

Summary

Week 20/2018 (14–20 May 2018)

- Influenza activity had returned to inter-season levels in most countries in the Region.
- 3% of the individuals sampled from primary health care settings tested positive for influenza viruses (compared to 10% in the previous week).

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 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 45% 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 24 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 37 Member States and areas reporting on intensity reported low intensity (Fig. 1).

Of the 36 Member States and areas reporting on geographic spread, 19 reported no activity, 15 sporadic and 2 (Sweden and the United Kingdom (Scotland)) reported local activity (Fig. 2).

Maps of qualitative indicators in the European Region

Fig. 1. Intensity in the European Region, week 20/2018

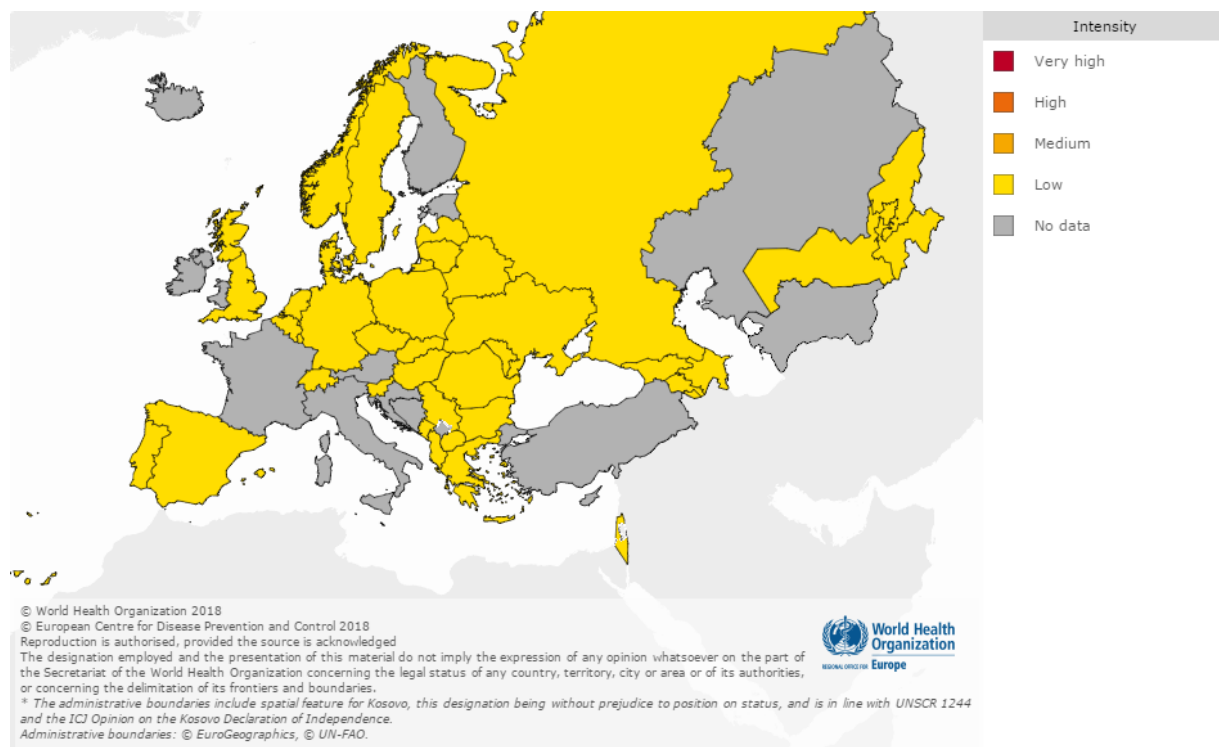
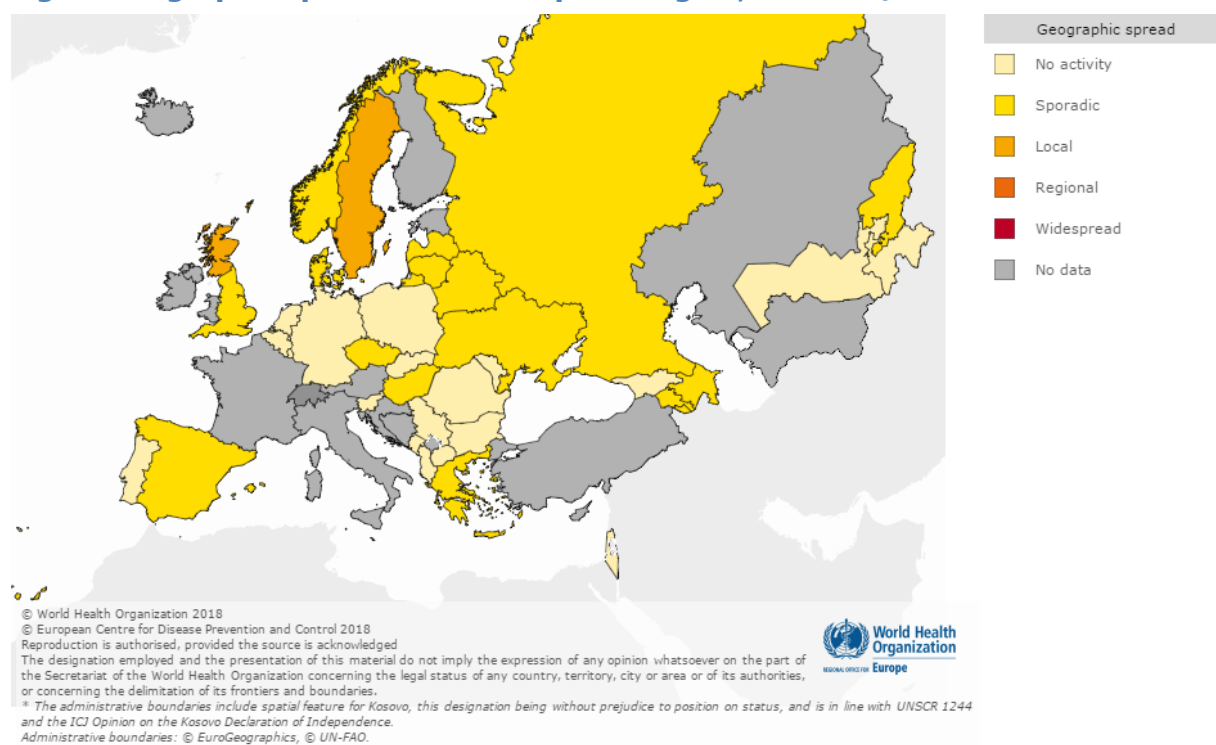


