

Summary

Week 05/2020 (27 January – 2 February 2020)

- Influenza activity continued to increase, with a number of Member States reporting very high (n=4) and high (n=5) intensity. Widespread influenza activity was reported by the majority of Member States and areas across the Region.
- The detection rate increased compared to the previous week. Of the individuals sampled who presented with ILI or ARI to sentinel primary healthcare sites, 54% tested positive for influenza viruses.
- Both influenza virus types A and B were co-circulating in sentinel source specimens with a higher proportion (65%) of type A viruses detected. Of the type A detections, A(H1N1)pdm09 viruses were detected more often (64%) and of the influenza B viruses, the vast majority (99%) were B/Victoria lineage.
- The distribution of viruses detected varied between Member States and areas and within sub-regions. Although the majority of reported influenza virus detections across the Region were type A, 4 Member States reported influenza type B dominance and 8 Member States and areas reported co-dominance of types A and B viruses.
- In the majority of specimens from severe cases admitted to ICU and non-ICU hospital wards, influenza type A viruses were detected.
- Pooled estimates of all-cause mortality from 23 countries or regions reporting to the [EuroMOMO](#) project indicated a small tendency of excess mortality over recent weeks from some countries.
- Data from [Influenzanet](#) indicated that influenza activity in the community was high in one reporting country, medium in 4 reporting countries and low in three reporting countries.

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 exceeded 50% in week 04/2020, one week later compared to the previous 2018–2019 influenza season.
- In sentinel sources, both influenza A virus subtypes, A(H1N1)pdm09 and A(H3N2), are co-circulating, 60% and 40% respectively. Increased influenza virus subtype A(H1N1)pdm09 detections have been reported since week 52/2019. Of the influenza B viruses, the vast majority (99%) have been B/Victoria lineage.
- Among hospitalized influenza virus-infected patients admitted to ICU wards since the beginning of the season, influenza type A viruses have been detected in the majority of cases (94%); of these 52% were A(H3N2) viruses. The same was reported for patients admitted to other wards, with 86% of cases being infected with type A viruses; of these 54% were A(H3N2) viruses.
- Among SARI cases, influenza type A viruses were detected most frequently (52%) in week 05/2020, prior to this type B viruses had been predominant.

- The majority of circulating viruses remain susceptible to neuraminidase inhibitors supporting early initiation of treatment or prophylactic use according to national guidelines.
- The effectiveness of vaccines in the population will be evaluated by vaccine effectiveness studies when there is a sufficient number of enrolled patients. 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 severe respiratory illness has been associated with a novel coronavirus first identified in Wuhan, China is spreading rapidly within China. 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 05/2020, 23 (70%) of the 33 Member States and areas that reported on influenza-like illness (ILI) and 10 (62%) of the 16 Member States and areas that reported on acute respiratory infection (ARI), registered activities above their baseline levels.

Influenza activity

Of 47 Member States and areas that reported on the intensity indicator, 9 reported activity at baseline levels (in eastern, northern and southern areas), 16 reported low (in eastern, northern and western areas), 13 reported medium (in eastern, southern and western areas), 5 reported high (in southern and western areas) and 4 reported very high (Albania, Greece, Luxembourg and Slovenia) intensity for week 05/2020 (Fig. 1).

Of 47 Member States and areas that reported on geographic spread, 2 reported no activity (Azerbaijan and Tajikistan), 5 reported sporadic spread (in eastern, southern and western areas), 2 reported local spread (Ireland and Slovakia), 6 reported regional spread (in eastern, northern and southern) and 32 reported widespread (across the Region) geographic activity for week 05/2020 (Fig. 2).

