

Summary

Week 12/2020 (16 – 22 March 2020)

- The novel coronavirus disease 2019 (COVID-19) outbreak in the Region seems to be affecting healthcare presentations and testing capacities in Member States, which impact both influenza epidemiologic and virologic data, and seasonal patterns.
- For the Region overall, influenza activity appears to be declining. High influenza intensity was reported by 1 Member State, and 7 Member States and areas reported medium influenza intensity. Widespread influenza activity was reported by less than half of the Member States and areas across the Region.
- However, influenza-like illness (ILI) and/or acute respiratory infection (ARI) notification rates continued to increase or remain high in some Member States this week, which might reflect the community transmission of COVID-19.
- The percentage of specimens from patients who presented with ILI or ARI to sentinel primary healthcare sites that tested positive for an influenza virus dropped from 30% last week to 14% this 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 (65%). Of the influenza B viruses, all were B/Victoria lineage.
- Pooled estimates of all-cause mortality show, overall, normal expected levels in the participating countries; however, increased excess mortality is notable in Italy.

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 maximum positivity rate of 55%. The peak phase with positivity levels above 50% lasted for just two weeks, 05/2020 and 06/2020, but reporting in subsequent weeks may have been adversely affected by Member State responses to the COVID-19 outbreak. In the previous influenza season, rates of influenza positivity exceeded 50% for six weeks.
- 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 in the northern hemisphere are available. Vaccination remains the best possible method for prevention of influenza and/or reducing the risk of serious complications.
- 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

The World Health Organization categorized the COVID-19 outbreak as a pandemic on 11 March 2020. The number of COVID-19 cases being reported within the European Region has continued to increase significantly. 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 12/2020, 12 (36%) of the 33 Member States and areas that reported on ILI registered activity above their baseline levels: 2 Member States in eastern areas, 6 in northern areas and 4 in western areas of the Region.

Of 16 Member States and areas that reported on ARI, 3 (19%) registered activity above their baseline levels: 2 Member States in eastern areas and 1 in the northern area of the Region.

Influenza activity

Of 38 Member States and areas that reported on the intensity indicator, 9 reported activity at baseline levels, 21 reported low, 7 reported medium, and 1 reported high (Ireland) intensity for week 12/2020 (Fig. 1).

Of 37 Member States and areas that reported on geographic spread, 3 reported no activity, 10 reported sporadic spread, 2 reported local spread, 7 reported regional spread and 15 reported widespread activity for week 12/2020 (Fig. 2).