Fig. 2. Geographic spread in the European Region, week 20/2018



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 20/2018, 7 (3%) of 229 sentinel specimens tested positive for influenza viruses; 4 were type A and 3 were type B (Table 1).

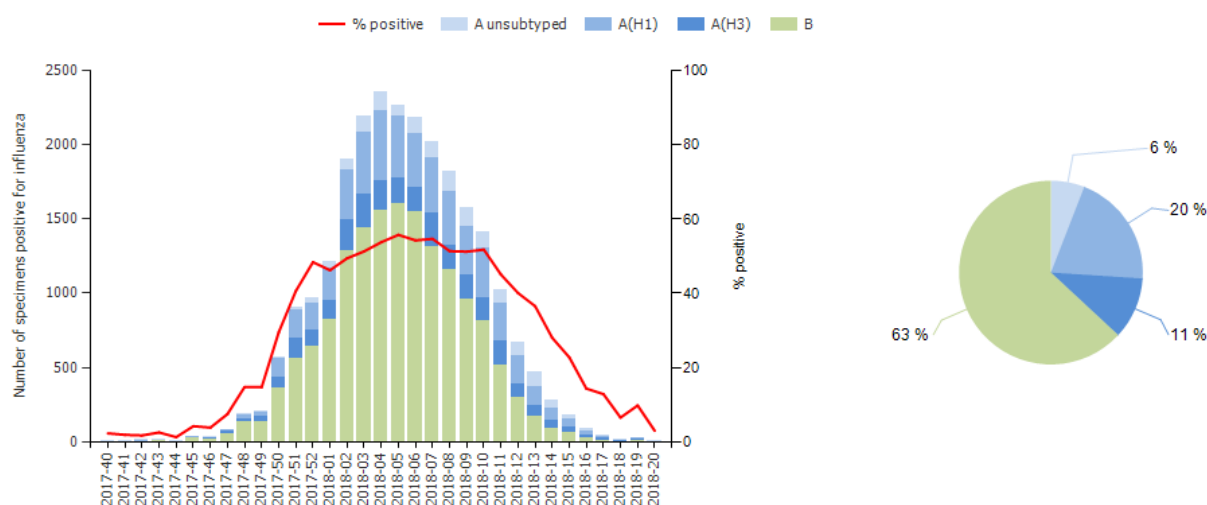
Of 7 countries across the region that each tested at least 10 sentinel specimens in week 20, none reported a rate of influenza virus detections above 8%.

