Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 50/2016 (12–18 December 2016)

- Influenza activity increased across the region with epidemic thresholds for the ILI/ARI rate being exceeded in ten countries.
- The proportion of virus detections among sentinel surveillance specimens increased to 38%.
- The great majority of influenza viruses detected this week were A(H3N2).
- Laboratory-confirmed influenza cases from hospital settings increased in some countries.
- It is possible that the season will peak during the holiday season in many countries, which will increase pressure on healthcare systems.

Season overview

- Sentinel specimen positivity reached 10% in week 46/2016, an indication of a slightly earlier start of the influenza season compared to previous seasons.
- Week 46/2016 was the earliest week in a season that the positivity rate reached 10% since the emergence of A(H1N1)pdm09 viruses in the 2009-2010 influenza season; during the last six seasons this occurred between weeks 48 and 51.
- Since week 40/2016, influenza A viruses have predominated; the great majority (99%) of subtyped influenza A viruses from sentinel sites have been A(H3N2).

Primary care data

Influenza activity

Influenza activity increased further in some countries in week 50/2016. Seasonal ILI/ARI epidemic thresholds were exceeded in ten countries which use the moving epidemic method for calculation of the threshold.

The percentage of influenza virus detections increased among sentinel specimens and influenza activity was at variable levels across the region with 27 countries reporting low intensity, twelve countries reporting medium and three reporting high intensity (Fig. 1). Of the 40 countries reporting any geographic spread of influenza, the majority (n=13) reported sporadic activity while other countries reported widespread (n=11), regional (n=7) or local activity (n=9) (Fig. 2).

