Flu News Europe
Joint ECDC–WHO/Europe weekly influenza update

Summary

Week 15/2019 (8–14 April 2019)

- Of 41 countries reporting on geographic spread, 5 reported widespread activity. Specimens collected from individuals presenting with ILI or ARI to sentinel primary health care sites yielded an influenza virus positivity rate of 20%, a further decrease for the fifth week in a row.

- Of 41 countries reporting on influenza activity, 40 reported baseline or low intensity levels and 1 reported medium intensity.

- Influenza type A viruses dominated with more A(H3N2) than A(H1N1)pdm09 viruses being detected among sentinel and non-sentinel source specimens. Very few influenza B viruses were detected.

- Of the subset of specimens from patients with severe acute respiratory infection (SARI) collected in week 15/2019 that were tested for influenza viruses, 16% were positive and all viruses were type A.

- Pooled data from 23 Member States and areas reporting to the EuroMOMO project indicated that the all-cause excess mortality observed in previous weeks has returned to normal levels.

2018–2019 season overview

- Influenza activity in the European Region, based on sentinel sampling, exceeded a positivity rate of 10% in week 49/2018, exceeded 50% between weeks 3/2019 and 7/2019, and peaked in week 5/2019.

- Both influenza A virus subtypes have circulated, with co-circulation in some countries while others reported dominance of either A(H1N1)pdm09 or A(H3N2) viruses.

- Among hospitalized influenza virus-infected patients admitted to ICU wards, 99% were infected with type A viruses, and of those subtyped, 67% were A(H1N1)pdm09. Among influenza virus-infected patients admitted to other wards, 99% were infected with type A viruses, with 56% of those subtyped being A(H1N1)pdm09.

- Of the patient specimens from SARI surveillance that tested positive for influenza, 99% were infected with influenza type A viruses, with 79% of those subtyped being A(H1N1)pdm09.

- A recent summary of regional activity from October 2018 to February 2019 was published in Eurosurveillance and can be found here.

- Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. For more detail, see the Vaccine effectiveness section.

- WHO has published recommendations for the composition of influenza vaccines to be used in the 2019–2020 northern hemisphere season. The recommendation was that type B lineage viruses remain unchanged, while the A(H1N1)pdm09 and A(H3N2) viruses were updated.

- Circulating viruses in the European Region remained susceptible to neuraminidase inhibitors supporting use of antiviral treatment according to national guidelines.

Primary care data

Syndromic surveillance data

For week 15/2019, of the 32 Member States reporting influenza-like illness (ILI) thresholds, none reported ILI activity above baseline levels.

Of the 18 Member States reporting acute respiratory infection (ARI) thresholds, only Armenia reported activity above baseline levels.

Influenza activity

For week 15/2019, of 41 Member States and areas reporting on intensity, 17 reported baseline (across the region), 23 reported low (across the region) and 1 reported medium intensity (Kazakhstan) for week 15/2019 (Fig. 1).

Of 41 Member States and areas reporting on geographic spread, 6 reported no activity (in eastern, southern, western areas), 18 reported sporadic (across the region), 6 reported local (in northern, southern areas), 6 reported regional (eastern, northern, southern areas) and 5 reported widespread activity (Croatia, Germany, Slovenia, Sweden, United Kingdom (England)) (Fig. 2).

