

## Summary

### Week 18/2018 (30 April–6 May 2018)

- Influenza activity was at inter-season levels in all but one reporting country.
- 6% of the individuals sampled from primary healthcare settings tested positive for influenza viruses (compared to 11% in the previous week).
- The number of influenza virus detections has further decreased compared to previous weeks.

### 2017–2018 season overview

- Influenza viruses circulated 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 20 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).

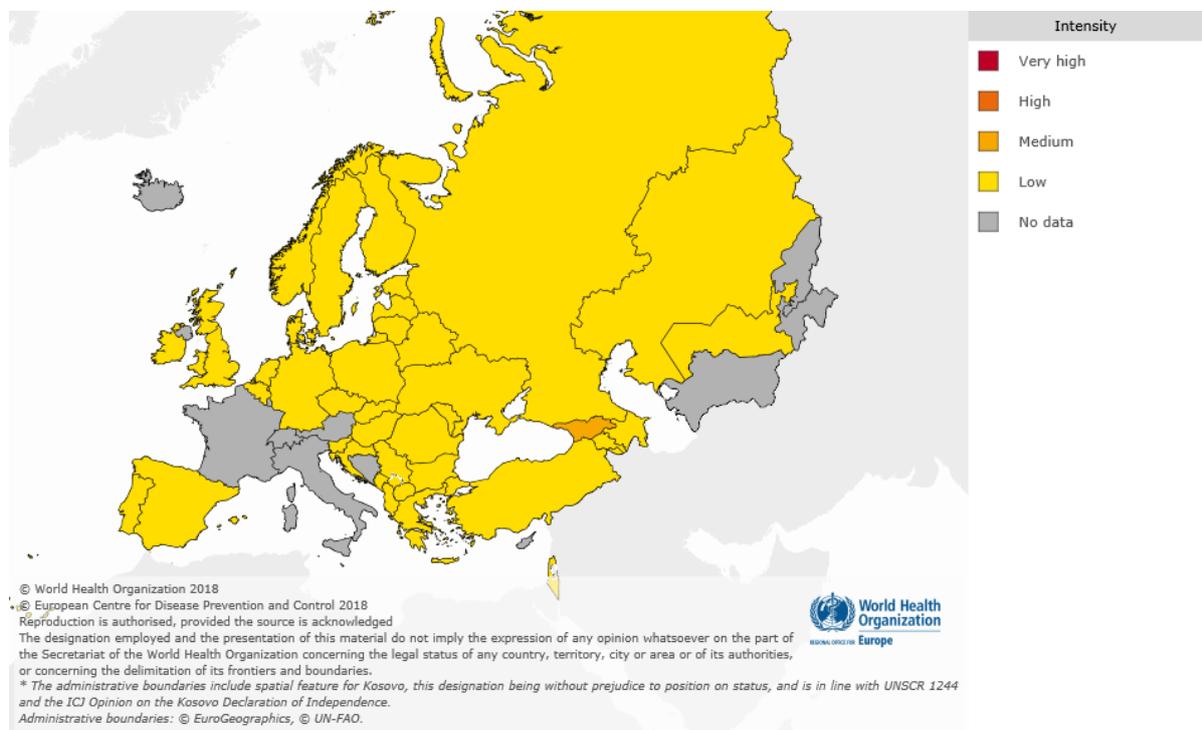
## Influenza activity

Of 39 Member States and areas reporting on intensity, 1 reported medium intensity (Georgia) and 38 reported low intensity (Fig. 1).

