Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 21–26/2017 (22 May–2 July 2017)

- Influenza activity has returned to out-of-season levels in all countries. All reporting countries continued to report low influenza intensity.
- Influenza viruses were detected sporadically both in sentinel and non-sentinel specimens, with influenza B predominating.
- As of week 26/2017, data from the 19 countries or regions reporting to the EuroMOMO project indicate that over recent months all-cause excess mortality has been at levels expected for the time of year.

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. Since week 12/2017, most countries reported decreased influenza activity with the proportion of sentinel detections returning to the epidemic threshold value (10%) in week 17/2017.
- A(H3N2) viruses predominated during the season.
- Significant excess all-cause mortality was observed in people aged 15–64 years, and markedly so in people aged 65 years 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 WHO CC London February 2017 report.
- Low levels of reduced susceptibility to oseltamivir and zanamivir were observed.

Primary care data

Influenza activity

For weeks 21–26/2017, a median of 26 countries (range 19 to 29) reported weekly epidemiological data. All reporting countries reported low intensity for the duration of this period. European intensity (Fig. 1) and geographic spread (Fig. 2) data are shown for week 26/2017.

Maps of qualitative indicators in the European Region

Fig. 1 Intensity in the European Region, week 26/2017

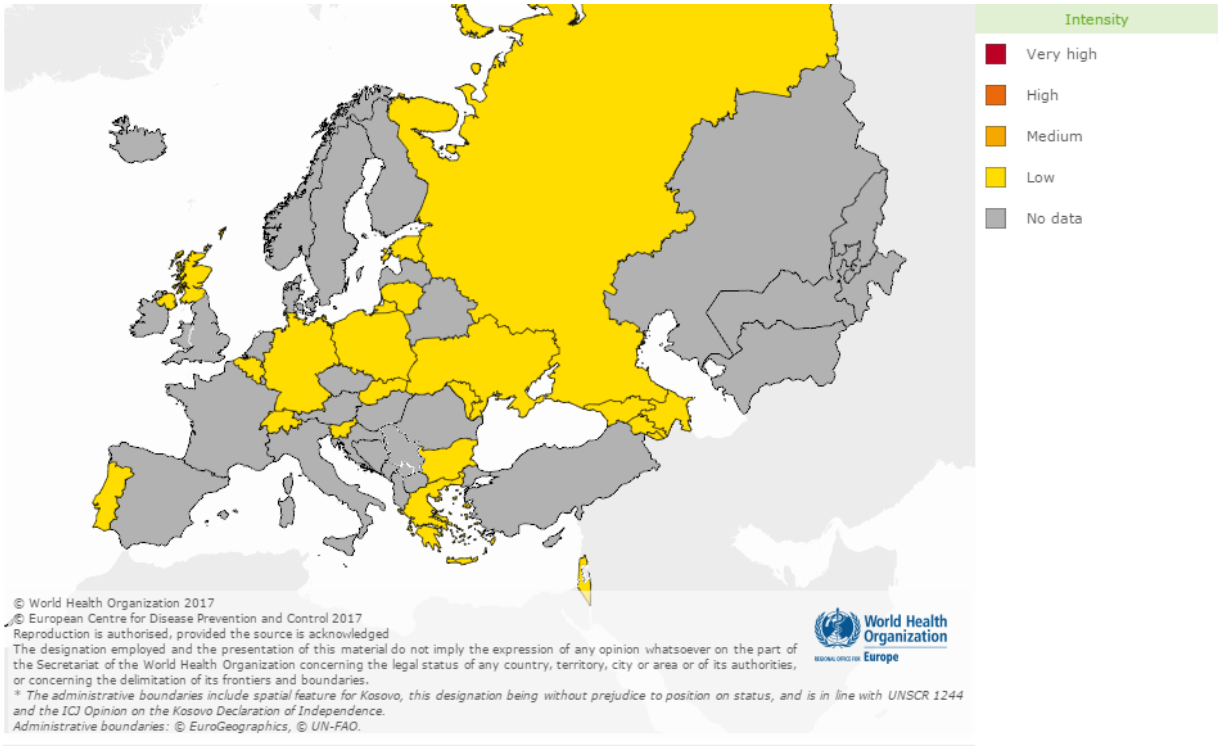
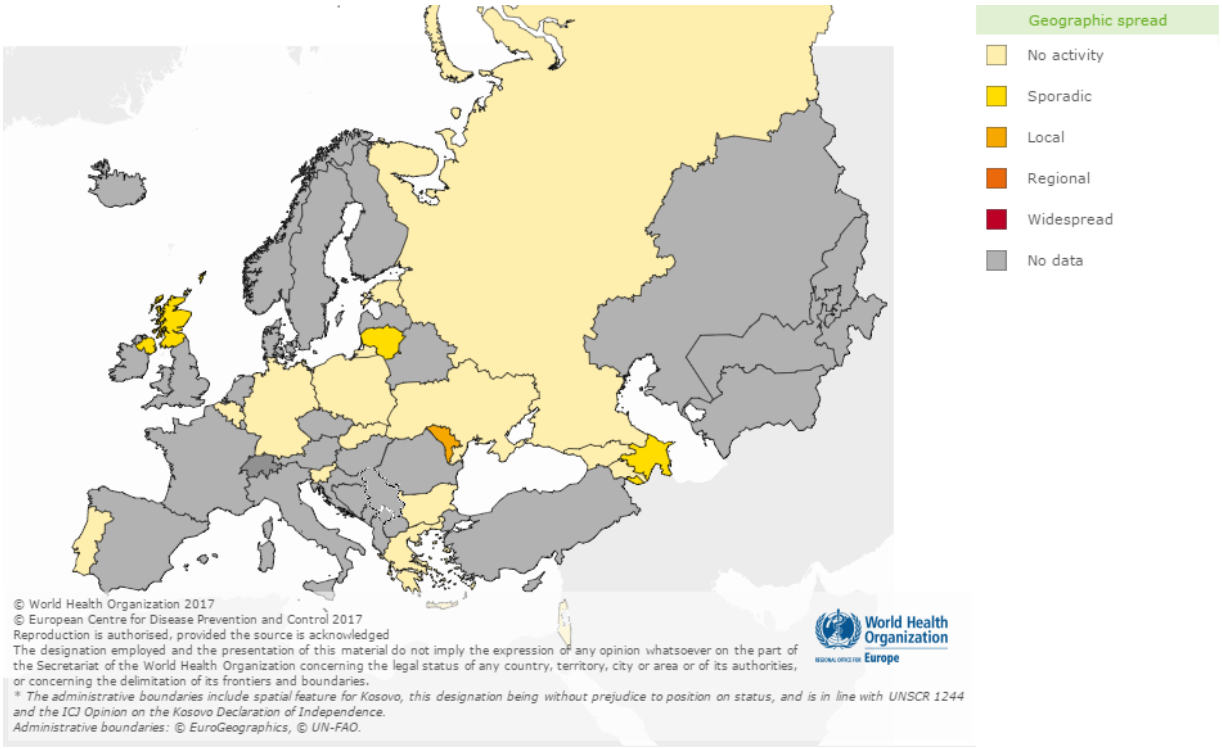


