

Summary

Week 08/2020 (17-23 February 2020)

- While no Member State reported very high intensity influenza activity for week 08/2020, 7 reported high intensity. Geographically widespread influenza activity was reported by the majority of Member States and areas across the Region.
- Of the individuals sampled who presented with influenza-like illness (ILI) or acute respiratory infection (ARI) to sentinel primary healthcare sites, 48% tested positive for influenza viruses, consistent with the previous week.
- Both influenza virus types A and B were co-circulating in sentinel source specimens with a higher proportion (61%) of type A viruses detected. Of the type A detections, A(H1N1)pdm09 viruses were detected most often (60%) and of the influenza B viruses, the vast majority were B/Victoria lineage.
- The distribution of viruses detected varied between Member States and areas and within sub-regions. Of 36 reports from across the Region: 19 reported dominance of type A viruses; 9 co-dominance of types A and B viruses; and 8 dominance of type B viruses.
- Pooled estimates of all-cause mortality from 24 countries or regions reporting to the [EuroMOMO](#) project show normal expected levels of mortality.

2019–2020 season overview

- For the Region as a whole, influenza activity commenced earlier than in recent years and, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019. The positivity rate crossed the 50% threshold in week 04, and the season peaked in week 05/2020 at 58%.
- The majority of circulating viruses were susceptible to neuraminidase inhibitors supporting early initiation of treatment or prophylactic use according to national guidelines.
- Member States should continue encouraging influenza vaccination.
- ECDC and WHO Regional Office published a joint [Regional Situation Assessment](#) for the 2019–2020 influenza season up to week 49/2019, which focused on disease severity and impact on healthcare systems to assist forward planning in Member States.

Other news

An ongoing outbreak of respiratory illness, associated with a novel coronavirus (SARS-CoV-2) infection causing infectious disease (COVID-19) first reported in Wuhan, China, is spreading rapidly within China. Additional cases have been identified in other international locations. For more information see:

- WHO: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>
- ECDC website: <https://www.ecdc.europa.eu/en/novel-coronavirus-china>

Primary care data

Syndromic surveillance data

For the 2019–2020 influenza season, ILI thresholds were defined for 35 Member States or areas and ARI thresholds for 17 Member States or areas.

For week 08/2020, 22 (76%) of the 29 Member States and areas that reported on ILI registered activities above their baseline levels. These include 2 Member States in eastern areas, 4 in northern areas, 7 in southern areas and 9 in western areas of the Region.

Of 13 Member States and areas that reported on ARI, 7 (54%) registered activities above their baseline levels. These include 3 Member States in eastern areas, 2 in southern areas and 2 in western areas of the Region.

Influenza activity

Of 45 Member States and areas that reported on the intensity indicator, 6 reported activity at baseline levels, 21 reported low, 11 reported medium, and 7 reported high intensity for week 08/2020 (Fig. 1).

Of 45 Member States and areas that reported on geographic spread, 4 reported no activity, 5 reported sporadic spread, 2 reported local spread, 5 reported regional spread and 29 reported widespread geographic activity for week 08/2020 (Fig. 2).