Fig. 1. Intensity in the European Region, week 05/2020

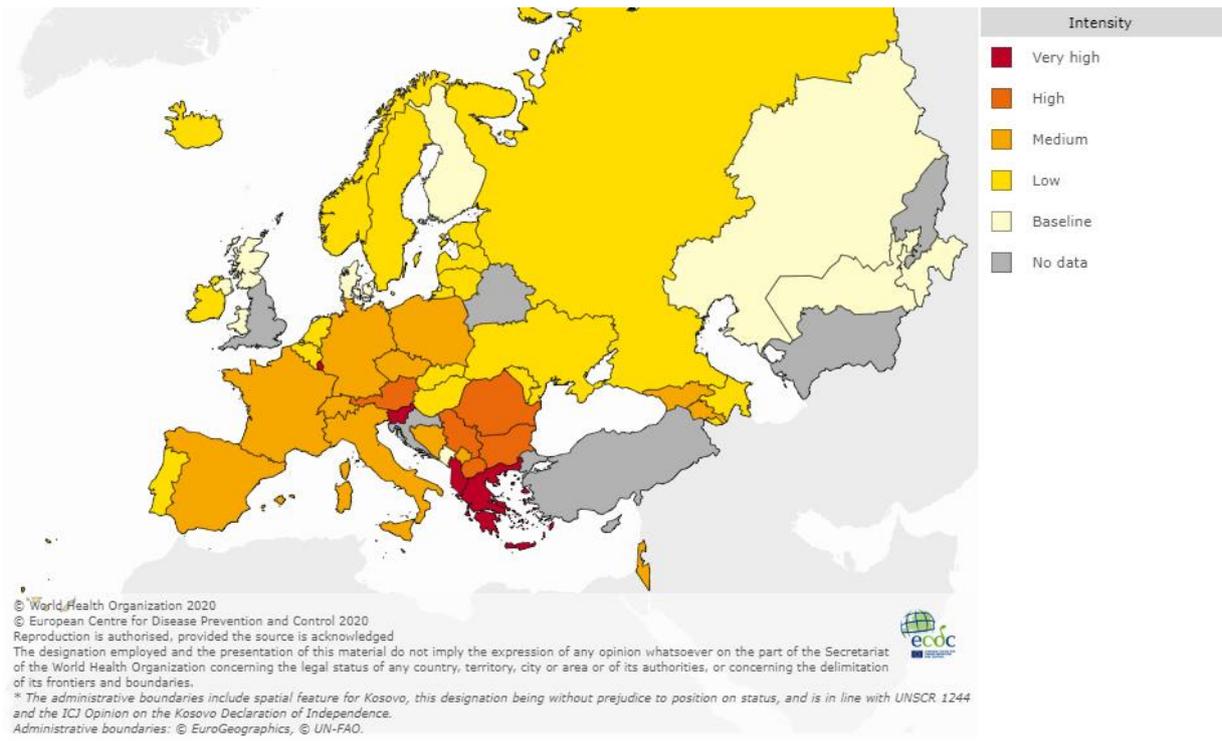
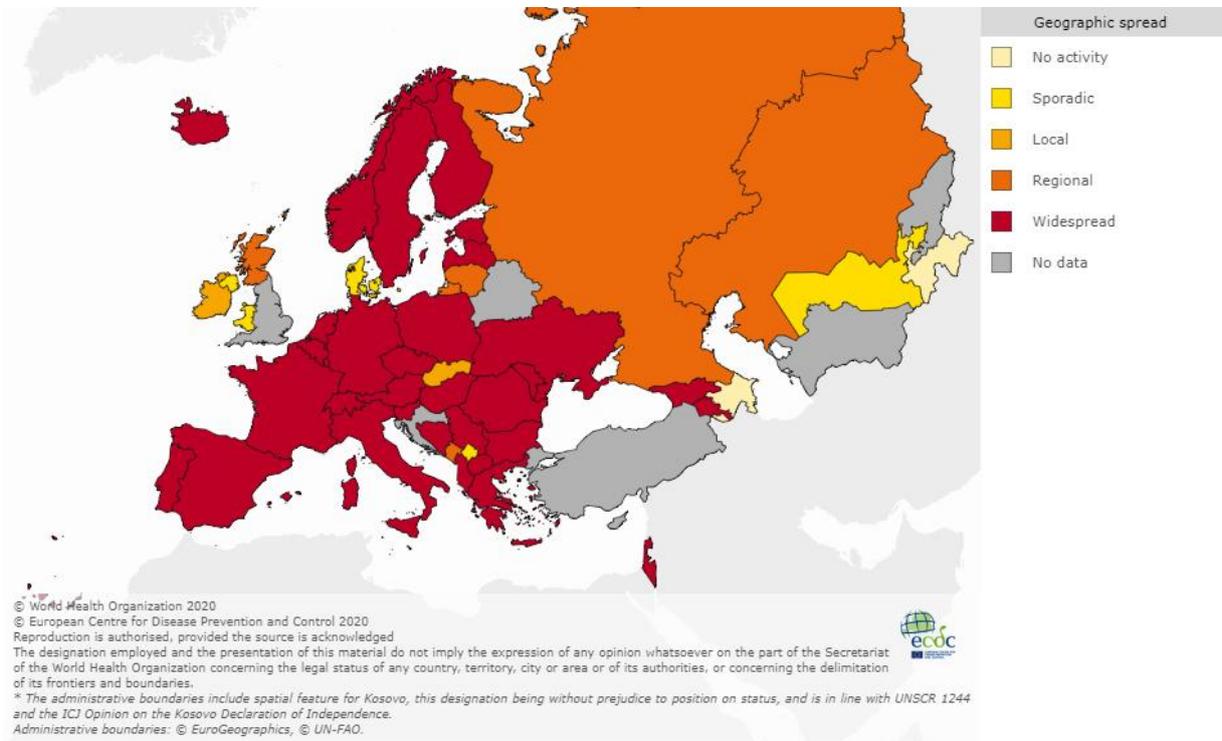