Map of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, week 50/2016

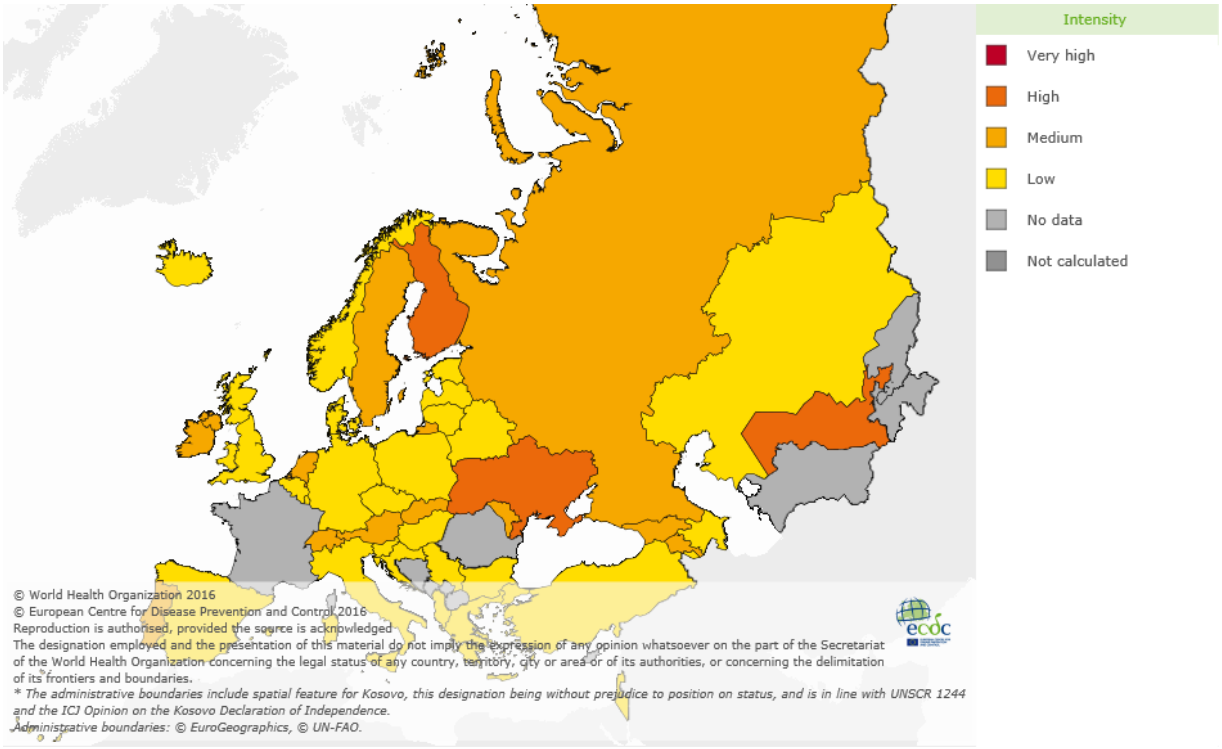
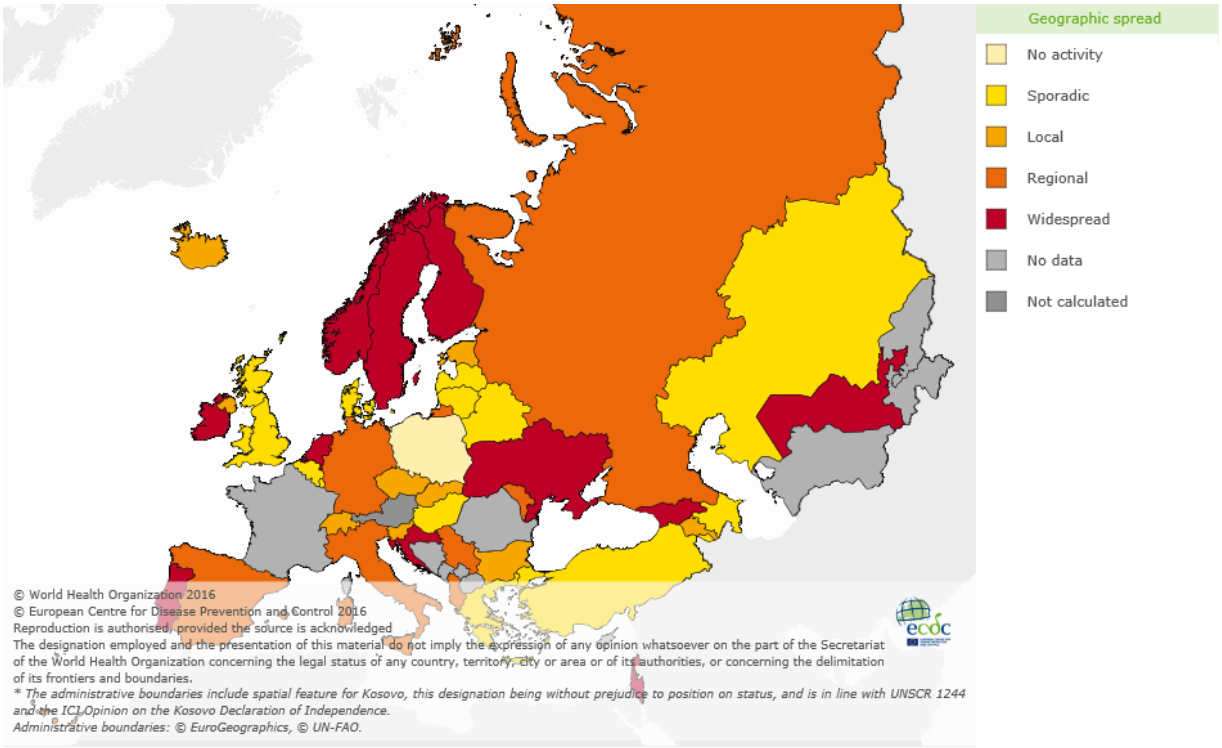


Fig. 2. Geographic spread in the European Region, week 50/2016



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 50/2016, 726 of 1 918 (38%) sentinel specimens tested positive for influenza virus (Table 1). Of these, 96% were type A and 4% were type B. The great majority (99.8%) of subtyped influenza A viruses were A(H3N2). The lineage of 17 influenza B viruses was determined and all were of B/Victoria lineage. Of 30 countries across the region that tested at least ten sentinel specimens, 27 reported proportions of influenza virus detections above 10%. Notably, Finland, Georgia, Portugal and Serbia reported high proportions (70% and above) of sentinel samples positive for influenza virus. Influenza virus detections have been reported by 36 countries across the Region.

