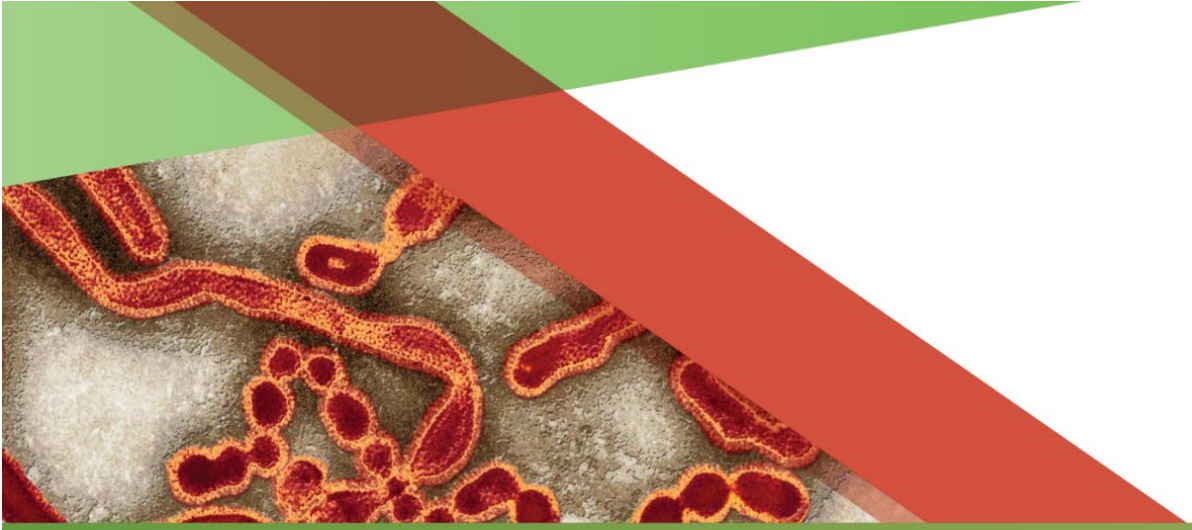

SURVEILLANCE REPORT

# Influenza virus characterisation

## Summary Europe, September 2020


## Summary

This is the 10th and final report for the 2019–2020 influenza season. As of week 39/2020, 164 917 influenza detections across the WHO European Region had been reported; 73% type A viruses, with A(H1N1)pdm09 prevailing over A(H3N2), and 27% type B viruses, with 4 480 (98%) of 4 569 ascribed to a lineage being B/Victoria.

Since the July 2020 characterisation report[1], two shipments of influenza-positive specimens from European Union/European Economic Area (EU/EEA) countries have been received at the London WHO Collaborating Centre, the Francis Crick Worldwide Influenza Centre (WIC). In total (since week 40/2019), 1 719 virus specimens, with collection dates after 31 August 2019, have been received.

Of the 33 A(H1N1)pdm09 viruses from EU/EEA countries characterised antigenically since the July report, 23 were well recognised by antisera raised against the 2019–20 vaccine virus, A/Brisbane/02/2018. The 10 viruses that showed poor reactivity generally carried amino acid substitutions (notably N156K) in the HA1 150-loop region. The 498 EU/EEA test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 455 6B.1A5A, 30 6B.1A5B, 1 6B.1A6 and 12 6B.1A7.

The majority (7) of the 10 A(H3N2) viruses from EU/EEA countries characterised antigenically since the July report were clade 3C.3a and were well recognised by antiserum raised against egg-propagated A/Kansas/14/2017, the current vaccine virus. Globally, approximately equal proportions of viruses in clade 3C.3a and subclade 3C.2a1b subgroups have been detected, but for viruses detected since 1 February 2020, subclade 3c.2a1b subgroup viruses have prevailed in many countries worldwide while those of clade 3C.3a and subgroup 3C.2a1b+T131K have dominated in Europe. In total, 512 viruses from EU/EEA countries have been characterised genetically at the WIC: 288 clade 3C.3a, 139 3C.2a1b+T131K, 64 3C.2a1b+T135K-A and 21 3C.2a1b+T135K-B.

Thirty-two B/Victoria-lineage viruses from EU/EEA countries were antigenically characterised since the July report. All but one were subclade 1A(Δ3)B and four of these viruses were not recognised well by antiserum raised against the vaccine virus for the 2020–2021 northern hemisphere influenza season, B/Washington/02/2019. Poor recognition was associated with HA1 amino acid substitutions of either N126K (n = 3) or N150K (n = 1). In total, 333 EU/EEA viruses have been characterised genetically at the WIC: 316 subclade 1A(Δ3)B and 17 subclade 1A(Δ2).


[1] European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, July 2020. Stockholm: ECDC; 2020. Available at: https://www.ecdc.europa.eu/sites/default/files/documents/influenza-virus-characterisation-july-2020.pdf


This report was prepared by Rod Daniels, Burcu Ermetal, Aine Rattigan and John McCauley (Crick Worldwide Influenza Centre) for the European Centre for Disease Prevention and Control under an ECDC framework contract.



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A single B/Yamagata-lineage virus from Norway, with a collection date in February 2020, was antigenically characterised in August. All nine EU/EEA viruses characterised genetically at the WIC since week 40/2019, 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.

Table 1 shows a summary of influenza virus detections in the WHO European Region reported to The European Surveillance System (TESSy) database for the whole of the 2019–2020 season (weeks 40/2019–39/2020), with a total of 164 917 detections over the period. Of the type B viruses ascribed to a lineage (n = 4 569) B/Victoria-lineage viruses (n = 4 480) have predominated over B/Yamagata-lineage viruses (n = 89) by a large margin, while for type A viruses subtyped (n = 47 203) A(H1N1)pdm09 viruses (56.0%) have predominated over A(H3N2) viruses (44.0%). Overall, in excess of 133 000 more samples have been tested in 2019-20 than in 2018-19 but there have been 41 030 (19.9%) less influenza detections reported than in 2018–19. This is probably due to two factors: (i) the increasing number of countries that either stopped influenza surveillance or stopped reporting (or reported sporadically) to TESSy from week 5/2020 due to responses to COVID–19, which WHO declared a pandemic on 11 March 2020 (week 11/2020) and (ii) significant numbers of samples taken from patients fulfilling Influenza Like Illness (ILI) and/or Acute Respiratory Infection (ARI) criteria being infected with other agents, possibly SARS-CoV-2 the virus responsible for the COVID-19 pandemic. With this caveat, the ratio of type A to type B detections is dramatically reduced compared with the 2018–19 season (86:1 to 2.7:1), and while proportions of influenza A subtypes are similar, B/Victoria-lineage viruses have predominated among the type B viruses compared to near equivalence with B/Yamagata-lineage viruses in the 2018–19 season.

**Table 1. Influenza virus detections in the WHO European Region from the start of reporting for the 2019–20 season (weeks 40/2019–39/2020)[a]**

| | Cumulative number of detections | | | Totals* | | Totals for 2018-19 season* | | |
|---|---|---|---|---|---|---|---|---|
| Virus type/subtype/lineage | Sentinel sources | Non-sentinel sources | Totals | % | Ratios | Number | % | Ratios |
| **Influenza A** | **11303** | **108968** | **120271** | **72.9** | **2.7:1** | **203564** | **98.8** | **86:1** |
| A(H1N1)pdm09 | 6126 | 20305 | 26431 | 56.0 | | 44179 | 57.2 | |
| A(H3N2) | 4175 | 16597 | 20772 | 44.0 | 0.79:1 | 33117 | 42.8 | 0.7:1 |
| A not subtyped | 1002 | 72066 | 73068 | | | 126271 | | |
| **Influenza B** | **6326** | 38320 | **44646** | **27.1** | | **2380** | **1.2** | |
| Victoria lineage | 2450 | 2030 | 4480 | 98.1 | | 79 | 47.9 | |
| Yamagata lineage | 23 | 66 | 89 | 1.9 | 0.02:1 | 86 | 52.1 | 1.1:1 |
| Lineage not ascribed | 3853 | 36224 | 40077 | | | 2215 | | |
| **Total detections (total tested)** | **17629 (53287)** | **147288 (>929614)** | **164917 (>982901)** | | | **205947 (>849439)** | | |

**[a] Numbers taken from Flu News Europe week 20/2020 and weeks 35-39/2020 reports**

*** Percentages are shown for total detections (types A & B [in bold type], and for viruses ascribed to influenza A subtype and influenza B lineage). Ratios are given for type A:B [in bold type], A(H3N2):A(H1N1)pdm09 and Yamagata:Victoria lineages.**

Since week 40/2019, 66 shipments of specimens (virus isolates and/or clinical specimens) have been received at the Crick Worldwide Influenza Centre (WIC), from 28 EU/EEA countries, two of which were received since the July report (one each from Hungary and Spain). The packages contained 1 719 virus-related samples with collection dates after 31 August 2019 and were made up of 1 227 type A viruses, with 598 and 619 subtyped as A(H1N1)pdm09 and A(H3N2), respectively, and 492 type B viruses, with 388 and 18 ascribed to B/Victoria and B/Yamagata lineages, respectively (Tables 2a/b). Genetic and antigenic characterisation data generated at the WIC for viruses with collection dates after 31 August 2019 and until 31 January 2020 contributed to the WIC virus characterisation report (the deadline for the report was 21 February 2020) that was presented at WHO's influenza vaccine composition meeting (VCM) in February 2020. At this meeting, recommendations were made for the northern hemisphere 2020–21 season. Recommendations for the now completed 2019–20 northern hemisphere, the ongoing 2020 southern hemisphere and the upcoming 2020–21 northern hemisphere seasons have been published [1, 2, 3].

During the lockdown imposed by the UK government due to the COVID-19 pandemic, WIC has been operating with reduced staff numbers. Consequently, only gene sequencing was performed to assess the emergence of any new genetic groups during March to May. Virus isolation and propagation for phenotypic analyses was reinstated in June following the relaxation of lockdown restrictions in the UK. Therefore, this report is based mainly on phylogenetic analyses of complete HA gene sequences submitted to the EpiFlu™ database of the Global Initiative on Sharing Avian Influenza Data (GISAID) during the months of August and September (inclusive of sequences generated at the WIC), with those from EU/EEA countries highlighted, together with antigenic and antiviral susceptibility data generated by the WIC.

WIC would like to thank those WHO-recognised national influenza centres (NICs) that responded to messages requesting sharing of influenza-positive samples with recent collection dates (after 31 January 2020). Virus characterisation data from the shared samples was used to inform the recent WHO VCM (held online from 16–24 September) to recommend viruses for inclusion in vaccines for the southern hemisphere 2021 influenza season. Results of these deliberations have been posted (https://www.who.int/influenza/vaccines/virus/recommendations/2021_south/en) and a full report published [4].

## Table 2a. Summary of clinical samples and virus isolates*, with collection dates from 1 September 2019, contained in packages received from EU/EEA Member States since week 40/2019: September to December 2019