Fig. 1. Intensity in the European Region, week 08/2020

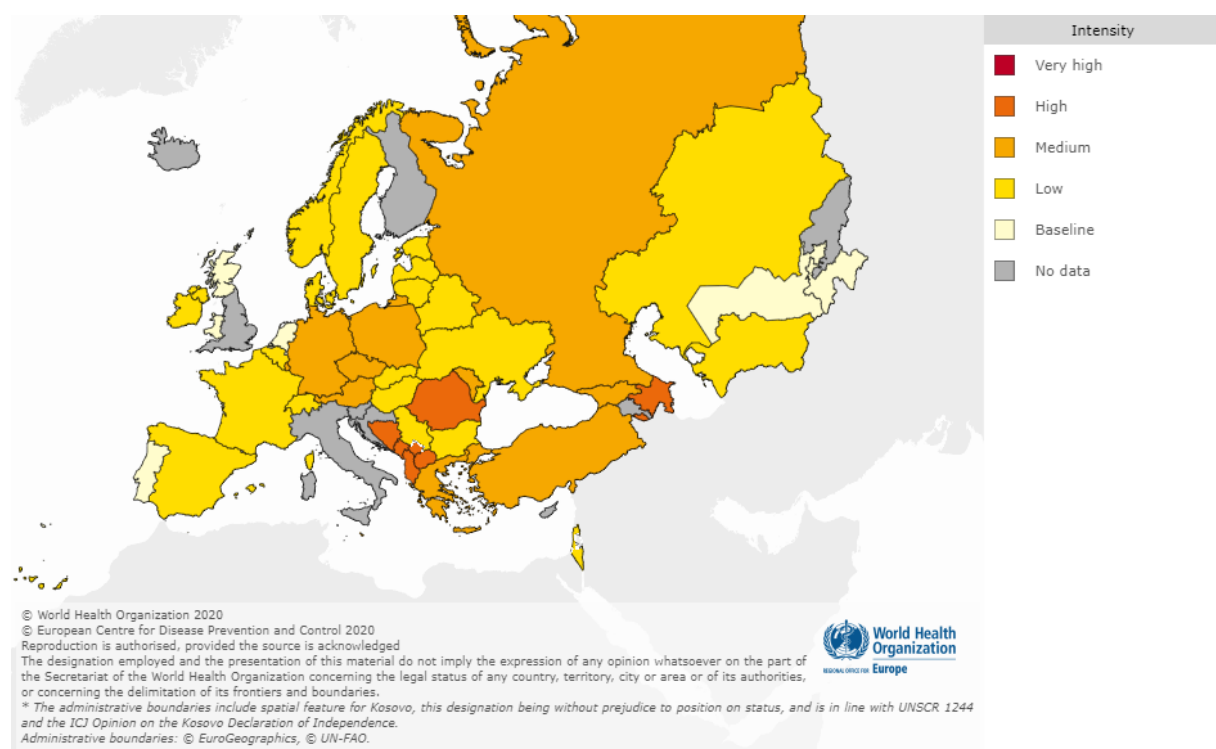
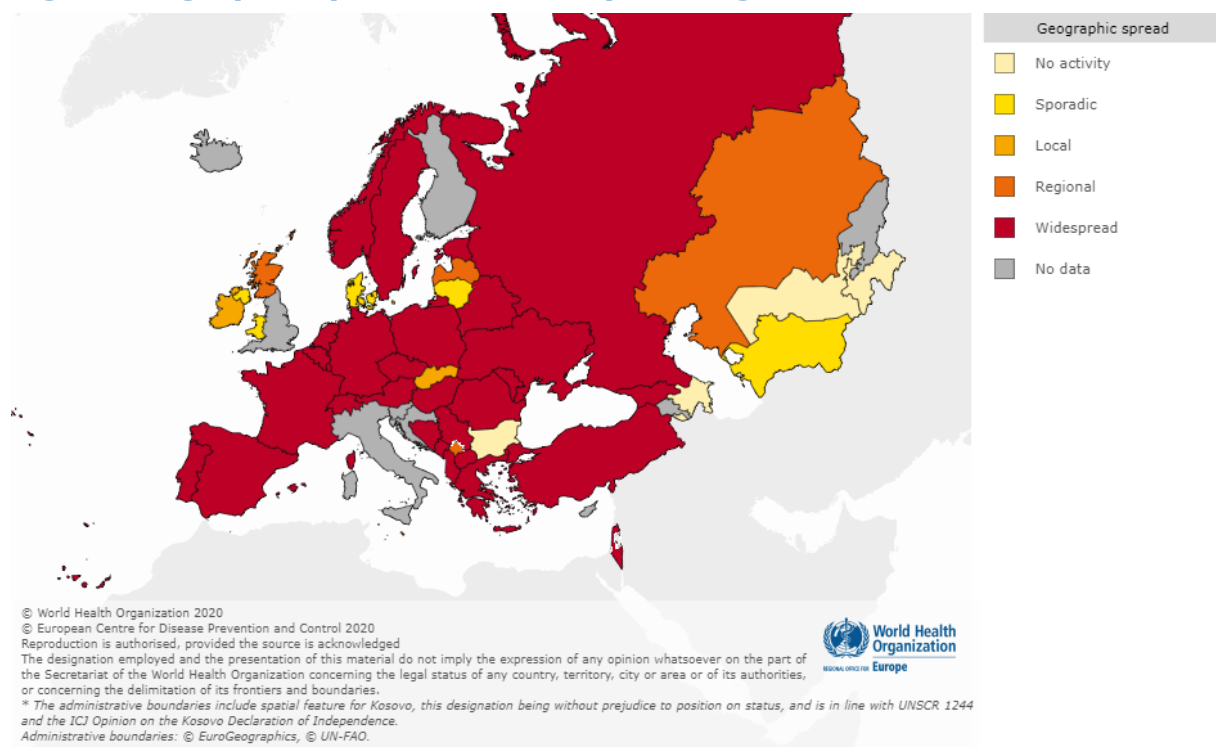


