

## Summary

### Week 2/2017 (9–15 January 2017)

- Influenza activity remained widespread across the region with high or very high intensity in 8 out of 44 reporting countries or regions and medium intensity in 26 countries.
- The proportion of influenza virus detections among sentinel surveillance specimens was 46%, a slight decline from 52% in the previous week.
- The great majority of influenza viruses detected were type A (97%) and, of those subtyped, 99% were A(H3N2).
- Most of the hospitalized laboratory-confirmed cases reported have occurred in people aged 65 years or more.
- Excess all-cause mortality among the elderly has been observed in the past 1 to 2 months in most of the 18 countries that take part in [EuroMOMO](#).

### Season overview

- Influenza activity started early this season compared to previous seasons.
- Week 46/2016 is the earliest week that the overall influenza-positivity rate in sentinel specimens reached 10% since the emergence of A(H1N1)pdm09 viruses in the 2009 season; during the last 6 seasons this occurred between weeks 48 and 51.
- Since week 40/2016, influenza A viruses have predominated, accounting for 96% of all sentinel detections; the great majority (99%) of subtyped influenza A viruses from sentinel sites has been A(H3N2).
- In an influenza season in which A(H3N2) viruses predominate, elderly populations can be expected to be most severely affected. Indeed, confirmed cases of influenza A infection reported from hospitals have predominantly been in adults aged over 65 years.
- So far, circulating A(H3N2) viruses are antigenically similar to the vaccine strain. While about two-thirds of the A(H3N2) viruses characterized belong to a new genetic subclade (3C.2a1), these viruses are antigenically similar to the vaccine strain (clade 3C.2a).
- Early monitoring of vaccine effectiveness in [Finland](#) and [Sweden](#) suggests levels of effectiveness similar to estimates from multi-country studies during the seasons 2011–2012 to 2014–2015 with 26% (95% CI 22% to 30%) and 24% (95% CI 11% to 34%) vaccine effectiveness, respectively, in persons aged 65 years and older with laboratory-confirmed influenza A. Given the partial effectiveness of influenza vaccines, rapid use of neuraminidase inhibitors for laboratory-confirmed or probable cases of influenza infection should be considered for vaccinated and non-vaccinated patients at risk of developing complications.
- No reduced antiviral susceptibility has been observed among the viruses tested.
- A [risk assessment](#) on seasonal influenza in EU/EEA countries was published by ECDC on 24 December 2016. The above summary is in line with the findings of the risk assessment.

