

Summary

Week 7/2019 (11–17 February 2019)

- Influenza activity is widespread in the European Region. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 53%.
- Influenza type A virus detections dominated with slightly more A(H1N1)pdm09 viruses than A(H3N2). Very few influenza B viruses were detected.
- 36% of specimens from patients hospitalized with severe acute respiratory infection (SARI) collected in week 7/2019 were positive for influenza virus, and almost all were type A.
- Pooled data from 22 Member States and areas reporting to the [EuroMOMO](#) project indicated excess mortality mostly among elderly people aged 65 years and above, but also in adults in the age group of 15–64 years.

2018–2019 season overview

- Influenza activity in the European region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018 and has exceeded 50% since week 3/2019.
- Both influenza A virus subtypes are circulating widely, with co-circulation in some countries while others report dominance of either A(H1N1)pdm09 or A(H3N2) viruses.
- Among hospitalized influenza virus-infected patients admitted to ICU wards, 37% of influenza A viruses were subtyped; of these 76.2% were A(H1N1)pdm09 virus. Among influenza virus-infected patients admitted to other wards, 31% of influenza A viruses were subtyped and 70% were A(H1N1)pdm09 virus.
- Over 90% of influenza A viruses detected from SARI surveillance since week 40/2018 were subtyped and 81.4% were A(H1N1)pdm09 virus.
- In general, current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. Preliminary vaccine effectiveness estimates continue to support the use of vaccines. Early data suggest the vaccines are effective, but estimates vary depending on the population studied and the proportions of circulating influenza A virus subtypes. See data from [six European studies](#), [Canada](#), [Finland](#), [Hong Kong](#), [Sweden](#), and the [United States](#).
- On 21 February 2019, [WHO published the recommendations](#) for the 2019–2020 northern hemisphere seasonal influenza vaccine composition.
- Circulating viruses remain susceptible to neuraminidase inhibitors supporting early initiation of treatment and prophylactic use according to national guidelines.

Primary care data

Syndromic surveillance data

For week 7/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, 25 (78%) reported ILI activity above baseline levels.

These include countries in eastern areas of the European Region (n=1; Russian Federation), northern areas (n=9; Denmark, Estonia, Iceland, Ireland, Latvia, Lithuania, Norway, United Kingdom (England and Wales)), southern areas (n=5; Greece, Israel, Montenegro, Republic of North Macedonia, Serbia) and western areas (n=10; Belgium, Czech Republic, Hungary, Luxembourg, Netherlands, Poland, Portugal, Slovakia, Spain, Switzerland).

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, 8 (44%) reported ARI above baseline levels.

These include countries in eastern areas of the European Region (n=2; Armenia, Russian Federation), northern areas (n=3; Estonia, Latvia, Lithuania), southern areas (n=1; Albania) and western areas (n=2; Czech Republic, Slovakia).

Influenza activity

For week 7/2019, of 48 Member States and areas reporting on intensity, 6 reported high (southern and western areas), 28 reported medium (across the region), 13 reported low (across the region), and 1 reported baseline (Austria) intensity (Fig. 1).

Of 48 Member States and areas reporting on geographic spread, 36 reported widespread (across the region), 4 reported regional spread (Belarus, Bulgaria, Ukraine, Kosovo*), 3 reported local spread (Azerbaijan, Ireland, Slovakia), 4 reported sporadic cases (Armenia, Lithuania, United Kingdom (Northern Ireland and Wales)), and 1 reported no activity (Uzbekistan) (Fig. 2).

*(*This designation is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence)*