Fig. 2. Geographic spread in the European Region, week 08/2020



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

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

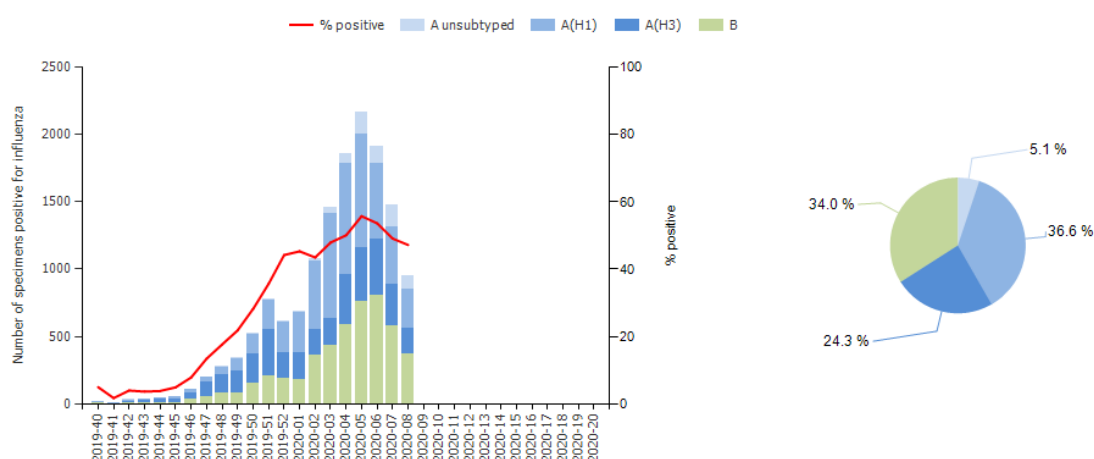
For week 08/2020, 950 (47%) of 2 002 sentinel specimens tested positive for an influenza virus; 61% were type A and 39% were type B (Fig. 3 and Table 1). Of 481 subtyped A viruses, 60% were A(H1N1)pdm09 and 40% were A(H3N2) (Fig. 3 and Table 1). Of 95 type B viruses ascribed to a lineage, all but one were of the B/Victoria lineage (Table 1).

Of 31 Member States or areas across the Region that each tested at least 10 sentinel specimens in week 08/2020, more than a third (n=12) reported rates of influenza virus detections of 50% and above.

