Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Weeks 21–25/2018 (21 May–24 June 2018)

- Influenza activity was at inter-season levels.
- 1% of the individuals sampled from primary health care settings tested positive for influenza viruses.

2017–2018 season overview

- Aggregated regional data indicated that influenza viruses circulated at high levels between weeks 52/2017 and 12/2018 (based on increased proportions - 40% and above - of sentinel specimens testing positive for influenza viruses). This is longer than in recent seasons and may have contributed to the severity seen this season.
- The majority of influenza viruses detected were type B, representing a high level of circulation of influenza B viruses compared to recent seasons. B/Yamagata lineage viruses greatly outnumbered those of the B/Victoria lineage. Click here for more information
- Different patterns of dominant influenza virus types and A subtypes were observed between the countries of the Region.
- While low in numbers, characterized A(H3N2) viruses fell mainly in clade 3C.2a (58%) and subclade 3C.2a1 (40%), while 48% of B/Victoria lineage viruses fell in a subclade of clade 1A viruses that are antigenically distinct from the 2017–2018 season trivalent vaccine component. Click here for more information
- The majority of severe cases were due to influenza type B virus infection and occurred mostly in persons older than 15 years of age. Click here for more information
- Mortality from all causes has now returned to levels expected for this time of year in all participating countries and regions that report to EuroMOMO. Click here for more information
- Interim results from 5 European studies indicate 25% to 52% vaccine effectiveness against any influenza. Click here for more information

Primary care data

All countries reported activity of respiratory infections below threshold levels, where thresholds existed, based on syndromic surveillance data for influenza-like illness (ILI) and/or acute respiratory infection (ARI).

Influenza activity

All 18 Member States and areas reporting on intensity reported low intensity for weeks 21–25/2018 (Fig. 1).

Of the 26 Member States and areas reporting on geographic spread for weeks 21–25/2018, most reported no activity, a few (3–5 countries) sporadic and one (the United Kingdom (Scotland)) reported local activity.