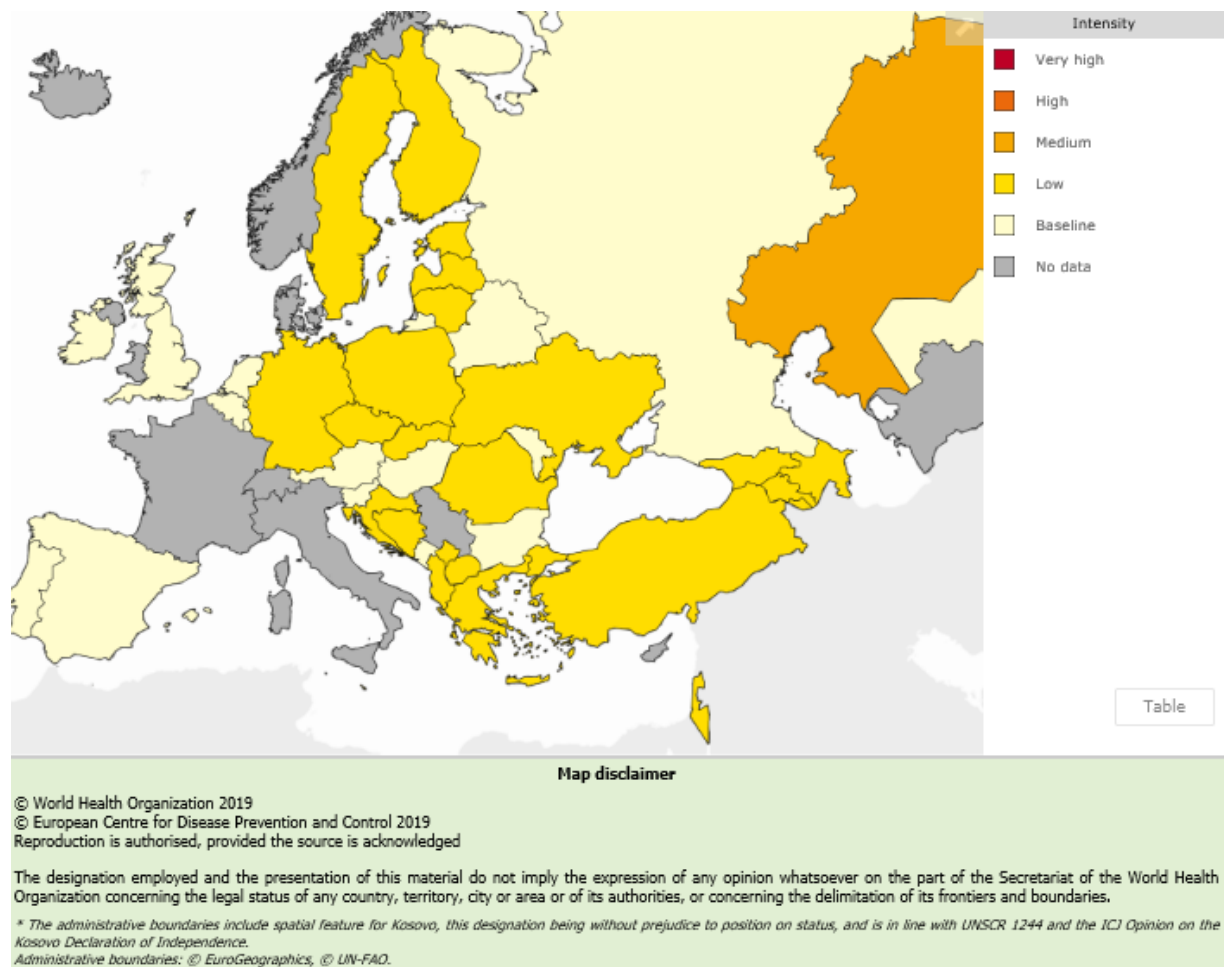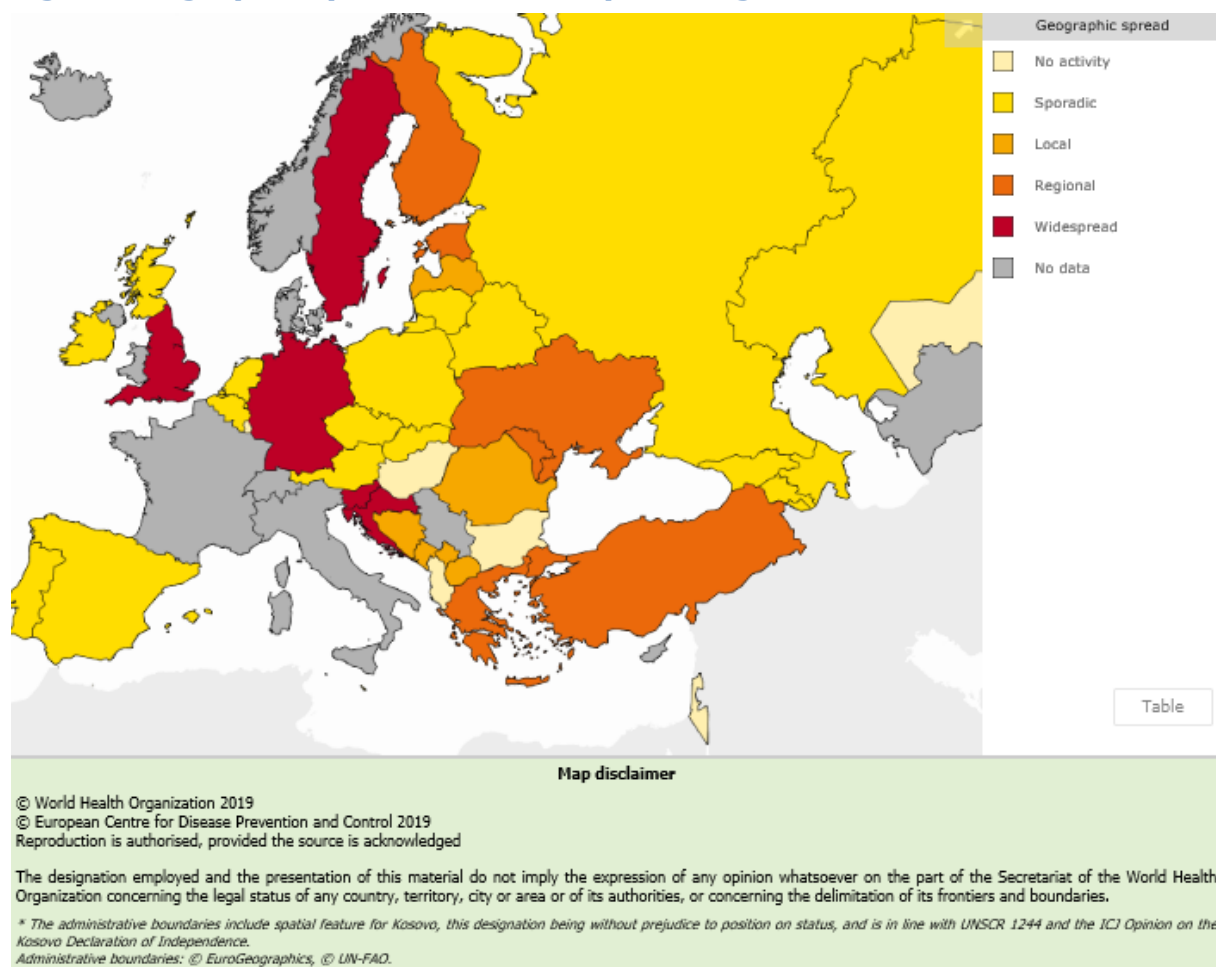# Fig. 1. Intensity in the European Region, week 15/2019

