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

Summary

Week 2/2018 (8–14 January 2018)

- Influenza activity was increasing in countries in northern, southern and western Europe.
- Both influenza types B and A viruses were co-circulating and different patterns of circulation were observed between countries in the Region.
- Of the individuals sampled, on presenting with ILI or ARI to sentinel primary healthcare sites, 46% tested positive for influenza viruses, similar to the previous weeks (42-50%).

2017–2018 season overview

- From sentinel sources for the Region overall, 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.
- From non-sentinel sources for the Region overall, a similar proportion of type B viruses compared to type A viruses has been detected. Of the type A detections, A(H3N2) viruses have outnumbered A(H1N1)pdm09 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.
- Different patterns of dominant type and A subtype were observed across the countries in the Region, an important cause of the observed differences between sentinel, non-sentinel and severe influenza sources of information.
- While low in number, 64% of the genetically characterized A(H3N2) viruses belonged to clade 3C.2a, the clade of the vaccine virus described in the WHO recommendations for vaccine composition for the northern hemisphere 2017–18, and 36% to clade 3C.2a1, with viruses in both clades being antigenically similar.
- 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.

Other news

- Based on data submitted to the EuroMOMO project there has, over the past weeks, been increased all-cause mortality among the elderly, notably in the southwestern part of the European Region and the United Kingdom (Scotland).
- 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, the majority of countries reported low intensity of activity of respiratory infections, based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI).

Influenza activity

Influenza activity was at variable levels across the region in week 2/2018. Of 46 Member States reporting intensity, Ireland, Luxembourg, Malta, Switzerland and the United Kingdom (Wales) reported high intensity, 15 medium and 27 low intensity (Fig. 1). Of the 46 Member States reporting on geographic spread, almost half (n=18) reported widespread activity similar to the previous week. Other Member States reported regional spread (n=4), local (n=7), sporadic activity (n=14), or no activity (n=3) (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 2/2018