Maps of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, weeks 25/2018

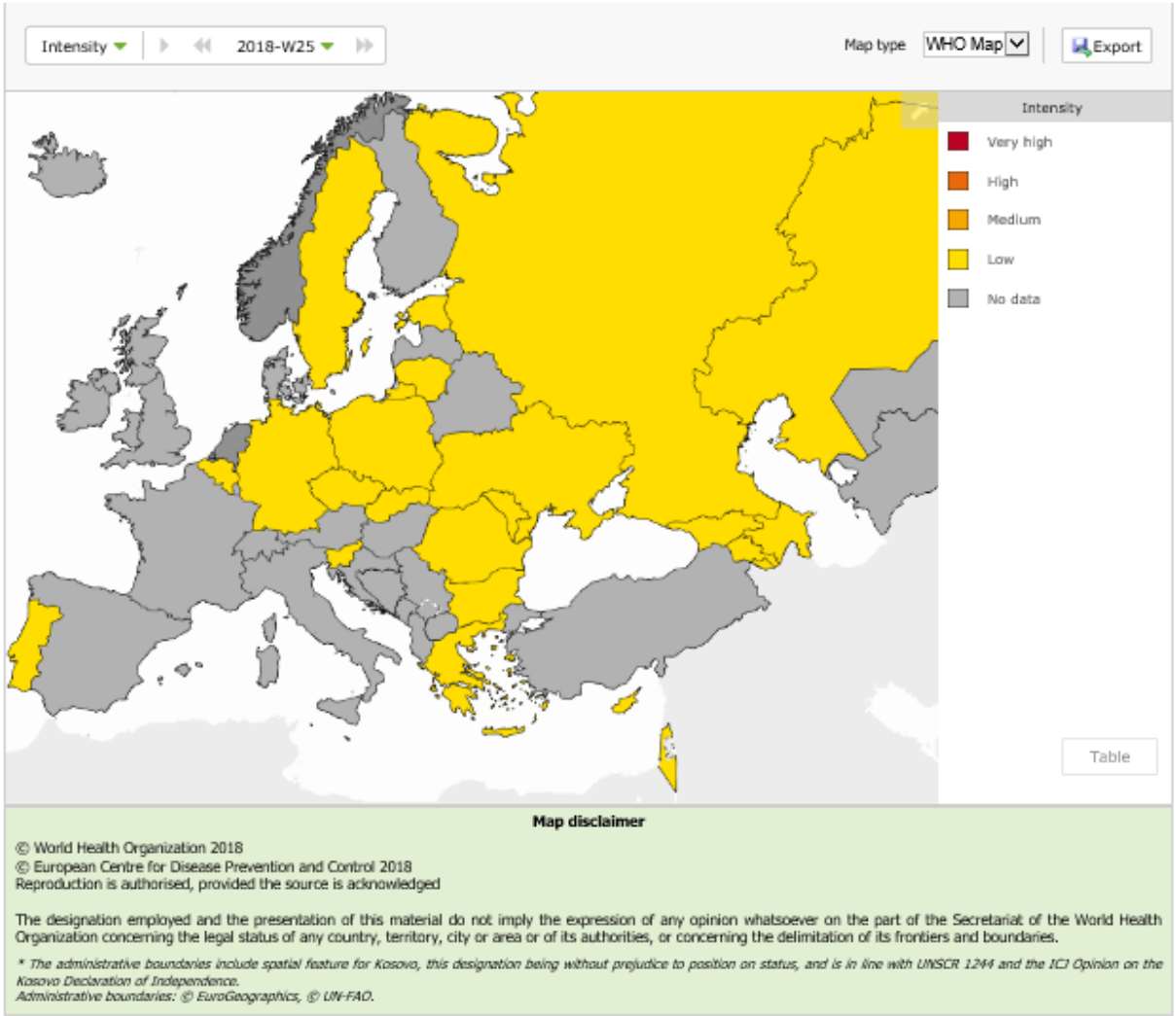
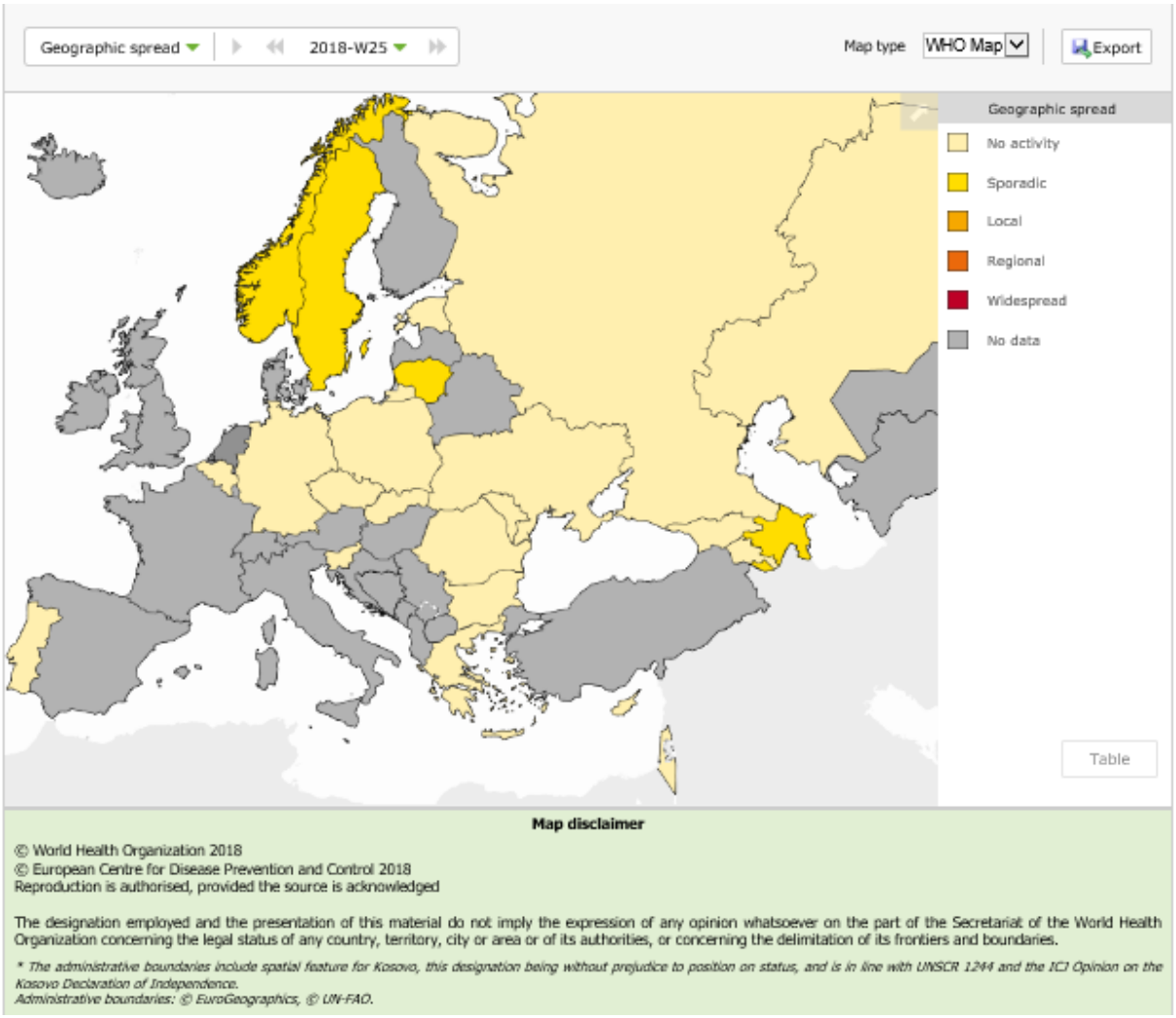