Intensity
- Very high
- High
- Medium
- Low
- Baseline
- No data

Table

Map disclaimer

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* The administrative boundaries include spatial feature for Kosovo, this designation being without prejudice to position on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.
Administrative boundaries: © EuroGeographics, © UN-FAO.

Fig. 2. Geographic spread in the European Region, week 15/2019

Geographic spread

- No activity
- Sporadic
- Local
- Regional
- Widespread
- No data

Table

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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 15/2019, 136 (20.4%) of 667 sentinel specimens tested positive for an influenza virus; 98% were type A and 2% were type B. Of 70 subtyped A viruses, 33% were A(H1N1)pdm09 and 67% A(H3N2) (Fig. 3 and Table 1).

Of 14 countries or areas across the region that each tested at least 10 sentinel specimens in week 15/2019, 9 reported a rate of influenza virus detections above 10%.

For the season to date, almost all viruses detected were influenza type A (99%) with type B accounting for only 1% of detections. Of subtyped A viruses, 55% were A(H1N1)pdm09 and 45% were A(H3N2). Of 60 influenza type B viruses ascribed to a lineage, 83% were B/Yamagata (71% of type B viruses were reported without a lineage) (Fig. 3 and 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]
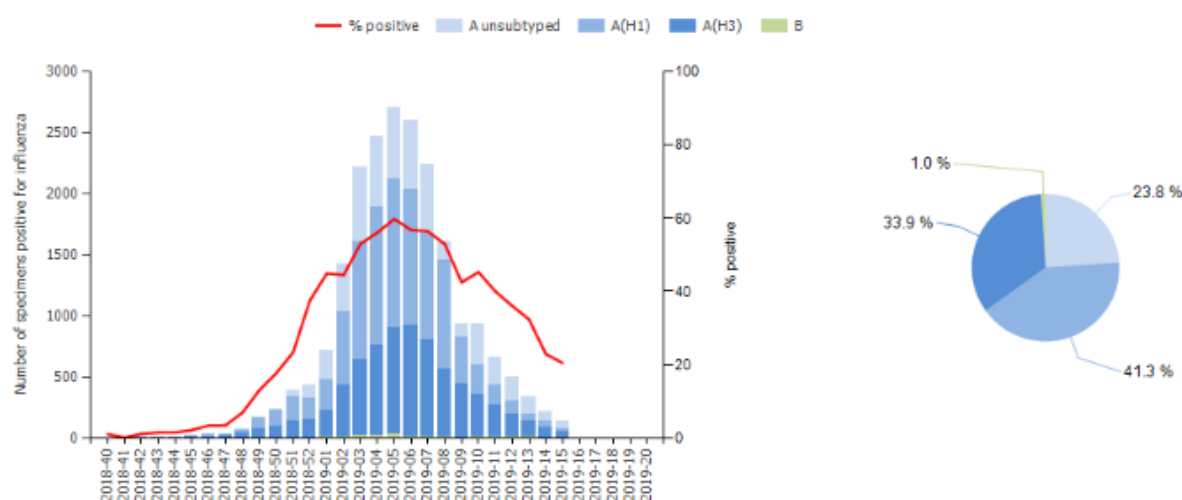
[a] Pie chart shows cumulative data for this period.

Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 15/2019 and cumulatively

Virus type and subtype	Current Week		Season 2018–2019	
	Number	%[a]	Number	%[a]
Influenza A	**133**	**97.8**	**20 917**	**99.0**
A(H1N1)pdm09	23	32.9	8 715	54.9
A(H3N2)	47	67.1	7 166	45.1
A not subtyped	63	-	5 036	-
Influenza B	**3**	**2.2**	**208**	**1.0**
B/Victoria lineage	0	0	10	16.7
B/Yamagata lineage	0	0	50	83.3
Unknown lineage	3	-	148	-
Total detections (total tested)	**136 (667)**	**20.4**	**21 125 (51 747)**	**40.8**

[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.

Severity

A subset of Member States and areas monitors severe disease related to influenza virus infection by surveillance of 1) hospitalized laboratory-confirmed influenza cases in ICUs (12 Member States or areas), or other wards (8 Member States or areas), or 2) severe acute respiratory infection (SARI; 17 Member States or areas).

1.1) Hospitalized laboratory-confirmed influenza cases – ICUs

Influenza type A viruses were detected in all of the laboratory-confirmed influenza cases reported in ICUs for week 15/2019 (n=46).

Since week 40/2018, more influenza type A (n=7 037, 99%) than type B (n=56, 1%) viruses were detected. Of 3 095 subtyped influenza A viruses, 67% were A(H1N1)pdm09 and 33% were A(H3N2). No influenza B viruses were ascribed to a lineage. Of 3 943 cases with known age, 47% were 65 years and older and 44% were 15-64 years old.

<u>1.2) Hospitalized laboratory-confirmed influenza cases – other wards</u>

Among laboratory-confirmed influenza cases reported in wards other than ICUs in week 15/2019 (n=43), all were influenza type A viruses.

Since week 40/2018, more influenza type A (n=9 377, 99%) than type B (n=66, 1%) viruses were detected. Of 3 652 subtyped influenza A viruses, 56% were A(H1N1)pdm09 and 44% were A(H3N2). Of 2 influenza B viruses ascribed to a lineage, 1 was B/Yamagata and 1 was B/Victoria. Of 9 443 cases with known age, 46% were 65 years and older and 32% were 15-64 years old.

<u>2. SARI surveillance</u>

For week 15/2019, 1 054 SARI cases were reported by 11 countries or areas. Of these cases, 127 specimens were tested for influenza viruses with 20 (16%) of them being positive. Of these, influenza type A viruses (n=19: 95%) were detected more frequently than influenza type B viruses (n=1: 5%).