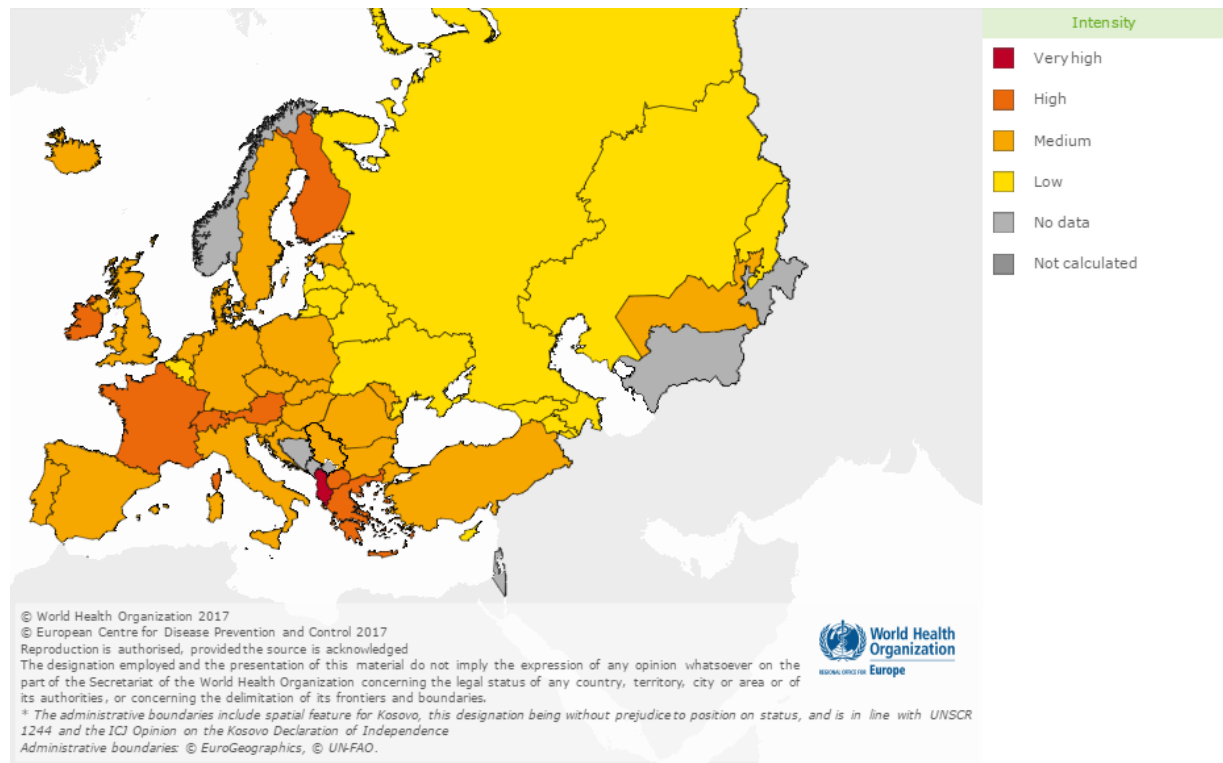
## Primary care data

### Influenza activity

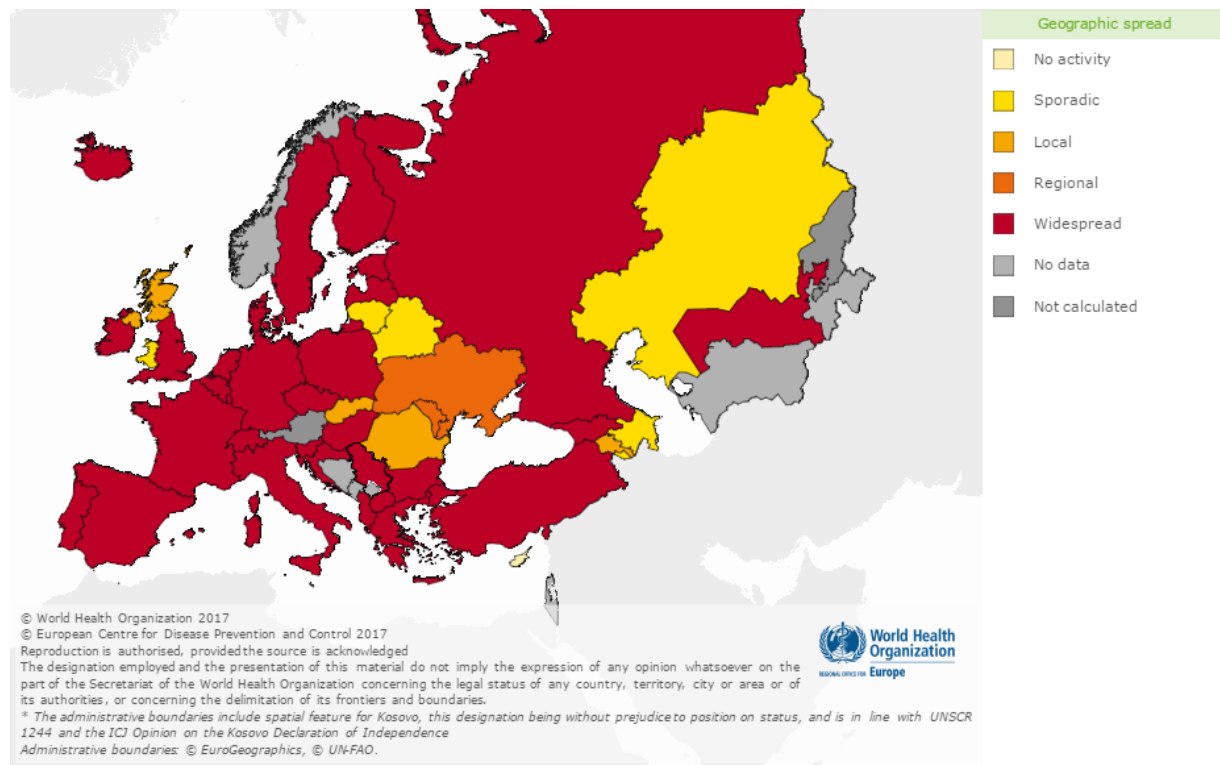
In week 2/2017 influenza activity was at variable levels across the region: Albania continued to report very high intensity for a third week, and 7, 26 and 12 countries or regions reported high, medium and low intensity, respectively (Fig. 1). The percentage of influenza virus detections among sentinel specimens was 46%, reduced compared to the previous week (52%). Of the 44 countries or regions reporting any geographic spread of influenza, the great majority (n=31) reported widespread activity similar to the previous week. Other countries reported regional (n=2), sporadic/local activity (n=10) or no activity (n=1) (Fig. 2).

