

## Summary

### Week 15/2020 (6 – 12 April 2020)

- The novel coronavirus disease 2019 (COVID-19) pandemic in the Region is affecting healthcare presentations and testing capacities in Member States, which has negative impact on influenza epidemiologic and virologic data, and seasonal patterns; therefore the data we present must be interpreted with caution.
- For the Region overall, influenza activity is declining: high or medium influenza intensity were reported by only 2 Member States and the majority reported baseline levels of intensity. No Member States or areas reported widespread influenza activity.
- The percentage of specimens from patients who presented with ILI or ARI to sentinel primary healthcare sites that tested positive for an influenza virus was 4% in week 15/2020, the third consecutive week with a positivity rate below 5%.
- Both influenza virus types A and B were co-circulating in sentinel source specimens: of 14 viruses detected, 3 were influenza type A and 11 were influenza type B.
- Pooled estimates of all-cause mortality show a marked increase in excess mortality within participating countries, related to the COVID-19 pandemic. This excess mortality is driven by a very substantial excess mortality in some countries, primarily seen in the age group 65 years and older, but also in the age group 15-64 years.

### 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 has been adversely affected by Member State responses to the COVID-19 pandemic. In the previous influenza season, the influenza positivity rate 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 the impact on healthcare systems, to assist forward planning in Member States.

## Other news

The World Health Organization categorized COVID-19 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 week 15/2020, 4 (22%) of the 18 Member States and areas that reported on ILI registered activity above their baseline levels: 1 in the northern area (Ireland), 1 in the southern area (Malta) and 2 in the western area (Belgium and Luxembourg) of the Region.

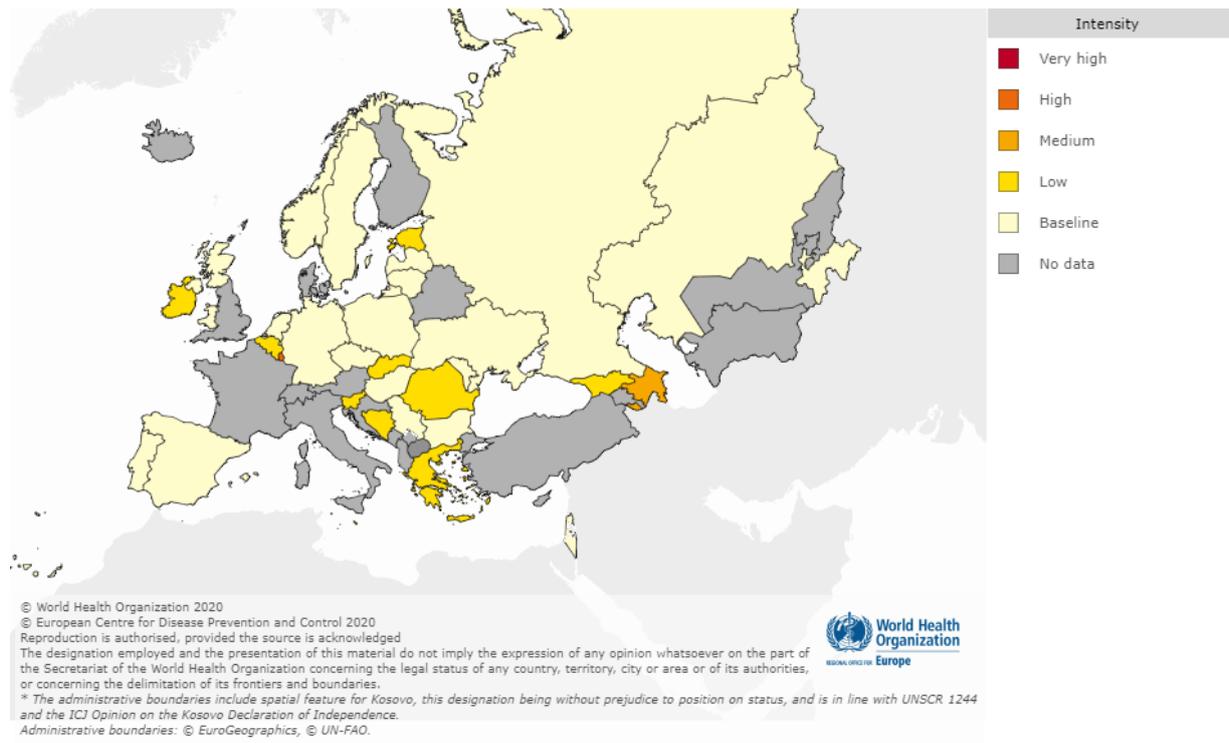
Of 13 Member States and areas that reported on ARI, only 1 (Luxembourg) registered activity above their baseline levels.