For the season to date, more influenza type A (n= 9 632, 66%) than type B (n=4 971, 34%) viruses have been detected (Fig. 3 and Table 1). Of 8 883 subtyped A viruses, 60% were A(H1N1)pdm09 and 40% were A(H3N2). Of 1 795 influenza type B viruses ascribed to a lineage, 99% were of the B/Victoria 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 the season 2019-2020^a



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^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 08/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	579	60.9	9 632	66
A(H1N1)pdm09	287	59.7	5 341	60.1
A(H3N2)	194	40.3	3 542	39.9
A not subtyped	98	-	749	-
Influenza B	371	39.1	4 971	34
B/Victoria lineage	94	98.9	1 775	98.9
B/Yamagata lineage	1	1.1	20	1.1
Unknown lineage	276	-	3 176	-
Total detections (total tested)	950 (2 002)	47.5	14 603 (39 424)	37

^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 monitor severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (11 Member States and areas) or other wards (7 Member States and areas), or 2) severe acute respiratory infection (SARI; 17 Member States and areas, mostly located in the eastern part of the Region).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Among laboratory-confirmed influenza cases reported in ICUs for week 08/2020 (n=161), influenza type A viruses (86%) were detected more frequently than influenza type B viruses (14%).

Since week 40/2019, more influenza type A (n=3 129, 92%) than type B (n=281, 8%) viruses were detected. Of 1 084 subtyped influenza A viruses, 55% were A(H1N1)pdm09 and 45% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 721 cases with known age, 49% were 15-64 years old and 38% 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 for week 08/2020 (n=120), influenza type A viruses (62%) were detected more frequently than influenza type B viruses (38%).

Since week 40/2019, more influenza type A (n=5 332, 89%) than type B (n=666, 11%) viruses were detected. Of 1 423 subtyped influenza A viruses, 54% were A(H1N1)pdm09 and 46% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 5 997 cases with known age, 45% were 65 years and older and 31% were 15-64 years old.

2. SARI surveillance

For week 08/2020, 1 429 SARI cases were reported by 12 Member States or areas. Of 346 specimens tested for influenza viruses, 42% (n=144) were positive for influenza virus, and influenza type A viruses (58%) were detected more frequently than influenza type B viruses (42%).

Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=2 266) were mostly infected by type A viruses (54%). Of the 1 081 influenza type A virus infected cases for which subtyping was performed, 62% were A(H1N1)pdm09 and 38% were A(H3N2) viruses. Of the 565 influenza type B viruses ascribed to a lineage, 98% were B/Victoria and 2% were B/Yamagata.

Of 27 687 SARI cases reported since week 40/2019, 27 439 had a recorded age and, of these, 54% were 0–4 years old and 26% were 15–64 years old.

Mortality monitoring

Pooled estimates of all-cause mortality from 24 countries or regions reporting to the [EuroMOMO](#) project showed normal expected levels of mortality.

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 08/2020, 8 756 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 influenza viruses; 66% were type A and 34% were type B. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage; 70% of all subtyped A viruses were A(H1N1)pdm09 and all influenza type B viruses ascribed to a lineage were B/Victoria (Table 2).

For the season to date, more influenza type A (77%) than type B (23%) viruses have been detected. Relatively low numbers of the viruses have been ascribed to a subtype or lineage; of subtyped A viruses, half were A(H3N2) and half A(H1N1)pdm09, and 96% of influenza type B viruses ascribed to a lineage were B/Victoria (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 08/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	5 752	65.7	86 915	77.2
A(H1N1)pdm09	1 486	69.5	14 487	51.5
A(H3N2)	653	30.5	13 651	48.5
A not subtyped	3 613	-	58 777	-
Influenza B	3 004	34.3	25 603	22.8
B/Victoria lineage	91	100	1 418	96.1
B/Yamagata lineage	0	0	58	3.9
Unknown lineage	2 913	-	24 127	-
Total detections (total tested)	8 756 (32 121)	-	112 518 (511 822)	-

^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

For specimens collected since week 40/2019, genetic characterization of 2 198 viruses has been reported (Table 3):

- 1 598 (73%) type A: 829 A(H3N2) and 769 A(H1N1)pdm09;
- 600 (27%) type B: 572 B/Victoria and 28 B/Yamagata.