Fig. 1. Intensity in the European Region, week 7/2019

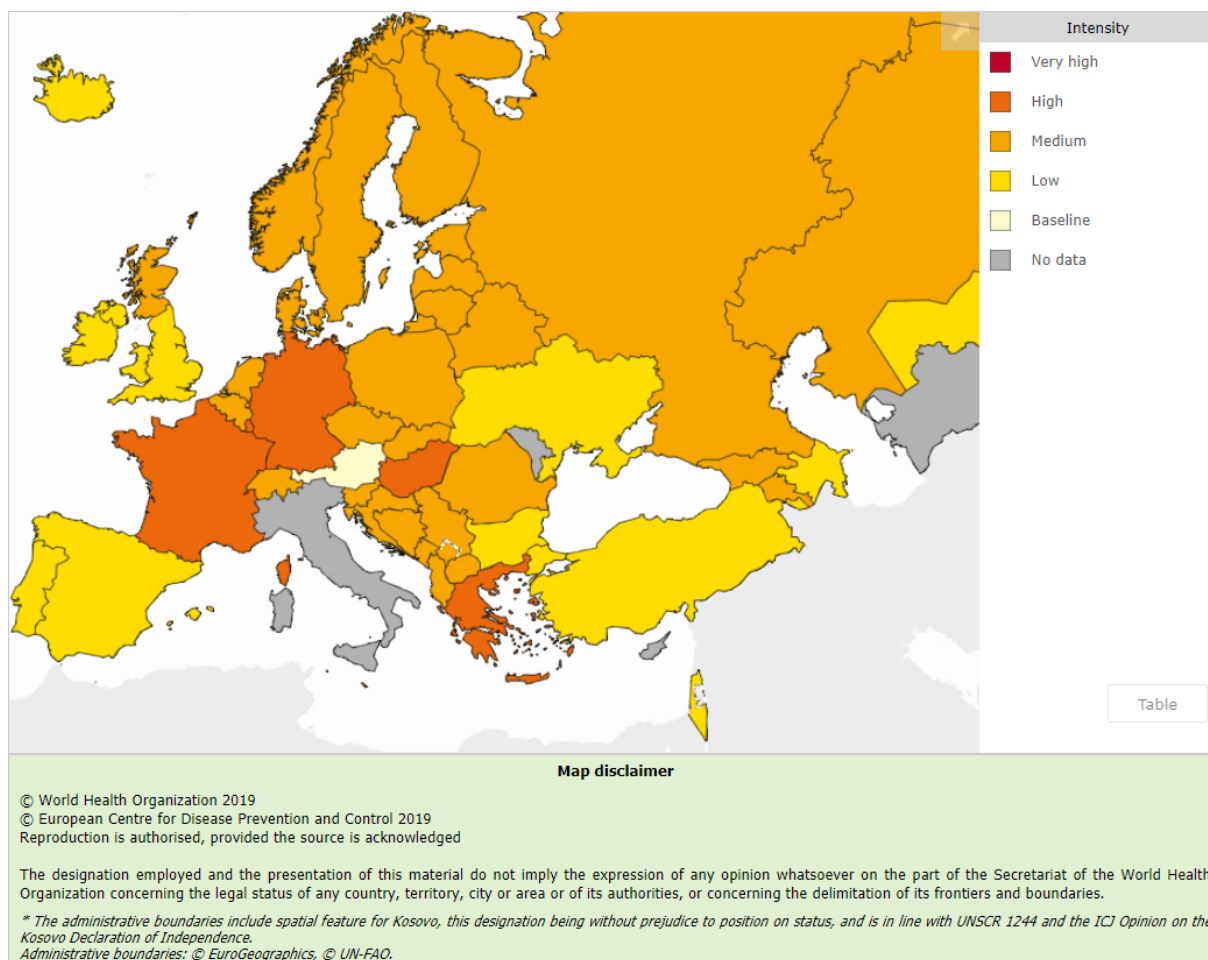
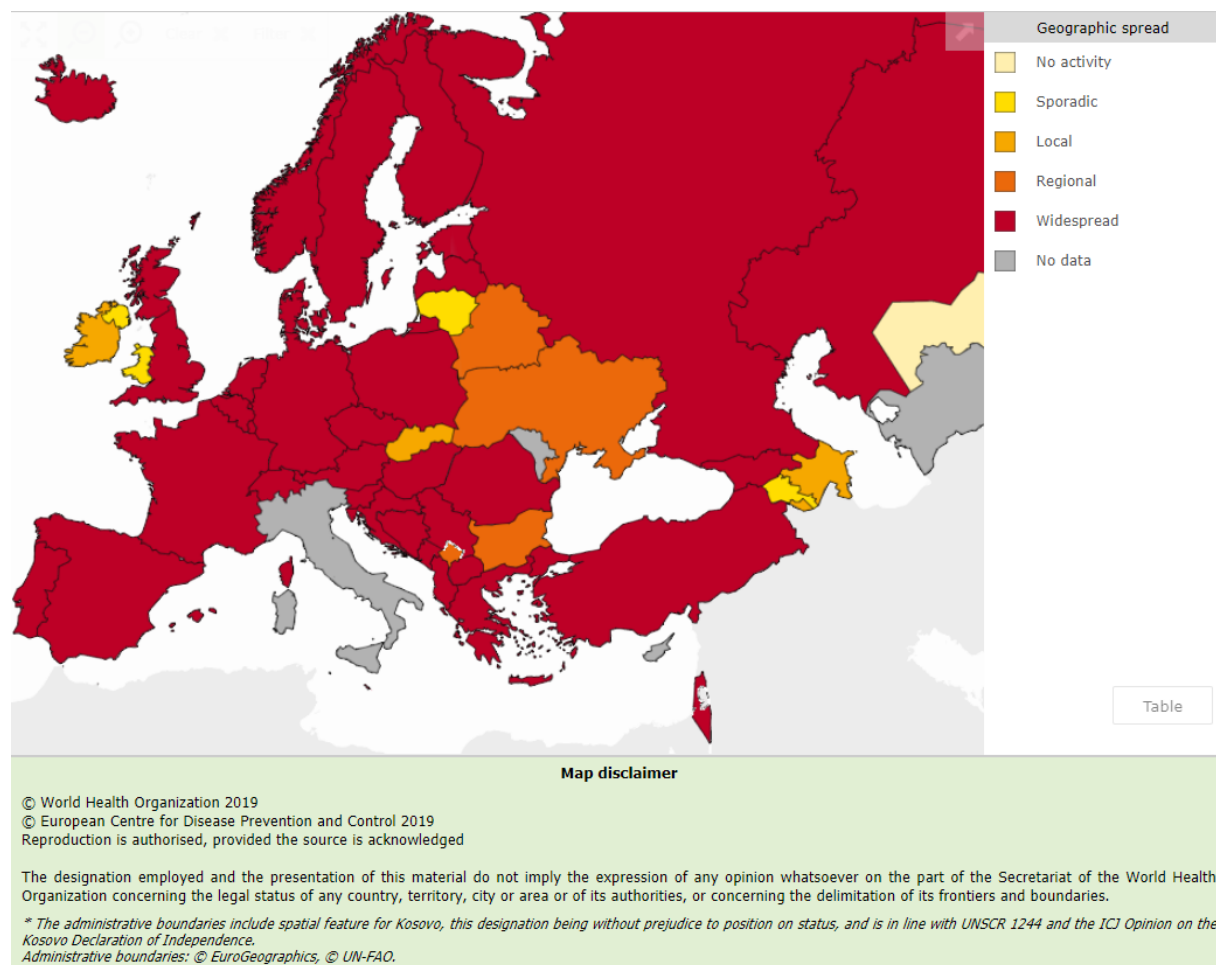