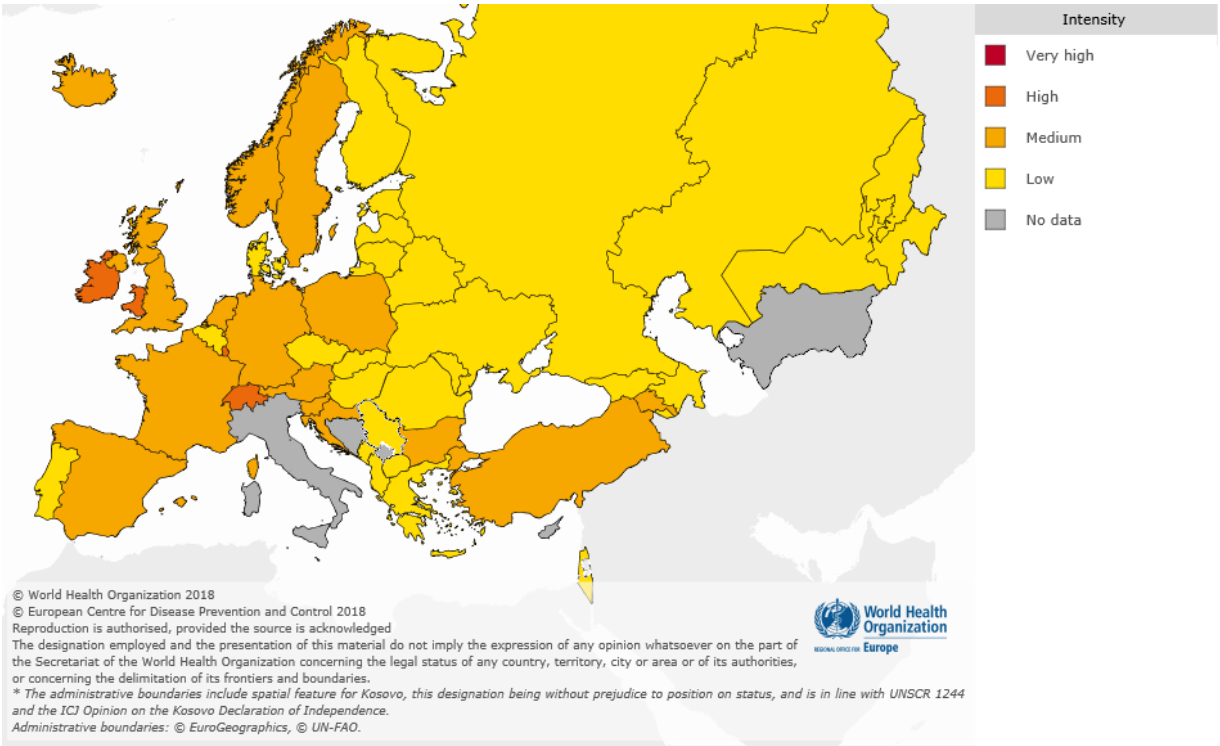
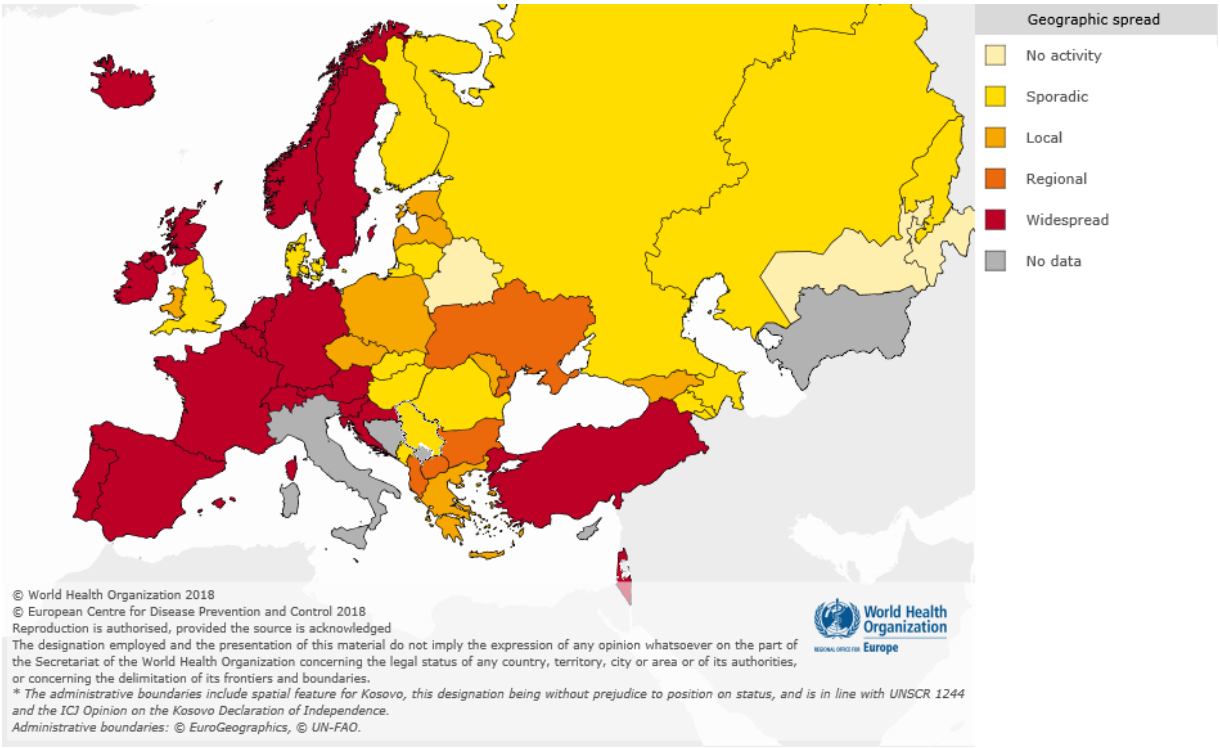


Fig. 2 Geographic spread in the European Region, week 2/2018



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 2/2018, 1 488 (46%) of 3 244 sentinel specimens tested positive for influenza viruses (

Table 1). Of these, 33% were type A and 67 % were type B. Out of 377 subtyped A viruses, 63% were influenza A(H1N1)pdm09 and 37% A(H3N2). Of 285 B viruses ascribed to a lineage, 99% were B/Yamagata and 1% B/Victoria (Fig. 3 and

Table 1).

