

## Summary

### Week 04/2020 (20-26 January 2020)

- Influenza activity continued to increase, with 1 Member State reporting very high, 3 high and 12 medium intensity. Widespread influenza activity was reported by the majority of Member States and areas across the Region.
- Of the individuals sampled who presented with ILI or ARI to sentinel primary healthcare sites, 47% tested positive for influenza viruses.
- Both influenza virus types A and B were co-circulating with a higher proportion (69%) of type A viruses detected.
- 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, 2 Member States reported influenza type B dominance and 4 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 number of deaths from 21 countries or regions reporting to the [EuroMOMO](#) project indicated an increasing trend in mortality over recent weeks.
- Data from [InfluenzaNet](#) indicated that influenza activity in the community was high in 1 reporting country, medium in 3 reporting countries and low in 4 reporting countries.

## Other news

There is an ongoing outbreak of respiratory illness, with a significant increase in geographic spread, linked to a novel coronavirus first identified in China. For more information see:

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

## 2019–2020 season overview

- For the Region as a whole, influenza activity commenced earlier than in recent years.
- Influenza activity in the Region, based on sentinel sampling, first exceeded a positivity rate of 10% in week 47/2019 and has remained over 10% for 10 weeks. There has been an overall increasing trend in the weekly positivity rate for influenza virus detections among sentinel ILI surveillance patients, following a dip in week 52.
- In sentinel sources, both influenza A virus subtypes, A(H1N1)pdm09 and A(H3N2), are co-circulating, 58% and 42% respectively. Increased influenza virus subtype A(H1N1)pdm09 detections have been reported since week 50/2019. Of the influenza B viruses, the vast majority (98%) 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 58% were A(H3N2) viruses. The same was reported for patients

admitted to other wards, with 94% of cases being infected with type A viruses; of these 65% were A(H3N2) viruses.

- Among SARI cases, influenza type B viruses were detected most frequently (57%).
- Circulating viruses remain susceptible to the 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.

## Primary care data

### Syndromic surveillance data

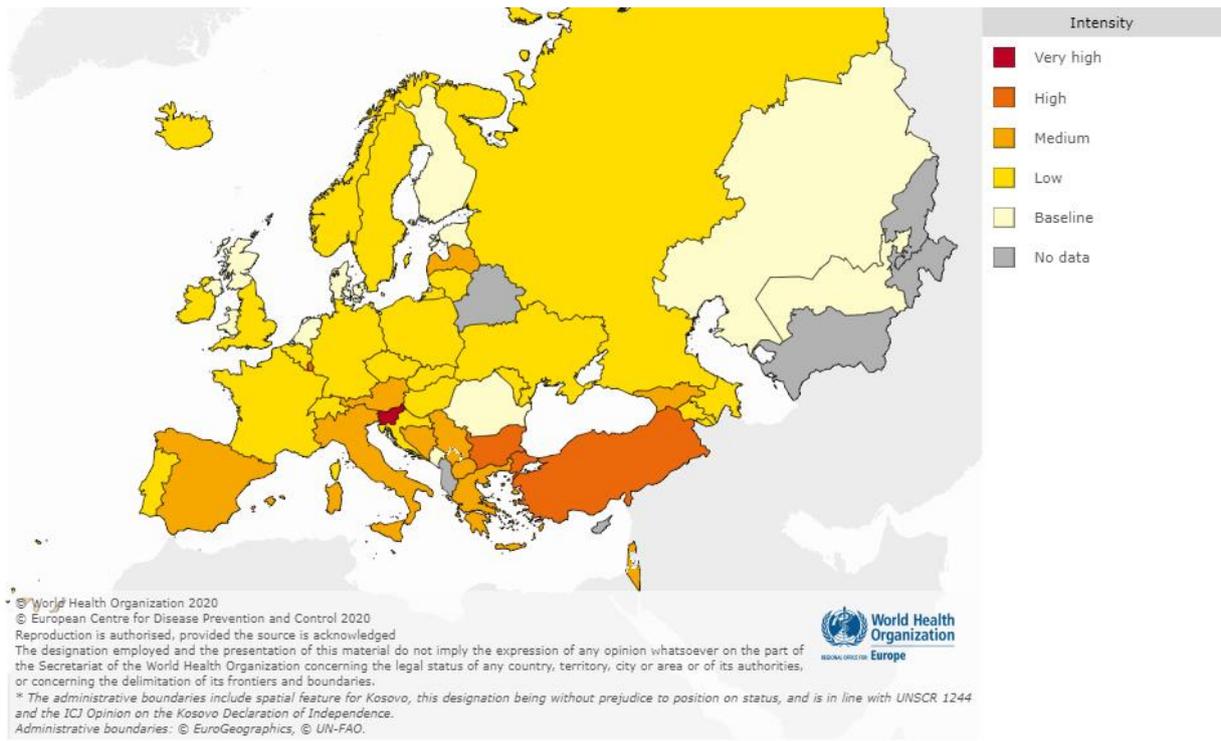
For the 2019-20 influenza season, ILI thresholds were defined for 35 Member States or areas and ARI thresholds for 17 Member States or areas. For week 04/2020, 21 (64%) of the 33 Member States and areas that reported on influenza-like illness (ILI) and 5 (31%) of the 16 Member States and areas that reported on acute respiratory infection (ARI), registered activities above their baseline levels.