### Influenza activity

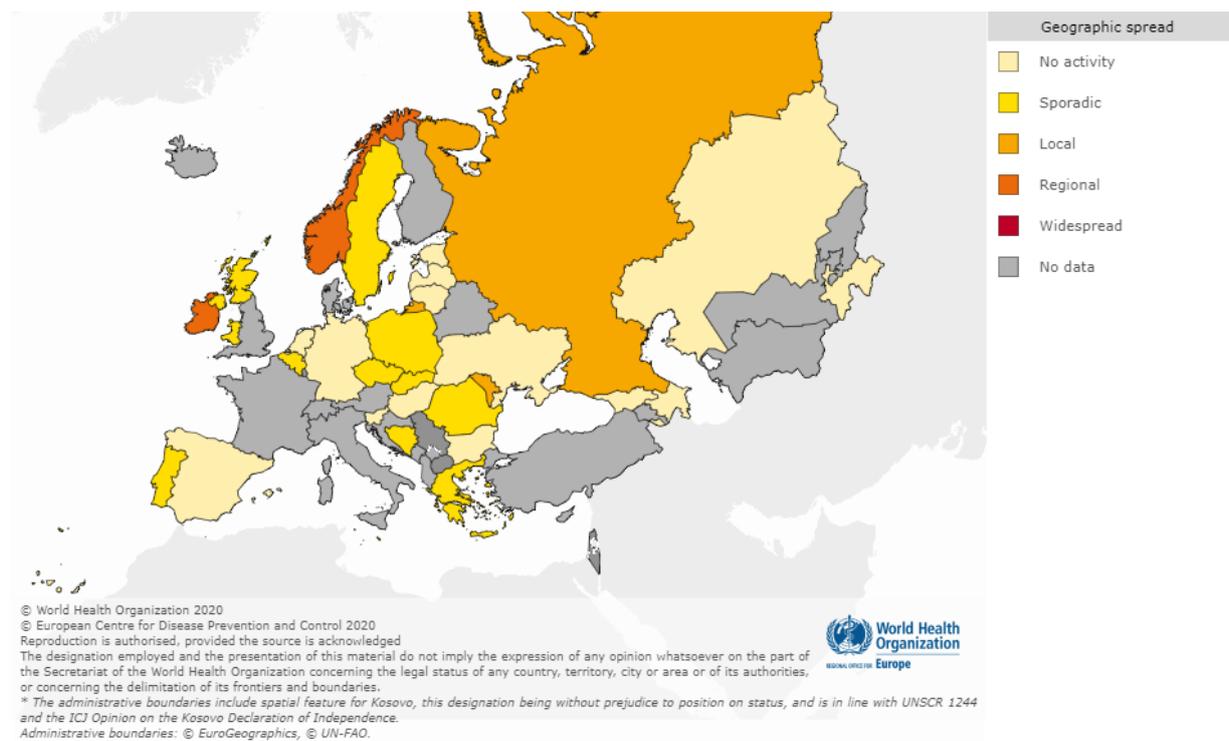
Of 34 Member States and areas that reported on the intensity indicator, 22 reported activity at baseline levels, 10 reported low, 1 reported medium (Azerbaijan), and 1 reported high (Luxembourg) intensity for week 15/2020 (Fig. 1).

Of 31 Member States and areas that reported on geographic spread, 14 reported no activity, 13 reported sporadic spread, 2 reported local spread and 2 reported regional spread for week 15/2020 (Fig. 2).

**Fig. 1. Intensity in the European Region, week 15/2020**



**Fig. 2. Geographic spread in the European Region, week 15/2020**



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

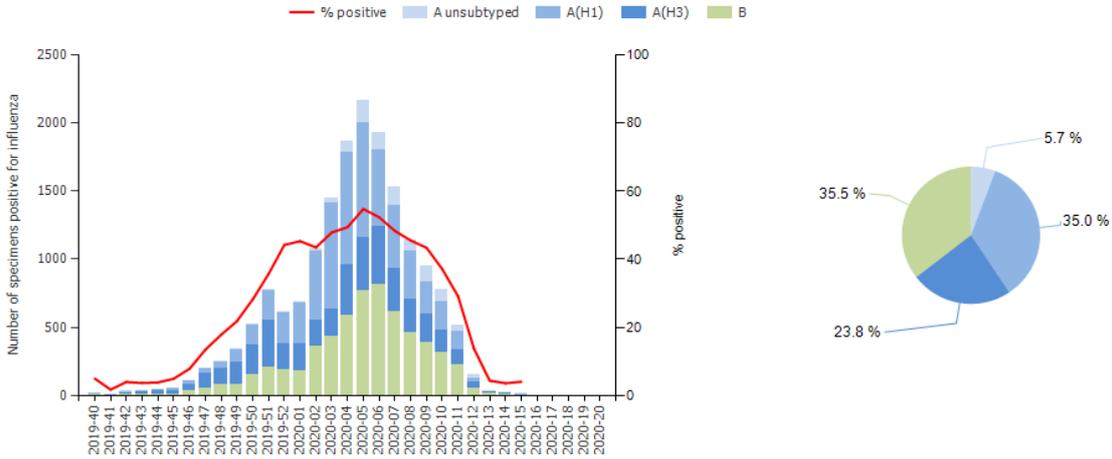
### Viruses detected in sentinel-source specimens (ILI and ARI)

