Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 17/2018 (23–29 April 2018)

- Influenza activity was at inter-season levels in all but one reporting country.
- While low in number, 11% of the individuals sampled from primary healthcare settings tested positive for influenza viruses (compared to 12% in the previous week).
- Both influenza virus types A and B were co-circulating with the majority being type A.

2017–2018 season overview

- Influenza viruses have been circulating at high levels in the Region 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 of 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 have 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 (57%) and subclade 3C.2a1 (42%), while 42% of B/Victoria lineage viruses fell in a subclade of clade 1A viruses that are antigenically distinct from the current trivalent vaccine component. Click here for more information
- The majority of severe cases were due to influenza type B virus infection and have mostly occurred in persons older than 15 years. Click here for more information
- Mortality from all causes now appears to have returned to normal expected levels in all 21 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

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

Influenza activity

Of 35 Member States and areas reporting on intensity, 1 reported medium intensity (Georgia) and 34 reported low intensity (Fig. 1).

Of the 35 Member States and areas reporting on geographic spread, 4 reported widespread activity, while others reported regional (n=2), local (n=5) or sporadic (n=16) activity and 8 reported no activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, week 17/2018

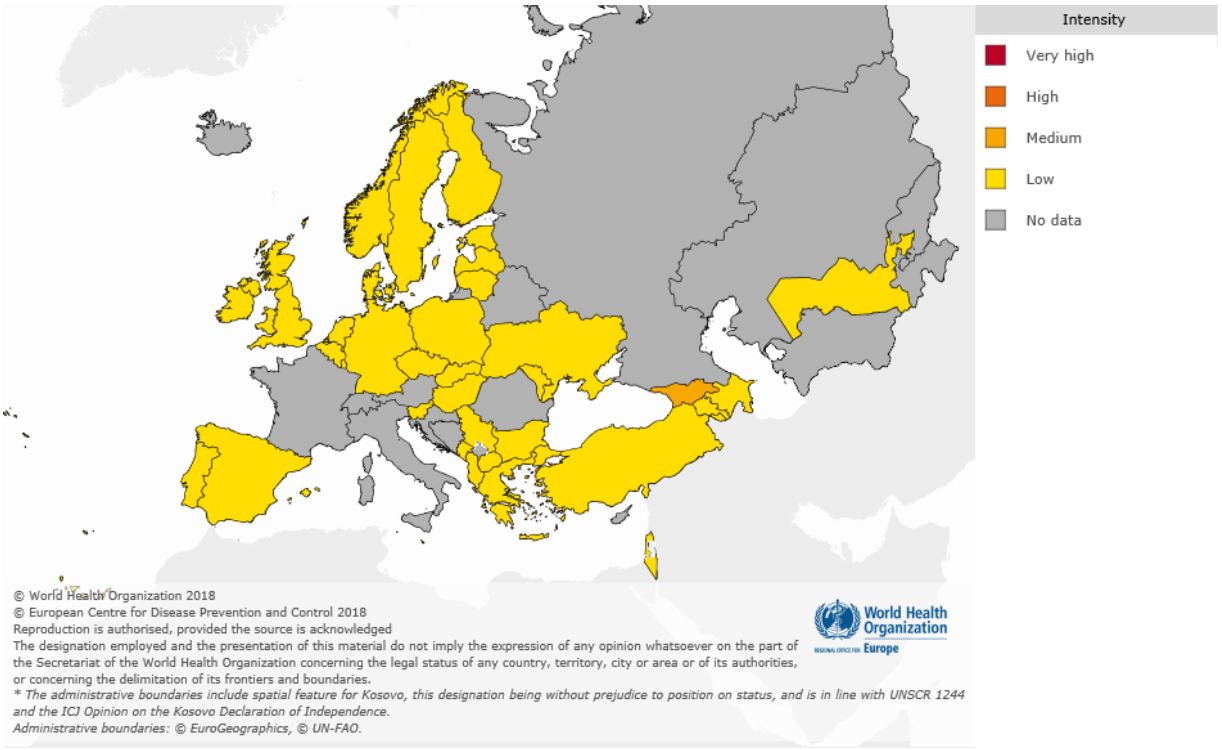
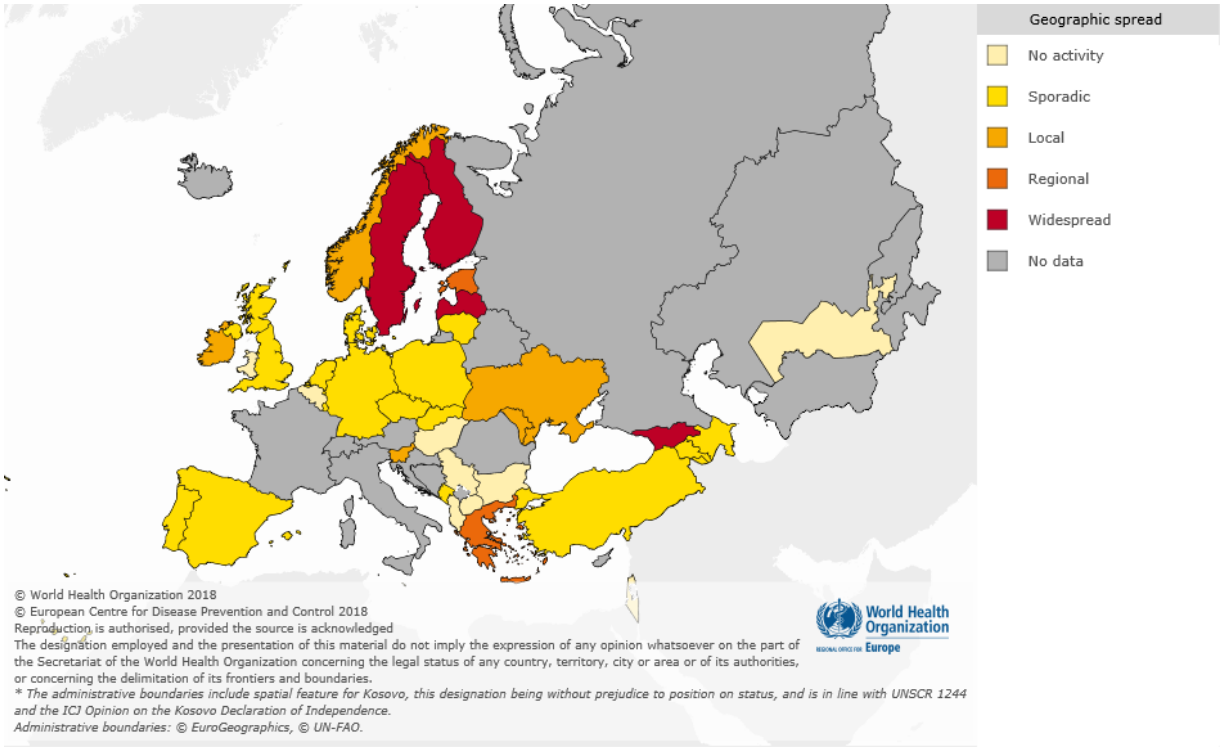


