

## Summary

### Weeks 30–34/2017 (24 July–27 August 2017)

- Influenza activity was at out-of-season levels in all countries. All reporting countries continued to report low intensity of influenza activity.
- Influenza viruses were detected sporadically both in sentinel and non-sentinel specimens, with both influenza type A and B viruses detected.
- For week 34/2017, data from the 20 countries or regions reporting to the EuroMOMO project indicated all-cause mortality to be at expected levels.

Additional information on global influenza activity is available from [WHO's biweekly global updates](#).

### 2016/17 season overview

- After an earlier start than usual (week 46/2016), influenza activity peaked between weeks 52/2016 and 4/2017. Between weeks 12 and 20/2017, most countries reported decreasing influenza activity with the proportion of sentinel detections returning to the epidemic threshold value (10%) in week 17/2017.
- A(H3N2) viruses predominated by a large margin during the season.
- Significant mortality from all causes was observed in people aged 15–64, and markedly so in people aged 65 or older, in the majority of the 20 reporting countries or regions. This is commonly seen when the predominant viruses circulating are A(H3N2).
- Two-thirds of the A(H3N2) viruses genetically characterized belonged to subclade 3C.2a1, but remained antigenically similar to the clade 3C.2a vaccine virus, as described in the [WHO recommendations for vaccine composition for the northern hemisphere 2017–18](#). See also the [ECDC summary report for June](#).

## Primary care data

### Influenza activity

For weeks 30–34/2017, 22 to 26 countries reported weekly epidemiological data. All reporting countries reported low intensity of influenza activity for the entire period. European intensity of influenza activity (Fig. 1) and geographic spread (Fig. 2) data are shown for week 34/2017.

# Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 34/2017

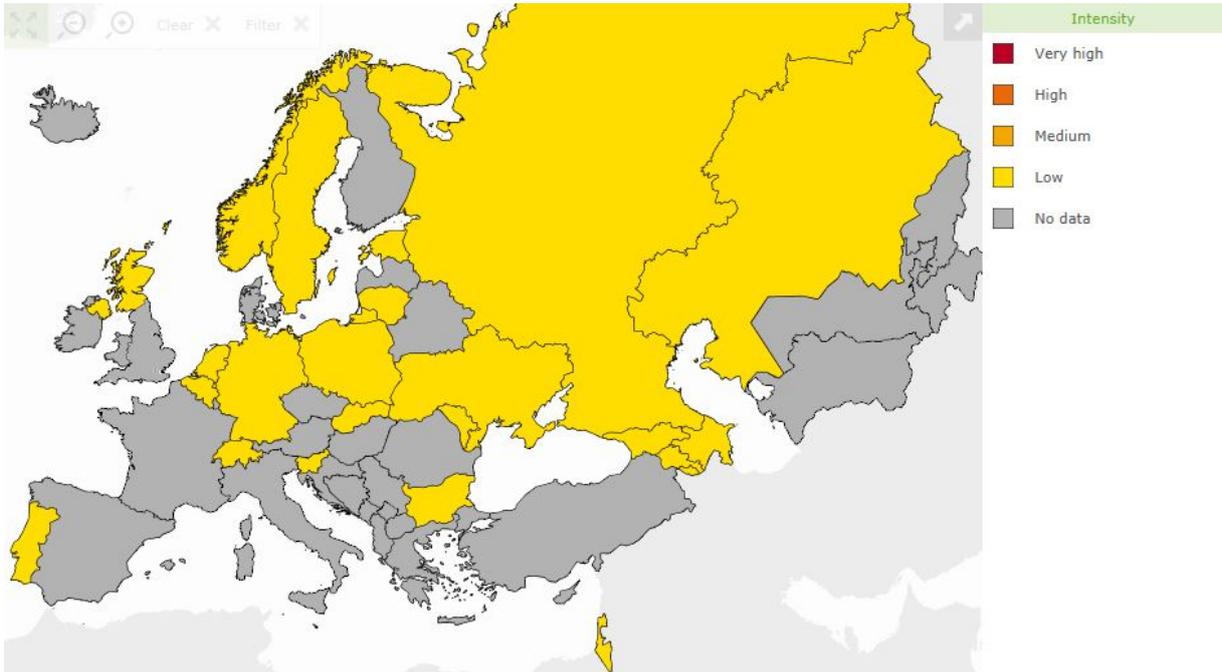
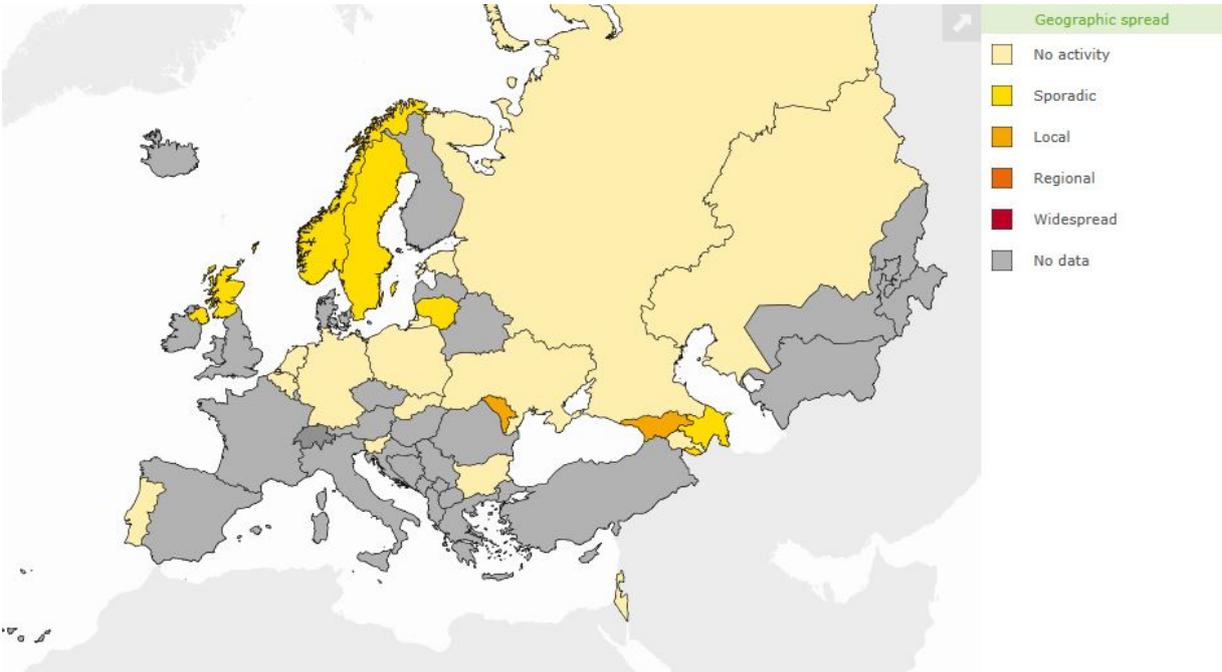