Fig. 2. Geographic spread in the European Region, weeks 25/2018



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

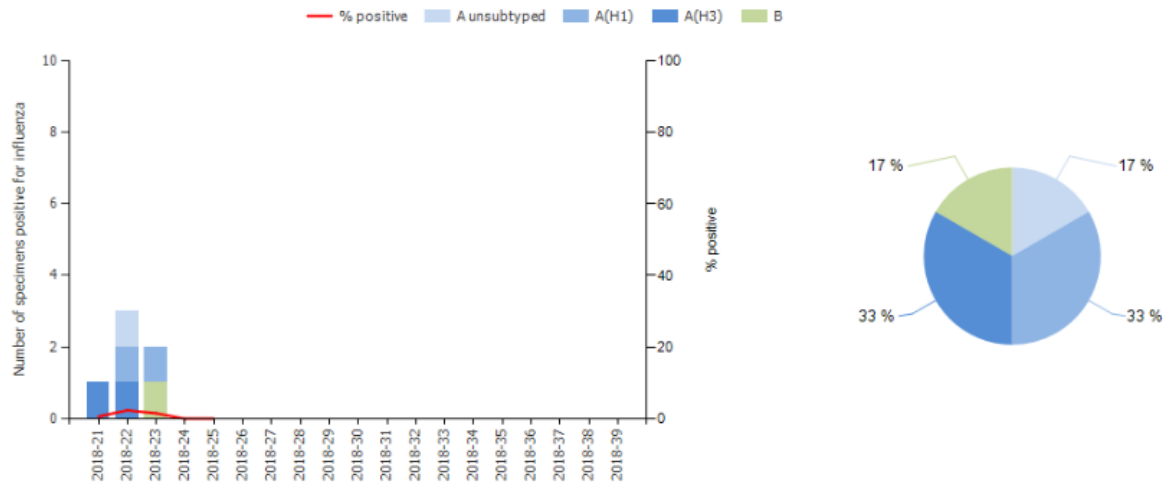
Viruses detected in sentinel-source specimens (ILI and ARI)

For weeks 21–25/2018, 6 (1%) of 576 sentinel specimens tested positive for influenza viruses; five type A and one type B (Table 1).

For the season overall, more influenza type B (63%) than type A (37%) viruses were detected, although between weeks 40/2017 and 44/2017 and since week 12/2018 the proportion of type A viruses detected has been higher than that of type B viruses. Of subtyped A viruses, 65% were A(H1N1)pdm09. While the majority of type B viruses was not ascribed to a lineage, 97% of those that were belonged to the B/Yamagata lineage (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 for weeks 21–25/2018 [a]



[a]Pie chart shows cumulative data.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, weeks 21–25/2018 and cumulatively for the season

	Current Weeks		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**5**	**-**	**9 164**	**36.9**
A(H1N1)pdm09	2	-	4 989	64.8
A(H3N2)	2	-	2 706	35.2
A not subtyped	1	-	1 469	-
Influenza B	**1**	**-**	**15 646**	**63.1**
B/Victoria lineage	0	-	209	2.8
B/Yamagata lineage	0	-	7 305	97.2
Unknown lineage	1	-	8 132	-
Total detections (total tested)	**6 (576)**	**1**	**24 810 (60 806)**	**40.8**

[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 in ICUs (n=12), or other wards (n=8), or 2) severe acute respiratory infections (SARI; n=16).