Fig. 1. Intensity in the European Region, week 12/2020

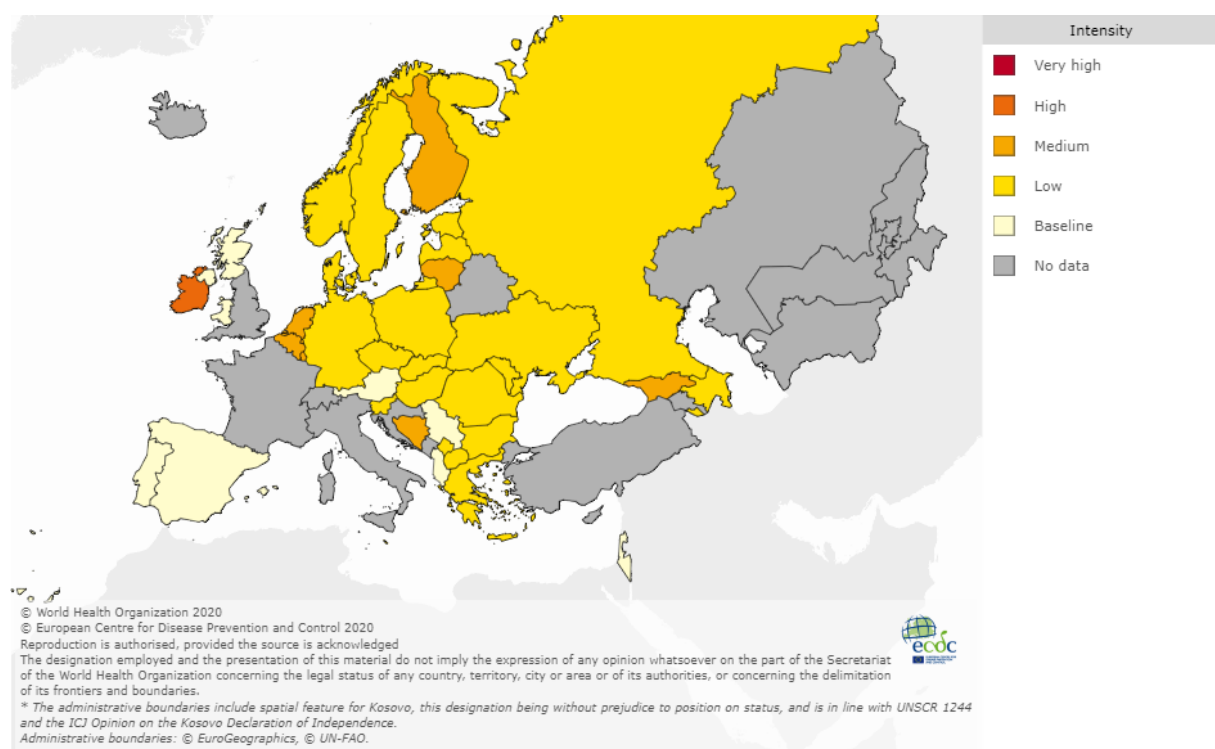
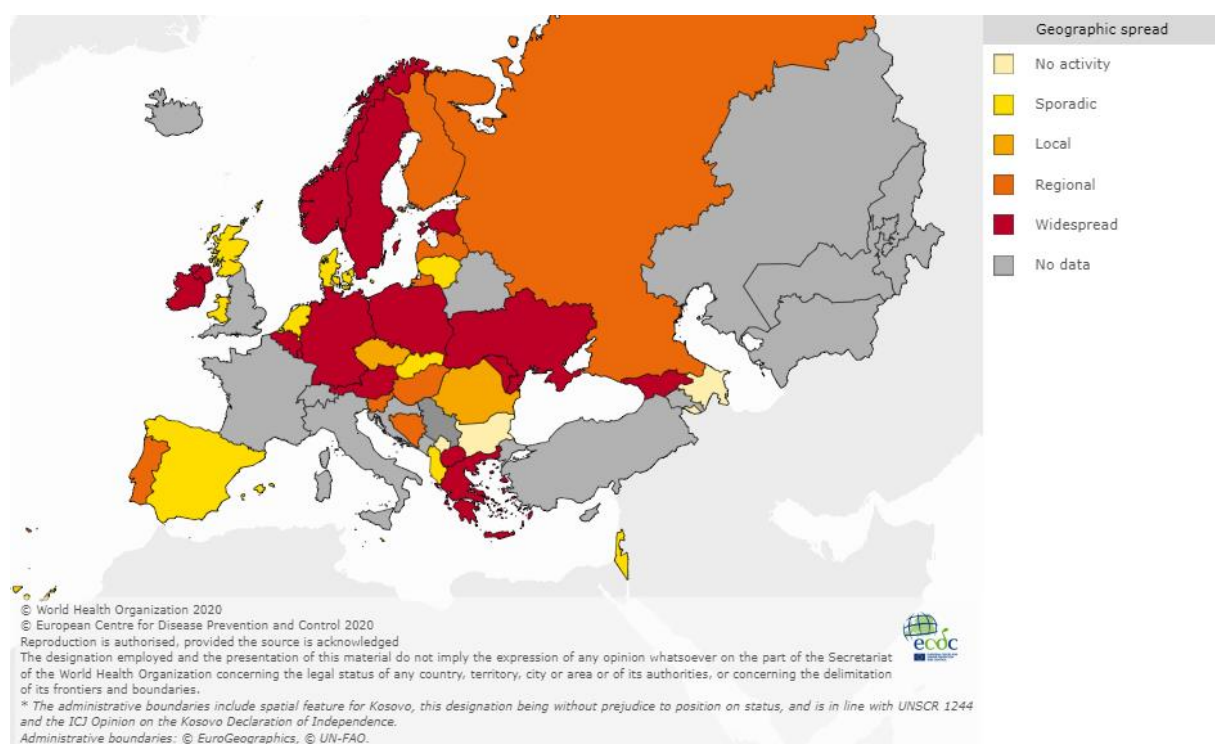