| MONTH / Country | TOTAL RECEIVED Seasonal viruses | A | | H1N1pdm09 | | H3N2 | | | B | | B Victoria lineage | | B Yamagata lineage | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Number received | Number propagated[1] | Number received | Number propagated[1] | Number received | Number propagated[2] | | Number received | Number propagated[1] | Number received | Number propagated[1] | Number received | Number propagated[1] |
| **2019** | | | | | | | | | | | | | | |
| **SEPTEMBER** | | | | | | | | | | | | | | |
| Czechia | 1 | | | | | 1 | 1 | | | | | | | |
| Finland | 1 | | | | | 1 | 1 | | | | | | | |
| France | 6 | | | 1 | 1 | 3 | 2 | 1 | | | 2 | 2 | | |
| Norway | 7 | | | 1 | 1 | 4 | 1 | 3 | | | 2 | 2 | | |
| Romania | 1 | | | | | 1 | 0 | 1 | | | | | | |
| Sweden | 3 | | | 2 | 2 | 1 | 1 | | | | | | | |
| United Kingdom | 4 | | | 2 | 2 | 2 | 0 | | | | | | | |
| **OCTOBER** | | | | | | | | | | | | | | |
| Denmark | 3 | | | 2 | 2 | 1 | 1 | | | | | | | |
| Finland | 2 | | | 1 | 1 | 1 | 1 | | | | | | | |
| France | 5 | | | 3 | 3 | | | | | | 2 | 2 | | |
| Germany | 6 | | | 2 | 2 | 4 | 2 | 1 | | | | | | |
| Greece | 1 | | | | | 1 | 1 | | | | | | | |
| Iceland | 9 | | | | | 8 | 4 | 4 | | | 1 | 1 | | |
| Ireland | 11 | | | 1 | 1 | 9 | 1 | 1 | | | | | 1 | 0 |
| Latvia | 3 | | | 1 | 1 | | | | | | 2 | 2 | | |
| Lithuania | 1 | | | | | | | | | | 1 | 1 | | |
| Netherlands | 3 | | | 1 | 1 | 2 | 0 | 2 | | | | | | |
| Norway | 28 | | | 5 | 4 | 19 | 3 | 15 | | | 3 | 2 | 1 | 0 |
| Poland | 1 | 1 | 0 | | | | | | | | | | | |
| Portugal | 7 | | | 2 | 2 | 2 | 1 | | 3 | 0 | | | | |
| Spain | 6 | | | 3 | 3 | 1 | 0 | | | | 2 | 2 | | |
| Sweden | 3 | | | | | 2 | 2 | | | | 1 | 1 | | |
| United Kingdom | 29 | | | 5 | 2 | 21 | 11 | 6 | | | 3 | 0 | | |
| **NOVEMBER** | | | | | | | | | | | | | | |
| Austria | 4 | | | 2 | 2 | 1 | 0 | 1 | | | | | 1 | 1 |
| Belgium | 3 | | | 2 | 1 | 1 | 1 | | | | | | | |
| Croatia | 3 | | | 2 | 2 | | | | | | 1 | 1 | | |
| Czechia | 2 | | | | | 2 | 2 | | | | | | | |
| Denmark | 16 | | | 7 | 7 | 6 | 3 | 3 | | | 3 | 3 | | |
| Finland | 1 | | | 1 | 1 | | | | | | | | | |
| France | 16 | | | 8 | 8 | 4 | 3 | 1 | | | 2 | 2 | 2 | 2 |
| Germany | 8 | | | 5 | 5 | 3 | 0 | 3 | | | | | | |
| Greece | 1 | | | | | 1 | 0 | | | | | | | |
| Iceland | 3 | | | | | 2 | 0 | 2 | | | 1 | 1 | | |
| Ireland | 49 | | | 18 | 12 | 22 | 7 | 5 | 2 | 0 | 7 | 6 | | |
| Italy | 7 | | | 2 | 2 | 3 | 1 | 2 | | | 2 | 2 | | |
| Latvia | 10 | | | 2 | 2 | 3 | 3 | | | | 5 | 5 | | |
| Lithuania | 2 | | | 2 | 2 | | | | | | | | | |
| Netherlands | 3 | | | 2 | 2 | 1 | 1 | | | | | | | |
| Norway | 22 | | | 6 | 5 | 9 | 3 | 4 | | | 4 | 4 | 3 | 1 |
| Poland | 1 | 1 | 0 | | | | | | | | | | | |
| Portugal | 102 | 1 | 0 | 13 | 11 | 3 | 0 | | 26 | 0 | 59 | 20 | | |
| Slovenia | 1 | | | 1 | 1 | | | | | | | | | |
| Spain | 20 | | | 9 | 2 | 5 | 2 | | 5 | 0 | 1 | 1 | | |
| Sweden | 8 | | | 5 | 5 | 1 | 0 | 1 | | | 2 | 2 | | |
| United Kingdom | 62 | | | 9 | 4 | 52 | 14 | 2 | | | 1 | 0 | | |
| **DECEMBER** | | | | | | | | | | | | | | |
| Austria | 18 | | | 5 | 5 | 9 | 7 | 2 | | | 4 | 4 | | |
| Belgium | 21 | | | 5 | 3 | 11 | 8 | | | | 5 | 3 | | |
| Bulgaria | 2 | | | 1 | 0 | 1 | 1 | | | | | | | |
| Croatia | 6 | | | 4 | 1 | 1 | 0 | 1 | | | 1 | 0 | | |
| Cyprus | 2 | | | | | 1 | 0 | | 1 | 0 | | | | |
| Czechia | 2 | | | | | 2 | 1 | 1 | | | | | | |
| Denmark | 1 | | | 1 | 0 | | | | | | | | | |
| Estonia | 1 | | | 1 | 1 | | | | | | | | | |
| Finland | 1 | | | 1 | 1 | | | | | | | | | |
| France | 39 | | | 14 | 14 | 9 | 5 | 4 | | | 16 | 15 | | |
| Germany | 13 | | | 6 | 6 | 6 | 4 | 2 | | | 1 | 1 | | |
| Greece | 6 | | | 4 | 0 | 2 | 0 | | | | | | | |
| Iceland | 5 | | | 2 | 2 | 2 | 0 | 1 | | | 1 | 1 | | |
| Italy | 12 | | | 2 | 2 | 6 | 2 | 4 | | | 4 | 4 | | |
| Latvia | 1 | | | | | 1 | 0 | 1 | | | | | | |
| Lithuania | 20 | 1 | 0 | 6 | 6 | 12 | 9 | 3 | | | 1 | 1 | | |
| Netherlands | 10 | | | 1 | 1 | 9 | 7 | 2 | | | | | | |
| Norway | 15 | | | 8 | 5 | 1 | 0 | | | | 1 | 0 | 5 | 2 |
| Poland | 5 | 2 | 0 | 1 | 0 | 2 | 1 | 0 | | | | | | |
| Portugal | 20 | | | 2 | 2 | 3 | 2 | 1 | | | 15 | 15 | | |
| Romania | 8 | | | | | | | | | | 8 | 8 | | |
| Slovenia | 9 | | | 5 | 5 | 3 | 3 | | | | 1 | 1 | | |
| Spain | 51 | | | 26 | 12 | 6 | 0 | 6 | 5 | 0 | 14 | 12 | | |
| United Kingdom | 18 | | | 4 | 3 | 11 | 9 | | | | 3 | 1 | | |

* Note: Where clinical sample and a virus isolate from the same patient were received, this is counted as one in the Total Received and following columns.

1. Propagated to sufficient titre to perform HI assay (the totalled number does not include any from batches that are in process)
2. Propagated to sufficient titre to perform HI assay in the presence of 20nM oseltamivir (the totalled number does not include any from batches that are in process)

Numbers in red indicate viruses recovered but with insufficient HA titre to permit HI assay

Includes clinical samples in lysis-mix from Northern Ireland and Scotland and RNA extracts from Greece and Portugal for which genetic characterisation only can be performed. In addition, some clinical samples from Bulgaria, Estonia, Greece, Ireland, Poland and Portugal were not cultured as either sequencing from the clinical sample failed or sequences generated were identical to those from other clinical samples.

Cells with an orange background indicate samples that were sequenced only (due either to restricted characterisation conducted during COVID-19 lockdown or the samples having collection dates before 2020-01-31 [but received in February or later] characterisation of which would not be used to inform the WHO VCM in September 2020).

As of 2020-10-06

## Table 2b. Summary of clinical samples and virus isolates*, with collection dates from 1 September 2019, contained in packages received from EU/EEA Member States since week 40/2019: January to April 2020

| MONTH / Country | TOTAL RECEIVED Seasonal viruses | A | | H1N1pdm09 | | H3N2 | | | B | | B Victoria lineage | | B Yamagata lineage | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Number received | Number propagated[1] | Number received | Number propagated[1] | Number received | Number propagated[2] | | Number received | Number propagated[1] | Number received | Number propagated[1] | Number received | Number propagated[1] |
| **2020** | | | | | | | | | | | | | | |
| **JANUARY** | | | | | | | | | | | | | | |
| Austria | 2 | 1 | 0 | | | | | | 1 | 0 | | | | |
| Belgium | 52 | | | 29 | 0 | 18 | 0 | | | | 5 | 0 | | |
| Bulgaria | 28 | | | 14 | 3 | 12 | 4 | | | | 2 | 0 | | |
| Cyprus | 27 | | | 4 | 0 | 22 | 1 | | | | 1 | 0 | | |
| Czechia | 5 | | | 2 | 2 | 3 | 3 | | | | | | | |
| Denmark | 10 | | | 4 | 0 | 5 | 0 | 0 | | | 1 | 1 | | |
| Estonia | 17 | | | 8 | 5 | 4 | 2 | 1 | | | 5 | 5 | | |
| Finland | 4 | | | 2 | 2 | 2 | 2 | | | | | | | |
| France | 8 | | | | | 4 | 4 | | | | 4 | 4 | | |
| Germany | 24 | | | 6 | 6 | 9 | 8 | 1 | | | 8 | 8 | 1 | 1 |
| Greece | 45 | | | 22 | 8 | 20 | 5 | 3 | 2 | 0 | 1 | 1 | | |
| Hungary | 1 | | | | | 1 | 1 | | | | | | | |
| Italy | 3 | | | 1 | 1 | 1 | 1 | | | | 1 | 1 | | |
| Lithuania | 2 | | | | | 2 | 1 | 1 | | | | | | |
| Norway | 22 | | | 1 | 0 | 14 | 2 | | | | 6 | 0 | 1 | 0 |
| Poland | 9 | 1 | 0 | 4 | 1 | 2 | 1 | 0 | 2 | 0 | | | | |
| Portugal | 7 | | | 1 | 0 | 1 | 0 | 0 | | | 5 | 0 | | |
| Romania | 15 | | | 4 | 3 | 7 | 1 | 0 | 1 | 0 | 3 | 3 | | |
| Slovakia | 1 | | | | | 1 | 0 | 0 | | | | | | |
| Slovenia | 7 | | | 4 | 2 | 2 | 1 | 0 | | | 1 | 1 | | |
| Spain | 40 | | | 35 | 13 | | | | 1 | 0 | 4 | 4 | | |
| United Kingdom | 38 | | | 18 | 0 | 11 | 0 | | 3 | 0 | 6 | 0 | | |
| **FEBRUARY** | | | | | | | | | | | | | | |
| Austria | 2 | 1 | 0 | | | | | | 1 | 0 | | | | |
| Belgium | 50 | | | 28 | 28 | 17 | 17 | | | | 5 | 5 | | |
| Bulgaria | 26 | | | 7 | 7 | 14 | 10 | 1 | | | 5 | 3 | | |
| Cyprus | 38 | | | 6 | 5 | 21 | 12 | | | | 11 | in process | | |
| Denmark | 9 | | | | | 6 | 4 | 2 | | | 3 | 3 | | |
| Estonia | 12 | | | 5 | 4 | 2 | 2 | | | | 5 | 4 | | |
| Finland | 8 | | | 5 | 5 | 1 | 1 | | | | 2 | 2 | | |
| France | 32 | | | 14 | 14 | 7 | 7 | | | | 9 | 9 | 2 | 1 |
| Germany | 25 | | | 13 | 13 | 7 | 5 | 2 | | | 5 | 5 | | |
| Hungary | 9 | | | 3 | 3 | 4 | 3 | 1 | | | 2 | 2 | | |
| Iceland | 10 | | | 4 | 4 | 2 | 2 | | | | 4 | 4 | | |
| Ireland | 12 | | | 1 | 0 | | | | 3 | 0 | 8 | 6 | | |
| Italy | 25 | | | 7 | 7 | 12 | 12 | | | | 6 | 6 | | |
| Norway | 13 | | | 4 | 2 | 5 | 2 | 0 | | | 3 | 0 | 1 | 1 |
| Poland | 22 | | | 8 | 2 | 11 | 4 | 0 | 1 | 0 | 2 | 2 | | |
| Portugal | 32 | | | 29 | 19 | 2 | 1 | 0 | | | 1 | 1 | | |
| Slovakia | 8 | | | 2 | 2 | 4 | 4 | 0 | | | 2 | 2 | | |
| Slovenia | 15 | | | 3 | 3 | 9 | 6 | 3 | | | 3 | 3 | | |
| Spain | 35 | 1 | 0 | 23 | 17 | 3 | 2 | 1 | | | 8 | 7 | | |
| Sweden | 18 | | | 8 | 8 | 5 | 3 | 2 | | | 5 | 5 | | |
| United Kingdom | 14 | | | 1 | 1 | 2 | 2 | | 7 | 0 | 4 | 4 | | |
| **MARCH** | | | | | | | | | | | | | | |
| Belgium | 6 | | | 4 | 4 | | | | | | 2 | 2 | | |
| Bulgaria | 9 | | | 2 | 2 | 1 | 1 | | | | 6 | 6 | | |
| Cyprus | 9 | | | 1 | 1 | 1 | 1 | | | | 7 | in process | | |
| Estonia | 5 | | | 1 | 1 | 3 | 2 | 0 | | | 1 | 1 | | |
| Finland | 4 | | | | | 2 | 2 | | | | 2 | 2 | | |
| France | 19 | | | 8 | 8 | 4 | 3 | 1 | | | 7 | 7 | | |
| Germany | 5 | | | 2 | 2 | 2 | 2 | | | | 1 | 1 | | |
| Hungary | 1 | | | | | 1 | 1 | | | | | | | |
| Iceland | 13 | | | 4 | 4 | 6 | 6 | | | | 3 | 3 | | |
| Ireland | 14 | | | 3 | 3 | 1 | 1 | | 4 | 0 | 6 | 4 | | |
| Norway | 37 | | | 5 | 4 | 18 | 15 | 0 | | | 14 | 9 | | |
| Poland | 4 | | | 4 | 2 | | | | | | | | | |
| Portugal | 4 | | | 3 | 2 | 1 | 1 | | | | | | | |
| Slovenia | 8 | | | | | 2 | 2 | | | | 6 | 6 | | |
| Spain | 7 | | | 4 | 3 | 1 | 1 | | 1 | 0 | 1 | 1 | | |
| United Kingdom | 19 | | | | | | | | 17 | 0 | 2 | 1 | | |
| **APRIL** | | | | | | | | | | | | | | |
| Iceland | 1 | | | | | | | | | | 1 | 1 | | |
| Norway | 1 | | | | | | | | | | 1 | 0 | | |
| **28 Countries** | 1719 | 10 | 0 | 598 | 397 | 619 | 306 | 105 | 86 | 0 | 388 | 273 | 18 | 9 |
| | | 0.58% | | 34.8% | | 36.0% | | | 5.0% | | 22.6% | | 1.0% | |
| | | 71.4% | | | | | | | 28.6% | | | | | |

*** Note: Where clinical sample and a virus isolate from the same patient were received, this is counted as one in the Total Received and following columns.**

1. Propagated to sufficient titre to perform HI assay (the totalled number does not include any from batches that are in process)
2. Propagated to sufficient titre to perform HI assay in the presence of 20nM oseltamivir (the totalled number does not include any from batches that are in process)

Numbers in red indicate viruses recovered but with insufficient HA titre to permit HI assay

Includes clinical samples in lysis-mix from Northern Ireland and Scotland and RNA extracts from Greece and Portugal for which genetic characterisation only can be performed. In addition, some clinical samples from Bulgaria, Estonia, Greece, Ireland, Poland and Portugal were not cultured as either sequencing from the clinical sample failed or sequences generated were identical to those from other clinical samples.

Cells with an orange background indicate samples that were sequenced only (due either to restricted characterisation conducted during COVID-19 lockdown or the samples having collection dates before 2020-01-31 [but received in February or later] characterisation of which would not be used to inform the WHO VCM in September 2020).