### Map of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, week 2/2017



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



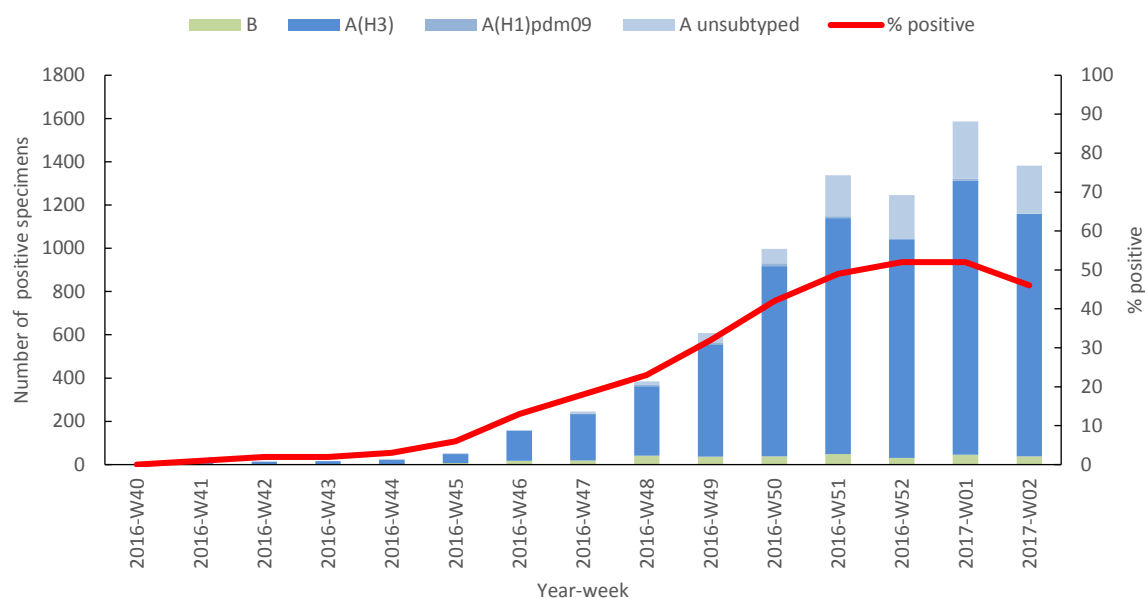
For interactive maps of influenza intensity and geographic spread, please see the Flu News Europe [website](#).

