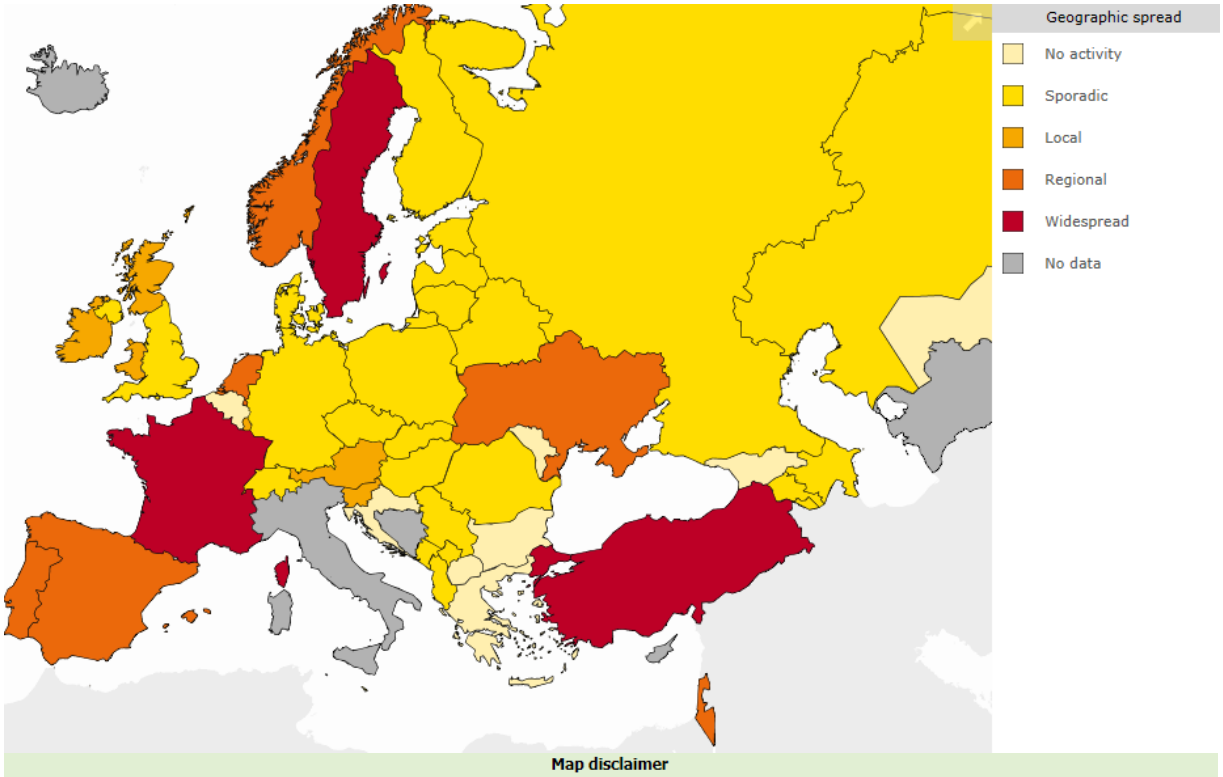


Fig. 2 Geographic spread in the European Region, week 50/2017



Map disclaimer

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** The administrative boundaries include spatial feature for Kosovo, this designation being without prejudice to position on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.*
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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)

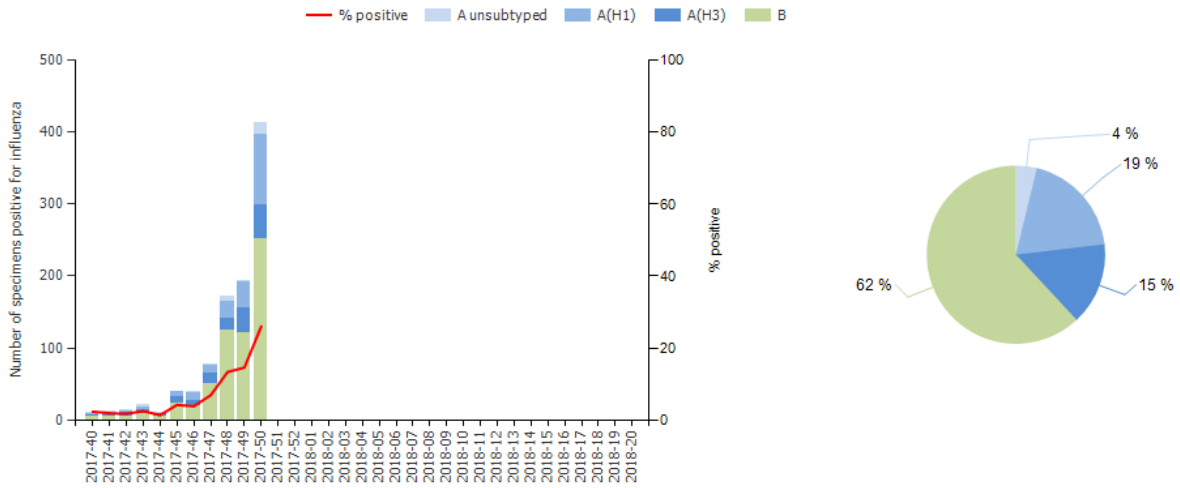
For week 50/2017, 412 (26.4%) of 1 561 sentinel specimens tested positive for influenza viruses (Table 1). Of these, 39% were type A and 61% were type B. Out of 146 subtyped viruses 67% were influenza A(H1N1)pdm09 and 33% A(H3N2). Of 46 B viruses ascribed to a lineage, 98% were B/Yamagata and 2% B/Victoria (Fig. 3 and Table 1).