While the A(H1N1)pdm09 viruses fall within subgroups of subclade 6B.1A5 and subclade 6B.1A7 that are different to that of the vaccine virus A/Brisbane/02/2018 (6B.1A1), it is anticipated that the vaccine virus will be effective based on HI assays conducted with post-infection ferret antisera raised against the vaccine virus.

As seen elsewhere in the world, there is significant genetic diversity among circulating A(H3N2) viruses in the European region for the 2019–20 influenza season to date, with 53% clade 3C.3a and 47% subclade 3C.2a. All subclade 3C.2a1 viruses fall in subgroup 3C.2a1b (with the latter splitting between 3 designated genetic clusters). The vaccine virus, A/Kansas/14/2017, falls within clade 3C.3a and viruses within this clade induce clade-specific antibodies in ferrets, so viruses falling in other clades/subclades may be less well covered by human immune responses to the vaccine.

For the B/Victoria-lineage, viruses in the B/Colorado/06/2017 vaccine virus double deletion clade (1A (del 162-163)) have been in the minority. However, there is evidence of some cross-reactivity with viruses in the triple deletion clade (1A (del 162-164)) by post-infection ferret antisera raised against the egg-propagated vaccine virus.

B/Yamagata lineage viruses have been detected in low numbers worldwide and, despite some genetic drift with associated HA amino acid substitutions, retain good reactivity with post-infection ferret antisera raised against the B/Phuket/3073/2013 vaccine virus.

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2019–08/2020

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	697
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	17
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	37
A(H1)pdm09 group 6B.1A1 representative A/Brisbane/02/2018 ^a	11
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	7
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	77
A(H3) clade 3C.3a representative A/Kansas/14/2017 ^a	435
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	55
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	261
A(H3) attributed to recognised group in the guidance but not listed here	1
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017 ^a	18
B(Vic)-lineage clade 1A (del162-164 subgroup) representative B/Hong Kong/269/2017	3
B(Vic) attributed to recognised group in the guidance but not listed here	40
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	511
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^b	26
B(Yam) attributed to recognised group in the guidance but not listed here	2

^a Vaccine component for 2019–2020 northern hemisphere.

^b Vaccine component of quadrivalent vaccines for use in 2019–2020 northern hemisphere season.

ECDC published a [report](#) in January that largely focused on viruses from across the world, with collection dates after 31 August, that had full length HA gene sequence data deposited in GISAID by 2 January 2020. Since the November 2019 characterisation report, 12 shipments of influenza-positive specimens from European Union/European Economic Area (EU/EEA) countries had been received by the WHO Collaborating Centre, London (the Francis Crick Institute). A total of 397 virus specimens had been received, with collection dates after 31 August. A summary of viruses from EU/EEA countries characterized in December is given below. Previously published [influenza virus characterisation reports](#) are also available on the ECDC website.

A(H1N1)pdm09 viruses

17 A(H1N1)pdm09 viruses from EU/EEA countries were characterized antigenically since the last report (for November, published in December), with 16 showing good reactivity with antiserum raised against the 2019–2020 vaccine virus, A/Brisbane/02/2018. The 21 viruses from EU/EEA countries characterized genetically fell within subclades of clade 6B.1A: 15 6B.1A5A, 3 6B.1A5B, 1 6B.1A6 and 2 6B.1A7.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. 17 A(H3N2) viruses were characterized antigenically since the last characterization report. Of the 17, 12 were clade 3C.3a viruses that were antigenically similar to the vaccine virus, A/Kansas/14/2017. The remaining five were subgroup 3C.2a1b+T135K viruses that were poorly recognised by the vaccine virus. Of the 57 viruses characterized genetically, 38 were

clade 3C.3a, 11 were subgroup 3C.2a1b+T131K, 3 were subgroup 3C.2a1b+T135K-A and 5 were subgroup 3C.2a1b+T135K-B.