Of 37 966 SARI cases reported since week 40/2018, 37 910 had a recorded age and, of these, 57% were 0-4 years old and 24% were 15-64 years old. For SARI cases testing positive for influenza virus since week 40/2018 (n=2 799), type A viruses have been the most common (99%). Of the 2 511 influenza type A infected cases for which subtyping was performed, 79% were infected by A(H1N1)pdm09 viruses and 21% were infected by A(H3N2) viruses. 1 type B virus ascribed to a lineage was B/Yamagata.

Mortality monitoring

For week 15/2019, the EuroMOMO project received data from 23 countries or areas that were included in pooled analyses. The pooled estimates indicated that the all-cause excess mortality observed in previous weeks has returned to normal levels.

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 15/2019, 1 834 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 an influenza virus; 96% were type A and 4% were type B. Of A viruses subtyped, 36% were A(H1N1)pdm09 and 64% were A(H3N2) (Table 2).

For the season to date, more influenza type A (99%) than type B (1%) viruses have been detected. Of A viruses subtyped, 59% were A(H1N1)pdm09 and 41% were A(H3N2). Of 48 influenza type B viruses ascribed to a lineage, 46% were B/Yamagata (97% of type B viruses were reported without a lineage) (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, week 15/2019 and cumulatively

	Current Week		Season 2018–2019	
Virus type and subtype	**Number**	**%ᵃ**	**Number**	**%ᵃ**
Influenza A	**1 766**	**96.3**	**176 751**	**99.1**
A(H1N1)pdm09	173	35.6	34 810	59.0
A(H3N2)	313	64.4	24 216	41.0
A not subtyped	1 280	-	117 725	-
Influenza B	**68**	**3.7**	**1607**	**0.9**
B/Victoria lineage	0	0	26	54.2
B/Yamagata lineage	0	0	22	45.8
Unknown lineage	68	-	1559	-
Total detections (total tested)	**1 834 (14 233)**	-	**178 358 (734 280)**	-

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

Genetic characterization of influenza viruses is routinely performed to understand how similar currently circulating influenza viruses are to the viruses used in influenza vaccines for an ongoing season.

Since week 40/2018, genetic characterizations of 3 477 viruses have been reported by the network laboratories.

Of the genetically characterized viruses, 1 728 were A(H1)pdm09 viruses belonging to the A/Michigan/45/2015 (6B.1) clade with a further 3 attributed to a subgroup not listed; 1 699 were A(H3) viruses, with 1 126 belonging to the A/Alsace/1746/2018 (3C.2a1b) subgroup, 65 to the A/Switzerland/8060/2017 (3C.2a2) subclade, 31 to the A/Cote d'Ivoire/544/2016 (3C.2a3) subclade, 57 to the A/Singapore-16-0019/2016 (3C.2a1) subclade, 9 to the A/Greece/4/2017 (3C.2a1a), 4 to the A/Hong Kong/4801/2014 (3C.2a) clade, 400 to the A/England/538/2018 (3C.3a) clade and 7 attributed to a subgroup not listed.

Of the 47 genetically characterized influenza B viruses, 24 were B/Yamagata viruses belonging to the B/Phuket/3073/2013 clade (clade 3). All 23 B/Victoria viruses characterized belonged to clade 1A (represented by B/Brisbane/60/2008); but of these, 5 fell in a subclade with a two amino acid deletion in HA (1A.Δ2; represented by B/Colorado/06/2017) and 13 fell in a subclade with a three amino acid deletion in HA (1A.Δ3; represented by B/Hong Kong/269/2017) (Table 3).

Table 3. Viruses attributed to genetic groups, cumulative for weeks 40/2018–15/2019

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1 representative A/Michigan/45/2015[a]	1 728
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	3
A(H3) clade 3C.2a1b representative A/Alsace/1746/2018 subgroup	1 126
A(H3) clade 3C.2a2 representative A/Switzerland/8060/2017 subgroup[b]	65
A(H3) clade 3C.2a3 representative A/Cote d'Ivoire/544/2016 subgroup	31
A(H3) clade 3C.3a representative A/England/538/2018 subgroup	400
A(H3) clade 3c.2a1 representative A/Singapore/INFIMH-16-0019/2016 subgroup[d]	57
A(H3) clade 3c.2a representative A/Hong Kong/4801/2014 subgroup	4
A(H3) attributed to recognized group in current guidance but not listed here	7
A(H3) clade 3C.2a1a representative A/Greece/4/2017 subgroup	9
B(Vic)-lineage clade 1A representative B/Brisbane/60/2008	5
B(Vic)-lineage clade 1A representative B/Colorado/06/2017[a]	5
B(Vic)-lineage clade 1A representative B/Hong Kong/269/2017	13
B(Yam)-lineage clade representative B/Phuket/3073/2013[c]	24

[a] Vaccine component for 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

[b] Vaccine component for 2019 southern hemisphere season.