As of 2020-10-06

# Influenza A(H1N1)pdm09 virus analyses

The first A(H1N1)pdm09 HA phylogeny is repeated from the July 2020 report and was generated based on sequences deposited in GISAID for recently circulating viruses, with collection dates from 1 February 2020, submitted to GISAID in July 2020 (Figure 1a). The second is based on viruses with collection dates from 1 March 2020, but with sequences deposited in GISAID during August and September 2020; a total of 163 sequences had been deposited (Figure 1b). All recently circulating viruses fell into clade 6B.1A, defined by the amino acid substitutions **S74R**, **S84N**, **S162N** (introducing a potential N-linked glycosylation site), **S164T** (which alters the glycosylation motif at residues 162 to 164), **I216T** and **I295V** in **HA1**. Within clade 6B.1A, clusters of viruses (genetic groups) encoding a range of **HA** amino acid substitutions have emerged, with most recently circulating viruses carrying the substitution **S183P** in **HA1**, although this is not retained in all genetic groups. Figures 1a and 1b are annotated with **HA1 S183P** substitution groups assigned for the February 2019 WHO Vaccine Consultation Meeting (6B.1A/183P-1 to -7, abbreviated to 6B.1A1 to 6B.1A7); the recommended vaccine viruses for the northern hemisphere 2019–2020 and 2020–2021 influenza seasons are shown in red [1, 3], together with those recently recommended for the southern hemisphere 2021 influenza season, A/Victoria/5270/2019 (egg-propagated) and A/Wisconsin/588/2019 (cell-propagated) [4]. The seven subclades are defined by the following HA amino acid substitutions:

1. Subclade **6B.1A1** viruses, represented by the current vaccine virus **A/Brisbane/02/2018**, carry an HA gene mutation encoding **HA1 S183P** amino acid substitution.
2. Subclade **6B.1A2** viruses, represented by **A/Denmark/2728/2019**, carry HA gene mutations encoding **HA1 S183P** and **L233I** with **HA2 V193A** amino acid substitutions – a subgroup within this subclade has emerged with additional **HA1** amino acid substitutions of **N129D, K130N, P137S, N156K** and **K211R** (e.g. **A/Hong Kong/110/2019**).
3. Subclade **6B.1A3** viruses, represented by **A/Norway/3737/2018**, carry HA gene mutations encoding **HA1 T120A** and **S183P** amino acid substitutions.
4. Subclade **6B.1A4** represented by **A/Hungary/20/2018** carries HA gene mutations encoding **HA1 N129D, A144E** and **S183P** amino acid substitutions.
5. Subclade **6B.1A5** viruses carry HA gene mutations encoding **HA1 S183P** and **N260D** amino acid substitutions and splits into two subgroups designated **6B.1A5A** represented by **A/Norway/3433/2018** with additional **HA1** amino acid substitutions of **N129D** and **T185A**, and **6B.1A5B** represented by **A/Switzerland/3330/2017** with additional amino acid substitutions of **HA1 E235D** and **HA2 V193A**.
6. Subclade **6B.1A6** viruses, represented by **A/Ireland/84630/2018**, carry HA gene mutations encoding **HA1 T120A** and **S183P** amino acid substitutions, like subclade **6B.1A3** viruses, but fall within a separate phylogenetic branch which is closer to subclade **6B.1A5** viruses.
7. Subclade **6B.1A7** viruses, represented by **A/Slovenia/1489/2019**, carry HA gene mutations encoding **HA1 K302T** and **HA2 I77M, N169S** and **E179D** amino acid substitutions sometimes with additional **HA1** substitutions of **E68D, S121N** and **L161I** (e.g. **A/Moscow/193/2019**). Note: a subgroup of this subclade has emerged with **P183S** (reversion)**, T185I, I240V** and **I286L** substitutions in **HA1** (e.g. **A/Estonia/120012/2019**).

The vast majority of recently circulating viruses have fallen in subgroup **6B.1A5A**, which contains a number of virus clusters, three of which have been detected in significant numbers defined by: (i) **HA1 D187A** and **Q189E** substitutions, (ii) **HA2 V193A** substitution and (iii) **HA1 N156K** substitution with the great majority in this cluster also having **HA1 K130N**, **L161V**, **V250A** and **HA2 E179D** substitutions. Relatively few viruses in subgroup **6B.1A5B** (with **HA1 K130N**, **K160M**, **T216K**, **E235D**, **H296N** and **HA2 V193A** substitutions) have also been detected and even fewer in subclade **6B.1A7**. Of the subgroup **6B.1A5A** viruses, there has been an approximately equal split between two of the genetic clusters defined above, (i) and (iii). This pattern was seen for viruses detected in the US and EU/EEA countries (Figures 1a and 1b) and is also true for countries in the southern hemisphere (Figure 1b). The two phylogenies have very similar profiles and are largely made up of sequences from viruses detected in February and March.

The great majority of viruses in the various subgroups characterised to date, with the exception of those in genetic cluster (iii), have remained antigenically similar to the northern hemisphere 2019–2020 vaccine virus, A/Brisbane/02/2018, as assessed with post-infection ferret antisera and shown in earlier characterisation reports; this is also the case for the viruses tested with antisera raised against A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like viruses (with **HA1 D187A** and **Q189E** amino acid substitutions) that were recommended for use in the northern hemisphere 2020–2021 influenza season [3].

Tables 3-1 to 3-3 show the results of haemagglutination inhibition (HI) assays of A(H1N1)pdm09 viruses performed, with a panel of post-infection ferret antisera, since the July 2020 report. The 33 test viruses are sorted by date of collection and genetic group/subgroup; 32 were subgroup **6B.1A5A** viruses and one was subgroup **6B.1A5B**.

The panel of post-infection ferret antisera was raised against 11 individual viruses, with titres against the homologous viruses indicated in red, three of which were egg-propagated viruses representing recently recommended vaccine viruses. Antisera raised against nine of the viruses showed similar HI reactivity recognising 17 to 23 (52-72%) test viruses at titres within twofold of respective homologous titres and 23 (70-72%) at titres within fourfold (Tables 3-1 to 3-3). The pattern of reactivity with antiserum raised against A/Bayern/69/2009, a virus with HA1 G155E amino acid substitution, was also similar with 18/23 (78%) test viruses being recognised at titres within twofold of the homologous titre. Antiserum raised against A/Denmark/3280/2019, representative of a cluster of viruses carrying HA1 amino acid

substitutions N156K, K130N, L161I and V250A, recognised only 10 (30%) test viruses at titres within fourfold (nine within twofold) of the homologous titre; all viruses recognised well by this antiserum carried the N156K substitution with additional HA1 amino acid substitutions (Tables 3-1 to 3-3). The viruses with HA1 N156K substitution showed poor reactivity with antisera raised against all three vaccine viruses. This observation, together with viruses containing the HAI N156K amino acid substitution spreading globally and representing an increasing proportion of A(H1N1)pdm09 viruses detected in recent months, resulted in recommendation of viruses in the **HA1 K130N**, **N156K**, **L161V**, **V250A** and **HA2 E179D** cluster for inclusion in vaccines for the 2021 southern hemisphere influenza season: A/Victoria/5270/2019 (egg-propagated) and A/Wisconsin/588/2019 (cell-propagated) [4].

**Figure 1a. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes (GISAID, July 2020)**

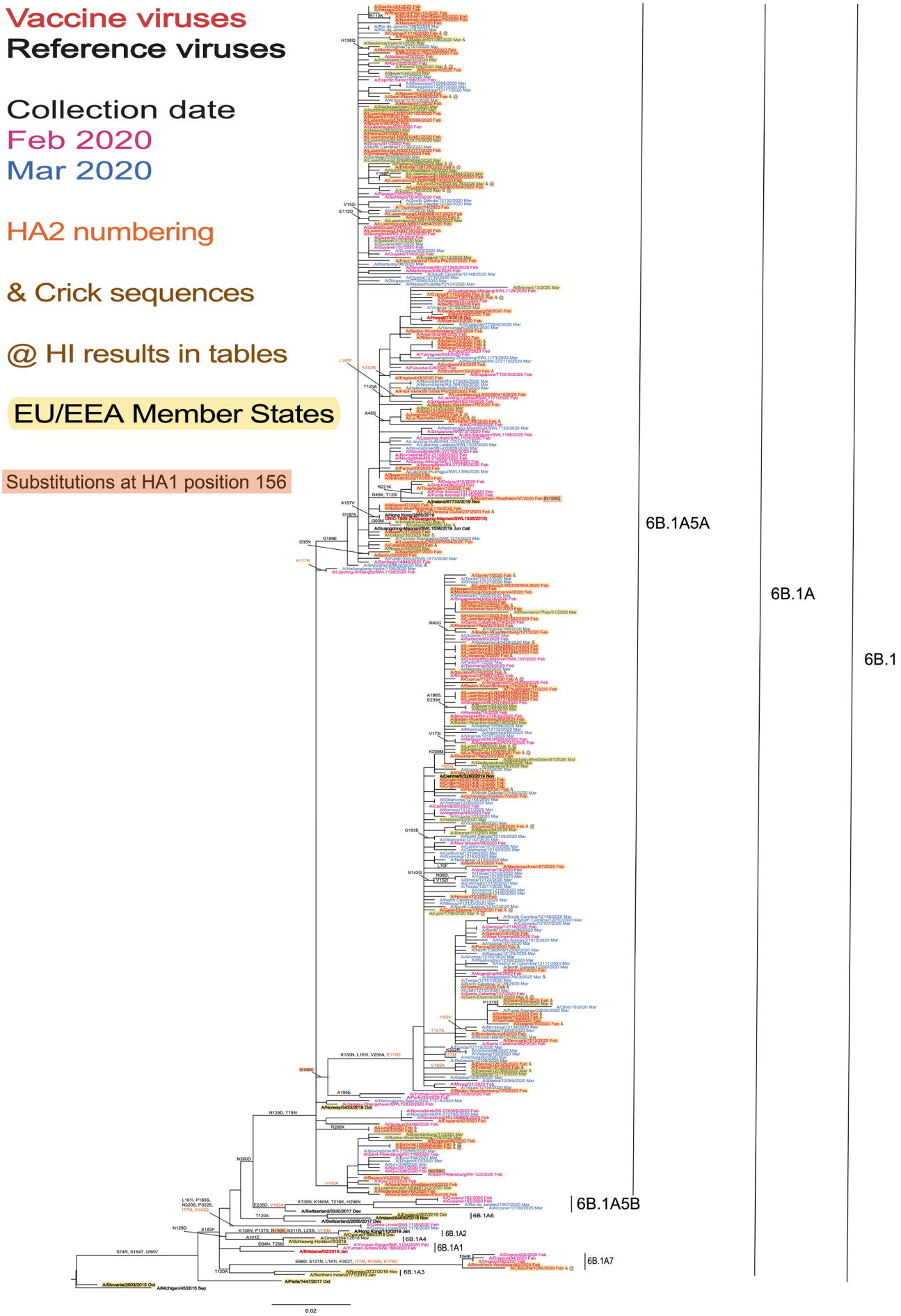
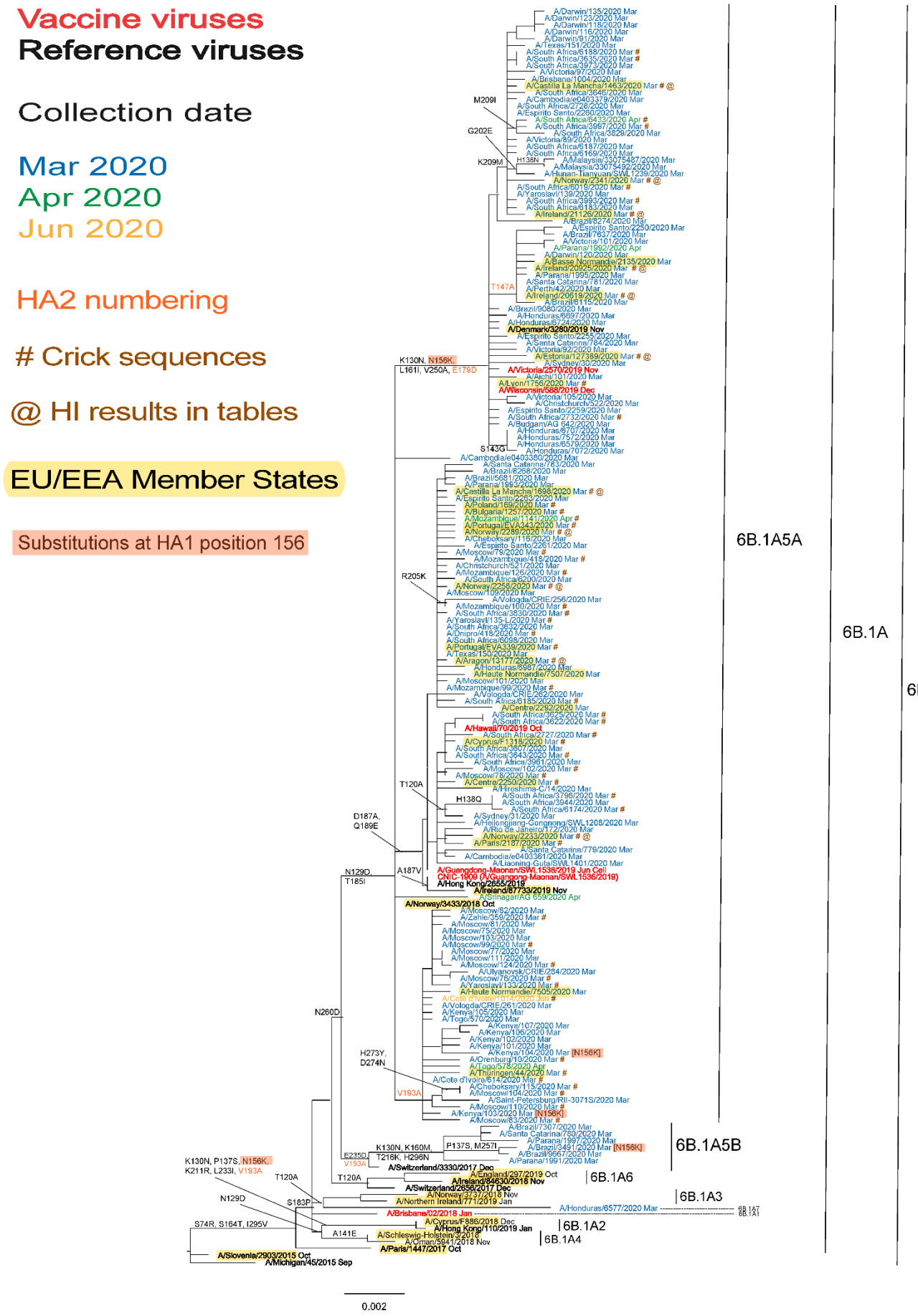