The majority of severe cases reported during the 2017–2018 season have been due to influenza type B and have occurred in persons above the age of 15 years. In laboratory-confirmed influenza cases in ICU, numbers of influenza type A infections were slightly higher than type B infections.

In laboratory-confirmed influenza cases reported in wards other than ICUs, influenza type B viruses were detected more frequently than influenza type A viruses, and more cases occurred among those older than 64 years compared with patients in the 15–64 years age group.

1.1) Hospitalized laboratory-confirmed influenza cases – Intensive care units (ICUs)

Numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs remained low during weeks 21–25/2018, with only the Czech Republic and Sweden reporting single cases.

For weeks 40/2017–20/2018, 12 countries reported laboratory-confirmed influenza cases admitted to either all ICUs in the country or a set of sentinel ICUs. Type A influenza viruses were detected in 53% and type B in 47% of cases in ICUs. Of 1 920 subtyped influenza A viruses, 58% were A(H1N1)pdm09 and 42% A(H3N2). Of 5 802 cases with known age, 44% were 15–64 years old and 48% were aged 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For weeks 21–25/2018, the Czech Republic and Spain reported sporadic cases from other wards.

For weeks 40/2017–20/2018, 8 countries reported laboratory-confirmed hospitalized influenza cases in other wards. Influenza type B infections accounted for 61% of these cases and 57% of all cases were in patients aged 65 years and older.

2. SARI surveillance

For weeks 21–25/2018, 2 094 SARI cases were reported by 7 countries, most (43%) by Kazakhstan. 10 (3%) of the 350 specimens tested were positive for influenza viruses.

Sixteen countries, the majority being located in the eastern part of the Region, reported on SARI cases for weeks 40/2017–20/2018. Of SARI cases testing positive for influenza viruses over this period, 62% were infected with type B viruses. Of the 1 082 influenza type A infected cases for which subtyping was performed, 66% were infected by A(H1N1)pdm09 viruses.

Mortality monitoring

For week 25/2018, the EuroMOMO project received data from 22 EU/EEA Member States or regions that were included in pooled analyses. Levels of all-cause mortality were at normal expected levels in all the participating countries.

Virus characteristics

Most influenza viruses detected in sentinel surveillance systems this season were type B with those assigned to a lineage being mainly B/Yamagata viruses, while most of the type A viruses subtyped were A(H1N1)pdm09. Details of the distribution of viruses detected in sentinel-source specimens can be found in the Primary care data section.

For the season overall, the majority of influenza virus detections in non-sentinel systems have been type B with B/Yamagata lineage viruses predominating, as seen in sentinel systems. However, in contrast to sentinel systems, in non-sentinel sources similar numbers of A(H3N2) and A(H1N1)pdm09 viruses were reported. This may be related to the higher proportion of non-sentinel specimens being derived from hospital-based settings or outbreaks in long-term care facilities for the elderly, with A(H3N2) viruses often causing more severe disease in the elderly, while A(H1N1)pdm09 viruses do so in middle-aged patients. Further details are given in the section below.

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

Viruses detected in non-sentinel-source specimens

For weeks 21–25/2018, 352 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, 72% were type A and 28% type B viruses (Table 2). The majority of typed viruses from non-sentinel specimens were not subtyped or assigned to a lineage, but 59% of the subtyped type A viruses were A(H3N2).

Table 2. Influenza virus detections in non-sentinel-source specimens by type and subtype, weeks 21–25/2018 and cumulatively for the season

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**255**	**72.4**	**95 315**	**44.5**
A(H1N1)pdm09	80	41.5	16 941	46.2
A(H3N2)	113	58.5	19 720	53.8
A not subtyped	62		58 654	-
Influenza B	**97**	**27.6**	**118 811**	**55.5**
B/Victoria lineage	0		90	1.1
B/Yamagata lineage	5	100	8 392	98.9
Unknown lineage	92	-	110 329	-
Total detections (total tested)	**352 (15 626)**	**-**	**214 126 (780 157)**	**-**

[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 2 146 viruses has been reported (Table 3).