For week 15/2020, 14 (4%) of 342 sentinel specimens from 14 Member States or areas across the Region tested positive for an influenza virus. Among these detections, 3 were type A and 11 were type B (Fig. 3 and Table 1). The subtyped A virus was A(H1N1)pdm09 (Fig. 3 and Table 1). No influenza type B viruses were ascribed to a lineage (Table 1).

For the season to date, more influenza type A (n=11 171, 65%) than type B (n=6 138, 35%) viruses have been detected (Fig. 3 and Table 1). Of 10 178 subtyped A viruses, 59% were A(H1N1)pdm09 and 41% were A(H3N2). Of 2 395 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<sup>a</sup>**



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<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 15/2020 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>3</b>        | <b>21.4</b>    | <b>11 171</b>          | <b>64.5</b>    |
| A(H1N1)pdm09                           | 1               | 100            | 6 050                  | 59.4           |
| A(H3N2)                                | 0               | 0              | 4 128                  | 40.6           |
| A not subtyped                         | 2               | -              | 993                    | -              |
| <b>Influenza B</b>                     | <b>11</b>       | <b>78.6</b>    | <b>6 138</b>           | <b>35.5</b>    |
| B/Victoria lineage                     | 0               | 100            | 2 374                  | 99.1           |
| B/Yamagata lineage                     | 0               | 0              | 21                     | 0.9            |
| Unknown lineage                        | 11              | -              | 3 743                  | -              |
| <b>Total detections (total tested)</b> | <b>14 (342)</b> | <b>4.1</b>     | <b>17 309 (49 299)</b> | <b>35.1</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](#) data were not reported for week 15/2020.

## 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 15/2020, 7 laboratory-confirmed influenza cases in intensive care units (ICUs) were reported by 2 Member States. Among these, 6 were infected with influenza type A viruses and 1 with an influenza type B virus.

Since week 40/2019, more influenza type A (n=3 590, 90%) than type B (n=389, 10%) viruses were detected. Of 1 249 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; France; and Spain. Of 2 443 cases with known age, 48% were 15-64 years old and 33% were 65 years and older.

### 1.2) Hospitalized laboratory-confirmed influenza cases – other wards

No laboratory-confirmed influenza cases in wards other than ICUs were reported for week 15/2020.

Since week 40/2019, more influenza type A (n=6 052, 84%) than type B (n=1 138, 16%) viruses were detected. Of 1 699 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 by Ireland and Spain. Of 7 143 cases with known age, 42% were 65 years and older and 31% were 15-64 years old.

## 2. SARI surveillance

For week 15/2020, 426 SARI cases were reported by 9 Member States or areas. Of 72 specimens tested for influenza viruses, 10% were positive. Among these cases, 6 were infected with influenza type A viruses and 1 with an influenza type B virus.

Of the SARI cases tested for influenza viruses since week 40/2019, those testing positive (n=2 914) were mostly infected by type A viruses (56%). Of the 1 374 influenza type A virus infected cases for which subtyping was performed, 61% were A(H1N1)pdm09 and 39% were A(H3N2) viruses. Of the 682 influenza type B viruses ascribed to a lineage, 99% were B/Victoria and 1% were B/Yamagata.

Of 36 092 SARI cases reported since week 40/2019, 35 772 had a recorded age and, of these, 50% were 0–4 years old and 28% were 15–64 years old.

## **Mortality monitoring**

Pooled estimates of all-cause mortality show a marked increase in excess mortality within participating countries, which coincides with the COVID-19 pandemic. This overall excess mortality is driven by a very substantial excess mortality in some countries, primarily seen in the age group of 65 years and older, but also in the age group 15-64 years.

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 15/2020, 262 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. Of 148 subtyped A viruses, 76% were A(H1N1)pdm09 and 24% were A(H3N2). No influenza type B viruses were ascribed to a lineage (Table 2).