**Figure 1b. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes (GISAID, September 2020)**



## Table 3-1. Antigenic analysis of A(H1N1)pdm09 viruses by HI

| Viruses | Other information | Passage history / Ferret number / Genetic group | Collection date | Passage history | Haemagglutination inhibition titre: Post-infection ferret antisera | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | A/Mich 45/15 Egg F31/16[-1] 6B.1 | A/Paris 1447/17 MDCK F03/18[-2] 6B.1A | A/Bris 02/18 Egg F09/19[-1] 6B.1A1 | A/Norway 3433/18 MDCK F04/19[-1] 6B.1A5A | A/Denmark 3280/19 MDCK F08/20[-1] 6B.1A5A | A/Ire 87733/19 Egg St Jude's F18/20 6B.1A5A | A/G-M SWL1536/19 Egg F12/20[-1] 6B.1A5A | A/G-M SWL1536/19 MDCK F09/20[-1] 6B.1A5A | A/Swit 3330/17 Egg F23/18[-1] 6B.1A5B | A/Ire 84630/18 MDCK F08/19[-1] 6B.1A6 |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | | | |
| A/Michigan/45/2015 | | 6B.1 | 2015-09-07 | E3/E3 | 1280 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 1280 | 1280 | 1280 |
| A/Paris/1447/2017 | | 6B.1A | 2017-10-20 | MDCK1/MDCK3 | 1280 | 2560 | 1280 | 2560 | < | 1280 | 1280 | 2560 | 640 | 2560 | 2560 |
| A/Brisbane/02/2018 | | 6B.1A1 | 2018-01-04 | E3/E1 | 1280 | 2560 | 1280 | 1280 | 40 | 640 | 1280 | 1280 | 640 | 1280 | 1280 |
| A/Norway/3433/2018 | | 6B.1A5A | 2018-10-30 | MDCK3 | 320 | 640 | 640 | 1280 | < | 640 | 640 | 640 | 320 | 640 | 640 |
| A/Denmark/3280/2019 | N156K | 6B.1A5A | 2019-11-10 | MDCK4/MDCK3 | 80 | 80 | 80 | 160 | 1280 | 80 | 80 | 80 | 80 | 40 | 40 |
| A/Ireland/87733/2019 | | 6B.1A5A | 2019-11-03 | E4 | 1280 | 1280 | 1280 | 2560 | 40 | 1280 | 1280 | 1280 | 1280 | 1280 | 1280 |
| A/Guangdong-Maonan/SWL1536/2019 | D187A, Q189E | 6B.1A5A | 2019-06-17 | E3/E1 | 640 | 1280 | 1280 | 2560 | < | 640 | 1280 | 1280 | 640 | 1280 | 1280 |
| A/Guangdong-Maonan/SWL1536/2019 | D187A, Q189E | 6B.1A5A | 2019-06-17 | C2/MDCK1 | 640 | 640 | 640 | 2560 | < | 640 | 1280 | 1280 | 640 | 640 | 640 |
| A/Switzerland/3330/2017 | clone 35 | 6B.1A5B | 2017-12-20 | E6/E2 | 640 | 640 | 1280 | 1280 | < | 320 | 640 | 640 | 640 | 640 | 640 |
| A/Ireland/84630/2018 | | 6B.1A6 | 2018-11-28 | MDCK1/MDCK3 | 640 | 1280 | 640 | 2560 | 40 | 640 | 1280 | 1280 | 1280 | 1280 | 1280 |
| *TEST VIRUSES* | | | | | | | | | | | | | | | |
| A/Ireland/20619/2020 | N156K, K130N, L161I, V250A | 6B.1A5A | 2020-03-03 | MDCK3 | 80 | 80 | 40 | 160 | 640 | 40 | 80 | 40 | 40 | < | 40 |
| A/Ireland/21126/2020 | N156K, T120I, K130N, L161I, K209M, V250A | 6B.1A5A | 2020-03-04 | MDCK3 | 40 | < | 40 | 80 | 640 | 40 | 40 | 40 | < | < | < |
| A/Ireland/20925/2020 | N156K, K130N, L161I, V250A | 6B.1A5A | 2020-03-04 | MDCK1 | 40 | 80 | 40 | 160 | 640 | < | 40 | 40 | 40 | < | < |
| | | | | | Vaccine NH 2018-19 SH 2019 | | Vaccine NH 2019-20 SH 2020 | | | | Vaccine NH 2020-21 | | | | |

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)
1 < = <40; 2 < = <80; ND =Not Done
Sequences in Phylogenetic tree (Fig.1b)

## Table 3-2. Antigenic analysis of A(H1N1)pdm09 viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Post-infection ferret antisera | | | | | | | | | | |
| | | | | A/Mich 45/15 Egg | A/Paris 1447/17 MDCK | A/Bris 02/18 Egg | A/Norway 3433/18 MDCK | A/Denmark 3280/19 MDCK | A/Ire 87733/19 Egg | A/G-M SWL1536/19 Egg | A/G-M SWL1536/19 MDCK | A/Swit 3330/17 Egg | A/Ire 84630/18 MDCK |
| Passage history | | | | | | | | | St Jude's | | | | |
| Ferret number | | | | F31/16[1] | F03/18[2] | F09/19[1] | F04/19[1] | F08/20[1] | F18/20 | F12/20[1] | F09/20[1] | F23/18[1] | F08/19[1] |
| Genetic group | | | | 6B.1 | 6B.1A | 6B.1A1 | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5B | 6B.1A6 |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | |
| A/Michigan/45/2015 | | 2015-09-07 | E3/E3 | 1280 | 1280 | 1280 | 2560 | 40 | 640 | 1280 | 1280 | 640 | 1280 |
| A/Paris/1447/2017 | | 2017-10-20 | MDCK1/MDCK3 | 640 | 1280 | 640 | 1280 | 40 | 320 | 640 | 640 | 320 | 1280 |
| A/Brisbane/02/2018 | | 2018-01-04 | E3/E2 | 1280 | 2560 | 1280 | 2560 | 40 | 640 | 1280 | 1280 | 1280 | 2560 |
| A/Norway/3433/2018 | | 2018-10-30 | MDCK3 | 320 | 640 | 320 | 640 | < | 160 | 640 | 320 | 160 | 640 |
| A/Denmark/3280/2019 | N156K | 2019-11-10 | MDCK4/MDCK2 | 80 | 80 | 80 | 160 | 640 | 40 | 80 | 80 | 40 | 40 |
| A/Ireland/87733/2019 | | 2019-11-03 | E4 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 640 | 320 | 640 |
| A/Guangdong-Maonan/SWL1536/2019 | D187A, Q189E | 2019-06-17 | E3/E1 | 640 | 1280 | 640 | 1280 | < | 320 | 1280 | 640 | 320 | 640 |
| A/Guangdong-Maonan/SWL1536/2019 | D187A, Q189E | 2019-06-17 | C2/MDCK1 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 320 | 1280 |
| A/Switzerland/3330/2017 | clone 35 | 2017-12-20 | E6/E2 | 640 | 1280 | 640 | 1280 | 40 | 320 | 640 | 640 | 640 | 640 |
| A/Ireland/84630/2018 | | 2018-11-28 | MDCK1/MDCK3 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 640 | 640 | 1280 |
| *TEST VIRUSES* | | | | | | | | | | | | | |
| A/Norway/941/2020 | | 2020-02-10 | MDCK1 | 320 | 320 | 320 | 640 | < | 320 | 640 | 640 | 160 | 640 |
| A/Norway/2258/2020 | | 2020-03-02 | MDCK1 | 640 | 640 | 1280 | 1280 | < | 640 | 1280 | 1280 | 640 | 1280 |
| A/Estonia/127389/2020 | N156K, K130N, L161I, V250A | 2020-03-11 | SIAT1/SIAT2 | 40 | 40 | 40 | 80 | 320 | 40 | < | < | < | ND |
| A/Norway/2233/2020 | | 2020-03-16 | MDCK1 | 640 | 320 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Norway/2289/2020 | | 2020-03-20 | MDCK1 | 320 | 320 | 320 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Norway/2341/2020 | N156K, E112K, K130N, L161I, K209M, V250A | 2020-03-21 | MDCK1 | < | < | < | 40 | 160 | < | < | < | < | < |
| A/Norway/729/2020 | | 2020-02-04 | MDCK2 | 640 | 640 | 640 | 1280 | 40 | 320 | 640 | 640 | 320 | 640 |
| | | | | Vaccine NH 2018-19 SH 2019 | | Vaccine NH 2019-20 SH 2020 | | | | Vaccine NH 2020-21 | | | |

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)
1 < = <40; 2 < = <80; ND =Not Done
Sequences in Phylogenetic tree (Fig.1b)

## Table 3-3. Antigenic analysis of A(H1N1)pdm09 viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Post-infection ferret antisera | | | | | | | | | | |
| | Passage history | | | A/Bayern 69/09 | A/Mich 45/15 | A/Paris 1447/17 | A/Bris 02/18 | A/Norway 3433/18 | A/Denmark 3280/19 | A/Ire 87733/19 | A/G-M SWL1536/19 | A/G-M SWL1536/19 | A/Swit 3330/17 | A/Ire 84630/18 |
| | | | | MDCK | Egg | MDCK | Egg | MDCK | MDCK | Egg | Egg | MDCK | Egg | MDCK |
| | Ferret number | | | F09/15$^{-1}$ | F31/16$^{-1}$ | F03/18$^{-2}$ | F09/19$^{-1}$ | F04/19$^{-1}$ | F08/20$^{-1}$ | St Jude's F18/20 | F12/20$^{-1}$ | F09/20$^{-1}$ | F23/18$^{-1}$ | F08/19$^{-1}$ |
| | Genetic group | | | | 6B.1 | 6B.1A | 6B.1A1 | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5A | 6B.1A5B | 6B.1A6 |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | | |
| A/Bayern/69/2009 | G155E | 2020-11-10 | MDCK5/MDCK2 | 160 | 80 | 160 | 80 | 160 | < | < | 40 | 40 | 40 | 40 |
| A/Michigan/45/2015 | 6B.1 | 2015-09-07 | E3/E3 | 320 | 640 | 1280 | 1280 | 1280 | 40 | 640 | 1280 | 640 | 640 | 1280 |
| A/Paris/1447/2017 | 6B.1A | 2017-10-20 | MDCK1/MDCK3 | 320 | 640 | 2560 | 1280 | 2560 | < | 640 | 1280 | 640 | 640 | 1280 |
| A/Brisbane/02/2018 | 6B.1A1 | 2018-01-04 | E3/E2 | 320 | 1280 | 2560 | 1280 | 2560 | 40 | 640 | 1280 | 1280 | 1280 | 1280 |
| A/Norway/3433/2018 | 6B.1A5A | 2018-10-30 | MDCK3 | 80 | 320 | 640 | 320 | 1280 | 40 | 160 | 640 | 320 | 320 | 640 |
| A/Denmark/3280/2019 | 6B.1A5A N156K | 2019-11-10 | MDCK4/MDCK4 | 40 | 40 | 80 | 40 | 80 | 320 | < | 80 | 40 | 40 | < |
| A/Ireland/87733/2019 | 6B.1A5A | 2019-11-03 | E4 | 320 | 640 | 1280 | 640 | 1280 | 40 | 640 | 1280 | 1280 | 320 | 1280 |
| A/Guangdong-Maonan/SWL1536/2019 | 6B.1A5A D187A, Q189E | 2019-06-17 | E3/E1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 1280 | 640 | 320 | 640 |
| A/Guangdong-Maonan/SWL1536/2019 | 6B.1A5A D187A, Q189E | 2019-06-17 | C2/MDCK1 | 320 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 640 | 1280 |
| A/Switzerland/3330/2017 | 6B.1A5B clone 35 | 2017-12-20 | E6/E2 | 320 | 640 | 1280 | 640 | 1280 | < | 320 | 1280 | 640 | 640 | 1280 |
| A/Ireland/84630/2018 | 6B.1A6 | 2018-11-28 | MDCK1/MDCK3 | 320 | 640 | 1280 | 1280 | 1280 | < | 320 | 1280 | 640 | 640 | 1280 |
| *TEST VIRUSES* | | | | | | | | | | | | | | |
| A/Hungary/71/2020 | 6B.1A5A | 2020-02-11 | MDCK1/MDCK1 | 160 | 320 | 1280 | 320 | 640 | < | 320 | 640 | 640 | 320 | 640 |
| A/Hungary/80/2020 | 6B.1A5A | 2020-02-13 | MDCK1/MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1089/2020 | 6B.1A5A | 2020-02-16 | MDCK1 | 320 | 1280 | 2560 | 1280 | 2560 | 40 | 640 | 1280 | 1280 | 640 | 1280 |
| A/Aragon/13165/2020 | 6B.1A5A | 2020-02-17 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 1280 | 320 | 640 |
| A/Melilla/995/2020 | 6B.1A5A | 2020-02-17 | MDCK1 | 320 | 640 | 1280 | 640 | 1280 | 40 | 640 | 640 | 1280 | 320 | 640 |
| A/Hungary/82/2020 | 6B.1A5A N156K, K130N, L161I, K209M, V250A | 2020-02-18 | MDCK1/SIAT1 | 40 | 40 | 80 | 40 | 80 | 320 | 40 | 40 | 40 | 40 | < |
| A/Pais Vasco/1081/2020 | 6B.1A5A | 2020-02-18 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 320 | 640 |
| A/Pais Vasco/1079/2020 | 6B.1A5A | 2020-02-18 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | 40 | 320 | 1280 | 1280 | 320 | 640 |
| A/Castilla La Mancha/1073/2020 | 6B.1A5A | 2020-02-18 | MDCK1 | 320 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 320 | 1280 |
| A/Castilla La Mancha/1169/2020 | 6B.1A5A | 2020-02-19 | MDCK2 | 160 | 320 | 640 | 320 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Navarra/1051/2020 | 6B.1A5A | 2020-02-20 | MDCK1 | 160 | 320 | 640 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1461/2020 | 6B.1A5A | 2020-02-21 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1464/2020 | 6B.1A5A | 2020-02-22 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1466/2020 | 6B.1A5A N156K, K130N, L161I, V250A | 2020-02-24 | MDCK1 | 40 | 40 | 80 | 40 | 80 | 320 | < | 40 | 40 | 40 | < |
| A/Castilla La Mancha/1465/2020 | 6B.1A5A | 2020-02-24 | MDCK1 | 320 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 320 | 1280 |
| A/Melilla/1083/2020 | 6B.1A5A | 2020-02-24 | MDCK1 | 320 | 640 | 1280 | 640 | 1280 | < | 640 | 1280 | 1280 | 320 | 1280 |
| A/Castilla La Mancha/1075/2020 | 6B.1A5A N156K, A48T, K130N, L161I, D187X, K209M, V250A, E283X | 2020-02-24 | MDCK1 | < | < | < | < | 40 | 160 | < | 40 | < | < | < |
| A/Melilla/1087/2020 | 6B.1A5A | 2020-02-25 | MDCK1 | 320 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1815/2020 | 6B.1A5A | 2020-02-27 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 1280 | 1280 | 320 | 640 |
| A/Castilla La Mancha/1411/2020 | 6B.1A5A N156K, K130N, L161I, V250A | 2020-02-29 | MDCK1 | < | < | < | < | 80 | 320 | < | < | < | < | < |
| A/Castilla La Mancha/1463/2020 | 6B.1A5A N156K, K130N, L161I, D187V, K209M, V250A | 2020-03-02 | MDCK1 | < | < | < | 40 | 40 | 320 | < | 40 | < | < | < |
| A/Aragon/13177/2020 | 6B.1A5A | 2020-03-03 | MDCK1 | 160 | 640 | 1280 | 640 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| A/Castilla La Mancha/1698/2020 | 6B.1A5A | 2020-03-04 | MDCK1 | 160 | 320 | 640 | 320 | 1280 | < | 320 | 640 | 640 | 320 | 640 |
| | | | | Vaccine NH 2018-19 SH 2019 | | Vaccine NH 2019-20 SH 2020 | | | | | Vaccine NH 2020-21 | | | |

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)

1 < = <40; 2 < = <80; ND =Not Done

Sequences in Phylogenetic tree (Fig.1b)

# Influenza A(H3N2) virus analyses

The first A(H3N2) HA phylogeny is repeated from the July 2020 report and was generated based on sequences deposited in GISAID for recently circulating viruses, with collection dates from 1 February 2020, submitted to GISAID in July 2020 (Figure 2a). The second is again based on viruses with collection dates from 1 February 2020, but with sequences deposited in GISAID during August and September 2020; a total of 152 sequences (Figure 2b).