Of 29 countries across the region that each tested at least 10 sentinel specimens in week 50, 10 countries reported detection proportions of 30% or more: Austria (34%), Croatia (42%), France (64%), Italy (30%), Norway (36%), Portugal (55%), Spain (40%), Sweden (32%), Switzerland (35%) and the United Kingdom (Scotland 33%).

Since week 40/2017, more influenza type B than type A viruses have been detected. Of 344 subtyped A viruses, 56% were A(H1N1)pdm09. The majority of B viruses were reported without lineage and of 186 influenza B viruses 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 50/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**161**	**39.1**	**382**	**38.1**
A(H1N1)pdm09	98	67.1	194	56.4
A(H3N2)	48	32.9	150	43.6
A not subtyped	15	-	38	-
Influenza B	**251**	**60.9**	**621**	**61.9**
B/Victoria lineage	1	2.2	7	3.8
B/Yamagata lineage	45	97.8	179	96.2
Unknown lineage	205	-	435	-
Total detections (total tested)	**412 (1 561)**	**26.4**	**1003 (10 596)**	**9.5**

[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 50/2017, slightly increased numbers of severe cases were reported by countries operating these surveillance systems.

For week 50/2017, 108 laboratory-confirmed influenza-infected cases from intensive care units (ICU) or other wards were reported by Denmark (n=13), Ireland (n=18), Spain (n=40), and the United Kingdom (n=37).

Since week 40/2017, 9 countries have reported laboratory-confirmed hospitalized influenza cases in ICU or other wards: 243 cases in ICU (142 in the United Kingdom, 53 in Spain, 37 in France, 7 in Sweden, 2 in Denmark and 1 each in the Czech Republic and Ireland), and 234 in other wards (96 in Spain, 81 in Ireland, 52 in Denmark, 2 each in the Czech Republic and Slovakia, and 1 in Romania).

Of 243 cases in ICU, 160 (66%) were infected with type A viruses (25 A(H1N1)pdm09, 33 A(H3N2), 102 A un-subtyped and 83 (34%) with type B viruses. A higher proportion of patients with influenza type B virus infection was observed in other wards: of 234 patients, 108 (46%) were infected with influenza type A (16 A(H1N1)pdm09, 27 A(H3N2), 65 A un-subtyped) and 126 (54%) with influenza B viruses.

For week 50/2017, 1 198 SARI cases were reported by 11 countries from which 300 specimens were tested with 13 (6 in Ukraine, 5 in Armenia and 2 in Belarus) testing positive for influenza viruses. Since week 40/2017, 10 275 SARI cases have been reported from 14 countries; of 2 444 specimens tested for influenza viruses, 55 were positive for influenza virus: 21 from Armenia (18 type B and 3 A(H1N1)pdm09), 20 from Ukraine (1 A(H1N1)pdm09, 1 un-subtyped and 18 type B), 9 from Kazakhstan (4 A(H3N2) and 5 type B), 3 from Tajikistan (1 type A and 2 type B), and 2 from Belarus (2 A(H3N2)).

Mortality monitoring

Data from 19 countries or regions reporting to the EuroMOMO project were received for week 50/2017 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 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. 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 50/2017, 2 345 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, 55% were type A and 45% 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 74% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage (n=215), 97% were B/Yamagata lineage and 3% were B/Victoria lineage.

The slightly 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 usually more common in non-sentinel cases as they are generally derived from hospital-based settings. In addition, the influenza virus subtypes may vary between countries which may lead to differences in (sub)type proportions for the Region as a whole.

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 50/2017 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**1290**	**55.0**	**4003**	**60.3**
A(H1N1)pdm09	162	36.2	438	26.1
A(H3N2)	285	63.8	1243	73.9
A not subtyped	843	-	2322	-
Influenza B	**1055**	**45.0**	**2635**	**39.7**
B/Victoria lineage	1	3.6	7	3.3
B/Yamagata lineage	27	96.4	208	96.7
Unknown lineage	1027	-	2420	-
Total detections (total tested)	**2345 (20 690)**	**-**	**6638 (146 350)**	**-**

[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 208 viruses has been reported (Table 3). Among 104 influenza A(H3N2) viruses, 62 (60%) 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. 3 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 40–50/2017

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	30
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
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	7
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	3
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	61
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 108 viruses (55 A(H3N2), 23 A(H1N1)pdm09 and 30 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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