For the season to date, more influenza type A (n=107 477, 74%) than type B (n=37 058, 26%) viruses have been detected but relatively low numbers have been ascribed to a subtype or lineage. Of 36 494 subtyped A viruses, 55% were A(H1N1)pdm09 and 45% were

A(H3N2). Of 2 083 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 15/2020 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>179</b>          | <b>68.3</b>    | <b>107 477</b>           | <b>74.4</b>    |
| A(H1N1)pdm09                           | 113                 | 76.4           | 20 060                   | 55.0           |
| A(H3N2)                                | 35                  | 23.6           | 16 434                   | 45.0           |
| A not subtyped                         | 31                  | -              | 70 983                   | -              |
| <b>Influenza B</b>                     | <b>83</b>           | <b>31.7</b>    | <b>37 058</b>            | <b>25.6</b>    |
| B/Victoria lineage                     | 0                   | -              | 2 017                    | 96.8           |
| B/Yamagata lineage                     | 0                   | -              | 66                       | 3.2            |
| Unknown lineage                        | 83                  | -              | 34 975                   | -              |
| <b>Total detections (total tested)</b> | <b>262 (17 062)</b> | <b>-</b>       | <b>144 535 (737 922)</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 2 642 viruses has been reported (Table 3):

- 1 981 (75%) type A: 1 019 A(H3N2) and 962 A(H1N1)pdm09;
- 661 (25%) type B: 633 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 54% clade 3C.3a and 46% 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 40/2019–15/2020**

| Phylogenetic group  | Number of viruses |
|---|-------------------|
| A(H1)pdm09 group 6B.1A5A representative A/Norway/3433/2018                            | 884               |
| A(H1)pdm09 group 6B.1A7 representative A/Slovenia/1489/2019                           | 19                |
| A(H1)pdm09 group 6B.1A5B representative A/Switzerland/3330/2018                       | 41                |
| A(H1)pdm09 group 6B.1A1 representative A/Brisbane/02/2018 <sup>a</sup>                | 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 <sup>a</sup>                        | 549               |
| 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                    | 324               |
| 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 <sup>a</sup>   | 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 <sup>b</sup> | 569               |
| B(Vic) attributed to recognised group in the guidance but not listed here             | 40                |
| B(Yam)-lineage clade representative B/Phuket/3073/2013 <sup>c</sup>                   | 26                |
| B(Yam) attributed to recognised group in the guidance but not listed here             | 2                 |

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

<sup>b</sup> Vaccine component for 2020-2021 northern hemisphere.

<sup>c</sup> Vaccine component of quadrivalent vaccines for use in 2019–2020 and 2020-2021 northern hemisphere seasons.

ECDC published a [report](#) in April 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 February 2020 characterization report, 3 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 1 076 virus specimens had been received, with collection dates after 31 August. A summary of viruses from EU/EEA countries characterized in March is given below. Previously published [influenza virus characterization reports](#) are also available on the ECDC website.

### **A(H1N1)pdm09 viruses**

Of 86 A(H1N1)pdm09 test viruses from EU/EEA countries characterised antigenically since the last report (for January and February, published in March 2020) 78 (91%) 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 219 test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 191 6B.1A5A, 20 6B.1A5B, 1 6B.1A6 and 7 6B.1A7.

## **A(H3N2) viruses**

55 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. Based on sequences available in GISAID from viruses detected since 1 February, viruses of clade 3C.3a and subgroup 3C.2a1b+T131k dominated in Europe. In total, 295 viruses have been characterised genetically at the WIC: 142 clade 3C.3a, 106 3C.2a1b+T131K, 35 3C.2a1b+T135K-A and 12 3C.2a1b+T135K-B.

## **B/Victoria viruses**

The great majority of the 62 B/Victoria-lineage viruses characterised in this reporting period gave antigenic profiles characteristic of subgroup 1A( $\Delta$ 3)B viruses represented by B/Washington/02/2019, the vaccine virus for the 2020-21 northern hemisphere season. Viruses detected in EU/EEA countries during February and March 2020, based on sequences available in GISAID, have all fallen in the 1A( $\Delta$ 3)B subgroup. In total, 172 viruses have been characterised genetically at the WIC: 159 subgroup 1A( $\Delta$ 3)B and 13 1A( $\Delta$ 2).

## **B/Yamagata viruses**

The single 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 6 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( $\Delta$ 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 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( $\Delta$ 3)B); 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( $\Delta$ 3)B); 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, 1 634 influenza viruses have been tested for susceptibility to neuraminidase inhibitors: 713 A(H1N1)pdm09, 586 A(H3N2) and 335 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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