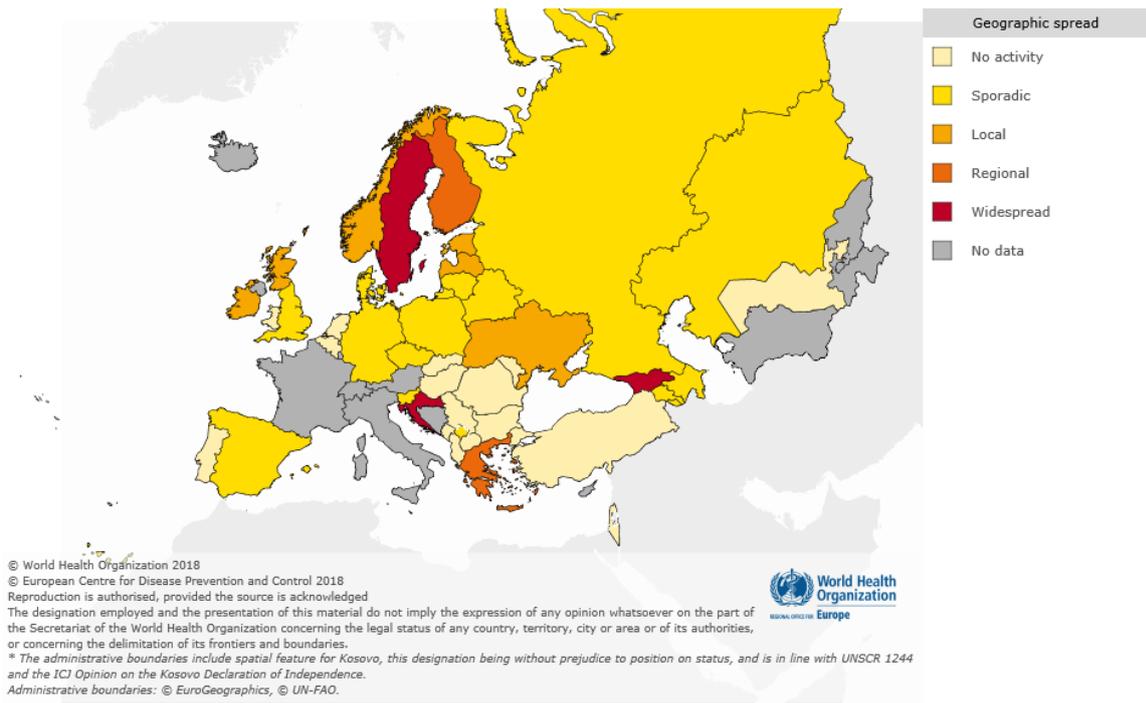
Of the 39 Member States and areas reporting on geographic spread, 15 reported no activity, 15 sporadic, 6 local, 1 regional and 2 reported widespread activity (Fig. 2).

## Maps of qualitative indicators in the European Region

**Fig. 1. Intensity in the European Region, week 18/2018**



**Fig. 2. Geographic spread in the European Region, week 18/2018**



**Erratum:** the report of geographic spread for Croatia is not correct; this should be local.

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 18/2018, 14 (6.4%) of 219 sentinel specimens tested positive for influenza viruses; 11 were type A and 3 were type B (Table 1).

Of 8 countries across the region that each tested at least 10 sentinel specimens in week 18, 2 countries (Armenia and Spain) reported proportions of influenza virus detections of more than 10% (19% for Armenia, and 30% for Spain).

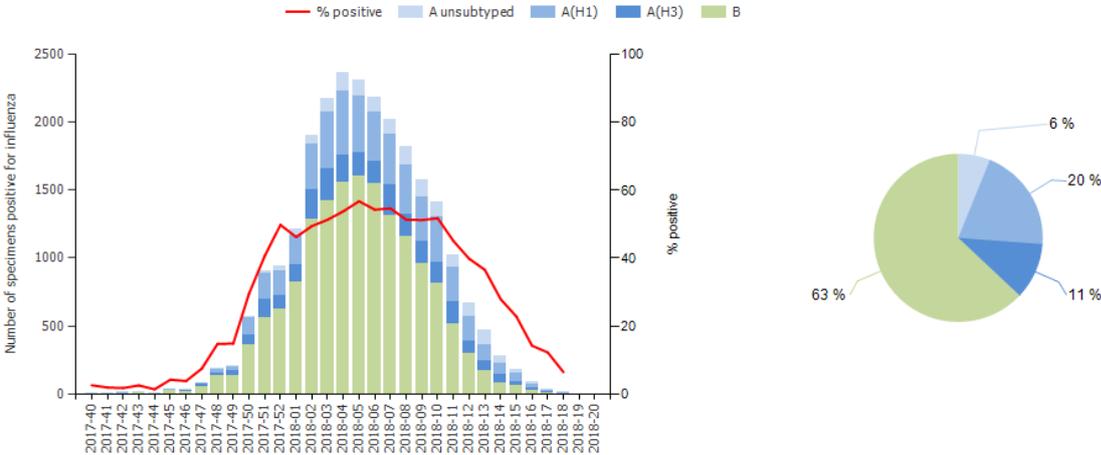
Of 10 subtyped A viruses, 40% were A(H1N1)pdm09 and 60% A(H3N2). The one type B virus ascribed to a lineage was B/Yamagata (