Fig. 2. Geographic spread in the European Region, week 12/2020



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

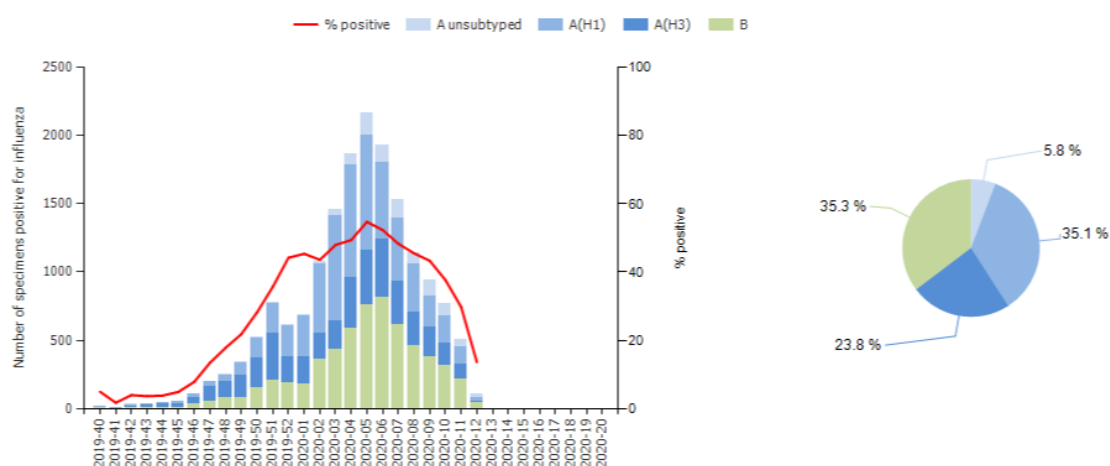
Viruses detected in sentinel-source specimens (ILI and ARI)

For week 12/2020, 105 (14%) of 760 sentinel specimens from 21 Member States or areas across the Region tested positive for an influenza virus. Among these detections, 60% were type A and 40% were type B (Fig. 3 and Table 1). Of 37 subtyped A viruses, 65% were A(H1N1)pdm09 and 35% were A(H3N2) (Fig. 3 and Table 1). All influenza type B viruses ascribed to a lineage were B/Victoria (Table 1).

For the season to date, more influenza type A (n=11 109, 65%) than type B (n=6 061, 35%) viruses have been detected (Fig. 3 and Table 1). Of 10 115 subtyped A viruses, 60% were A(H1N1)pdm09 and 40% were A(H3N2). Of 2 362 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



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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 12/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	63	60.0	11 109	64.7
A(H1N1)pdm09	24	64.9	6 030	59.6
A(H3N2)	13	35.1	4 085	40.4
A not subtyped	26	-	994	-
Influenza B	42	40.0	6 061	35.3
B/Victoria lineage	15	100.0	2 341	99.1
B/Yamagata lineage	0	0.0	21	0.9
Unknown lineage	27	-	3 699	-
Total detections (total tested)	105 (760)	13.8	17 170 (46 859)	36.6

^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 ILI in the general population using citizens' self-reported symptoms. For week 12/2020, per 1 000 active participants, Ireland and Italy reported between 0 and 5 ILI cases; France, Portugal, Spain and Switzerland reported between 5 and 10 ILI cases; Denmark and the United Kingdom reported between 15 and 20 ILI cases.

Based on this system, ILI activity is low (below the first quartile of historical data for this week) in France, Ireland, Italy and Portugal; and medium (between the first and third quartile of historical data) in Denmark, 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 12/2020, 14 laboratory-confirmed influenza cases in intensive care units (ICUs) were reported by 3 Member States. Among these cases 12 were infected with influenza type A viruses and 2 with influenza type B viruses.