### Influenza activity

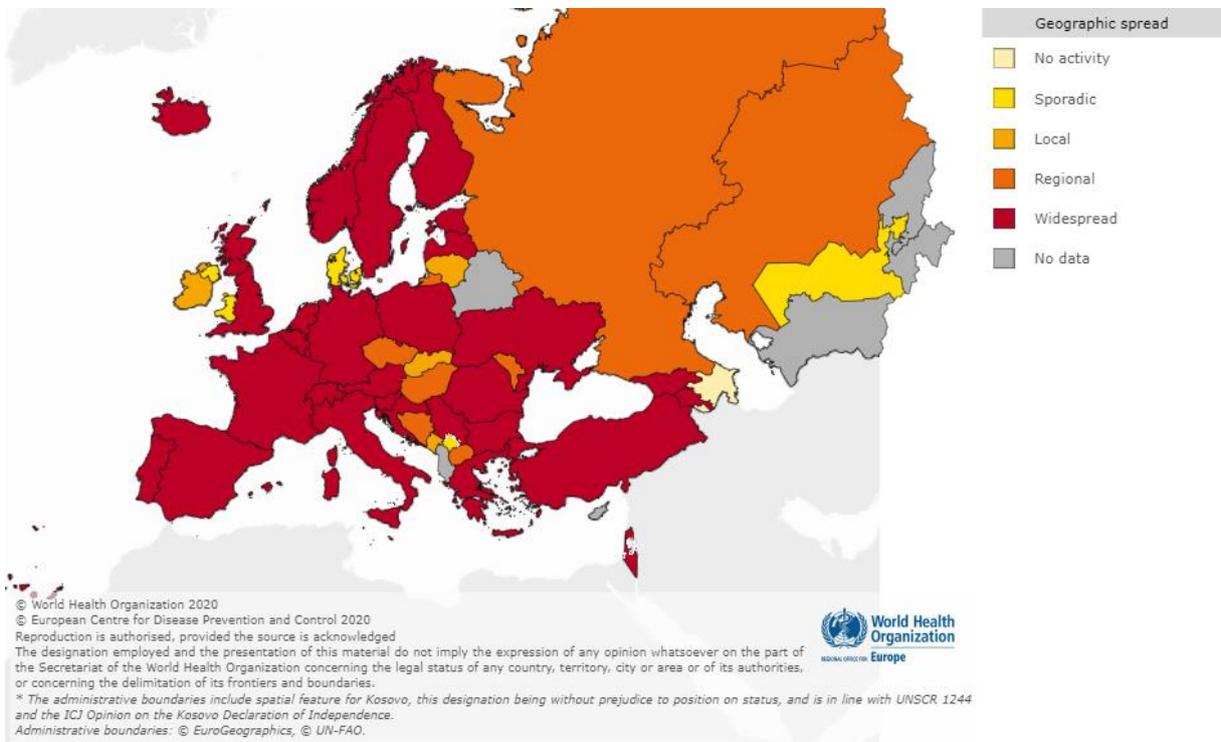
Of 48 Member States and areas that reported on the intensity indicator, 11 reported activity at baseline levels (across the Region), 21 reported low (across the Region), 12 reported medium (across the Region), 3 reported high (Bulgaria, Luxemburg, Turkey) and 1 reported very high (Slovenia) intensity for week 04/2020 (Fig. 1).

Of 48 Member States and areas that reported on geographic spread, 1 reported no activity (Azerbaijan), 5 reported sporadic spread (across the Region), 4 reported local spread (Ireland, Lithuania, Montenegro, Slovakia), 8 reported regional spread (in eastern, southern and western areas) and 30 reported widespread (across the Region) geographic activity (Fig. 2).