Fig. 2. Geographic spread in the European Region, week 17/2018



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 week 17/2018, 22 (11%) of 197 sentinel specimens tested positive for influenza viruses; 68% were type A and 32% were type B (Table 1).

Of 5 countries across the region that each tested at least 10 sentinel specimens in week 17, 3 countries (Armenia, the Republic of Moldova and Spain) reported proportions of influenza virus detections of more than 10% (50% for Armenia, and 15% for the Republic of Moldova and Spain).

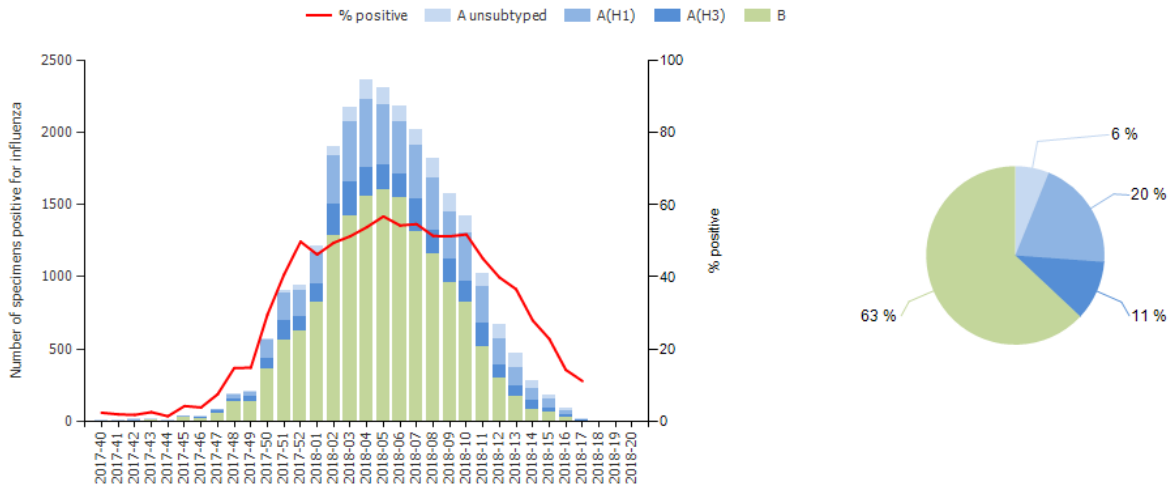
Of 14 subtyped type A viruses, 79% were A(H1N1)pdm09 and 21% A(H3N2). Of 3 type B viruses ascribed to a lineage, all were B/Yamagata (

