Flu News Europe

Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 09/2020 (24 February – 1 March 2020)

- Influenza activity remained elevated, with 6 Member States and areas reporting high and 14 medium influenza 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, 44% 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 (60%) of type A viruses being detected. Of the type A detections, A(H1N1)pdm09 viruses were the most common (52%). 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 31 reports from across the Region: 18 reported dominance of type A viruses; 7 co-dominance of types A and B viruses; and 6 dominance of type B viruses.
- Pooled estimates of all-cause mortality from 21 countries or regions reporting to the EuroMOMO project showed 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 influenza season for the Region as a whole peaked in week 05/2020 reaching a positivity rate of 55%.
- The majority of circulating viruses were susceptible to neuraminidase inhibitors supporting early treatment or prophylactic use according to national guidelines.
- Interim estimates of 2019–2020 seasonal influenza vaccine effectiveness from 4 studies in the northern hemisphere are available. Vaccination remains the best possible method for prevention of influenza and/or reducing the risk of serious complications. Member States should continue to promote vaccination while influenza viruses continue to circulate in the community.
- WHO has published recommendations for the composition of influenza vaccines to be used in the 2020–2021 northern hemisphere season. Based on these recommendations the influenza A(H1N1)pdm09, A(H3N2) and B/Victoria-lineage virus components should be updated for the 2020–2021 influenza vaccine.
- ECDC and WHO Regional Office for Europe 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 outbreak of respiratory illness associated with a novel coronavirus (SARS-CoV-2) infection causing infectious disease (COVID-19) first reported in Wuhan, China, continues to spread rapidly. Cases of COVID-19 are reported in a growing number in the European Region. For more information visit:

- WHO website: 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 09/2020, 19 (58%) of the 33 Member States and areas that reported on ILI registered activities above their baseline levels. These include 2 Member States in eastern areas, 2 in northern areas, 7 in southern areas and 8 in western areas of the Region.

Of 19 Member States and areas that reported on ARI, more than half (n=9) registered activities above their baseline levels. These include 3 Member States in eastern areas, 4 in southern areas and 2 in western areas of the Region.

Influenza activity

Of 43 Member States and areas that reported on the intensity indicator, 8 reported activity at baseline levels, 15 reported low, 14 reported medium, and 6 reported high intensity for week 09/2020 (Fig. 1).

Of 43 Member States and areas that reported on geographic spread, 3 reported no activity, 5 reported sporadic spread, 2 reported local spread, 6 reported regional spread and 27 reported widespread geographic activity for week 09/2020 (Fig. 2).