Since week 40/2019, more influenza type A (n=3 543, 90%) than type B (n=373, 10%) viruses were detected. Of 1 228 subtyped influenza A viruses, 58% were A(H1N1)pdm09 and 42% A(H3N2). No influenza B viruses were ascribed to a lineage. The majority of cases were

reported from three countries, the United Kingdom (n=1 775), France (n=881) and Spain (n=741). Of 2 141 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 12/2020, 53 laboratory-confirmed influenza cases in wards other than ICUs were reported by 5 Member States. Among these cases 51% were infected with influenza type B viruses and 49% with influenza type A viruses.

Since week 40/2019, more influenza type A (n=5 907, 85%) than type B (n=1 042, 15%) viruses were detected. Of 1 587 subtyped influenza A viruses, 57% were A(H1N1)pdm09 and 43% A(H3N2). No influenza B viruses were ascribed to a lineage. The majority of cases were reported by two countries, Ireland (n=4 132) and Spain (n=2 309). Of 6 948 cases with known age, 43% were 65 years and older and 31% were 15-64 years old.

2. SARI surveillance

For week 12/2020, 616 SARI cases were reported by 7 Member States or areas. Of 295 specimens tested for influenza viruses, 11% were positive for influenza virus. Among these cases, 16 were infected with influenza type A viruses and 2 with influenza type B viruses.

Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=2 877) were mostly infected by type A viruses (56%). Of the 1 356 influenza type A virus infected cases for which subtyping was performed, 61% were A(H1N1)pdm09 and 39% were A(H3N2) viruses. Of the 681 influenza type B viruses ascribed to a lineage, 99% were B/Victoria and 1% were B/Yamagata.

Of 33 588 SARI cases reported since week 40/2019, 33 307 had a recorded age and, of these, 51% were 0–4 years old and 28% were 15–64 years old.

Mortality monitoring

Pooled estimates of all-cause mortality show, overall, normal expected levels in the participating countries; however, increased excess mortality is notable in Italy.

The number of deaths reported to the [EuroMOMO](#) project in recent weeks should be interpreted with caution as adjustments for delayed registrations may be imprecise. Furthermore, results of pooled analyses may vary dependent on which countries reported and were therefore included in weekly analyses, despite pooled analyses being adjusted for variation between the included countries and for differences in the local delay in reporting.

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 12/2020, 2 764 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; 68% were type A and 32% were type B. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage. Of 852 subtyped A viruses, 65% were A(H1N1)pdm09 and 35% 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=105 386, 75%) than type B (n=35 558, 25%) viruses have been detected but relatively low numbers have been ascribed to a subtype or lineage. Of 35 436 subtyped A viruses, 54% were A(H1N1)pdm09 and 46% were A(H3N2). Of 2 020 influenza type B viruses ascribed to a lineage, 97% were B/Victoria (Table 2).

Table 2. Influenza virus detections in non-sentinel source specimens by type and subtype, for week 12/2020 and cumulatively for the season

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% ^a	Number	% ^a
Influenza A	1 885	68.2	105 386	74.8
A(H1N1)pdm09	552	64.8	19 278	54.4
A(H3N2)	300	35.2	16 158	45.6
A not subtyped	1 033	-	69 950	-
Influenza B	879	31.8	35 558	25.2
B/Victoria lineage	5	100.0	1 960	97.0
B/Yamagata lineage	0	0.0	60	3.0
Unknown lineage	874	-	33 538	-
Total detections (total tested)	2 764 (28 984)	-	140 944 (656 041)	-

^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 2 553 viruses has been reported (Table 3):

- 1 909 (75%) type A: 993 A(H3N2) and 916 A(H1N1)pdm09;
- 644 (25%) type B: 616 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 still 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 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 40/2019–12/2020

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	839
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	18
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	41
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	81
A(H3) clade 3C.3a representative A/Kansas/14/2017 ^a	528
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	63
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	320
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	552
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 March relating to viruses circulating globally, with collection dates after 31 August, but focusing on those from European Union/European Economic Area (EU/EEA) countries. Since the December 2019 characterization report, 25 shipments of influenza-positive specimens from EU/EEA countries had been received by the WHO Collaborating Centre, London (the Francis Crick Institute, Worldwide Influenza Centre (WIC)). A total of 954 virus specimens had been received, with collection dates after 31 August. A summary of viruses from EU/EEA countries characterized in the period January to February is given below. Previously published [influenza virus characterization reports](#) are also available on the ECDC website.