Viruses in clade 3C.2a have been dominant since the 2014–15 influenza season, and subgroup 3C.2a1b viruses predominated over the course of the 2018–19 season, but the HA gene sequences of viruses in both clades 3C.2a and 3C.3a continue to diverge. Notably, clade 3C.3a viruses have evolved to carry **HA1** amino acid substitutions of **L3I, S91N**, **N144K** (loss of a N-linked glycosylation motif at residues 144-146), **F193S** and **K326R**, and **D160N** in **HA2**, compared with cell culture-propagated A/Stockholm/6/2014, and levels of detection since January 2019 had increased in a number of WHO European Region countries and North America. Greater variation has been observed among clade 3C.2a viruses, resulting in the designation of new subclades/subgroups. Amino acid substitutions that define these subclades/subgroups are:

- Subclade **3C.2a1**: Those in clade **3C.2a** plus **N171K** in **HA1** and **I77V** and **G155E** in **HA2**, most also carry **N121K** in **HA1**, e.g. **A/Singapore/INFIMH-16-0019/2016** (a former vaccine virus).
- Subgroup **3C.2a1a**: Those in subclade **3C.2a1** plus **T135K** in **HA1**, resulting in the loss of a potential glycosylation site, and **G150E** in **HA2**, e.g. **A/Greece/4/2017.**
- Subgroup **3C.2a1b**: Those in subclade **3C.2a1** plus **E62G, R142G** and **H311Q** in **HA1**, often with additional amino acid substitutions – notably **HA1 T131K** and **HA2 V200I**, the **3C.2a1b+T131K** cluster (e.g. **A/South Australia/34/2019**) or **HA1 T135K** (resulting in the loss of a potential glycosylation site) commonly with **T128A** (resulting in the loss of a potential glycosylation site), the **3C.2a1b+T135K-A** cluster (e.g. **A/La Rioja/2202/2018**) or a recently emerged, antigenically distinct group with **HA1 T135K, T128A, S137F, A138S** and **F193S**, the **3C.2a1b+T135K-B** cluster (e.g. **A/Hong Kong/2675/2019**).
- Clade **3C.3a**: represented by **A/Switzerland/9715293/2013** (see above), but recently a resurgence of clade **3C.3a** viruses, carrying additional substitutions of **S91N, N144K** (resulting in the loss of a potential glycosylation site)**, and F193S** in **HA1** and **D160N** in **HA2**, e.g. **A/England/538/2018** and **A/Kansas/14/2017**, the A(H3N2) vaccine virus for the 2019–20 influenza season.

The HA phylogeny generated for the July report, based on sequences recently deposited in GISAID, showed numbers of sequences to be approximately equally distributed between viruses in the **3C.2a1b** subgroup and clade **3C.2a** with sequences from viruses detected in EU/EEA countries being the majorities in clade **3C.3a** and clusters **3C.2a1b+T131K** and **3C.2a1b+T135K-A**, but with viruses having collection dates in February and March (Figure 2a). The significant geographic spread of viruses in the antigenically distinct **3C.2a1b+T135K-B** cluster, influenced the selection of an A/Hong Kong/2671/2019-like virus as the A(H3N2) component of vaccines for the 2020–2021 northern hemisphere and 2021 southern hemisphere influenza seasons [3, 4]. The geographic distribution of clade **3C.3a** viruses was more restricted with the great majority of recently detected viruses being reported from the European Region (Figure 2a). The updated phylogeny, for sequences deposited in August and September, again contains large numbers of sequences from viruses detected in EU/EEA and other European countries with collection dates in February and March, but with many sequences derived from viruses detected in non-European countries, notably Australia, Brazil, Cambodia, Honduras and Togo (Figure 2b). The great majority of sequences from viruses detected in non-European countries, including some with collection dates in April to September, fall in subgroup **3C.2a1b** and are approximately equally distributed among the three HA genetic clusters identified above. Overall, the two phylogenies are very similar with regards to distribution of virus clades/subclades/subgroups.

The locations of A/Kansas/14/2017 (**3C.3a**), the A(H3N2) virus recommended for inclusion in vaccines for the northern hemisphere 2019–20 influenza season [1], and A/South Australia/34/2019 (**3C.2a1b+T131K**), the A(H3N2) virus recommended for inclusion in vaccines for the southern hemisphere 2020 influenza season [2], are indicated in Figures 2a and 2b in red. The location of the A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) virus and its cell culture-equivalent A/Hong Kong/45/2019, recently recommended for egg- and cell culture-generated vaccines to be used in the 2020–2021 northern hemisphere [3] and 2021 southern hemisphere [4] seasons, are also indicated.

As described in many previous reports[2], influenza A(H3N2) viruses have continued to be difficult to characterise antigenically by HI assay due to variable agglutination of red blood cells (RBCs) from guinea pigs, turkeys and humans, often with the loss of ability to agglutinate any of these RBCs. As was highlighted first in the November 2014 report[3], this has been a significant problem for most viruses that fall in genetic clade **3C.2a**, though there has been some alleviation of this over the 2020-21 season.

Since the July 2020 characterisation report of the viruses recovered, based on positive neuraminidase activity, 10 retained sufficient HA activity to allow antigenic analysis by HI (Tables 4-1 to 4-2). Test viruses are sorted by date of

[2] For example, the September 2013 report: European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, September 2013. Stockholm: ECDC; 2013. Available at: https://ecdc.europa.eu/sites/portal/files/media/en/publications/Publications/influenza-virus-characterisation-sep-2013.pdf

[3] European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, November 2014. Stockholm: ECDC; 2014. Available at: https://www.ecdc.europa.eu/sites/default/files/media/en/publications/Publications/ERLI-Net%20report%20November%202014.pdf

collection and genetic group/subgroup where known at the time of writing this report; seven were clade **3C.3a** viruses, two were subgroup **3C.2a1b** viruses (one each in clusters **T131K** and **T135K-A**) and one has not been sequenced (but gave an HI reactivity profile like that of clade **3C.3a** viruses).

The panel of antisera were raised against seven individual clade **3C.2a** viruses and three clade **3C.3a** viruses (Tables 4-1 and 4-2). Those raised against tissue culture-propagated A/Hong Kong/5738/2014 (**3C.2a**), A/Denmark/3264/2019 (**3C.2a1b+T135K-A**) and A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) recognised nine (90%), six (60%) and two (20%) test viruses, respectively, at titres within fourfold of their homologous titres. Antisera raised against tissue culture-propagated A/Norway/3275/2018 (**3C.2a1b+T131K**) and A/La Rioja/2202/2018 (**3C.2a1b+T135K-A**), for which homologous titres were not available, recognised 1 (10%) and no test viruses respectively at titres of 160 or above. Antisera raised against a previous egg-propagated vaccine virus, A/Singapore/INFIMH-16-0019/2016 (**3C.2a1**), recognised nine (90%) test viruses at titres within fourfold of its homologous titre. The antiserum raised against egg-propagated A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**), the vaccine virus for the 2020-21 northern hemisphere [3] and 2021 southern hemisphere [4] influenza seasons, recognised no test viruses at titres within fourfold of its homologous titre.

Antisera raised against two cell culture-propagated clade **3C.3a** viruses, A/England/538/2018 and A/Kansas/14/2017, each recognised nine (90%) test viruses at titres within fourfold of homologous titres. Antiserum raised against the egg-propagated clade **3C.3a** vaccine virus, NYMC X-327 (A/Kansas/14/2017), had a high homologous titre and only three (30%) test viruses were recognised at titres within fourfold of the homologous titre; however, the absolute titres with many of the test viruses matched those seen with antisera raised against cell culture-propagated A/England/538/2018 and A/Kansas/14/2017 which yielded significantly lower homologous titres. The nine test viruses genetically characterised fell in the following clades/subclades: **3C.3a** (n = 7), **3C.2a1b+T131K** (n = 1) and **3C.2a1b+T135K-A** (n = 1).

Overall, the HI data presented here and in earlier recent reports show strong clade/subclade-specific recognition of test viruses by post-infection ferret antisera raised against cell culture-propagated reference viruses. For antisera raised against the three egg-propagated vaccine viruses and based on test virus recognition fourfold reduced compared to homologous titres: A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) had a homologous titre of 640 and showed poor recognition of test viruses (0%); NYMC X-327 (A/Kansas/14/2017, **3C.3a**) had a high homologous titre (640-1280) and showed significant clade-specificity in recognition of test viruses; and A/Singapore/INFIMH-16-0019/2016 (**3C.2a1**) had the lowest homologous titre (320) and showed the greatest cross-clade/subclade recognition with the majority of titres with test viruses being 80 (fourfold reduced compared to the homologous titre).