Fig. 3 and Table 1).

Overall, since week 40/2017, more influenza type B (63%) than type A (37%) viruses have been detected. Of 7 631 subtyped type A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 7 493 ascribed to a lineage, 97% were B/Yamagata (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.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 17/2018 and cumulatively

	Current Week		Season 2017-2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**15**	**68.2**	**9147**	**37.0**
A(H1N1)pdm09	11	78.6	4954	64.9
A(H3N2)	3	21.4	2677	35.1
A not subtyped	1	-	1516	-
Influenza B	**7**	**31.8**	**15585**	**63.0**
B/Victoria lineage	0	0.0	209	2.8
B/Yamagata lineage	3	100.0	7283	97.2
Unknown lineage	4	-	8093	-
Total detections (total tested)	**22 (197)**	**11.2**	**24732 (59 554)**	**41.5**

[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 this 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, slightly more cases were infected with influenza type A compared to type B viruses (n=4 853 and 4 412, respectively).

In laboratory-confirmed influenza cases reported in wards other than ICUs, influenza type B viruses were detected more frequently than influenza type A viruses (11 067 vs. 6 815), and more cases occurred among those older than 64 years compared with patients in the 15–64 years age group (10 194 vs. 5 452).

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

Since week 40/2017, 12 countries have reported laboratory-confirmed influenza cases admitted to either all ICUs in the country or a set of sentinel ICUs (Table 2).

Overall, numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs decreased further in week 17/2018, reflecting the decreasing influenza activity in the Region. There were 12 laboratory-confirmed influenza cases in ICUs, with half of these being in the United Kingdom (n=6, 50%). For weeks 15/2018 and 16/2018, the same countries reported 116 and 44 cases, respectively.

Since week 40/2017, type A influenza viruses have been detected in 52% and type B in 48% of cases in ICUs. Of 1 853 subtyped influenza A viruses, 58% were A(H1N1)pdm09 and 42% A(H3N2). Of 5 725 cases with known age, 44% were 15–64 years old and 49% were aged 65 years and older.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–17/2018

Country	Total Cases	A unsub.	A(H1N1) pdm09	A(H3N2)	B total	0-4 yrs	5-14 yrs	15-64 Yrs	>64 yrs	UNK
Czech Republic	308	45	64	6	193	12	10	130	156	0
Denmark	512	94	44	37	337	11	8	170	323	0
Finland	64	0	4	29	31	1	1	19	43	0
France	2914	1230	519	59	1106	72	48	1376	1364	54
Ireland	166	42	16	28	80	18	16	62	70	0
Netherlands	15	5	0	0	10	0	0	8	7	0
Romania	54	1	25	1	27	4	2	24	24	0
Russian Federation	8	0	2	6	0	0	0	3	5	0
Spain	1240	304	149	156	631	103	36	541	560	0
Sweden	439	130	8	14	287	9	19	183	228	0
Ukraine	59	1	1	2	55	16	20	23	0	0
United Kingdom	3486	1148	243	440	1655	0	0	0	0	3486
TOTAL	**9265**	**3000**	**1075**	**778**	**4412**	**246**	**160**	**2539**	**2780**	**3540**

UNK = age unknown, *from either sentinel hospitals or all hospitals per country

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 17/2018, 7 cases were reported from other wards. Numbers of cases in other wards decreased in week 17/2018 compared to week 16/2018 (n=112).

Since week 40/2017, 8 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (62%) of these cases were infected by influenza type B viruses and 57% of all cases were in patients aged 65 years and older.