Fig. 2 Geographic spread in the European Region, week 26/2017

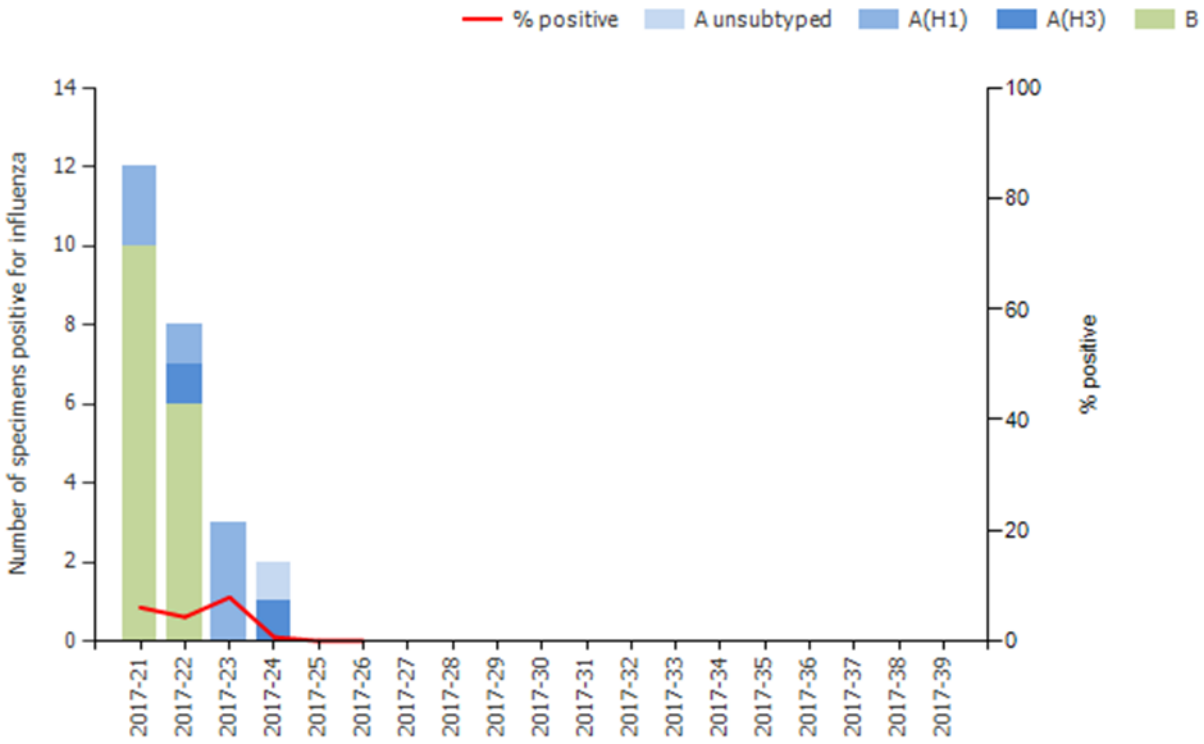


For interactive maps of influenza intensity and geographic spread, please see the Flu News Europe website.

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

For weeks 21–26/2017, 31 (4%) of 820 sentinel specimens tested positive for influenza viruses (Table 1) and the number of detections showed a decreasing trend over this period (Fig. 3). Of all typed viruses, 71% were type B and most of these have not been ascribed to a lineage.

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



* No specimens were tested positive for weeks 25 and 26/2017

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, cumulatively for weeks 21–26/2017

Virus type and subtype	Weeks 21–26/2017	
	Number	%[a]
Influenza A	**9**	**29**
A(H1N1)pdm09	6	75
A(H3N2)	2	25
A not subtyped	1	-
Influenza B	**22**	**71**
B/Victoria lineage	5	83
B/Yamagata lineage	1	17
Unknown lineage	16	-
Total detections / Total tested	**31 / 820**	**4**

[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

For weeks 21–26/2017, eight countries reported data on severe acute respiratory infection (SARI), with low numbers of influenza detections among hospitalized cases. Of 9 countries that conduct surveillance of hospitalized laboratory-confirmed influenza cases, Ireland and Sweden each reported one ICU case due to influenza B virus infection during this period. Ireland also reported five cases in other wards due to influenza B virus infection.