Fig. 2 Geographic spread in the European Region, week 34/2017

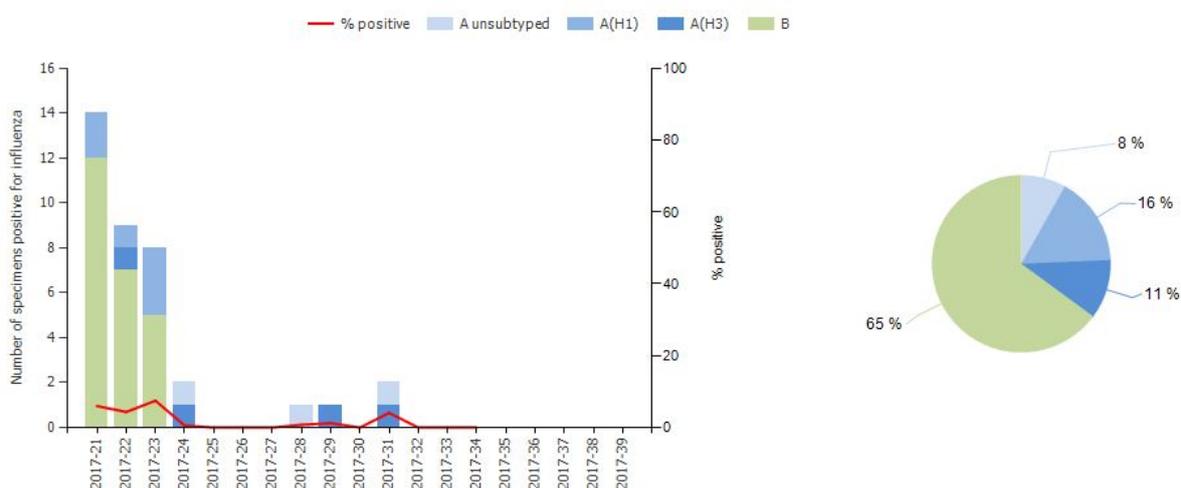


For interactive maps of influenza intensity and geographic spread, please see the [Flu News Europe website](#).

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

For weeks 30–34/2017, 2 (<1%) of 225 sentinel specimens tested positive for influenza viruses (Fig. 3 and Table 1). Both were type A viruses and one was subtyped as A(H3N2).

**Fig. 3 Influenza virus detections in sentinel-source specimens by type and subtype, for weeks 21–34/2017**



**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, cumulatively for weeks 30–34/2017**

Virus type and subtype	Weeks 30–34/2017	
	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>2</b>	<b>100</b>
A(H1N1)pdm09	0	0
A(H3N2)	1	100
A not subtyped	1	-
<b>Influenza B</b>	<b>0</b>	<b>0</b>
B/Victoria lineage	0	0
B/Yamagata lineage	0	0
Unknown lineage	0	-
<b>Total detections / Total tested</b>	<b>2 / 225</b>	<b>&lt;1</b>

<sup>a</sup>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

For weeks 30–34/2017, of 67 specimens tested by countries reporting data on severe acute respiratory infection (SARI), none were positive for influenza virus. No hospitalized laboratory-confirmed influenza cases were reported by the 9 countries that conduct this surveillance.