**Figure 2a. Phylogenetic comparison of influenza A(H3N2) HA genes (GISAID, July 2020)**

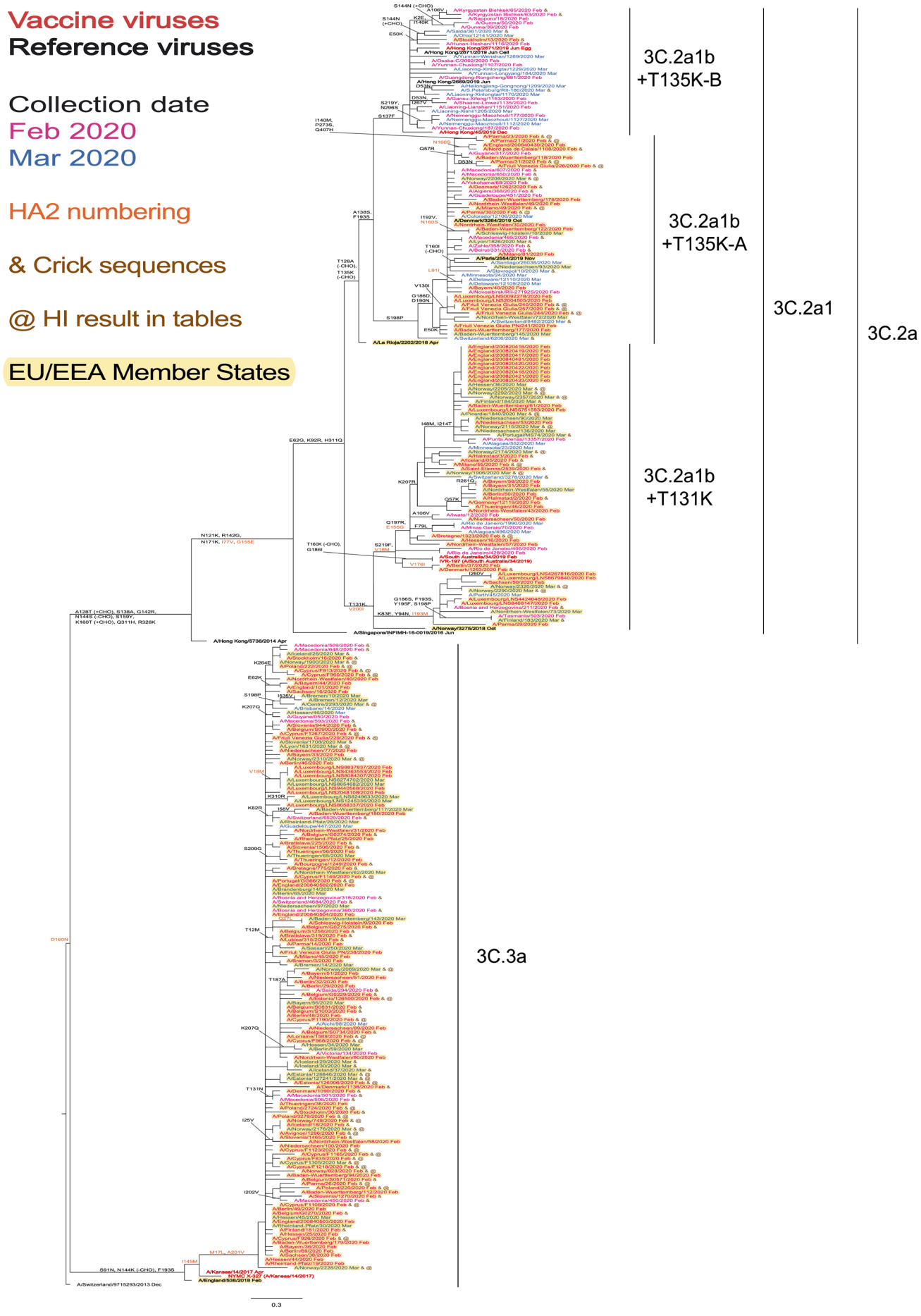
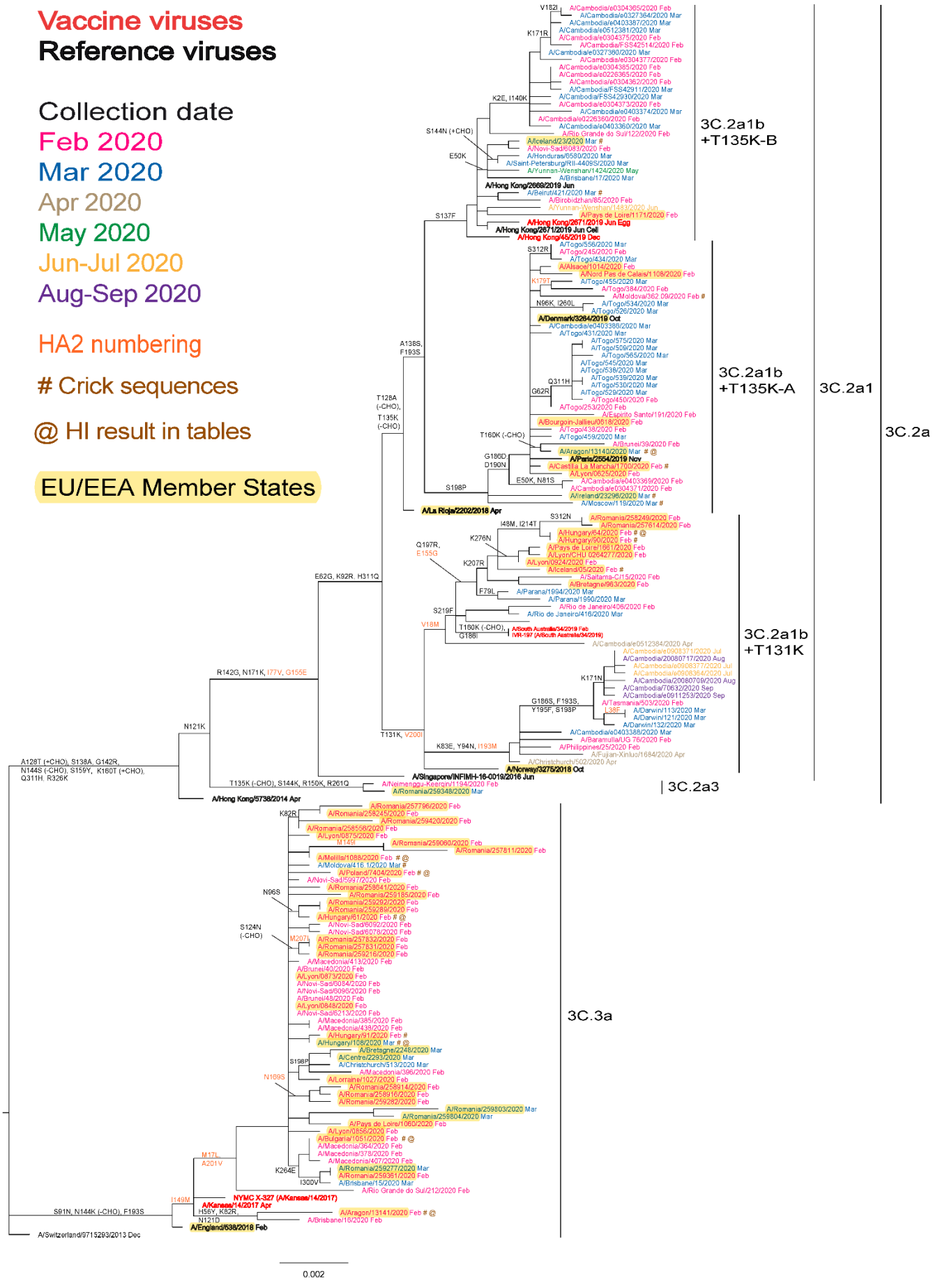


**Figure 2b. Phylogenetic comparison of influenza A(H3N2) HA genes (GISAID, September 2020)**



## Table 4-1. Antigenic analysis of A(H3N2) viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Post-infection ferret antisera | | | | | | | | | | |
| | Passage history | | | A/HK 5738/14 MDCK | A/Singapore 0019/16 Egg $10^{-4}$ | A/Norway 3275/18 SIAT | A/La Rioja 2202/18 SIAT | A/Denmark 3264/19 SIAT | A/HK 2671/19 Egg | A/HK 2671/19 Cell | A/Eng 538/18 SIAT | NYMC X-327 A/Kansas/14 Egg | A/Kansas 14/17 SIAT |
| | Ferret number | | | St Judes F60/17$^{-1}$ | F13/19$^{-1}$ | F03/19$^{-1}$ | F26/18$^{-1}$ | F19/20$^{-1}$ | F44/19$^{-1}$ | St Judes F21/20$^{-1}$ | F31/18$^{-1}$ | F16/19$^{-1}$ | F17/19$^{-1}$ |
| | Genetic group | | | 3C.2a | 3C.2a1 | 3C.2a1b+T131K | 3C.2a1b+T135K-A | 3C.2a1b+T135K-A | 3C.2a1b+T135K-B | 3C.2a1b+T135K-B | 3C.3a | 3C.3a | 3C.3a |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | |
| A/Hong Kong/5738/2014 | 3C.2a | 2014-04-30 | MDCK1/MDCK3/SIAT2 | 160 | 160 | 160 | 80 | < | < | 160 | 160 | 160 | 80 |
| A/Singapore/INFIMH-16-0019/2016 | 3C.2a1 | 2016-04-14 | E5/E2 | 80 | 320 | 40 | 160 | 80 | 80 | < | 40 | 40 | < |
| A/Denmark/3264/2019 | 3C.2a1b+T135K-A | 2019-10-25 | SIAT3/SIAT2 | ND | ND | ND | ND | 320 | ND | ND | ND | ND | ND |
| A/Hong Kong/2671/2019 | 3C.2a1b+T135K-B | 2019-06-17 | E8/E2 | 40 | 160 | < | 40 | 160 | 640 | 160 | 160 | 320 | 80 |
| A/Hong Kong/2671/2019 | 3C.2a1b+T135K-B | 2019-06-17 | MDCK1/SIAT4 | 80 | 160 | 160 | 160 | 160 | 160 | 160 | 80 | 80 | 80 |
| A/England/538/2018 | 3C.3a | 2018-02-26 | MDCK1/SIAT4 | < | 40 | < | < | 40 | 40 | < | 320 | 160 | 320 |
| NYMC X-327 (A/Kansas/14/17) | 3C.3a | 2017-12-14 | Ex/E1 | < | < | < | < | 40 | 160 | < | 160 | 640 | 320 |
| A/Kansas/14/2017 | 3C.3a | 2017-12-14 | SIAT3/SIAT2 | 40 | 80 | < | < | 40 | 40 | < | 320 | 160 | 320 |
| *TEST VIRUSES* | | | | | | | | | | | | | |
| A/Hungary/104/2020 | 3C.3a | 2020-01-27 | MDCK1/SIAT1 | 40 | 80 | < | < | 40 | < | < | 320 | 160 | 320 |
| A/Hungary/91/2020 | No seq | 2020-02-18 | MDCK1/SIAT1 | 40 | 80 | < | < | 40 | < | 40 | 320 | 160 | 160 |
| A/Hungary/61/2020 | 3C.3a | 2020-02-05 | MDCK1/SIAT1 | < | 40 | < | < | 40 | 40 | < | 320 | 160 | 320 |
| A/Hungary/64/2020 | 3C.2a1b+T131K | 2020-02-08 | MDCK1/SIAT1 | 80 | 80 | 160 | 80 | 80 | < | 80 | 40 | 40 | 40 |
| | | | | | Vaccine NH 2018-19 | | | | Vaccine NH 2020-21 | | | Vaccine NH 2019-20 | |

Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used) 1 < = <40
ND = Not Done
Sequences in Phylogenetic tree (Fig.2b)

## Table 4-2. Antigenic analysis of A(H3N2) viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Post-infection ferret antisera | | | | | | | | | | |
| | Passage history | | | A/HK 5738/14 MDCK | A/Singapore 0019/16 Egg $10^{-4}$ | A/Norway 3275/18 SIAT | A/La Rioja 2202/18 SIAT | A/Denmark 3264/19 SIAT | A/HK 2671/19 Egg | A/HK 2671/19 Cell | A/Eng 538/18 SIAT | NYMC X-327 A/Kansas/14 Egg | A/Kansas 14/17 SIAT |
| | Ferret number | | | St Judes F60/17 $^{+1}$ | F13/19 $^{+1}$ | F03/19 $^{+1}$ | F26/18 $^{+1}$ | F19/20 $^{-1}$ | F44/19 $^{+1}$ | St Judes F21/20 $^{+1}$ | F31/18 $^{+1}$ | F16/19 $^{+1}$ | F17/19 $^{+1}$ |
| | Genetic group | | | 3C.2a | 3C.2a1 | 3C.2a1b+T131K | 3C.2a1b+T135K-A | 3C.2a1b+T135K-A | 3C.2a1b+T135K-B | 3C.2a1b+T135K-B | 3C.3a | 3C.3a | 3C.3a |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | |
| A/Hong Kong/5738/2014 | 3C.2a | 2014-04-30 | MDCK1/MDCK2/SIAT2 | 160 | 320 | 160 | 80 | 40 | < | 40 | 160 | 160 | 160 |
| A/Singapore/INFIMH-16-0019/2016 | 3C.2a1 | 2016-04-14 | E5/E2 | 160 | 320 | 40 | 160 | 80 | 80 | < | 40 | 40 | < |
| A/Denmark/3264/2019 | 3C.2a1b+T135K-A | 2019-10-25 | SIAT3/SIAT3 | 160 | 160 | 160 | 160 | 160 | 40 | 80 | 80 | 80 | 40 |
| A/Hong Kong/2671/2019 | 3C.2a1b+T135K-B | 2019-06-17 | E8/E2 | < | 80 | < | 40 | 80 | 640 | 80 | 80 | 320 | 80 |
| A/Hong Kong/2671/2019 | 3C.2a1b+T135K-B | 2019-06-17 | MDCK1/SIAT4 | 80 | 320 | 160 | 160 | 320 | 160 | 320 | 160 | 160 | 160 |
| A/England/538/2018 | 3C.3a | 2018-02-26 | MDCK1/SIAT4 | 40 | 40 | < | < | 40 | < | < | 320 | 160 | 320 |
| NYMC X-327 (A/Kansas/14/17) | 3C.3a | 2017-12-14 | Ex/E1 | < | 40 | < | < | 40 | 160 | < | 160 | 1280 | 320 |
| A/Kansas/14/2017 | 3C.3a | 2017-12-14 | SIAT3/SIAT2 | 40 | 80 | < | < | 40 | 40 | 40 | 320 | 160 | 320 |
| *TEST VIRUSES* | | | | | | | | | | | | | |
| A/Poland/7404/2020 | 3C.3a | 2020-02-12 | MDCK3 | 40 | 80 | < | < | 40 | 40 | < | 640 | 160 | 320 |
| A/Bulgaria/1051/2020 | 3C.3a | 2020-02-21 | SIAT2/MDCK2 | 40 | 80 | < | < | 40 | 40 | < | 320 | 160 | 320 |
| A/Melilla/1088/2020 | 3C.3a | 2020-02-24 | SIAT1 | 40 | 80 | < | < | 40 | 40 | < | 320 | 160 | 320 |
| A/Aragon/13141/2020 | 3C.3a | 2020-02-25 | SIAT1 | 40 | 80 | < | < | 40 | < | < | 320 | 160 | 320 |
| A/Hungary/108/2020 | 3C.3a | 2020-03-06 | MDCK1/SIAT1 | 40 | 80 | < | < | < | < | < | 320 | 160 | 160 |
| A/Aragon/13140/2020 | 3C.2a1b+T135K-A | 2020-03-05 | SIAT1 | 40 | 80 | < | 40 | 160 | 80 | 40 | 160 | 80 | 80 |
| | | | | | Vaccine NH 2018-19 | | | | Vaccine NH 2020-21 | | | Vaccine NH 2019-20 | |

Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used) 1 < = <40

Sequences in Phylogenetic tree (Fig.2b)

# Influenza B virus analyses

A total of 492 influenza type B viruses with collection dates after 31 August 2019 have been received at the WIC (Table 2). Of these, 406 were sent with pre-assignment to a lineage: 388 B/Victoria and 18 B/Yamagata.

## Influenza B/Victoria-lineage

All recently circulating B/Victoria-lineage viruses have fallen in genetic **clade 1A**, represented by **B/Brisbane/60/2008**, a former vaccine virus, but with additional **HA1** amino acid substitutions of **I117V, N129D** and **V146I** (e.g. **B/Ireland/3154/2016**). Viruses retaining full-length HAs have remained antigenically similar to B/Brisbane/60/2008. However, three genetic groups (described below with amino acid substitutions/deletions relative to B/Brisbane/60/2008 indicated) containing deletions of HA gene codons have emerged and the viruses in these groups are antigenically distinct from B/Brisbane/60/2008 and each other (as noted in the September 2018 characterisation report[4] and earlier ones), such that four antigenically distinguishable groups had been circulating:

- A group with double deletion of **HA1** residues **162** and **163** (**subclade △162-163** or **1A(△2)**) with amino acid substitutions of **D129G** and **I180V**, and **HA2 R151K** that spread worldwide and is represented by the current vaccine virus, **B/Colorado/06/2017**.
- A group with triple deletion of **HA1** residues **162** to **164** (**subclade △162-164A** or **1A(△3)A**), first detected in Asia, with amino acid substitutions of **I180T** and **K209N** that showed limited spread worldwide (with no detections having been made recently) and is represented by **B/Hong Kong/269/2017**.
- A group with triple deletion of **HA1** residues **162** to **164** (**subclade △162-164B** or **1A(△3)B**), first detected in Africa, with amino acid substitution **K136E** often with **G133R** that showed geographic spread and dominance in recent months being represented by **B/Washington/02/2019**, the vaccine virus recommended after WHO VCMs in February and September 2020.