**Fig. 1. Intensity in the European Region, week 04/2020**



**Fig. 2. Geographic spread in the European Region, week 04/2020**



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

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

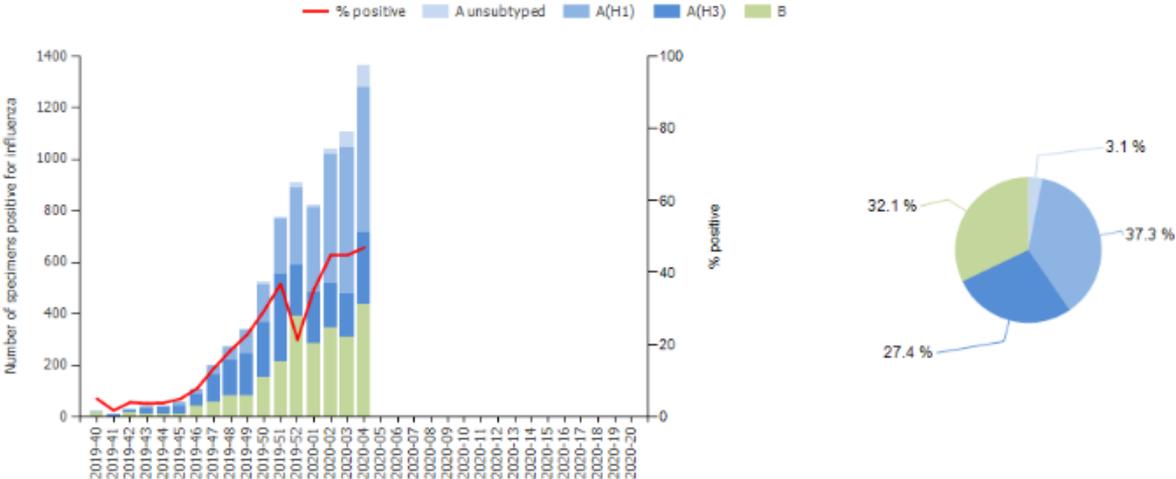
For week 04/2020, 1 364 (47%) of 2 910 sentinel specimens tested positive for an influenza virus; 68% were type A and 32% were type B (Fig. 3 and Table 1). Of 841 subtyped A viruses, 67% were A(H1N1)pdm09 and 33% were A(H3N2) (Fig. 3 and Table 1). Of 119 type B viruses ascribed to a lineage, 99% were 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 04/2020, 25 reported rates of influenza virus detections of 30% and above.

For the season to date, more influenza type A (n=5 193, 68%) than type B (n=2 457, 32%) viruses have been detected (Fig. 3 and Table 1). Of 4 955 subtyped A viruses, 2 856 (58%) were A(H1N1)pdm09 and 2 099 (42%) were A(H3N2). Of 730 influenza type B viruses ascribed to a lineage, 98% 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 2019-20<sup>a</sup>**



<sup>a</sup> Pie chart shows cumulative data for this period.

**Table 1. Influenza virus detections in sentinel-source specimens by type and subtype, week 04/2020 and cumulatively for the season**

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>930</b>	<b>68.2</b>	<b>5 193</b>	<b>67.9</b>
A(H1N1)pdm09	560	66.6	2 856	57.6
A(H3N2)	281	33.4	2 099	42.4
A not subtyped	89	-	238	-
<b>Influenza B</b>	<b>434</b>	<b>31.8</b>	<b>2 457</b>	<b>32.1</b>
B/Victoria lineage	118	99.2	719	98.5
B/Yamagata lineage	1	0.8	11	1.5
Unknown lineage	315	-	1727	-
<b>Total detections (total tested)</b>	<b>1 364 (2 910)</b>	<b>46.9</b>	<b>7 650 (28 686)</b>	<b>26.7</b>

<sup>a</sup>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 04/2020, Denmark, France and Switzerland reported between 10 and 15 ILI cases per 1 000 active participants. UK reported 21 ILI cases per 1 000 active participants. Ireland and Portugal reported between 30 and 35 ILI cases per 1 000 active participants. Italy reported 47 ILI cases per 1 000 active participants.

Spain reported 80 ILI cases per 1 000 active participants. Based on this system, activity is still low (below the first quartile of historical data for this week) in the UK, Denmark, Switzerland and France, medium (between the first and third quartile of historical data) in Portugal, Italy and Ireland, 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 04/2020 (n=107), influenza type A viruses (n=99, 93%) were detected more frequently than influenza type B viruses (n=8, 7%).

Since week 40/2019, more influenza type A (n=2 059, 94%) than type B (n=126, 6%) viruses were detected. Of 660 subtyped influenza A viruses, 58% were A(H3N2) and 42%

A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 665 cases with known age, 51% 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 04/2020 (n=183), influenza type A viruses (n=123, 67%) were detected more frequently than influenza type B viruses (n=17, 33%).