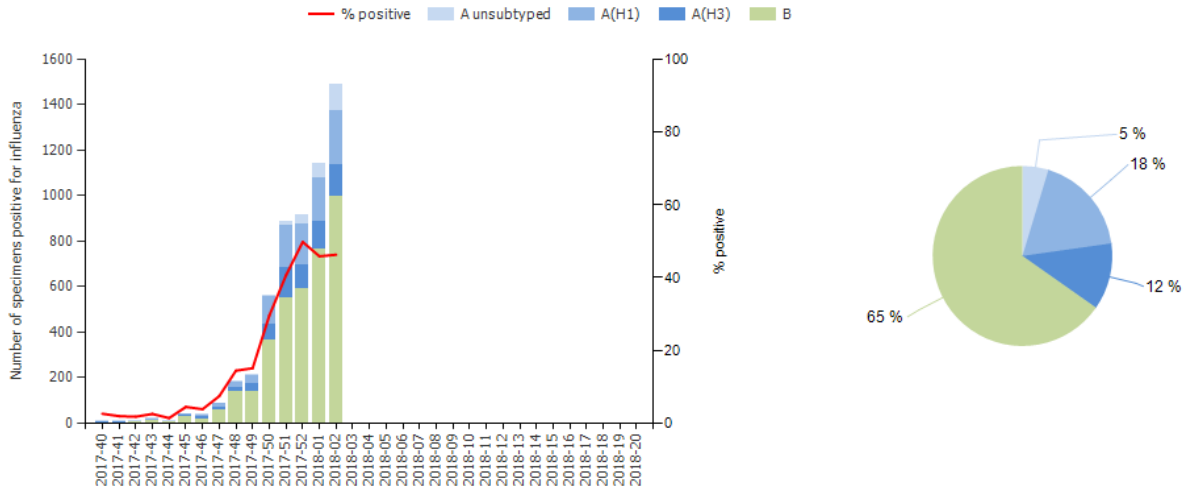
Of 39 Member States across the region that each tested at least 10 sentinel specimens in week 2/2018, 24 reported proportions of influenza virus detections of at least 30% or more (median of 51%, range of 36% to 71%).

Since week 40/2017, more influenza type B (65%) than type A (35%) viruses have been detected. Of 1 690 subtyped A viruses, 60% were A(H1N1)pdm09, mainly detected from France. The majority of type B viruses were reported without lineage, but of the 1 225 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 2/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**491**	**33**	**1953**	**34.7**
A(H1N1)pdm09	237	62.9	1017	60.2
A(H3N2)	140	37.1	673	39.8
A not subtyped	114	-	263	-
Influenza B	**997**	**67**	**3671**	**65.3**
B/Victoria lineage	3	1.1	41	3.3
B/Yamagata lineage	282	98.9	1184	96.7
Unknown lineage	712	-	2 446	-
Total detections (total tested)	**1 488 (3 244)**	**45.9**	**5 624 (20 884)**	**26.9**

[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

A subset of Member States monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases (n=10), or 2) severe acute respiratory infections (SARI; n=15).

1) Hospitalized laboratory-confirmed influenza

Overall numbers of reported hospitalized laboratory-confirmed influenza cases in intensive care units (ICUs) and other wards from nine reporting countries decreased in week 2/2018. Data are, however, preliminary and week 3 data is required to see if this trend is continued.

For week 2/2018, 408 laboratory-confirmed influenza-infected cases from ICUs were reported, with the majority reported by the United Kingdom (49%) and France (36%). A total of 469 cases were reported from other wards, with the majority of cases reported by Ireland (49%) and Spain (37%) (Table 2).

Table 2. Lab-confirmed hospitalised cases summary table by Member State and ward type.

		Cases in recent weeks		*Current week*	*Cumulative since week 40/2017*				
Member State		week 52	week 1	week 2	Total cases	A Total	A(H1) pdm09	A(H3)	B Total
Czech Republic	ICU	1	2	4	7	4	3	1	3
	Other wards	-	3	3	8	5	3		3
Denmark	ICU	8	3	1	16	6	1	2	10
	Other wards	103	87	65	379	144	10	45	235
Spain	ICU	105	73	46	365	136	28	36	229
	Other wards	285	346	172	1068	309	41	50	759
Finland	ICU	1	3	1	6	2		2	4
	Other wards	-	-	-					
France	ICU	330	384	148	1166	914	243	21	252
	Other wards	-	-	-					
Ireland	ICU	11	20	5	44	25	1	6	19
	Other wards	173	391	229	999	435	26	70	564
Romania	ICU	-	-	1	1	1	1		
	Other wards	-	1	3	6	4		1	2
Sweden	ICU	13	18	5	55	16		6	39
	Other wards	-	-	-					
United Kingdom	ICU	202	300	198	952	529	66	133	423
	Other wards	-	-	-					
Total	ICU	671	803	408	2611	1632	342	207	979
Total	Other wards	561	827	469	2454	893	80	165	1561

Since week 40/2017, 9 countries have reported laboratory-confirmed hospitalized influenza cases in ICUs or other wards (Table 2). Influenza A was more common in cases admitted to ICUs (62.5%), and influenza B more common in other wards (63.6%). Of the subtyped influenza A viruses, A(H1N1)pdm09 was more common (62%) in ICU cases compared to cases in other wards (33%). However, different patterns of virus circulation and total numbers reported between countries may be (partly) explaining these differences between ICU and other wards. Of cases reported since the start of the season, the largest number was among the older age groups and notably those aged 65 years and above, in particular for other wards.