A(H1N1)pdm09 viruses

Of 151 A(H1N1)pdm09 viruses characterised antigenically from EU/EEA countries since the last report (for December, published in January 2020) 129 (85%) showed good reactivity with antiserum raised against the 2019–20 vaccine virus, A/Brisbane/02/2018, with those viruses showing poor reactivity carrying amino acid substitutions (notably N156K) in the HA1 150-loop region. The 159 test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 139 6B.1A5A, 12 6B.1A5B, 1 6B.1A6 and 7 6B.1A7.

A(H3N2) viruses

122 A(H3N2) viruses have been characterised antigenically, the majority of which showed reduced recognition by antiserum raised against the current vaccine virus, egg-propagated A/Kansas/14/2017. While circulation of A(H3N2) viruses has varied considerably between countries in terms of numbers and genetic clades, globally there have been approximately equal proportions of clade 3C.3a and subgroups 3C.2a1b+T131K and 3C.2a1b+T135K viruses detected. In total, 191 viruses have been characterised genetically at the WIC: 103 clade 3C.3a, 62 3C.2a1b+T131K, 19 3C.2a1b+T135K-A and seven 3C.2a1b+T135K-B.

B/Victoria viruses

The great majority of the 104 B/Victoria-lineage viruses characterised in this reporting period gave antigenic profiles characteristic of subgroup 1A(Δ 3)B viruses represented by B/Washington/02/2019, the vaccine virus for the 2020 southern hemisphere season. A minority of viruses gave a profile characteristic of 1A(Δ 2) viruses represented by the 2019–20 northern hemisphere vaccine virus B/Colorado/06/2017. In total, 125 viruses have been characterised genetically at the WIC: 118 subgroup 1A(Δ 3)B and seven 1A(Δ 2).

B/Yamagata viruses

The five B/Yamagata-lineage virus characterised antigenically in this reporting period reacted well with antiserum raised against the vaccine virus B/Phuket/3073/2013 (clade 3). All five viruses characterised genetically at the WIC, as for all recently circulating B/Yamagata-lineage viruses, belong to genetic clade 3 and contain at least two HA amino acid substitutions (HA1 L172Q and M251V) compared to B/Phuket/3073/2013, the antigenic effects of which have been minimal as assessed in earlier reports.

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) for the northern hemisphere have been published based on [six European studies](#) (see below) and independent studies conducted in [Finland](#), [Canada](#) and [the United States of America](#). 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 type/subtype/lineage of circulating viruses. Vaccination against influenza remains the best method for prevention of influenza infection and/or development of severe disease during the ongoing 2019-2020 influenza season.

Interim 2019-2020 influenza VE estimates from the six European studies for all ages ranged from 29% to 61% against any influenza in the primary care setting and 35% to 60% in hospitalized older adults (aged 65 years and over). The VE point estimates against influenza A(H1N1)pdm09 (all ages, both settings) was 48% to 75%, and against influenza A(H3N2) ranged from –58% to 57% (primary care) and –16% to 60% (hospital). Against influenza type B, VE for all ages was 62% to 83% (primary care only).

Antiviral susceptibility testing

Since the beginning of the season, 1 382 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 603 A(H1N1)pdm09, 531 A(H3N2) and 248 type B viruses. Three A(H1N1)pdm09 viruses carried amino acid substitution H275Y in NA, with one of them also having H295S substitution, both of which are indicative of highly reduced inhibition (HRI) by oseltamivir. One A(H3N2) virus carried amino acid substitution R292K in NA and showed evidence of HRI by oseltamivir and reduced inhibition (RI) by 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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