## Viruses detected in sentinel-source specimens (ILI and ARI)

For week 2/2017, 1 382 of 3 009 (46%) sentinel specimens tested positive for influenza viruses (Table 1). Of these, 97% were type A and 3% were type B. The great majority (>99%) of subtyped influenza A viruses were A(H3N2). The lineage of seven influenza B viruses was determined with 5 being B/Yamagata lineage. Of 32 countries across the region that each tested at least 10 sentinel specimens, 24 reported proportions of influenza virus detections above 30% (median 55%, range 37% to 75%).

Similar cumulative distributions of types and subtypes have been observed since week 40/2016: of all typed viruses, 96% were type A, with 99% of those subtyped being A(H3N2) (Fig. 3, Table 1). Of the 168 influenza B viruses which have been ascribed a lineage, 122 (73%) were of the B/Victoria lineage and 46 (27%) were of the B/Yamagata lineage.

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



**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 2/2017 and cumulatively**

Virus type and subtype	Number of detections	
	Current Week	Season 2016-2017
<b>Influenza A</b>	<b>1 343</b>	<b>7 729</b>
A(H1N1)pdm09	1	50
A(H3N2)	1 120	6 650
A not subtyped	222	1029
<b>Influenza B</b>	<b>39</b>	<b>334</b>
B/Victoria lineage	2	122
B/Yamagata lineage	5	46
Unknown lineage	32	166
<b>Total detections (total tested)</b>	<b>1 382 (3 009)</b>	<b>8 063 (24 318)</b>

## Severity

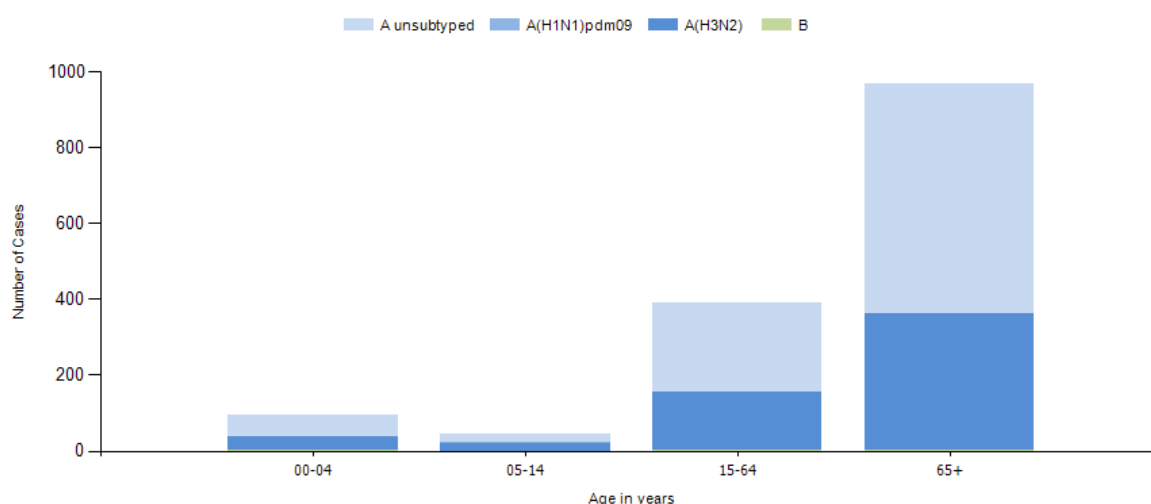
For week 2/2017, of the 15 countries that conduct sentinel surveillance on severe acute respiratory infection (SARI), 12 reported data and all 8 countries that conduct surveillance on hospitalized laboratory-confirmed influenza cases reported data.

Of 1 416 SARI cases reported, 336 were tested for influenza and 129 (38%) were positive: 98 A(H3N2), 24 untyped influenza type A viruses and 7 influenza type B viruses were detected. Since week 40/2016, 18 737 SARI cases have been reported from 15 countries with 4 814 being tested for influenza, of which 1 822 (38%) were positive: 1 578 (87%) were infected by type A and 244 (13%) by type B viruses. Of the influenza A viruses, 1 487 (94%) were A(H3N2) and 91 (6%) were untyped.