2. SARI surveillance

Since week 40/2017, SARI cases have been reported from 15 countries, of which the majority is located in the eastern part of the Region.

For week 2/2018, 1 571 SARI cases were reported by 10 countries from which 452 specimens were tested for influenza viruses with 59 (13%) being positive. Although numbers are still low, the proportion positive has gradually increased over recent weeks. In particular, data from Albania, Armenia and Serbia showed an increase in influenza detections for week 2/2018, possibly indicating that the incidence of influenza will further increase in these countries in the coming weeks.

For SARI cases reporting positive for influenza, influenza B is also common with 52% B in week 2/2018, and 68% overall for the period weeks 40/2017–2/2018.

Mortality monitoring

Data from 20 Member States or regions reporting to the EuroMOMO project were received for week 2/2018 and included in the pooled analyses of all-cause excess mortality. Over the past few weeks, there has been increased all-cause mortality among the elderly, notably in the southwestern part of the European Region (Portugal and Spain) and the United Kingdom (Scotland).

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 this season have been influenza type A viruses, and of those typed most were A(H3N2). This may be related to the higher proportion of non-sentinel specimens being derived from hospital-based settings or outbreaks in long-term care homes for elderly, with A(H3N2) viruses often causing more severe disease in the elderly and A(H1N1)pdm09 in middle-aged patients. However, since week 1/2018 influenza type B detections have been in the majority for non-sentinel specimens with the B/Yamagata lineage viruses predominating, as seen in sentinel systems. Further details are given in the section below.

Differences in the relative contributions of sentinel and non-sentinel specimen sources to influenza surveillance between countries may lead to variation in (sub)type proportions in countries within the Region.

Viruses detected in non-sentinel-source specimens

For week 2/2018, 8 033 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, 43% were type A and 57% type B viruses (Table 2); this is the second week in which more type B viruses than type A viruses were detected in non-sentinel specimens. 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 66% were A(H3N2) (Table 2). Of influenza type B viruses ascribed to a lineage, 98% were B/Yamagata lineage and 2% were B/Victoria lineage.

Table 3. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 2/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**3 439**	**42.8**	**21 784**	**50.3**
A(H1N1)pdm09	696	44.6	2 955	33.7
A(H3N2)	864	55.4	5 813	66.3
A not subtyped	1 879	-	13 016	-
Influenza B	**4 594**	**57.2**	**21 484**	**49.7**
B/Victoria lineage	3	1.3	25	1.9
B/Yamagata lineage	230	98.7	1 324	98.1
Unknown lineage	4 361	-	20 135	-
Total detections (total tested)	**8 033 (33 471)**	**-**	**43 268 (267 993)**	**-**

[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 661 viruses has been reported (Table 4).

Among 303 influenza A(H3N2) viruses, 171 (56%) fell in the vaccine virus component clade (3C.2a), and 113 (37%) 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 A(H1N1)pdm09, 1 A(H3N2) and 88 B/Yamagata viruses were not attributed to any clade.

15 of the 28 B/Victoria-lineage viruses belonged to a subgroup of clade 1A viruses, represented by B/Norway/2409/2017, which carry the HA1 double amino acid deletion, Δ162-163, characteristic of the new antigenically distinct subgroup of genetic clade 1A viruses that are circulating in several countries.

For more information on virus characterizations for EU/EEA countries, see the WHO CC London December 2017 report.

Table 4. Viruses attributed to genetic groups, cumulative for weeks 40/2017–2/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	50
A(H1N1)pdm09 not attributable to any clade	2
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	171
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	113
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	18
A(H3N2) not attributable to any clade	1
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	10
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	15
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	190
B(Vic) lineage not attributed to clade	3
B/Yamagata lineage not attributed to any clade	88

[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 187 viruses (72 A(H3N2), 42 A(H1N1)pdm09 and 73 type B) with collection dates since week 40/2017. 1 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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