Fig. 1. Intensity in the European Region, week 09/2020

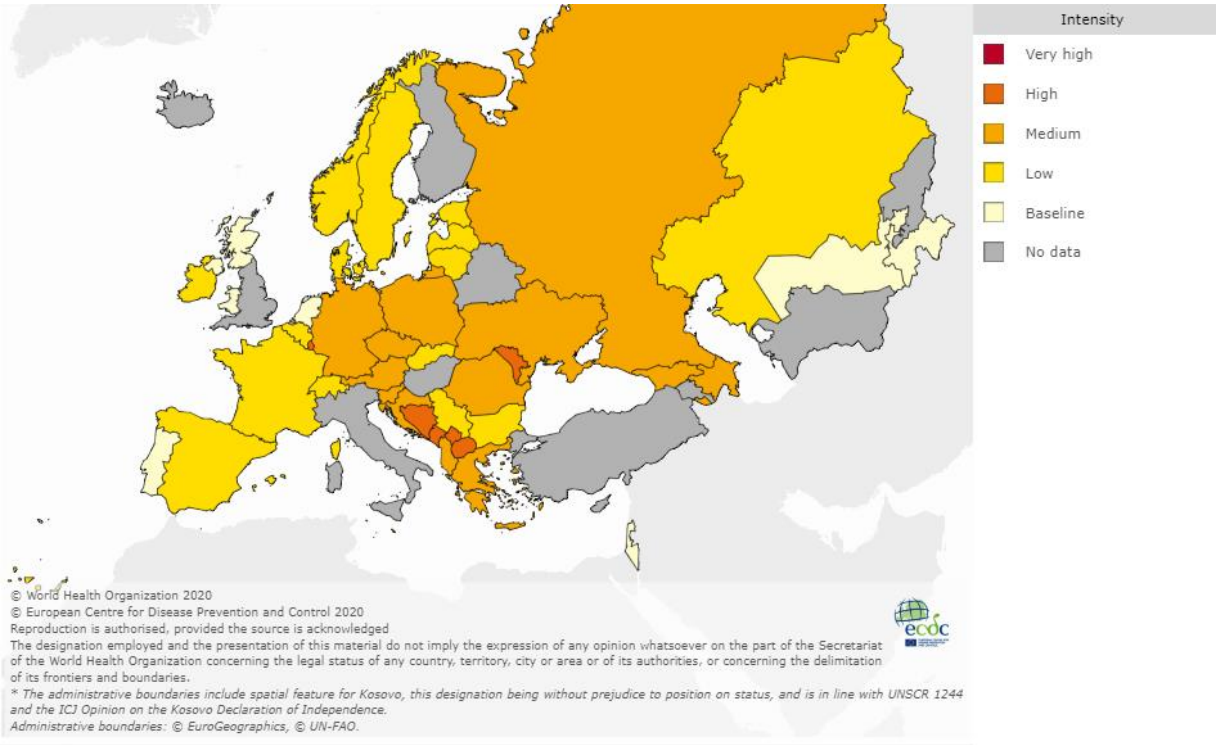
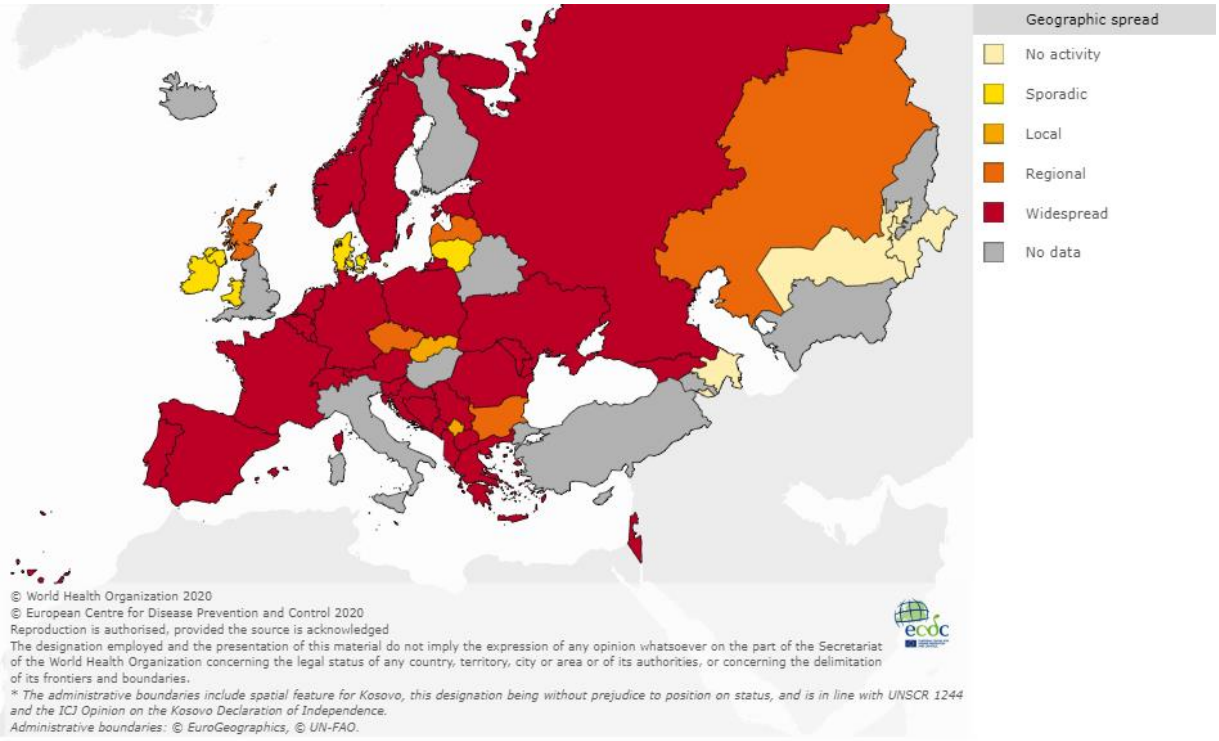


Fig. 2. Geographic spread in the European Region, week 09/2020



For interactive maps of influenza intensity and geographic spread, see the Flu News Europe website.