Fig. 2. Geographic spread in the European Region, week 7/2019



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

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

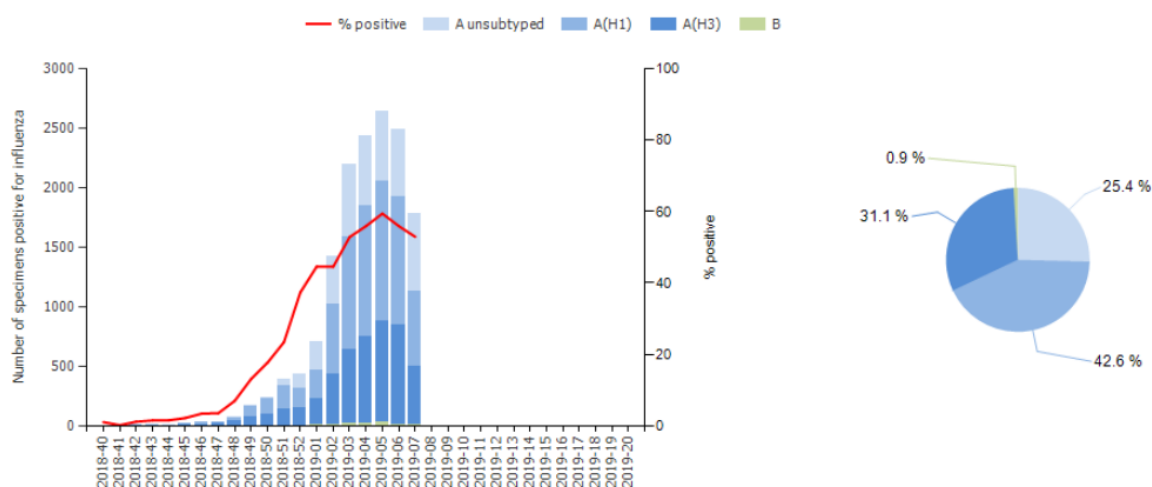
For week 7/2019, 1 775 (52.9%) of 3 356 sentinel specimens tested positive for an influenza virus; 1 768 (99.6%) were type A and 7 (0.4%) were type B. Of 1 120 subtyped A viruses, 56.1% were A(H1N1)pdm09 and 43.9% were A(H3N2). Of 4 type B viruses ascribed to a lineage, all were Yamagata lineage (Fig. 3 and Table 1).