Since week 40/2019, more influenza type A (n=3 663, 94%) than type B (n=253, 6%) viruses were detected. Of 844 subtyped influenza A viruses, 65% were A(H3N2) and 35% A(H1N1)pdm09. No influenza B viruses were ascribed to a lineage. Of 3 915 cases with known age, 47% were 65 years and older and 28% were 15-64 years old.

## 2. SARI surveillance

For week 04/2020, 1 623 SARI cases were reported by 12 Member States or areas. In total, specimens from 417 SARI cases were tested for influenza viruses and 46% were positive for influenza virus: 68% (n=131) type A and 32% (n=62) type B.

Of 17 966 SARI cases reported since week 40/2019, 17 769 had a recorded age and, of these, 57% were 0–4 years old and 24% were 15–64 years old. Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=930) were mostly infected by type B viruses (n=530, 57%). Of the 366 influenza type A virus infected cases for which subtyping was performed, 78% (n=285) were A(H1N1)pdm09 and 22% (n=81) were A(H3N2) viruses. Of the 189 influenza type B viruses ascribed to a lineage, 96% (n=181) were B/Victoria and 4% (n=8) were B/Yamagata.

## **Mortality monitoring**

Pooled estimates of all-cause number of deaths from 21 countries or regions reporting to the [EuroMOMO](#) project indicated an increasing trend in mortality over recent weeks.

## **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 04/2020, 7 949 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; 74% were type A and 26% were type B. The majority of viruses from non-sentinel specimens were not subtyped or assigned to a lineage; 63% 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 (84%) than type B (16%) viruses have been detected. Relatively low numbers of the viruses have been ascribed to a subtype or lineage; 59% of all subtyped A viruses were A(H3N2) and 93% 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 04/2020 and cumulatively for the season**

Virus type and subtype	Current Week		Season 2019–2020	
	Number	% <sup>a</sup>	Number	% <sup>a</sup>
<b>Influenza A</b>	<b>5 887</b>	<b>74.1</b>	<b>53 633</b>	<b>83.5</b>
A(H1N1)pdm09	1 103	63.1	6 501	40.7
A(H3N2)	646	36.9	9 453	59.3
A not subtyped	4 138	-	37 679	-
<b>Influenza B</b>	<b>2 062</b>	<b>25.9</b>	<b>10 615</b>	<b>16.5</b>
B/Victoria lineage	69	100.0	653	93.3
B/Yamagata lineage	0	0.0	47	6.7
Unknown lineage	1 993	-	9915	-
<b>Total detections (total tested)</b>	<b>7 949 (30 867)</b>	<b>-</b>	<b>64 248 (347 926)</b>	<b>-</b>

<sup>a</sup> 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 1 035 viruses has been reported (Table 3):

- 781 (75%) type A: 487 A(H3N2) and 294 A(H1N1)pdm09;
- 254 (25%) type B: 233 B/Victoria and 21 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 2019–2020 influenza season to date, with 51% subclade 3C.2a. and 49% clade 3C.3a. 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 40/2019–04/2020**

Phylogenetic group	Number of viruses
A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018	264
A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019	8
A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018	21
A(H1)pdm09 attributed to recognised group in the guidance but not listed here	1
A(H3) clade 3C.2a1b+T135K-B representative A/Hong Kong/2675/2019	50
A(H3) clade 3C.3a representative A/Kansas/14/2017 <sup>a</sup>	251
A(H3) clade 3C.2a1b+T135K-A representative A/La Rioja/2202/2018	26
A(H3) clade 3C.2a1b+T131K representative A/South Australia/34/2019	160
B(Vic)-lineage clade 1A (del162-163) representative B/Colorado/06/2017 <sup>a</sup>	4
B(Vic)-lineage clade 1A(del162-164 subgroup) representative B/Hong Kong/269/2017	1
B(Vic)-lineage clade 1A (del162-164) representative B/Washington/02/2019	228
B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>b</sup>	21

<sup>a</sup> Vaccine component for 2019–2020 northern hemisphere.

<sup>b</sup> 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 were 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 2019–20 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( $\Delta$ 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\_ $\Delta$ 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 2020/21 northern hemisphere influenza season will be held in Geneva, Switzerland 24–27 February 2020.

### **Antiviral susceptibility testing**

Since the beginning of the season, 463 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 201 A(H1N1)pdm09, 196 A(H3N2) and 66 type B viruses. All showed normal inhibition (NI) by both oseltamivir and 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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