The HA phylogeny generated for the July report, largely made up of viruses detected in the USA and Europe, showed continued dominance of **subclade 1A(△3)B** viruses having **HA1 K136E,** often with **G133R** substitution, and several virus clusters had emerged defined by specific amino acid substitutions, e.g. **HA1 N126K** or **E128K** or **D129N** or **N150K** with **G184E** or **N233K** (loss of a glycosylation site), and relatively few **subclade 1A(△2)** viruses had been detected (Figure 3a). The updated phylogeny for sequences deposited in GISAID during August and September is largely made up of viruses detected in Europe and countries of the southern hemisphere, with very few viruses having collection dates after March (Figure 3b); the phylogeny profile is very similar to that of Figure 3a.

Following the spread of **1A(Δ2)** viruses, a representative – B/Colorado/06/2017 – was recommended for use in trivalent influenza vaccines for the 2019–20 northern hemisphere season [1]. Recent predominance of **1A(Δ3)B** viruses led to the recommendation of a representative (B/Washington/02/2019) for use in trivalent influenza vaccines for the 2020 and 2021 southern hemisphere [2, 4] and northern hemisphere 2020–2021 [3] seasons.

Of the B/Victoria-lineage viruses from EU/EEA countries received, 29 were assessed by HI assay since the July 2020 report (Tables 5-1 and 5-2). Test viruses are sorted by date of collection and 26 were subclade **1A(Δ3)B**, one subclade **1A(Δ2)** and two were not sequenced.

Poor test virus reactivity with ferret antisera raised against viruses in **clade 1A** (n=4) was observed, but for B/Hungary/69/2020 which had an unusual combination of HA1 amino acid substitutions (V117I, N126K, A127T AND A169X). Antisera raised against three **subclade 1A(△2)** viruses, tissue culture-propagated B/Norway/2409/2017, tissue culture- and egg-propagated cultivars of B/Colorado/06/2017, recognised 1 (3%), 14 (48%) and 4 (14%) test viruses, respectively, at titres within fourfold of their respective homologous titres, indicative of limited cross-reactivity with **subclade 1A(△3)B** viruses. Antisera raised against two **subclade 1A(△3)B** viruses, tissue culture- and egg-propagated cultivars of B/Washington/02/2019, recognised 26 (90%) and 24 (83%) test viruses, respectively, at titres within fourfold of their corresponding homologous titres. Three of four **subclade 1A(△3)B** test viruses showing eightfold or greater reductions in titre with antiserum raised against egg-propagated B/Washington/02/2019, compared to the homologous titre, carried HA1 N126K amino acid substitution (two with additional substitutions) while B/Navarra/1052/2020 contained multiple substitutions in HA1 (N150K, G184E, N197D [encoding loss of a glycosylation site], V220M, P241Q and R279K) (Tables 5-1 and 5-2) .

## Influenza B/Yamagata-lineage

One B/Yamagata-lineage virus was characterised antigenically (Table 6) and genetically at the WIC since the July report. The HA phylogeny, for viruses with collection dates from 1 January 2020, has been updated from the July report to contain five sequences submitted to GISAID in the August-September period, three for viruses from France and one each from Norway and Honduras, with the latter virus having the most recent collection date in March (Figure 4). As for other recently detected B/Yamagata-lineage viruses, the HA genes fall in genetic **clade 3**, the B/Wisconsin/1/2010–B/Phuket/3073/2013 clade, within a subgroup defined by **HA1 L172Q** and **M251V** amino acid substitutions compared to B/Phuket/3073/2013. Some sub-clustering of sequences from recently collected viruses, defined by specific amino acid substitutions (e.g. **HA1 N164K, K211R, D229N** or **D232N** [introducing a potential N-linked glycosylation site]

[4] European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, September 2018. Stockholm: ECDC; 2018. Available at: https://ecdc.europa.eu/sites/portal/files/documents/ECDC-Flu-Characterisation-Report-Sep-2018.pdf

sometimes with **R48K**), has occurred. A majority (57%) of the viruses with collection dates in 2020 encode the **D232N** substitution. As noted in previous characterisation reports for 2018, none of these amino acid substitutions have any obvious antigenic effects based on HI assays using post-infection ferret antisera raised against egg-propagated B/Phuket/3073/2013 which has been recommended for inclusion in quadrivalent vaccines for the 2019–2020 and 2020–2021 [1, 3] northern hemisphere and the 2020 and 2021 [2, 4] southern hemisphere seasons. This remains the case for the virus, B/Norway/993/2020, which was antigenically characterised in August (Table 6).

**Figure 3a. Phylogenetic comparison of influenza B/Victoria-lineage HA genes (GISAID, July 2020)**

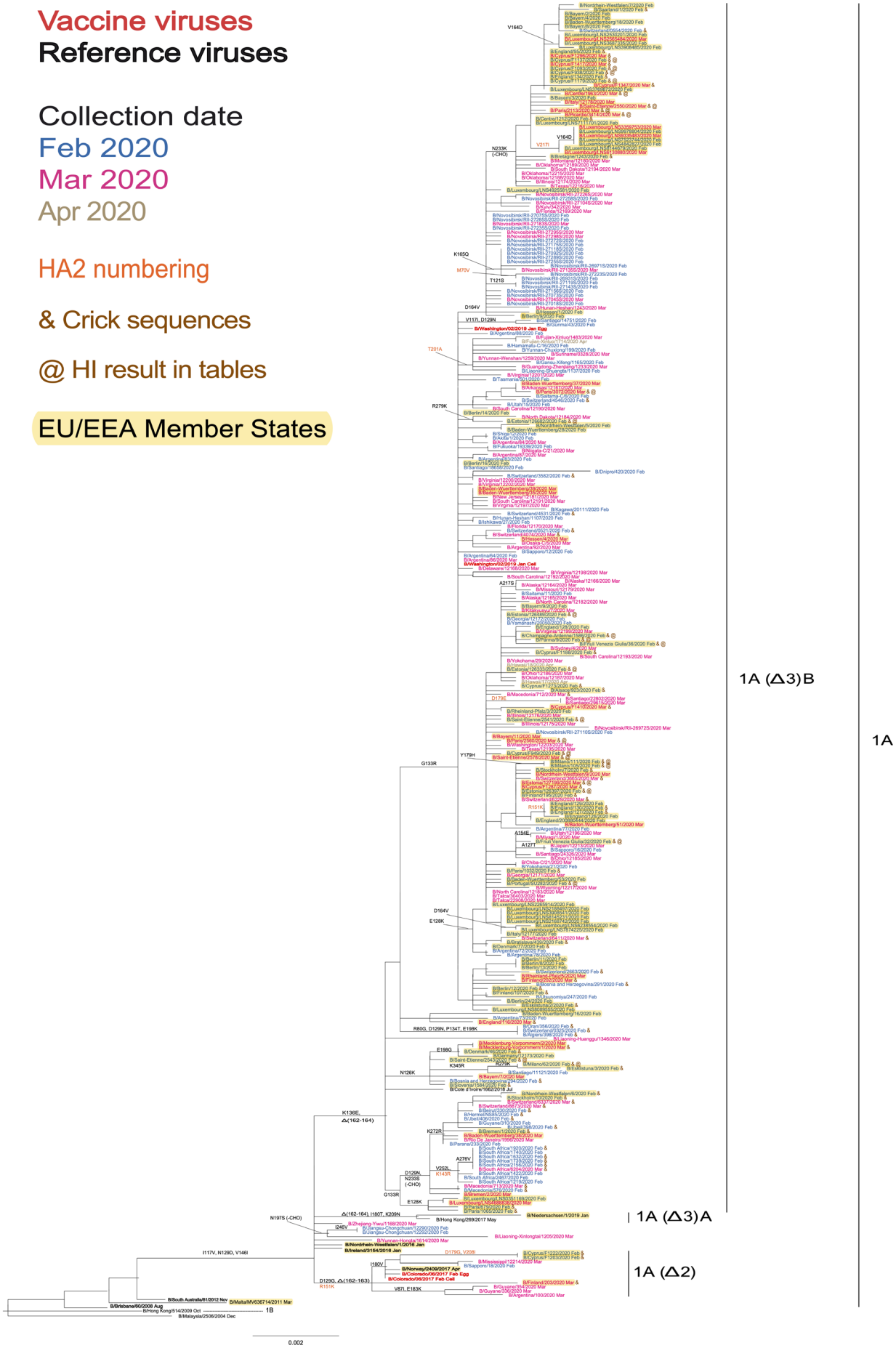
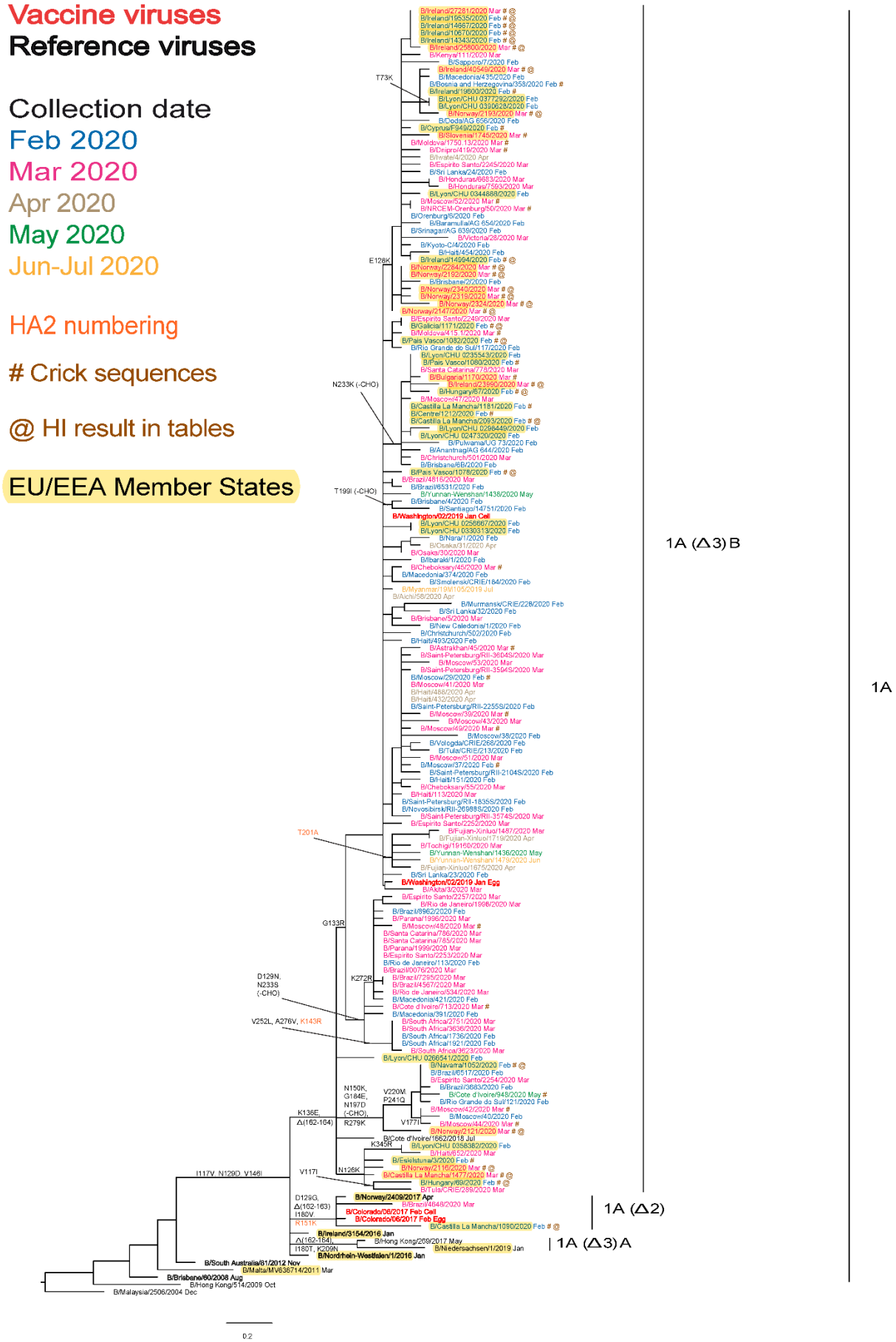