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 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 <sup>a</sup>**



<sup>a</sup>Pie chart shows cumulative data.

**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 18/2018 and cumulatively**

Virus type and subtype	Current Week		Season 2017-2018	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>11</b>	<b>78.6</b>	<b>9173</b>	<b>37.1</b>
A(H1N1)pdm09	4	40	4967	64.9
A(H3N2)	6	60	2692	35.1
A not subtyped	1	-	1514	-
<b>Influenza B</b>	<b>3</b>	<b>21.4</b>	<b>15585</b>	<b>62.9</b>
B/Victoria lineage	0	-	209	2.8
B/Yamagata lineage	1	100	7283	97.2
Unknown lineage	2	-	8093	-
<b>Total detections (total tested)</b>	<b>14 (219)</b>	<b>6.4</b>	<b>24 758 (59 888)</b>	<b>41.3</b>

<sup>a</sup>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=4 890 and 4 422, 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 (11 112 vs. 6 899), and more cases occurred among those older than 64 years compared with patients in the 15–64 years age group (10 260 vs. 5 496).

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

Since week 40/2017, 13 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 18/2018, reflecting the decreasing influenza activity in the Region. There were 8 laboratory-confirmed influenza cases in ICUs, with the majority being in the United Kingdom (n=6, 75%). For weeks 16/2018 and 17/2018, the same countries reported 54 and 17 cases, respectively.

Since week 40/2017, type A influenza viruses have been detected in 53% and type B in 47% of cases in ICUs. Of 1 870 subtyped influenza A viruses, 58% were A(H1N1)pdm09 and 42% A(H3N2). Of 5 759 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 40/2017–18/2018**

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	535	99	52	39	345	12	8	187	328	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	1246	308	149	158	631	103	36	543	564	0
Sweden	444	132	10	14	288	10	19	185	230	0
Ukraine	59	1	1	2	55	16	20	23	0	0
United Kingdom	3499	1157	243	443	1656	0	0	0	0	3499
<b>TOTAL</b>	<b>9312</b>	<b>3020</b>	<b>1085</b>	<b>785</b>	<b>4422</b>	<b>248</b>	<b>160</b>	<b>2560</b>	<b>2791</b>	<b>3553</b>

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

### 1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 18/2018, 10 cases were reported from other wards. Numbers of cases in other wards decreased in week 18/2018 compared to week 17/2018 (n=38).

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 60% of all cases were in patients aged 65 years and older.

**Table 3. Laboratory-confirmed hospitalized cases in other wards\* by country, cumulatively weeks 40/2017–18/2018**

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	341	65	88	6	182	6	4	132	199	0
Denmark	7960	1253	496	693	5518	427	284	2651	4598	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	4592	1243	255	520	2574	247	52	1026	3267	0
Ukraine	259	10	6	8	235	35	44	175	5	0
<b>TOTAL</b>	<b>18011</b>	<b>3844</b>	<b>1153</b>	<b>1902</b>	<b>11112</b>	<b>1405</b>	<b>848</b>	<b>5496</b>	<b>10260</b>	<b>2</b>

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 18/2018, 782 SARI cases were reported by 10 countries, most (52%) by Kazakhstan. 88 specimens were tested for influenza viruses with 8 being positive, indicating a decrease to week 17/2018 when 11 of 35 specimens tested positive.