Similar distributions of types and subtypes have been observed since week 40/2016: of all typed viruses, 93% were type A, with 99% of those subtyped being A(H3N2) (Fig. 3, Table 1). Of the 83 influenza B viruses which have been ascribed a lineage, 54 (65%) were of the B/Victoria lineage and 29 (35%) were of the B/Yamagata lineage.

Fig. 3. Influenza virus detections in sentinel-source specimens by type and subtype, by week and cumulatively

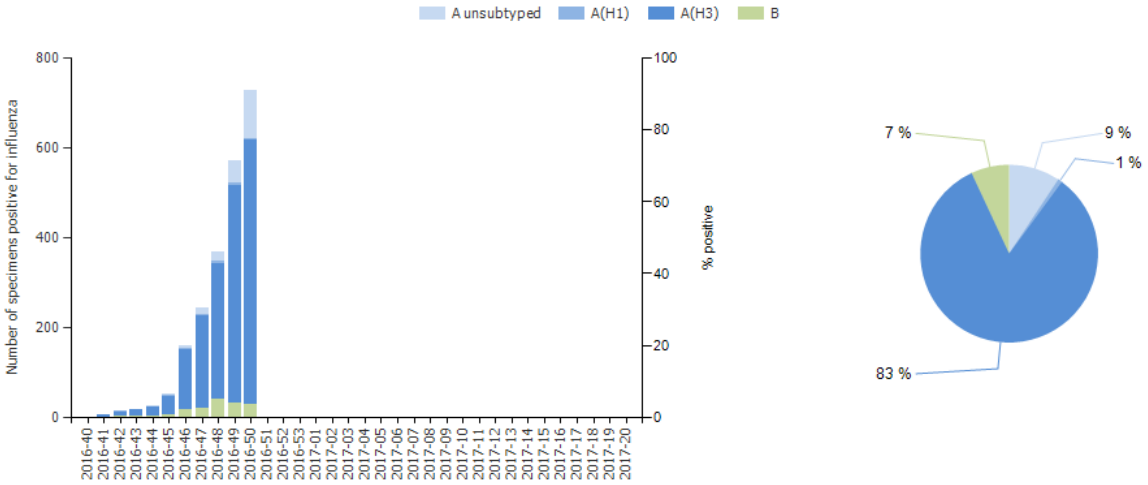


Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 50/2016 and cumulatively

	Number of detections	
Virus type and subtype	**Current Week**	**Season 2016-2017**
Influenza A	**698**	**2 030**
A(H1N1)pdm09	1	17
A(H3N2)	590	1 810
A not subtyped	107	203
Influenza B	**28**	**152**
B/Victoria lineage	17	54
B/Yamagata lineage	0	29
Unknown lineage	11	69
Total detections (total tested)	**726 (1 918)**	**2 182 (12 501)**

Severity

For week 50/2016, 15 countries reported laboratory-confirmed influenza cases based on hospital surveillance.

Of those countries, territories and regions that conduct surveillance based on sentinel severe acute respiratory infection (SARI), 1 061 SARI cases were reported of which 110 were positive for influenza A(H3N2) virus.

Of those countries, territories and regions that conduct surveillance based on hospitalized laboratory-confirmed influenza cases in intensive care units (ICU) or other wards, 17 cases were reported in ICU by Finland, Romania, Spain and Sweden, ten with type A, six with A(H3N2) and one with type B influenza virus infection. From other wards, 77 cases were reported by Ireland, Romania and Spain; 55 with type A and 22 with A(H3N2) influenza virus infection.

Since week 40/2016, 11 220 SARI cases were reported from 15 countries of which 672 (27%) of 2531 tested were positive for influenza virus infection. Of all influenza cases reported, 582 (87%) were infected by type A and 90 by type B viruses. Of the influenza A viruses 535 were A(H3N2) and 47 were not subtyped.