Of 3 subtyped A viruses, 2 were A(H1N1)pdm09 and 1 A(H3N2). No type B viruses were ascribed to a lineage (Fig. 3 and 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 7 689 subtyped A viruses, 65% were A(H1N1)pdm09. The majority of type B viruses were reported without lineage, but of the 7 513 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



^aPie chart shows cumulative data.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 20/2018 and cumulatively

Virus type and subtype	Current Week		Season 2017-2018	
	Number	% ^a	Number	% ^a
Influenza A	4	57.1	9 156	36.9
A(H1N1)pdm09	2	66.7	4 987	64.9
A(H3N2)	1	33.3	2 702	35.1
A not subtyped	1	-	1 467	-
Influenza B	3	42.9	15 647	63.1
B/Victoria lineage	0	-	209	2.8
B/Yamagata lineage	0	-	7 304	97.2
Unknown lineage	3	-	8 134	-
Total detections (total tested)	7 (229)	3.1	24 803 (60 658)	40.9

^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 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=4 937 and 4 448, 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 (11 155 vs. 7 020), and more cases occurred among those older than 64 years compared with patients in the 15–64 years age group (10 319 vs. 5 550).

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).

Numbers of reported hospitalized laboratory-confirmed influenza cases in ICUs remained low in week 20/2018, with only the United Kingdom reporting cases (n=7) which represents a further decrease in this country compared to recent weeks (16 and 19 in weeks 18/2018 and 19/2018, respectively).

Since week 40/2017, type A influenza viruses have been 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.

Table 2. Laboratory-confirmed ICU admitted cases* by country, cumulatively weeks 40/2017–20/2018

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	43	66	6	193	12	10	130	156	0
Denmark	550	105	55	40	350	13	8	195	334	0
Finland	64	0	4	29	31	1	1	19	43	0
France	2 925	1 199	548	62	1 116	73	47	1 382	1 368	55
Ireland	169	43	16	29	81	18	16	62	73	0
Netherlands	15	5	0	0	10	0	0	8	7	0
Romania	55	1	26	1	27	4	2	25	24	0
Russian Federation	9	0	3	6	0	0	0	3	6	0
Spain	1 256	312	149	160	635	104	36	545	571	0
Sweden	447	136	9	14	288	10	19	185	233	0
Ukraine	59	1	1	2	55	16	20	23	0	0
United Kingdom	3 528	1 172	246	448	1 662	0	0	0	0	3 528
TOTAL	9 385	3 017	1 123	797	4 448	251	159	2 577	2 815	3 583

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

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 20/2018, 3 cases were reported from other wards. Numbers of cases in other wards decreased in week 20/2018 compared to week 19/2018 (n=23).