Table 3. Laboratory-confirmed hospitalized cases in other wards* by country, cumulatively weeks 40/2017–17/2018

Country	Total Cases	A unsub.	A(H1N1) pdm09	A(H3N2)	B total	0-4 yrs	5-14 yrs	15-64 yrs	>64 yrs	UNK
Czech Republic	338	64	87	6	181	6	4	131	197	0
Denmark	7841	1227	476	663	5475	413	280	2609	4539	0
Ireland	4395	1268	214	485	2428	587	418	1258	2130	2
Romania	101	3	43	6	49	23	13	51	14	0
Russian Federation	359	0	50	184	125	80	33	199	47	0
Slovakia	4	2	1	0	1	0	0	4	0	0
Spain	4585	1240	256	516	2573	246	52	1025	3262	0
Ukraine	259	10	6	8	235	35	44	175	5	0
TOTAL	**17882**	**3814**	**1133**	**1868**	**11067**	**1390**	**844**	**5452**	**10194**	**2**

UNK = age unknown, *from either sentinel hospitals or all hospitals per country

2. SARI surveillance

Since week 40/2017, SARI cases have been reported by 16 countries, the majority being located in the eastern part of the Region.

For week 17/2018, 321 SARI cases were reported by 10 countries, most (51%) by the Republic of Moldova; 35 specimens were tested for influenza viruses with 31% being positive, indicating an increase compared to week 16/2018 when 20% were positive from 132 tested specimens.

For SARI cases testing positive for influenza virus, type B viruses have been the most common; 57% overall for weeks 40/2017–17/2018, and 55% in week 17/2018. A(H1N1)pdm09 viruses were detected in 45% of influenza virus-positive SARI cases in week 17/2018.

Mortality monitoring

Data from 18 EU/EEA Member States or regions reporting to the EuroMOMO project were received for week 17/2018 and included in pooled analyses. Mortality has been significantly elevated in many European countries over the past months, mainly affecting elderly people. However, mortality now appears be have returned to 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.

Since week 40/2017, 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 week 17/2018, 681 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, 73% were type A and 27% type B viruses (Table 4). The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage.

While relatively few of the viruses detected in non-sentinel specimens since week 40/2017 have been ascribed to a subtype or lineage, 52% of all subtyped A viruses were A(H3N2) and 99% of influenza type B viruses ascribed to a lineage were B/Yamagata (Table 4).

Table 4. Influenza virus detections in non-sentinel-source specimens by type and subtype, week 17/2018 and cumulatively

	Current Week		Season 2017–2018	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**497**	**73.0**	**94388**	**44.4**
A(H1N1)pdm09	52	44.8	17358	47.8
A(H3N2)	64	55.2	18964	52.2
A not subtyped	381	-	58066	-
Influenza B	**184**	**27.0**	**118062**	**55.6**
B/Victoria lineage	0	0.0	92	1.1
B/Yamagata lineage	1	100.0	8221	98.9
Unknown lineage	183	-	109749	-
Total detections (total tested)	**681 (8 969)**	**-**	**212 450 (743 993)**	**-**

[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 of 2 821 viruses has been reported (Table 5).

Among 891 influenza A(H3N2) viruses attributed to a clade, 502 (56%) fell in the vaccine virus component clade (3C.2a), 383 (43%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 6 (1%) in clade 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, thereby requiring continued monitoring of antigenic characteristics. 3 A(H3N2) viruses were not attributed to any clade.

All 496 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

54 (41%) of the 133 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. All of the 1 298 B/Yamagata lineage viruses belonged to clade 3, represented by B/Phuket/3073/2013. For more information on virus characterizations for EU/EEA countries, see the WHO CC London February 2018 report.

Table 5. Viruses attributed to genetic groups, cumulative for weeks 40/2017–17/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1)[a]	496
A(H1N1)pdm09 not attributable to any clade	0
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a)[b]	502
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1)[c]	383
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	6
A(H3N2) not attributable to any clade	3*
B/Brisbane/60/2008 (Victoria lineage clade 1A)[b, d]	79
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163)[e]	54
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3)[c, f]	1 298
B/Yamagata lineage not attributed to any clade	0

[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
* A(H3) attributed to recognised group in current guidance but not listed in TESSy

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 1 974 viruses with collection dates since week 40/2017: 913 type B, 576 A(H3N2), and 485 A(H1N1)pdm09). 2 type B viruses carried the amino acid substitution D198N in neuraminidase and D197N and showed evidence of reduced inhibition by oseltamivir and zanamivir. 2 A(H1N1)pdm09 viruses carried the amino acid substitution H275Y and showed evidence of reduced inhibition by oseltamivir and zanamivir and 8 for oseltamivir only. 2 A(H3N2) viruses carried amino acid substitution R292K in neuraminidase and showed evidence of reduced inhibition by oseltamivir and zanamivir.

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