Fig. 2. Geographic spread in the European Region, week 05/2020



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

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

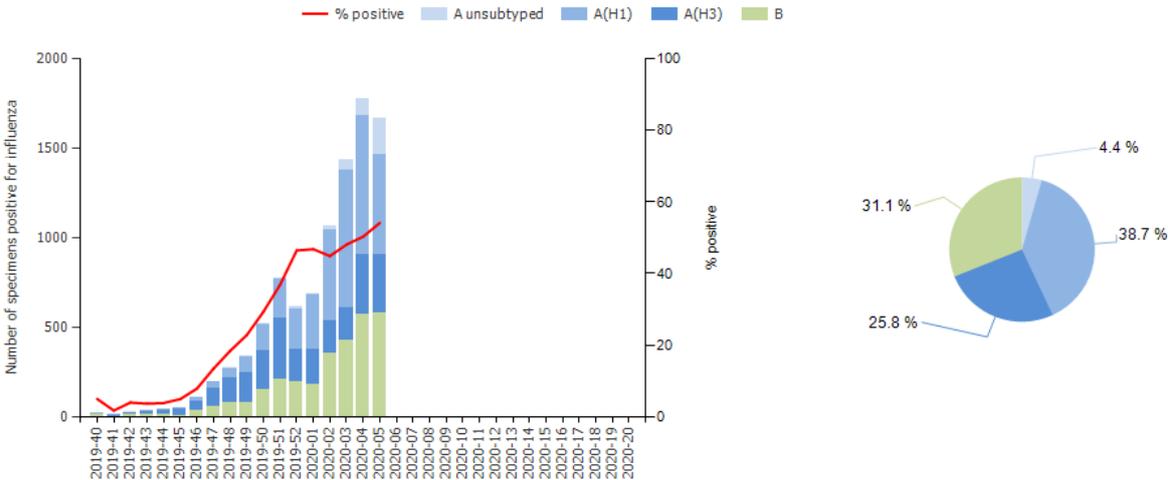
For week 05/2020, 1 664 (54%) of 3 077 sentinel specimens tested positive for an influenza virus; 65% were type A and 35% were type B (Fig. 3 and Table 1). Of 885 subtyped A viruses, 64% were A(H1N1)pdm09 and 36% were A(H3N2) (Fig. 3 and Table 1). Of 214 type B viruses ascribed to a lineage, 99% were of the B/Victoria lineage (Table 1).

Of 34 Member States or areas across the Region that each tested at least 10 sentinel specimens in week 05/2020, 20 reported rates of influenza virus detections of 50% and above.

For the season to date, more influenza type A (n=6 645, 69%) than type B (n=3 000, 31%) viruses have been detected (Fig. 3 and Table 1). Of 6 222 subtyped A viruses, 60% were A(H1N1)pdm09 and 40% were A(H3N2). Of 980 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



^a Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 05/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	1 084	65.1	6 645	68.9
A(H1N1)pdm09	562	63.5	3 731	60.0
A(H3N2)	323	36.5	2 491	40.0
A not subtyped	199	-	423	-
Influenza B	580	34.9	3 000	31.1
B/Victoria lineage	211	98.6	966	98.6
B/Yamagata lineage	3	1.4	14	1.4
Unknown lineage	366	-	2 020	-
Total detections (total tested)	1 664 (3 077)	54.1	9 645 (29 308)	32.9

^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.

Influenzanet

[Influenzanet](#) is a European wide initiative providing surveillance of influenza-like illness (ILI) in the general population using citizens self-reported symptoms. For week 05/2020, per 1 000 active participants, Italy, Switzerland and the United Kingdom reported between 15 and 20 cases; France reported between 20 and 25 cases; Denmark and Portugal reported between 25 and 30 cases; Ireland reported between 35 and 40 cases; and Spain reported between 75 and 80 ILI cases.

Based on this system, ILI activity is still low (below the first quartile of historical data for this week) in the Denmark, Switzerland and the United Kingdom medium (between the first and third quartile of historical data) in France, Ireland, Italy and Portugal, and high (above the third quartile of historical data) in Spain.

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 (12 Member States and areas) or other wards (8 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 05/2020 (n=152), influenza type A viruses (n=140, 92%) were detected more frequently than influenza type B viruses (n=12, 8%).