Among 1 118 influenza A(H3N2) viruses attributed to a clade, 650 (58%) fell in the vaccine virus component clade (3C.2a), 448 (40%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 20 (2%) in clades 3.C3 and 3C.3a. Viruses in the first 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 (see the latest WHO CC London Influenza virus characterisation reports), thereby requiring continued monitoring of antigenic characteristics.

Of 814 A(H1N1)pdm09 viruses attributed to a clade, 812 fell in the A/Michigan/45/2015 vaccine component clade (6B.1) and 2 fell in clade 6B represented by A/South Africa/3626/2013.

74 (48%) of the 154 B/Victoria-lineage clade 1A viruses belonged to a subgroup represented by B/Norway/2409/2017, which carries HA1 double amino acid deletion, Δ162-163, characteristic of a new antigenically distinct subgroup of viruses that has been detected in several countries. For B/Yamagata lineage viruses, 1 782 belonged to clade 3 (represented by B/Phuket/3073/2013) and 1 belonged to clade 2 (represented by B/Massachusetts/02/2012). For more information on virus characterizations for EU/EEA countries, see the latest WHO CC London Influenza virus characterisation reports).

Countries that reported viruses falling into clades not represented in current reporting categories or that were not attributed to a clade are contacted for further clarification.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2017–25/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	812
A(H1N1)pdm09 group 6B representative A/South Africa/3626/2013	2
A(H1N1)pdm09 attributed to recognised group in the guidance but not listed here	2*
A(H1N1)pdm09 not attributable to any clade	1*
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	650
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	448
A(H3N2) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	11
A(H3N2) clade 3C.3 representative A/Samara/73/2013 subgroup	9
A(H3N2) attributed to recognised group in current guidance but not listed here	35*
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	80
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	74
B(Victoria) lineage not attributed to clade	1
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	1 782
B/Massachusetts/01/2012 (Yamagata lineage clade 2)	1
B(Yamagata) lineage not attributed to clade	20*

[a] Vaccine component of vaccines for northern (2017–2018 and 2018-2019 seasons) and southern (2018 season) hemispheres
[b] Vaccine component for northern hemisphere 2017–2018 season
[c] Vaccine component for southern hemisphere 2018 and northern hemisphere 2018-2019 seasons
[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 2017-2018 vaccine component: B/Norway/2409/2017 is B/Colorado/06/2017-like (trivalent vaccine component for the northern hemisphere 2018-2019 season).
[f] Vaccine component of quadrivalent vaccines for use in northern hemisphere 2017–2018 and 2018-2019 seasons
* reporting countries are contacted for clarification

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 21 February 2018 WHO published influenza vaccine recommendations for the 2018–2019 season in the northern hemisphere. 2 changes were recommended compared to the current trivalent and quadrivalent vaccines recommended for the 2017–2018 season in the northern hemisphere. Similar to the recommended composition for the 2018 southern hemisphere vaccine, the A(H3N2) component was changed to an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus. In trivalent vaccines the B component was switched to a B/Colorado/06/2017-like virus, representing the emergent strain of B/Victoria-lineage viruses with deletion of K162 and N163 in the HA1 subunit. The A(H1N1)pdm09 component in

trivalent and quadrivalent vaccines and the B/Yamagata component in quadrivalent vaccines remained the same.

Vaccine effectiveness

Interim results from 5 European studies indicate that influenza vaccine effectiveness in all age groups was 25 to 52% against any influenza, 55 to 68% against influenza A(H1N1)pdm09, -47 to 7% against influenza A(H3N2) and 36 to 54% against influenza B. This is consistent with earlier estimates from Canada, Finland, Germany, Spain, Stockholm County and the United States of America.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility has been assessed for 3 703 viruses with collection dates since week 40/2017: 1 539 type B, 990 A(H3N2), and 1 174 A(H1N1)pdm09). 2 type B viruses carried the neuraminidase (NA) amino acid substitution D197N and showed evidence of reduced inhibition (RI) by oseltamivir and zanamivir, and 2 type B viruses showed RI by oseltamivir only. 19 A(H1N1)pdm09 viruses carried the NA amino acid substitution H275Y and showed evidence of highly reduced inhibition by oseltamivir and 2 showed RI by zanamivir only. 2 A(H3N2) viruses carried NA amino acid substitution R292K and showed evidence of RI by 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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Tables and figures should be referenced:

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