Countries that conduct surveillance on hospitalized laboratory-confirmed influenza cases in intensive care units (ICU) or other wards, reported 145 cases admitted to ICU in week 2/2017 by the Czech Republic, Finland, France, Ireland, Romania, Spain, Sweden and the United Kingdom (75 were type A not subtyped, 58 were A(H3N2), 11 were A(H1N1)pdm09 and 1 was type B). From other wards, 240 cases were reported in week 2/2017 by the Czech Republic, Ireland, Romania, and Spain (160 were type A not subtyped, 78 were A(H3N2), 1 was A(H1N1)pdm09 and 1 was type B).

Since week 40/2016, the Czech Republic, Ireland, Romania and Spain have reported 1 540 laboratory-confirmed influenza cases admitted to non-ICU wards; 939 infected with untyped A virus, 593 with A(H3N2), 2 with A(H1N1)pdm09 and 6 with type B influenza viruses. In total, the Czech Republic, Finland, France, Ireland, Romania, Spain, Sweden and the United Kingdom have reported 1 464 cases admitted to ICU; 922 infected with untyped influenza A virus, 445 with A(H3N2), 73 with A(H1N1)pdm09 and 24 with type B influenza viruses.

**Fig. 4. Distribution of virus (sub)type in influenza-confirmed cases admitted to ICU by age-group, cumulatively**



Since the start of the season, most of the hospitalized laboratory-confirmed cases reported have occurred in people aged 65 years or more. Information on patient age and influenza virus (sub)type was available for 997 cases admitted to ICU; the majority (67%) of cases (n=670) were aged ≥65 years, 287 (29%) were aged 15–64 years and 40 (4%) were aged

under 15 years. A(H3N2) viruses predominated and accounted for 299 cases, 97% of the subtyped influenza A viruses in cases admitted to ICUs. 221 fatal cases have been reported, 125 from ICUs and 96 from other wards (100 A(H3N2), 119 type A not subtyped, and 2 type B) with 184 (83%) being in patients aged  $\geq 65$  years.

## Mortality monitoring

Pooled analysis of data from 18 EU/EEA countries or regions reporting to the [EuroMOMO](#) project indicated that most participating countries saw marked increases in excess all-cause mortality among elderly over the past one to two months. This is probably due to circulation of influenza A(H3N2) viruses.

## Virus characteristics

### Viruses detected in non-sentinel-source specimens

For week 2/2017, 9 027 specimens from non-sentinel sources (such as hospitals, schools, non-sentinel primary care facilities, nursing homes and other institutions) tested positive for influenza viruses (Table 2). Of these, 97% were type A (with more than 99% of the subtyped viruses being A(H3N2)), and 3% type B.

Similar cumulative distributions of types and subtypes as seen in the sentinel detections have been observed since week 40/2016 with A(H3N2) viruses being dominant throughout Europe (Table 2). The distribution of typed viruses is similar to that of sentinel surveillance data with 97% type A and 3% type B influenza viruses. For the majority of viruses, no subtype or lineage was determined; however, for those that were, 99% of the subtyped influenza A viruses were A(H3N2), while of 204 type B viruses ascribed to a lineage, 64% were B/Yamagata lineage and 36% were B/Victoria lineage, which differs from sentinel detections where B/Victoria lineage viruses have dominated so far this season. The difference is mainly driven by the proportions of influenza B lineage detections in sentinel specimens in Kyrgyzstan (B/Victoria lineage predominant) and detections among non-sentinel specimens in Estonia and Norway (B/Yamagata lineage predominant).