Of 34 Member States or areas across the region that each tested at least 10 sentinel specimens in week 7/2019, 28 reported a rate of influenza virus detections above 30% (median 58.0%; range 30.1% – 89.3%)

For the season to date, almost all viruses detected were influenza type A (n=14 954, 99.1%) with type B accounting for only 0.9% (n=143). Of 11 121 subtyped A viruses, 6 429 (57.8%) were A(H1N1)pdm09 and 4692 (42.2%) were A(H3N2). Of 50 influenza type B viruses ascribed to a lineage, 84% were B/Yamagata (65% type B viruses were reported without a lineage) (Fig. 3 and 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^a



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 7/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	1 768	99.6	14 954	99.1
A(H1N1)pdm09	628	56.1	6 429	57.8
A(H3N2)	492	43.9	4 692	42.2
A not subtyped	648	-	3 833	-
Influenza B	7	0.4	143	0.9
B/Victoria lineage	0	0	8	16
B/Yamagata lineage	4	100	42	84
Unknown lineage	3	-	93	-
Total detections (total tested)	1 775 (3 356)	52.9	15 097 (37 800)	39.9

^aFor 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 and areas monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (12 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infections (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs in week 7/2019 (n = 546), almost exclusively influenza type A viruses (n=545, 99.8%) were detected.

Since week 40/2018, overwhelmingly more influenza type A (n=4 962, 99.1%) than type B (n=44, 0.9%) viruses were detected. Of 1 858 subtyped influenza A viruses, 76.2% were A(H1N1)pdm09 and 23.8% were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 2 537 cases with known age, 47% were 15-64 years old and 44.2% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

Among laboratory-confirmed influenza cases reported in wards other than ICUs in week 7/2019 (n=302), almost exclusively influenza type A viruses (99.7%) were detected.

Since week 40/2018, more influenza type A (n=6 209, 99.2%) than type B (n=49, 0.8%) viruses were detected. Of 1 921 subtyped influenza A viruses, 70.0% were A(H1N1)pdm09 and 30.0% A(H3N2). 1 influenza B virus ascribed to a lineage was B/Yamagata. Of 6 258 cases with known age, 41.9% were 65 years and older and 35.2% were 15-64 years old.

2. SARI surveillance

For week 7/2019, 1 507 SARI cases were reported by 12 Member States or areas. Of 587 specimens tested for influenza viruses, 36.1% were positive. Only influenza type A viruses were detected.

Of 26 753 SARI cases reported since week 40/2018, 26 321 had a recorded age and, of these, 59.4% were 0-4 years old and 23.1% were 15-64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 056), almost all were type A viruses (99.9%). Of the 1 885 influenza type A virus infected cases for which subtyping was performed, 81.4% were infected by A(H1N1)pdm09 viruses and 18.6% were infected by A(H3N2) viruses. 1 influenza B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 7/2019, the [EuroMOMO](#) project received data from 22 Member States or areas that were included in pooled analyses. The pooled estimates indicated excess mortality mostly among elderly aged 65 years and above, but also in adults in the age group of 15-64 years.