[c] Vaccine component of quadrivalent vaccines for use in 2018–2019 northern hemisphere and 2019 southern hemisphere seasons.

[d] Vaccine component for 2018-2019 northern hemisphere season

A [report](#) detailing influenza virus characterization data conducted in January and February 2019 by the WHO Collaborating Centre, London (the Francis Crick Institute), on influenza positive specimens received from EU/EEA countries, was published by the European Centre for Disease Prevention and Control. A summary is given below.

A(H1N1)pdm09 viruses

The great majority (203/204) of A(H1N1)pdm09 viruses characterized were antigenically similar to the vaccine virus for use in the 2018–2019 northern hemisphere (A/Michigan/45/2015, clade 6B.1) and fell in subclade 6B.1A. Within this subclade, there has been increasing genetic diversity of the HA genes with several emerging genetic subgroups. Most viruses carried the HA1 amino acid substitution of S183P.

A(H3N2) viruses

Antigenic characterization of A(H3N2) viruses remains technically difficult. Since the previous report published in December 2018, only 33 A(H3N2) viruses have had a sufficient HA titre to allow antigenic characterization by haemagglutination inhibition (HI) assay. By HI assay, all viruses belonging to subgroups within clades 3C.2a and 3C.3a were poorly recognized by antisera raised against egg-propagated A/Singapore/INFIMH-16-0019/2016, the current vaccine virus.

B/Victoria viruses

Only 5 B/Victoria lineage viruses were characterized antigenically. Of these, 2 were antigenically similar to the current vaccine virus, B/Colorado/06/2017, which belongs to a subclade with a two amino acid deletion in HA (Δ162-163, 1A.Δ2). The other 3 were antigenically similar to a virus of African origin with a three amino acid deletion in HA1 (Δ162-164, 1A.Δ3).

B/Yamagata viruses

Only 7 B/Yamagata lineage viruses were characterized antigenically. HI analyses with post-infection ferret antisera raised against B/Phuket/3072/2013, the virus recommended for inclusion in quadrivalent vaccines for the current and subsequent northern hemisphere influenza seasons, indicated that all 7 viruses were antigenically similar to the vaccine virus.

Vaccine composition

The recommended composition of the trivalent influenza vaccine for the current northern hemisphere 2018–2019 season included an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus and a B/Colorado/06/2017-like virus (B/Victoria lineage). For quadrivalent vaccines, a B/Phuket/3073/2013-like virus (B/Yamagata lineage) was recommended. The full report can be found here.

On 21 February 2019, WHO published recommendations for the components of influenza vaccines for use in the 2019–2020 northern hemisphere influenza season, and on 21 March it was updated. Vaccines should contain the following

- an A/Brisbane/02/2018 (H1N1)pdm09-like virus;

- an A/Kansas/14/2017 (H3N2)-like virus;

- a B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage); and

- a B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage).

It is 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" are available for the 21 February decision and the 21 March addendum on the WHO website.

Vaccine effectiveness

Current influenza vaccines tend to work better against influenza A(H1N1)pdm09 and influenza B viruses than against influenza A(H3N2) viruses. Preliminary vaccine effectiveness estimates continue to support the use of vaccines. Early data suggest that vaccines are moderately effective, with estimates varying depending on the population studied and the proportions of circulating influenza A virus subtypes. See data from a European study (6 countries), Canada, Finland, Hong Kong (China), Sweden, and the United States of America.

Antiviral susceptibility testing

Neuraminidase inhibitor susceptibility was assessed for 2 195 viruses with collection dates since week 40/2018 [1 316 A(H1N1)pdm09, 849 A(H3N2), and 30 type B]. 8 A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA indicative of highly reduced inhibition (HRI) by oseltamivir and 3 of them were confirmed by phenotypic testing. 1 type B virus showed evidence of RI by oseltamivir and zanamivir.

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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Tables and figures should be referenced:

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