**Table 2. Influenza viruses detected in non-sentinel-source specimens, by virus (sub)type, week 2/2017 and cumulatively**

Virus type and subtype	Number of detections	
	Current Week	Season 2016-2017
<b>Influenza A</b>	<b>8 770</b>	<b>49 024</b>
A(H1N1)pdm09	15	122
A(H3N2)	3 128	17 123
A not subtyped	5 627	31 779
<b>Influenza B</b>	<b>257</b>	<b>1 326</b>
B/Victoria lineage	4	73
B/Yamagata lineage	12	131
Unknown lineage	241	1122
<b>Total detections (total tested)</b>	<b>9 027 (31 407)</b>	<b>50 350 (257 570)</b>

\* 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 682 viruses has been reported (Table 3). Among A(H3N2) viruses, 200 fall in the vaccine component clade (3C.2a), and 432 in a subclade of clade 3C.2a viruses (3C.2a1) defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin. Viruses in these 2 clades are antigenically similar, though the 3C.2a1 clade is evolving rapidly with emergence of numerous virus clusters defined by additional amino acid substitutions in haemagglutinin.

**Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2016–2/2017**

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1) <sup>b</sup>	5
A(H1N1)pdm09 A/South Africa/3626/2013 (subgroup 6B)	2
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) <sup>a,b</sup>	200
A(H3N2) A/Bolzano/7/2016 (clade 3C.2a1)	432
A(H3N2) A/Switzerland/9715293/2013 (clade 3C.3a)	2
B/Brisbane/60/2008 (Victoria lineage clade 1A) <sup>a,b</sup>	13
B/Phuket/3073/2013 (Yamagata lineage clade 3) <sup>c</sup>	28

<sup>a</sup> Vaccine component for Northern Hemisphere 2016–2017 season

<sup>b</sup> Vaccine component for Southern Hemisphere 2017 season

<sup>c</sup> Vaccine component of quadrivalent vaccines for both northern and southern hemisphere

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)pdm09-like virus, the first update since A(H1N1)pdm09 viruses emerged in 2009.

Early monitoring of vaccine effectiveness in [Finland](#) and [Sweden](#) suggests levels of effectiveness similar to estimates from multi-country studies during the seasons 2011–2012 to 2014–2015 with 26% (95% CI 22% to 30%) and 24% (95% CI 11% to 34%) vaccine effectiveness, respectively, in persons aged 65 years and older with laboratory-confirmed influenza A. Given the partial effectiveness of influenza vaccines, rapid use of neuraminidase inhibitors for laboratory-confirmed or probable cases of influenza infection should be considered for vaccinated and non-vaccinated at-risk patients.

## Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 413 viruses (389 A(H3N2), 8 A(H1N1)pdm09 and 16 type B) with collection dates since week 40/2016. None showed evidence of reduced inhibition (Table 4).

**Table 4. Antiviral susceptibility (combined phenotypic and genotypic susceptibility information) by influenza virus type and subtype, cumulative for weeks 40/2016–2/2017**

Subtype	Oseltamivir					Zanamivir				
	Viruses tested	RI	HRI	RI+HRI	RI+HRI%	Viruses tested	RI	HRI	RI+HRI	RI+HRI%
A(H1)pdm09	8	0	0	0	0.0%	7	0	0	0	0.0%
A(H3)	389	0	0	0	0.0%	377	0	0	0	0.0%
B	16	0	0	0	0.0%	16	0	0	0	0.0%

For phenotypic analysis, reduced inhibition, RI, was defined as 10 to 100-fold above normal inhibition and highly reduced inhibition, HRI as >100-fold above normal inhibition for influenza A viruses, and 5 to 50-fold and >50-fold for influenza B viruses, respectively. For genotypic analysis, the summary table of neuraminidase amino acid substitutions associated with RI by neuraminidase inhibitors published by WHO was used ([http://www.who.int/influenza/gisrs\\_laboratory/antiviral\\_susceptibility/nai\\_overview/en/](http://www.who.int/influenza/gisrs_laboratory/antiviral_susceptibility/nai_overview/en/)).

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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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