## Mortality monitoring

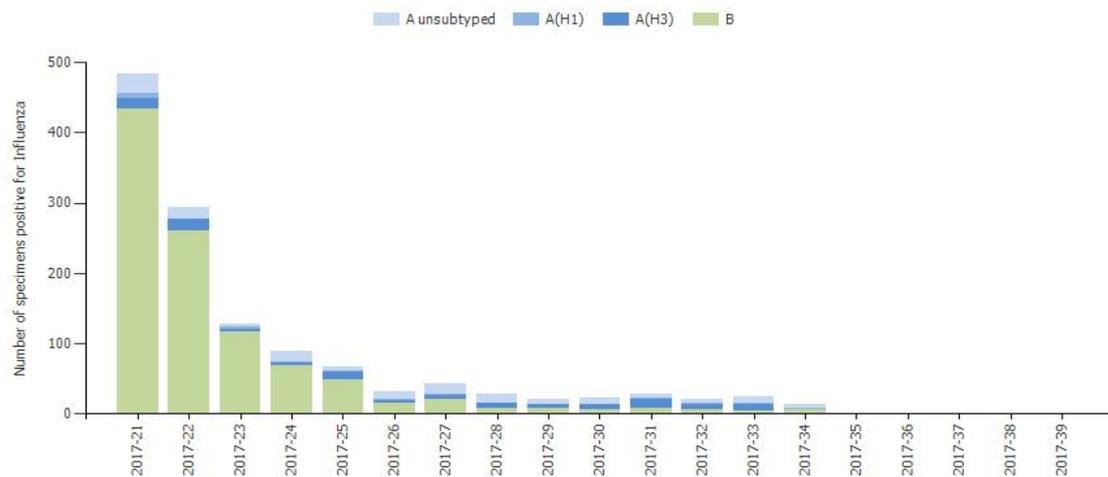
Data from 20 countries or regions reporting to the [EuroMOMO](#) project were received for week 34/2017 and included in the pooled analyses of excess all-cause mortality. Levels of all-cause mortality have been at expected levels in the past few weeks in the participating European countries.

## Virus characteristics

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

For weeks 30–34/2017, 5 593 specimens from non-sentinel sources were tested (such as hospitals, schools, non-sentinel primary care facilities, nursing homes and other institutions), of which 109 were positive for influenza viruses (Fig. 4, Table 2). Of the 109 detections, 74% were type A (85% of all subtyped viruses being A(H3N2)) and 26% type B.

**Fig. 4 Influenza virus detections in non-sentinel-source specimens by type and subtype, for weeks 21-34/2017**



**Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, cumulatively for weeks 30–34/2017**

Virus type and subtype	Weeks 30–34/2017	
	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>81</b>	<b>74</b>
A(H1N1)pdm09	7	15
A(H3N2)	39	85
A not subtyped	35	
<b>Influenza B</b>	<b>28</b>	<b>26</b>
B/Victoria lineage	0	0
B/Yamagata lineage	2	100
Unknown lineage	26	
<b>Total detections / Total tested</b>	<b>109 / 5 593</b>	<b>2</b>

<sup>a</sup>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

Since week 21/2017, genetic characterization of 5 viruses has been reported. Of these, 3 were B/Yamagata lineage viruses (clade 3), 1 A(H3N2) fell into the 3C.2a1 subclade defined by N171K amino acid substitution, often with N121K, in the haemagglutinin. Viruses in this clade have been antigenically similar to the vaccine component clade (3C.2a), but both clades 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. Additionally, 1 A(H1N1)pdm09 virus was genetically characterised and fell in the sub-group 6B.1. See also the [ECDC summary report for June](#).

The recommended composition of trivalent influenza vaccines for the 2016–2017 season in the [northern hemisphere](#) was 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) was recommended. On 2 March 2017, WHO announced the recommended vaccine composition for the 2017–2018 season in the [northern hemisphere](#). The recommendations matched those for the 2017 southern hemisphere season, with a changed A(H1N1)pdm09 component to an A/Michigan/48/2015-like virus (clade 6B.1).

Overall vaccine effectiveness of influenza vaccines for the 2016–2017 season was estimated at 44% in European primary care settings ([I-MOVE](#)) and 49% in the United States of America ([CDC](#)).

## Antiviral susceptibility testing

No viruses with collection dates from week 30/2017 through week 34/2017 have been tested for antiviral susceptibility.

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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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, weeks 30–34/2017.

Tables and figures should be referenced:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 30–34/2017.

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