Since week 40/2017, 8 countries have reported laboratory-confirmed hospitalized influenza cases in other wards (Table 3). The majority (61%) 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 40/2017–20/2018

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	344	66	89	6	183	6	4	133	201	0
Denmark	7 989	1 251	507	703	5 528	429	285	2 662	4 613	0
Ireland	4 487	1 313	227	497	2 450	611	427	1 289	2 158	2
Romania	101	3	43	6	49	23	13	51	14	0
Russian Federation	388	0	59	197	132	94	34	206	54	0
Slovakia	4	2	1	0	1	0	0	4	0	0
Spain	4 603	1 248	255	523	2 577	247	52	1 030	3 274	0
Ukraine	259	10	6	8	235	35	44	175	5	0
TOTAL	18 175	3 893	1 187	1 940	11 155	1 445	859	5 550	10 319	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 20/2018, 726 SARI cases were reported by 10 countries, most (41%) by Kazakhstan. In total, 101 specimens were tested for influenza viruses and 10% were positive.

For SARI cases testing positive for influenza virus since week 40/2017, type B viruses have been the most common (55%). Of the 787 influenza type A infected cases for which subtyping was performed, 60% were infected by A(H1N1)pdm09 viruses.

Mortality monitoring

Data from 24 EU/EEA Member States or regions reporting to the [EuroMOMO](#) project were received for week 20/2018 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 to have returned to normal expected levels in all 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 week 20/2018, 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, 70% were type A and 30% type B viruses (Table 4). The majority of typed viruses from non-sentinel specimens were not subtyped or assigned to a lineage and of type A viruses 60% were A(H3N2).

Compared to sentinel surveillance systems, lower proportions of the viruses detected in non-sentinel specimens since week 40/2017 have been ascribed to a subtype or lineage, but 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 20/2018 and cumulatively

Virus type and subtype	Current Week		Season 2017–2018	
	Number	% ^a	Number	% ^a
Influenza A	245	69.6	96 353	44.8
A(H1N1)pdm09	62	40.0	17976	47.7
A(H3N2)	93	60.0	19697	52.3
A not subtyped	90	-	58680	-
Influenza B	107	30.4	118 830	55.2
B/Victoria lineage	0	0.0	90	1.1
B/Yamagata lineage	1	100.0	8387	98.9
Unknown lineage	106	-	110353	-
Total detections (total tested)	352 (7 746)	-	215 183 (779 071)	-

^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; 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 3 363 viruses has been reported (Table 5).

Among 1 038 influenza A(H3N2) viruses attributed to a clade, 585 (56%) fell in the vaccine virus component clade (3C.2a), 440 (42%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 8 (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 (see the [WHO CC London February 2018 report](#)), thereby requiring continued monitoring of antigenic characteristics. 5 A(H3N2) viruses were not attributed to any clade.

All 613 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

68 (45%) of the 152 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. 1 559 B/Yamagata lineage viruses belonged to clade 3, represented by B/Phuket/3073/2013, and one B/Yamagata lineage virus belonged to clade 2, represented by B/Massachusetts/02/2012. 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 40/2017–20/2018

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1) ^a	613
A(H1N1)pdm09 not attributable to any clade	0
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) ^b	585
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1) ^c	440
A(H3) representative A/Switzerland/9715293/2013 subgroup (clade 3C.3a)	8
A(H3N2) not attributable to any clade	5*
B/Brisbane/60/2008 (Victoria lineage clade 1A) ^{b, d}	84
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163) ^e	68
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3) ^{c, f}	1 559
B/Massachusetts/01/2012 (Yamagata lineage clade 2)	1

^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 2 192 viruses with collection dates since week 40/2017: 1 016 type B, 610 A(H3N2), and 566 A(H1N1)pdm09). 3 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. 11 A(H1N1)pdm09 viruses carried the NA amino acid substitution H275Y and showed evidence of highly reduced inhibition by oseltamivir. 2 A(H3N2) viruses carried NA amino acid substitution R292K and showed evidence of RI by oseltamivir and zanamivir and 1 A(H3N2) virus by oseltamivir 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.

Suggested citation:

European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC–WHO weekly influenza update, week 20/2018.

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 20/2018.

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