Since week 40/2019, more influenza type A (n=2 400, 94%) than type B (n=153, 6%) viruses were detected. Of 807 subtyped influenza A viruses, 52% were A(H3N2) and 48%

A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 990 cases with known age, 51% were 15-64 years old and 37% 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 05/2020 (n=266), influenza type A viruses (n=230, 86%) were detected more frequently than influenza type B viruses (n=36, 14%).

Since week 40/2019, more influenza type A (n=4 246, 92%) than type B (n=392, 8%) viruses were detected. Of 1 082 subtyped influenza A viruses, 54% were A(H3N2) and 46% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 4 637 cases with known age, 45% were 65 years and older and 30% were 15-64 years old.

2. SARI surveillance

For week 05/2020, 2 011 SARI cases were reported by 13 Member States or areas. Of 541 specimens tested for influenza viruses, 44% were positive for influenza virus: 80% (n=190) type A and 20% (n=47) type B.

Of 20 272 SARI cases reported since week 40/2019, 20 048 had a recorded age and, of these, 55% were 0–4 years old and 25% were 15–64 years old. Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=1 252) were mostly infected by type A viruses (n=651, 52%). Of the 570 influenza type A virus infected cases for which subtyping was performed, 74% (n=419) were A(H1N1)pdm09 and 26% (n=151) were A(H3N2) viruses. Of the 233 influenza type B viruses ascribed to a lineage, 97% (n=226) were B/Victoria and 3% (n=7) were B/Yamagata.

Mortality monitoring

Pooled estimates of all-cause mortality from 23 countries or regions reporting to the [EuroMOMO](#) project indicated a small tendency of excess mortality over the past few weeks in some of the participating countries.

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 05/2020, 9 003 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; 70% were type A and 30% were type B. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage; 67% of all subtyped A viruses were A(H1N1)pdm09 and 99% of all influenza type B viruses ascribed to a lineage were B/Victoria (Table 2).

For the season to date, more influenza type A (81%) than type B (19%) viruses have been detected. Relatively low numbers of the viruses have been ascribed to a subtype or lineage; 55% of all subtyped A viruses were A(H3N2) and 94% 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 05/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	6 303	70.0	60 962	81.5
A(H1N1)pdm09	1 467	66.6	8 472	44.9
A(H3N2)	735	33.4	10 406	55.1
A not subtyped	4 101	-	42 084	-
Influenza B	2 700	30.0	13 848	18.5
B/Victoria lineage	80	98.8	807	94.4
B/Yamagata lineage	1	1.2	48	5.6
Unknown lineage	2 619	-	12 993	-
Total detections (total tested)	9 003 (35 058)	-	74 810 (39 1526)	-

^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 1 726 viruses has been reported (Table 3):

- 1 285 (74%) type A: 722 A(H3N2) and 563 A(H1N1)pdm09;
- 441 (26%) type B: 415 B/Victoria and 26 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 52% clade 3C.3a and 48% 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 40/2019–05/2020

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	510
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	13
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	34
A(H1)pdm09 group 6B.1A1 representative A/Brisbane/02/2018 ^a	2
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	4
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	72
A(H3) clade 3C.3a representative A/Kansas/14/2017 ^a	379
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	43
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	227
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	11
B(Vic)-lineage clade 1A(del162-164 subgroup) representative B/Hong Kong/269/2017	3
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	401
B(Yam)-lineage clade representative B/Phuket/3073/2013 ^b	26

^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_ Δ 2); 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.

Antiviral susceptibility testing

Since the beginning of the season, 727 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 276 A(H1N1)pdm09, 309 A(H3N2) and 142 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 type B virus showed evidence of reduced inhibition by oseltamivir.

This weekly update was prepared by an editorial team at the European Centre for Disease Prevention and Control (Angeliki Melidou, Nick Bundle, Silvia Funke, Lucia Pastore Celentano, Andrew Amato-Gauci, and Oksana Martinuka) and the WHO Regional Office for Europe (Sonja Olsen, James Fielding, Dmitriy Pereyaslov, and Miriam Sneiderman). It was reviewed by country experts (Ana Paula Rodrigues, National Institute of Health Dr Ricardo Jorge (INSA), Portugal and Božidarka Rakočević, Centre for Disease Control, Institute of Public Health, Montenegro) and by experts from the network (Adam Meijer, National Institute for Public Health and the Environment (RIVM), the Netherlands; Rod Daniels and John McCauley, WHO Collaborating Centre for Reference and Research on Influenza, Francis Crick Institute, United Kingdom).

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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