Mortality monitoring

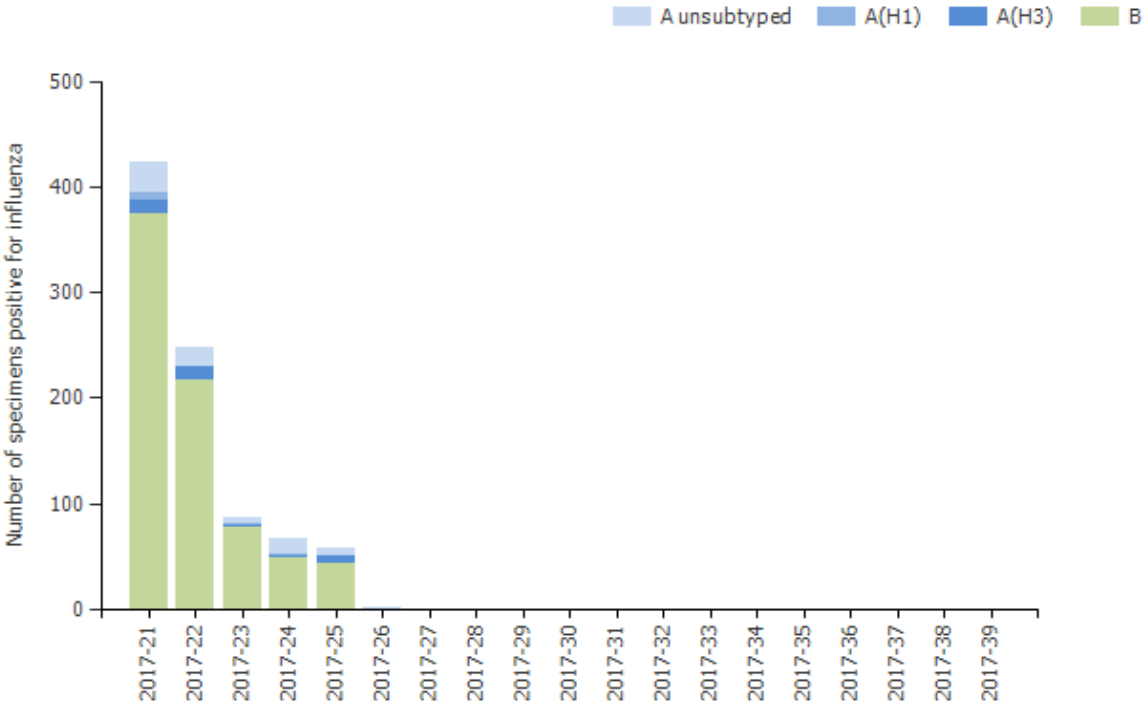
Data from 19 countries or regions reporting to the EuroMOMO project were received for week 26/2017 and included in the pooled analyses of excess all-cause mortality. These data indicate that over recent months all-cause excess mortality has been at levels expected for the time of year.

Virus characteristics

Viruses detected in non-sentinel-source specimens

For weeks 21–26/2017, 1 029 specimens from non-sentinel sources (such as hospitals, schools, non-sentinel primary care facilities, nursing homes and other institutions) tested positive for influenza viruses (Fig. 4, Table 2) and the number of detections showed a decreasing trend over this period. Of these detections, 12% were type A (81% of all subtyped viruses being A(H3N2)) and 88% type B (95% of those which have been ascribed to a lineage were Yamagata lineage).

Fig. 4 Influenza virus detections in non-sentinel-source specimens by type and subtype, by week*



*One specimen tested positive for week 26/2017

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, cumulatively for weeks 21–26/2017

Virus type and subtype	Weeks 21–26/2017	
	Number	%[a]
Influenza A	**122**	**12**
A(H1N1)pdm09	9	19
A(H3N2)	38	81
A not subtyped	75	-
Influenza B	**907**	**88**
B/Victoria lineage	8	5
B/Yamagata lineage	139	95
Unknown lineage	760	-
Total detections / Total tested	**1 029 / 21 507**	**-**

[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 between weeks 21/2017 and 26/2017, genetic characterization of 3 viruses has been reported. Two were B/Yamagata lineage viruses and one fell into the A(H3N2) 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. See also the WHO CC London February 2017 report.

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 2016–2017 season, but for the A(H1N1)pdm09 component being changed to an A/Michigan/48/2015-like virus (clade 6B.1).

Mid-season vaccine effectiveness (VE) estimates for all age groups against A(H3N2) illness from Canada (42%), from the US (43%) and from Europe (38%) were consistent with early estimates from Finland and Sweden.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 3 influenza viruses (1 A(H3N2) and 2 type B) with collection dates between week 21/2017 and 26/2017. None showed evidence of reduced inhibition to either oseltamivir or zanamivir.

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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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Tables and figures should be referenced:

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