Virus characteristics

Details of the distribution of viruses detected in sentinel-source specimens can be found in the [Primary care data](#) section.

Viruses detected in non-sentinel source specimens

For week 7/2019, 18 037 specimens from non-sentinel sources (such as hospitals, schools, primary care facilities not involved in sentinel surveillance, or nursing homes and other institutions) tested positive for an influenza virus; 99.5% were type A and 0.5% were type B.

Of 4 966 subtyped A viruses, 58.5% were A(H1N1)pdm09 and 41.5% were A(H3N2) (Table 2).

For the season to date, more influenza type A (n=111 106, 99.2%) than type B (n=933, 0.8%) viruses have been detected. Of 36 805 subtyped A viruses, 23 958 (65.1%) were A(H1N1)pdm09 and 12 847 (34.9%) were A(H3N2). Of 35 influenza type B viruses ascribed to a lineage, 54.3% were B/Yamagata (96.2% of type B viruses were reported without a lineage) (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 7/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	% ^a	Number	% ^a
Influenza A	17 948	99.5	111 106	99.2
A(H1N1)pdm09	2 907	58.5	23 958	65.1
A(H3N2)	2 059	41.5	12 847	34.9
A not subtyped	12 982	-	74 301	-
Influenza B	89	0.5	933	0.8
B/Victoria lineage	0	-	16	45.7
B/Yamagata lineage	0	-	19	54.3
Unknown lineage	89	-	898	-
Total detections (total tested)	18 037 (46 669)	-	112 039 (488 453)	-

^a For 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 and antigenic characterization

Genetic and antigenic characterization of influenza viruses is routinely performed to understand how similar currently circulating influenza viruses are to the viruses used in influenza vaccines for an ongoing season.

Since week 40/2018, genetic characterizations of 1 690 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 001 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade; 655 were A(H3) viruses, with 425 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 40 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 16 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 105 to the A/England/538/2018 (3C.3a) clade, 37 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 3 to the A/Hong Kong/4801/2014 (3C.2a) clade, 3 attributed to a subgroup not listed, and 26 not attributed to a clade. Of the 31 genetically characterized influenza B viruses, 18 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). Of the 13 B/Victoria viruses characterized, 1 was not attributed to a clade. All others belonged to clade 1A, but 6 fell in subclades with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 5 fell in subclades with a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–7/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015 ^a	1 001
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	3
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	425
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup ^b	40
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	16
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	105
A(H3) clade 3c.2a1 representative A/Singapore-16-0019/2016 subgroup ^d	37
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	3
A(H3) attributed to recognized group in current guidance but not listed here	3
A(H3) not attributed to a clade	26
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	2
B(Vic)-lineage clade 1A representative B/Colorado/06/2017 ^a	4
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	6
B(Vic) lineage not attributed to a clade	1
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^c	18

^a Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^b Vaccine component for 2019 southern hemisphere season.

^c Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

^d Vaccine component for 2018–2019 northern hemisphere season.

Vaccine composition

The recommended composition of the trivalent influenza vaccine for the current northern hemisphere 2018–2019 season included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and a B/Colorado/06/2017-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. The full report can be found [here](#).

This week, on 21 February 2019, WHO published the recommendations for quadrivalent vaccines for use in the 2019–2020 northern hemisphere influenza season to contain the following:

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;
- an A(H3N2) virus to be announced on 21 March 2019*;
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).

It is recommended that the influenza B virus component of trivalent vaccines for use in the 2019-2020 northern hemisphere influenza season be a B/Colorado/06/2017-like virus of the B/Victoria/2/87-lineage.

* In light of recent changes in the proportions of genetically and antigenically diverse A(H3N2) viruses, the recommendation for the A(H3N2) component has been postponed.

The full report and a "Frequently Asked Questions" document are available on the WHO website at:

http://www.who.int/influenza/vaccines/virus/recommendations/2019_20_north/en/

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 966 viruses with collection dates since week 40/2018 [649 A(H1N1)pdm09, 304 A(H3N2), and 13 type B]. 3 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 2 of them were confirmed by phenotypic test. 1 A(H3N2) virus showed evidence of reduced inhibition (RI) by oseltamivir only. 1 type B virus showed evidence of RI by zanamivir only.

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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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