Since week 40/2016, Ireland, Romania, Spain and the United Kingdom have reported 255 cases in other wards; 141 infected with type A, 98 with A(H3N2), 7 with A(H1N1)pdm09 and 9 with type B influenza virus. In total, Finland, France, Ireland, Romania, Spain and Sweden

have reported 69 cases from ICU; 39 infected with type A, 25 with A(H3N2), 1 with A(H1N1)pdm09 and 4 with type B influenza virus. Since the start of the season, most of the hospitalized laboratory-confirmed cases reported have occurred in people aged 65 years or more and been associated with type A influenza virus infection. Information on patient age and influenza virus (sub)type was available for 69 cases in ICUs; 65 (94%) were infected with type A viruses. Most (n=45, 65%) were aged 65 years or more, 19 (28%) were aged 15–64 years and 5 (7%) were aged under 15 years. A(H3N2) was the dominant influenza virus subtype and accounted for 96% of the subtyped A viruses in cases admitted to ICUs. 8 fatalities have been reported, 4 from ICU and 4 from other wards, 3 infected by an A(H3N2) and 5 by unsubtyped type A influenza virus.

Mortality monitoring

Pooled analysis of data from 19 EU/EEA countries or regions reporting to the EuroMOMO project indicated that all-cause mortality was within normal, expected levels during recent weeks.

Virus characteristics

Viruses detected in non-sentinel-source specimens

For week 50/2016, 4 693 specimens from non-sentinel sources (such as hospitals, schools, non-sentinel primary care units, nursing homes and other care institutions) tested positive for influenza viruses (Table 1). Of these, 98% were type A and 2% type B, with 98% of the subtyped influenza A viruses being A(H3N2).

Similar distributions of types and subtypes have been observed since week 40/2016 with A(H3N2) viruses being dominant throughout Europe (Table 1). The distribution of viruses is similar to that of sentinel surveillance data with 96% type A and 4% type B viruses. For the majority of viruses, no subtype or lineage was determined; however, 96% of the subtyped influenza A viruses were A(H3N2). Of 49 type B viruses ascribed to a lineage, 65% were B/Yamagata lineage and 35% were B/Victoria lineage, which is different from the sentinel detections where the B/Victoria lineage has dominated the season this far. The difference is mainly driven by the 47 B/Victoria and 22 B/Yamagata detections from sentinel specimens in Kyrgyzstan and 15 B/Victoria and 22 B/Yamagata detections from non-sentinel sources in Norway.

Table 2. Influenza viruses detected in non-sentinel-source specimens, by virus (sub)type, week 50/2016 and cumulatively

	Number of detections	
Virus type and subtype	**Current Week**	**Season 2016-2017**
Influenza A	**4 603**	**11 060**
A(H1N1)pdm09	9	65
A(H3N2)	1 425	3 722
A not subtyped	3 169	7 273
Influenza B	**90**	**411**
B/Victoria lineage	0	17
B/Yamagata lineage	5	32
Unknown lineage	85	362
Total detections (total tested*)	**4 693 (20 634)**	**11 471 (132 016)**

* Not all countries have a true non-sentinel testing denominator and these figures are likely to be an underestimate.

Genetic characterization

For specimens collected since week 40/2016, genetic characterization of 234 viruses has been reported (Table 3). Among A(H3N2) viruses, 89 fall in the vaccine component clade (3C.2a), and 129 in a subclade of clade 3C.2a viruses (3C.2a1) defined by N171K, often with N121K, amino acid substitution in haemagglutinin. These two clades are antigenically similar.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40–50/2016

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[b]	4
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[a,b]	89
A(H3N2) A/Bolzano/7/2016 (clade 3C.2a1)	129
A(H3N2) A/Perth/16/2009grA/Switzerland/9715293/2013 (clade 3C.3a)	1
B/Brisbane/60/2008 (Victoria lineage clade 1A)[a,b]	4
B/Phuket/3073/2013 (Yamagata lineage clade 3)	7

[a] Vaccine component for Northern Hemisphere 2016-2017 season

[b] Vaccine component for Southern Hemisphere 2017 season

The ECDC summary report for September 2016 provides detailed genetic and antigenic analyses of viruses collected between January and June 2016.

The recommended composition of trivalent influenza vaccines for the 2016-2017 season in the northern hemisphere is for inclusion of an A/California/7/2009 (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) virus is recommended. The recommended influenza A(H1N1)pdm09 component of the 2017 southern hemisphere influenza vaccine is an A/Michigan/48/2015 (H1N1)pdm09like virus, the first update since A(H1N1)pdm09 viruses emerged in 2009.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 141 viruses (133 A(H3N2), 4 A(H1N1)pdm09 and 4 type B) with collection dates from week 40/2016. None showed evidence of reduced inhibition.

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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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