B/Victoria viruses

14 B/Victoria-lineage viruses were characterised in December. All gave antigenic profiles characteristic of the triple deletion subgroup 1A(Δ 3)B, represented by B/Washington/02/2019, the vaccine virus for the 2020 southern hemisphere season. The subgroup has been confirmed for nine of the viruses.

B/Yamagata viruses

1 B/Yamagata-lineage virus was characterised antigenically in December. It reacted poorly with antiserum raised against the vaccine virus B/Phuket/3073/2013 (clade 3) and only reacted well with an antiserum raised against a B/Yamagata-lineage virus carrying multiple unusual substitutions in HA1.

Vaccine composition

On 21 February 2019, WHO published recommendations for the components of influenza vaccines for use in the 2019–2020 northern hemisphere influenza season; the recommendations were finalized on 21 March. Vaccines should contain the following:

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus (Clade 6B.1A1);
- an A/Kansas/14/2017 (H3N2)-like virus (Clade 3C.3a);
- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage) (Clade 1A_Δ2); and
- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage) (Clade 3).

It was 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.

The full report and Frequently Asked Questions for the 21 February decision and the 21 March addendum are available on the [WHO website](#).

The report from the [Vaccine Composition Meeting for the southern hemisphere](#) 2020 season can be found [here](#).

The WHO consultation on the composition of influenza virus vaccines for use in the 2020–2021 northern hemisphere influenza season will be held in Geneva, Switzerland 24–27 February 2020.

Vaccine effectiveness

Interim estimates of 2019–20 seasonal influenza vaccine effectiveness (VE) in the United States have been [published](#). Overall, VE against any influenza virus associated with medically attended ARI was 45% (95% CI: 36%–53%). VE was estimated to be 50% (95% CI: 39%–59%) against influenza B/Victoria viruses and 37% (95% CI: 19%–52%) against influenza A(H1N1)pdm09. VE among children and adolescents aged 6 months–17 years was 55% (95% CI: 42%–65%).

Interim influenza VE estimates for the 2019/20 season in Canada have also been [published](#). Overall VE was 58% (95% CI: 47%–66%), with higher point estimates among children 1–19 years (74%; 95% CI: 59%–84%) but lower among adults aged ≥65 years (18%; 95% CI: –59%–58%). VE against influenza A(H1N1)pdm09 was 44% (95% CI: 26%–58%) overall; VE against influenza A(H3N2) was 62% (95% CI: 37%–77%) overall; and VE against influenza B was 69% (95% CI: 57%–77%)

Preliminary influenza VE estimates from [Sweden](#) and [Finland](#) suggest that overall 2019-2020 VE 39% and 41% (adjusted VE CI 95%: 29%–50%) respectively among adults 65 years and older, and 70% (adjusted VE CI 95%: 47%–70%) among children from 6 months to 6 years of age for both influenza virus types.

Influenza vaccine effectiveness estimates can vary depending on several factors, for example, study methods, health facility type, population, disease outcome, influenza vaccine types, influenza activity and circulating viruses.

Antiviral susceptibility testing

Since the beginning of the season, 879 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 365 A(H3N2), 336 A(H1N1)pdm09 and 178 type B viruses. One A(H3N2) virus carried amino acid substitution R292K in neuraminidase and showed evidence of highly reduced inhibition by oseltamivir and reduced inhibition by zanamivir. One A(H1N1)pdm09 virus carried amino acid substitution H275Y in NA indicative of highly reduced inhibition by oseltamivir. One type B virus showed evidence of reduced inhibition by oseltamivir.

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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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