For SARI cases testing positive for influenza virus, type B viruses have been the most common; 57% overall for weeks 40/2017–18/2018. Of the 880 influenza type A infected cases for which subtyping was performed, 66% were infected by A(H1N1)pdm09 viruses.

## **Mortality monitoring**

Data from 20 EU/EEA Member States or regions reporting to the [EuroMOMO](#) project were received for week 18/2018 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 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 18/2018, 714 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, 77% were type A and 23% 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 18/2018 and cumulatively**

Virus type and subtype	Current Week		Season 2017–2018	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>547</b>	<b>76.6</b>	<b>95 660</b>	<b>44.7</b>
A(H1N1)pdm09	125	48.8	17 802	47.8
A(H3N2)	131	51.2	19 417	52.2
A not subtyped	291	-	58 441	-
<b>Influenza B</b>	<b>167</b>	<b>23.4</b>	<b>118 519</b>	<b>55.3</b>
B/Victoria lineage	0	0.0	90	1.1
B/Yamagata lineage	5	100.0	8 385	98.9
Unknown lineage	162	-	110 044	-
<b>Total detections (total tested)</b>	<b>714 (8 700)</b>	<b>-</b>	<b>214 179 (757 591)</b>	<b>-</b>

<sup>a</sup>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 3 007 viruses has been reported (Table 5).

Among 904 influenza A(H3N2) viruses attributed to a clade, 513 (56.7%) fell in the vaccine virus component clade (3C.2a), 385 (42.6%) in subclade 3C.2a1 with viruses defined by N171K, often with N121K, amino acid substitutions in the haemagglutinin, and 6 (0.7%) 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 571 A(H1N1)pdm09 viruses fell in the A/Michigan/45/2015 vaccine component clade (6B.1).

57 (42%) of the 136 B/Victoria-lineage clade 1A viruses belonged to a subgroup represented by B/Norway/2409/2017, which carries HA1 double amino acid deletion,  $\Delta$ 162-163, characteristic of a new antigenically distinct subgroup of viruses that has been detected in several countries. All of the 1 393 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 40/2017–18/2018**

Phylogenetic group	Number of viruses
A(H1N1)pdm09 A/Michigan/45/2015 (clade 6B.1) <sup>a</sup>	571
A(H1N1)pdm09 not attributable to any clade	0
A(H3N2) A/Hong Kong/4801/2014 (clade 3C.2a) <sup>b</sup>	513
A(H3N2) A/Singapore/INFIMH-16-0019/2016 (clade 3C.2a1) <sup>c</sup>	385
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) <sup>b, d</sup>	79
B/Norway/2409/2017 (Victoria lineage clade 1A Δ162-163) <sup>e</sup>	57
B(Victoria) lineage not attributed to clade	0
B/Phuket/3073/2013 (Yamagata lineage clade 3) <sup>c, f</sup>	1 393
B/Yamagata lineage not attributed to any clade	0

<sup>a</sup> Vaccine component of vaccines for northern (2017–2018 and 2018-2019 seasons) and southern (2018 season) hemispheres

<sup>b</sup> Vaccine component for northern hemisphere 2017–2018 season

<sup>c</sup> Vaccine component for southern hemisphere 2018 and northern hemisphere 2018-2019 seasons

<sup>d</sup> Vaccine component of quadrivalent vaccines for use in southern hemisphere 2018 season

<sup>e</sup> 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).

<sup>f</sup> 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 1 970 viruses with collection dates since week 40/2017: 906 type B, 570 A(H3N2), and 494 A(H1N1)pdm09). 2 type B viruses carried the neuraminidase (NA) amino acid substitution D198N and D197N and showed evidence of reduced inhibition (RI) by oseltamivir and zanamivir. 2 A(H1N1)pdm09 viruses carried the NA amino acid substitution H275Y and showed evidence of highly reduced inhibition by oseltamivir and zanamivir, while another 8 (no NA amino acid substitution identified) showed RI by oseltamivir only. 2 A(H3N2) viruses carried NA amino acid substitution R292K and showed evidence of RI by oseltamivir and 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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