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

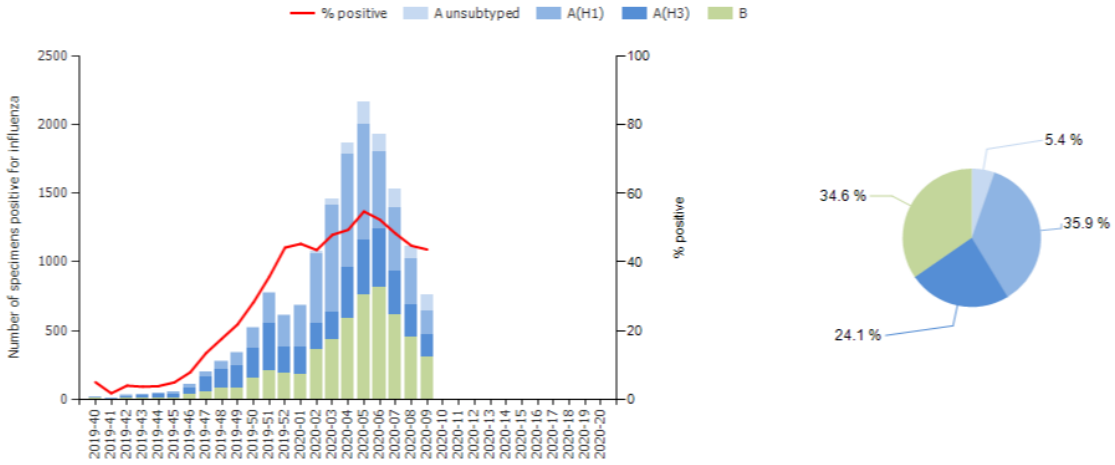
For week 09/2020, 764 (44%) of 1 755 sentinel specimens tested positive for an influenza virus; 60% were type A and 40% were type B (Fig. 3 and Table 1). Of 338 subtyped A viruses, 52% were A(H1N1)pdm09 and 48% were A(H3N2) (Fig. 3 and Table 1). All influenza type B viruses ascribed to a lineage were B/Victoria (Table 1).

Of 28 Member States or areas across the Region that each tested at least 10 sentinel specimens in week 09/2020, 10 countries reported rates of influenza virus detections of 50% and above.

For the season to date, more influenza type A (n=10 201, 65%) than type B (n=5 402, 35%) viruses have been detected (Fig. 3 and Table 1). Of 9 366 subtyped A viruses, 60% were A(H1N1)pdm09 and 40% were A(H3N2). Of 1 980 influenza type B viruses ascribed to a lineage, 99% were B/Victoria (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 09/2020 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**457**	**59.8**	**10 201**	**65.4**
A(H1N1)pdm09	176	52.1	5 609	59.9
A(H3N2)	162	47.9	3 757	40.1
A not subtyped	119	-	835	-
Influenza B	**307**	**40.2**	**5 402**	**34.6**
B/Victoria lineage	115	100	1 960	99.0
B/Yamagata lineage	0	-	20	1.0
Unknown lineage	192	-	3 422	-
Total detections (total tested)	**764 (1 755)**	**43.5**	**15 603 (42 079)**	**37.1**

[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.

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 09/2020, per 1 000 active participants, Ireland and Portugal reported between 0 and 5 ILI cases; France reported between 5 and 10 cases; Italy reported between 10 and 15 cases; the United Kingdom and Switzerland reported between 15 and 20 cases; Denmark and Spain reported between 30 and 35 cases.

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

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

For week 09/2020, 108 laboratory-confirmed influenza cases in intensive care units (ICUs) were reported by 8 Member States. Among these cases influenza type A viruses (90%) were detected more frequently than influenza type B viruses (10%).

Since week 40/2019, more influenza type A (n=3 325, 91%) than type B (n=312, 9%) viruses were detected. Of 1 160 subtyped influenza A viruses, 57% were A(H1N1)pdm09 and

43% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 1 915 cases with known age, 49% were 15-64 years old and 37% were 65 years and older.

1.2) Hospitalized laboratory-confirmed influenza cases – other wards

For week 09/2020, 89 laboratory-confirmed influenza cases in wards other than ICUs were reported by 5 Member States. Among these cases influenza type A viruses (62%) were detected more frequently than influenza type B viruses (38%).

Since week 40/2019, more influenza type A (n=5 569, 88%) than type B (n=745, 12%) viruses were detected. Of 1 534 subtyped influenza A viruses, 57% were A(H1N1)pdm09 and 44% A(H3N2). No influenza B viruses were ascribed to a lineage. Of 6 313 cases with known age, 45% were 65 years and older and 31% were 15-64 years old.

2. SARI surveillance

For week 09/2020, 1 559 SARI cases were reported by 13 Member States or areas. Of 593 specimens tested for influenza viruses, 36% were positive for influenza virus, and influenza type A viruses (57%) were detected more frequently than influenza type B viruses (43%).

Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=2 552) were mostly infected by type A viruses (55%). Of the 1 206 influenza type A virus infected cases for which subtyping was performed, 61% were A(H1N1)pdm09 and 39% were A(H3N2) viruses. Of the 609 influenza type B viruses ascribed to a lineage, 99% were B/Victoria and 1% were B/Yamagata.

Of 29 612 SARI cases reported since week 40/2019, 29 344 had a recorded age and, of these, 53% were 0–4 years old and 26% were 15–64 years old.

Mortality monitoring

Pooled estimates of all-cause mortality from 21 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 09/2020, 8 449 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; 63% were type A and 37% were type B. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage. Of 2 048 subtyped A viruses, 70% were A(H1N1)pdm09 and 30% were A(H3N2). All influenza type B viruses ascribed to a lineage were B/Victoria (Table 2).

For the season to date, more influenza type A (n=96 691, 76%) than type B (n= 29 524, 24%) viruses have been detected. Relatively low numbers of the viruses have been ascribed to a subtype or lineage; of subtyped A viruses, 53% were A(H1N1)pdm09 and 47% were A(H3N2). Of influenza type B viruses ascribed to a lineage, 96% were B/Victoria (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 09/2020 and cumulatively for the season

	Current Week		Season 2019–2020	
Virus type and subtype	**Number**	**%[a]**	**Number**	**%[a]**
Influenza A	**5 306**	**62.8**	**93 691**	**76.0**
A(H1N1)pdm09	1 442	70.4	16 133	52.7
A(H3N2)	606	29.6	14 468	47.3
A not subtyped	3 258	-	63 090	-
Influenza B	**3 143**	**37.2**	**29 524**	**24.0**
B/Victoria lineage	97	100	1 582	96.4
B/Yamagata lineage	0	-	59	3.6
Unknown lineage	3 046	-	27 883	-
Total detections (total tested)	**8 449 (32 894)**	-	**123 215 (549 695)**	-

[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 2 395 viruses has been reported (Table 3):

- 1 771 (74%) type A: 918 A(H3N2) and 853 A(H1N1)pdm09;
- 624 (26%) type B: 596 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 from 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 2019–2020 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 40/2019–09/2020

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	777
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	18
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	40
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	78
A(H3) clade 3C.3a representative A/Kansas/14/2017[a]	480
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	61
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	298
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]	19
B(Vic)-lineage clade 1A (del162-164 subgroup) representative B/Hong Kong/269/2017	5
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	532
B(Vic) attributed to recognised group in the guidance but not listed here	40
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 characterization 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 characterization 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 characterized in December. All gave antigenic profiles characteristic of the triple deletion subgroup 1A(Δ3)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 characterized 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

Based on WHO published recommendations on 21 February 2019, the composition of influenza vaccines for use in the **2019–2020 northern hemisphere influenza season** 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 2019 decision and the 21 March 2019 addendum are available on the WHO website.

The report from the Vaccine Composition Meeting for the southern hemisphere 2020 season can be found here.

On 28 February 2020, WHO published recommendations for the components of influenza vaccines for use in the **2020–2021 northern hemisphere influenza season**.

Egg-based vaccines should contain following:

- an A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus (Clade 6B.1A5A);

- an A/Hong Kong/2671/2019 (H3N2)-like virus (Clade 3C.2a1b+T135K-B);
- a B/Washington/02/2019 (B/Victoria lineage)-like virus (Clade 1A_Δ3B); and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus (Clade 3).

Cell- or recombinant-based vaccines should contain following:

- an A/Hawaii/70/2019 (H1N1)pdm09-like virus (Clade 6B.1A5A);
- an A/Hong Kong/45/2019 (H3N2)-like virus (Clade 3C.2a1b+T135K-B);
- a B/Washington/02/2019 (B/Victoria lineage)-like virus (Clade 1A_Δ3B); and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus (Clade 3).

It is recommended that the influenza B virus component of both trivalent vaccine types for use in the 2020–2021 northern hemisphere influenza season should be a B/Washington/02/2019-like virus of the B/Victoria-lineage.

The full report and Frequently Asked Questions for the 28 February 2020 decision are available on the WHO website.

Vaccine effectiveness

Interim estimates of 2019–2020 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 2019–2020 season in Canada have also been published. Overall VE was 58% (95% CI: 47%–66%), with higher point estimates among children aged 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 was 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, 1 164 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 480 A(H1N1)pdm09, 472 A(H3N2) and 212 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. Two type B/Victoria viruses showed evidence of reduced inhibition, one of them by oseltamivir and the other by zanamivir.

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).

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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