**Figure 3b. Phylogenetic comparison of influenza B/Victoria-lineage HA genes (GISAID, September 2020)**



## Table 5-1. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre: Post-infection ferret antisera | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | B/Bris 60/08 Egg Sh 539, 540, 543, 544, 570, 571, 574[1,3] | B/Bris 60/08 Egg | B/Sth Aus 81/12 Egg | B/Ireland 3154/16 MDCK | B/Nord-West 1/16 MDCK | B/Norway 2409/17 MDCK | B/Colorado 06/17 MDCK | B/Colorado 06/17 Egg | B/Wash'ton 02/19 MDCK | B/Wash'ton 02/19 Egg |
| | Passage history | | | 1A | 1A | 1A | 1A | 1A | 1A(Δ2) | 1A(Δ2) | 1A(Δ2) | 1A(Δ3)B | 1A(Δ3)B |
| | Ferret number | | | F44/17[2] | | F25/16[2] | F15/16[2] | F38/17[2] | F40/17[2] | F21/18[2] | F11/18[2] | F37/19[2] | F38/19[2] |
| | Genetic group | | | | | | | | | | | | |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | |
| B/Brisbane/60/2008 | 1A | 2008-08-04 | E4/E4 | 1280 | 640 | 640 | 40 | 80 | < | 10 | 160 | < | 160 |
| B/South Australia/81/2012 | 1A | 2012-11-28 | E4/E2 | 1280 | 640 | 320 | 40 | 80 | < | 10 | 80 | < | 160 |
| B/Ireland/3154/2016 | 1A | 2016-01-14 | MDCK1/MDCK4 | 1280 | 80 | 40 | 80 | 160 | < | < | < | < | < |
| B/Nordrhein-Westfalen/1/2016 | 1A | 2016-01-04 | C2/MDCK2 | 1280 | 80 | 40 | 80 | 160 | < | < | < | < | < |
| B/Norway/2409/2017 | 1A(Δ2) | 2017-04-27 | MDCK1/MDCK3 | 40 | 10 | 10 | < | < | 40 | 40 | 160 | < | < |
| B/Colorado/06/2017 | 1A(Δ2) | 2017-02-05 | MDCK1/MDCK2 | 40 | 10 | 10 | < | < | 40 | 40 | 80 | < | < |
| B/Colorado/06/2017 | 1A(Δ2) | 2017-02-05 | E5/E2 | 640 | 160 | 40 | < | < | 20 | 40 | 320 | < | 80 |
| B/Washington/02/2019 | 1A(Δ3)B | 2019-01-19 | C2/MDCK3 | 1280 | 160 | 160 | < | < | < | 10 | 320 | 40 | 320 |
| B/Washington/02/2019 | 1A(Δ3)B | 2019-01-19 | E3/E2 | 640 | 160 | 80 | < | < | < | 20 | 160 | 40 | 320 |
| *TEST VIRUSES* | | | | | | | | | | | | | |
| B/Hungary/67/2020 | 1A(Δ3)B | 2020-02-06 | MDCK1/MDCK1 | 160 | 40 | 20 | < | < | < | 10 | 40 | 20 | 160 |
| B/Hungary/69/2020 | V117I, N126K, A127T, A169X | 1A(Δ3)B | 2020-02-10 | MDCK1/MDCK1 | 80 | 40 | 20 | < | < | < | 20 | 40 | 20 | 40 |
| B/Norway/2121/2020 | 1A(Δ3)B | 2020-03-10 | MDCK1 | 640 | 160 | 160 | < | < | < | < | 160 | < | 160 |
| B/Norway/2193/2020 | 1A(Δ3)B | 2020-03-16 | MDCK1 | 160 | 10 | 10 | < | < | < | < | 10 | 40 | 160 |
| B/Norway/2192/2020 | 1A(Δ3)B | 2020-03-17 | MDCK1 | 160 | 40 | 10 | < | < | < | < | 20 | 40 | 160 |
| B/Norway/2147/2020 | 1A(Δ3)B | 2020-03-17 | MDCK1 | 40 | 10 | 10 | < | < | < | < | 10 | 40 | 160 |
| B/Norway/2116/2020 | N126K, E198G | 1A(Δ3)B | 2020-03-18 | MDCK1 | 160 | 40 | 20 | < | < | < | 10 | 20 | 10 | 40 |
| B/Norway/2324/2020 | 1A(Δ3)B | 2020-03-23 | MDCK1 | 160 | 20 | 20 | < | < | < | 10 | 20 | 40 | 160 |
| B/Norway/2319/2020 | 1A(Δ3)B | 2020-03-23 | MDCK1 | 160 | 40 | 20 | < | < | < | 10 | 20 | 40 | 160 |
| B/Norway/2284/2020 | 1A(Δ3)B | 2020-03-23 | MDCK1 | 160 | 40 | 20 | < | < | < | 20 | 40 | 40 | 320 |
| B/Norway/2340/2020 | 1A(Δ3)B | 2020-03-26 | MDCK2 | 160 | 20 | 20 | 10 | < | < | 20 | 20 | 40 | 160 |

| Vaccine | Vaccine |
|---|---|
| SH 2019 | SH 2020 |
| NH 2019-20 | NH 2020-21 |

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used):
[1] < = <40; [2] < = <10; [3] hyperimmune sheep serum; [4] < = <20; ND = Not Done

Sequences in Phygenetic tree (Fig. 3b)

## Table 5-2. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

| Viruses | Other information | Collection date | Passage history | Haemagglutination inhibition titre Post-infection ferret antisera | | | | | | | | | | | NEW | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Passage history | | | | B/Bris 60/08 Egg | B/Bris 60/08 Egg | B/Sth Aus 81/12 Egg | B/Ireland 3154/16 MDCK | B/Nord-West 1/16 MDCK | B/Norway 2409/17 MDCK | B/Colorado 06/17 MDCK | B/Colorado 06/17 Egg | B/Wash'ton 02/19 MDCK | B/Wash'ton 02/19 Egg | B/Wash'ton 02/19 Egg |
| Ferret number | | | | Sh 539, 540, 543, 544, 570, 571, 574[1,3] | F44/17[*2] | F25/16[*2] | F15/16[*2] | F38/17[*2] | F40/17[*2] | F21/18[*2] | F11/18[*2] | F37/19[*2] | F38/19[*4] | F20/20[*2] |
| Genetic group | | | | 1A | 1A | 1A | 1A | 1A | 1A(Δ2) | 1A(Δ2) | 1A(Δ2) | 1A(Δ3)B | 1A(Δ3)B | 1A(Δ3)B |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | | |
| B/Brisbane/60/2008 | 1A | 2008-08-04 | E4/E4 | 2560 | 640 | 640 | 40 | 160 | < | 10 | 160 | < | 320 | 160 |
| B/South Australia/81/2012 | 1A | 2012-11-28 | E4/E2 | 2560 | 640 | 640 | 40 | 80 | < | 10 | 160 | < | 160 | 80 |
| B/Ireland/3154/2016 | 1A | 2016-01-14 | MDCK1/MDCK4 | 2560 | 160 | 40 | 80 | 160 | < | < | < | < | < | < |
| B/Nordrhein-Westfalen/1/2016 | 1A | 2016-01-04 | C2/MDCK3 | 2560 | 160 | 40 | 80 | 160 | < | < | < | < | < | < |
| B/Norway/2409/2017 | 1A(Δ2) | 2017-04-27 | MDCK1/MDCK3 | 80 | < | 10 | < | < | 80 | 80 | 160 | < | < | < |
| B/Colorado/06/2017 | 1A(Δ2) | 2017-02-05 | MDCK1/MDCK2 | 80 | < | 10 | < | < | 40 | 40 | 160 | < | < | < |
| B/Colorado/06/2017 | 1A(Δ2) | 2017-02-05 | E5/E2 | 640 | 80 | 40 | < | < | 20 | 40 | 320 | < | 160 | 80 |
| B/Washington/02/2019 | 1A(Δ3)B | 2019-01-19 | C2/MDCK3 | 640 | 80 | 80 | < | < | < | 10 | 160 | 40 | 320 | 160 |
| B/Washington/02/2019 | 1A(Δ3)B | 2019-01-19 | E3/E2 | 640 | 80 | 80 | < | < | < | 20 | 160 | 20 | 320 | 160 |
| *TEST VIRUSES* | | | | | | | | | | | | | | |
| B/Castilla La Mancha/1181/2020 | No seq | 2020-02-18 | MDCK1 | 160 | 10 | 20 | < | < | < | 10 | 40 | 20 | 160 | 80 |
| B/Ireland/19600/2020 | No seq | 2020-02-28 | MDCK1 | 160 | < | < | < | < | < | < | 10 | 40 | 160 | 80 |
| B/Ireland/10670/2020 | 1A(Δ3)B | 2020-02-03 | MDCK2 | 80 | < | < | < | < | < | < | 20 | 20 | 160 | 80 |
| B/Ireland/14667/2020 | 1A(Δ3)B | 2020-02-11 | MDCK1 | 80 | < | < | < | < | < | < | 10 | 40 | 160 | 80 |
| B/Ireland/14994/2020 | 1A(Δ3)B | 2020-02-12 | MDCK1 | 160 | < | < | < | < | < | < | 20 | 40 | 160 | 80 |
| B/Ireland/14343/2020 | 1A(Δ3)B | 2020-02-13 | MDCK2 | 80 | < | < | < | < | < | < | 20 | 40 | 160 | 80 |
| B/Galicia/1171/2020 | 1A(Δ3)B | 2020-02-16 | MDCK1 | 320 | 40 | 44 | < | < | < | 10 | 80 | 40 | 320 | ND |
| B/Pais Vasco/1082/2020 | 1A(Δ3)B | 2020-02-18 | MDCK1 | 160 | < | 10 | < | < | < | 10 | 40 | 20 | 160 | 80 |
| B/Pais Vasco/1078/2020 | 1A(Δ3)B | 2020-02-18 | MDCK1 | 160 | < | 20 | < | < | < | 10 | 40 | 20 | 160 | 80 |
| B/Navarra/1052/2020 | 1A(Δ3)B | 2020-02-19 | MDCK1 | 320 | 40 | 40 | < | < | < | < | 40 | < | < | 40 |
| B/Castilla La Mancha/2093/2020 | 1A(Δ3)B | 2020-02-21 | MDCK1 | 80 | < | 10 | < | < | < | < | 40 | 10 | 160 | 80 |
| B/Ireland/19535/2020 | 1A(Δ3)B | 2020-02-28 | MDCK1 | 160 | < | < | < | < | < | < | 40 | 40 | 320 | 160 |
| B/Castilla La Mancha/1477/2020 | 1A(Δ3)B | 2020-03-02 | MDCK1 | 80 | < | < | < | < | < | < | 40 | 10 | < | 20 |
| B/Ireland/23990/2020 | 1A(Δ3)B | 2020-03-06 | MDCK3 | 160 | < | 10 | < | < | < | < | 20 | 20 | 160 | 80 |
| B/Ireland/25800/2020 | 1A(Δ3)B | 2020-03-12 | MDCK2 | 80 | < | < | < | < | < | < | 10 | 40 | 160 | 80 |
| B/Ireland/27281/2020 | 1A(Δ3)B | 2020-03-13 | MDCK2 | 320 | 40 | 10 | < | < | < | 10 | 40 | 40 | 160 | 80 |
| B/Ireland/40549/2020 | 1A(Δ3)B | 2020-03-23 | MDCK1 | 320 | 40 | 20 | < | < | < | 10 | 80 | 40 | 160 | 80 |
| B/Castilla La Mancha/1090/2020 | 1A(Δ2) | 2020-02-22 | MDCK1 | 80 | < | < | < | < | 40 | 40 | 80 | < | < | < |

| Other information | Vaccine SH 2019 NH 2019-20 | Vaccine SH 2020 NH 2020-21 |
|---|---|---|
| N190K, G184E, N197D(-CHO), V220M, P241Q, R279K | | |
| N126K | | |

*Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used):
[1] < = <40; [2] < = <10; [3] hyperimmune sheep serum; [4] < = <20; ND = Not Done

Sequences in Phyogenetic tree (Fig. 3b)

**Figure 4. Phylogenetic comparison of influenza B/Yamagata-lineage HA genes (GISAID, September 2020)**

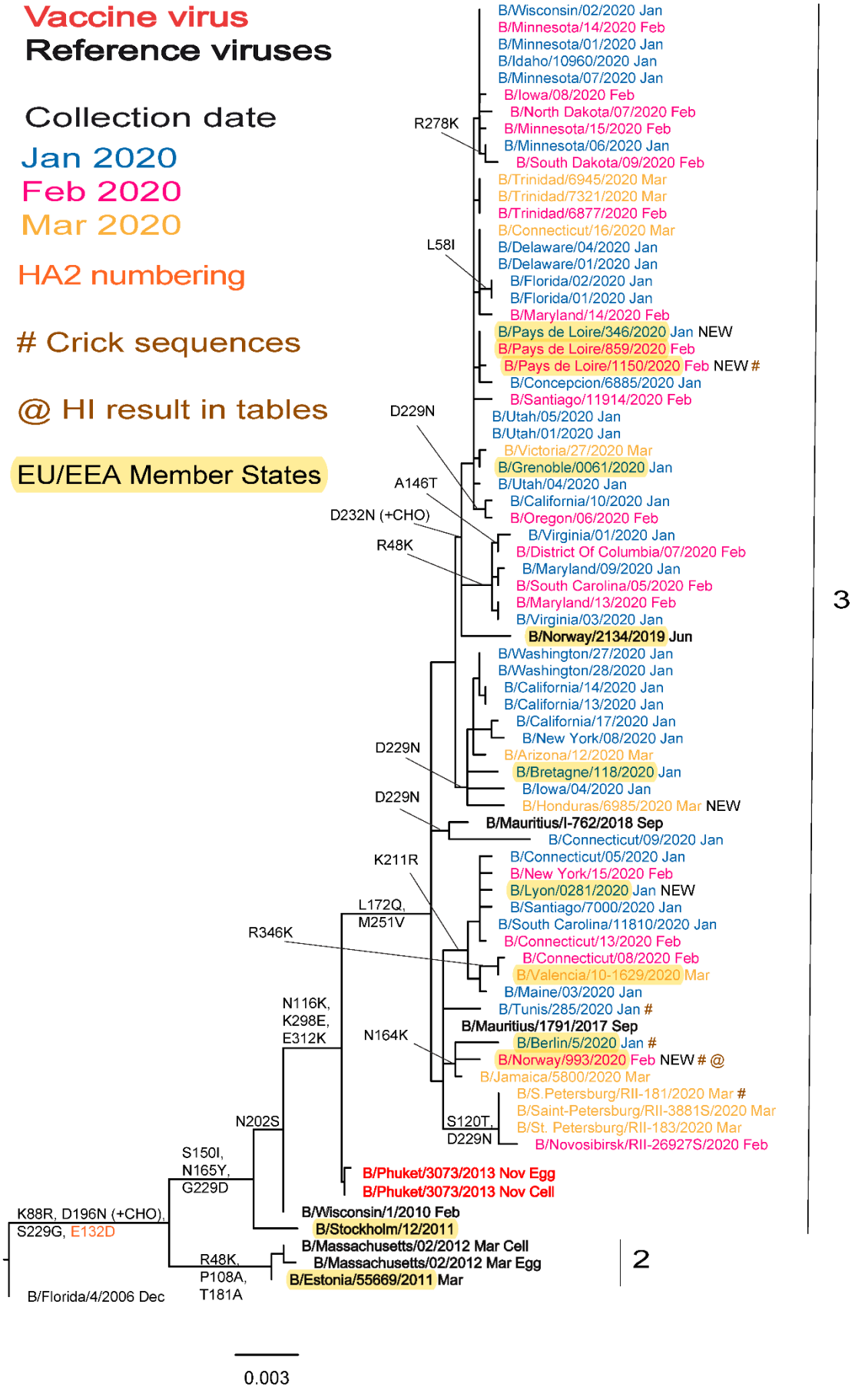


**Table 6. Antigenic analysis of influenza B/Yamagata-lineage viruses by HI**

| Viruses | Other information | Passage history / Ferret number / Genetic Group | Collection date | Passage history | Haemagglutination inhibition titre | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Post-infection ferret antisera | | | | | | | |
| | | | | | B/Phuket 3073/13 Egg SH614*1,3 | B/Estonia 55669/11 MDCK F39/17*2 | B/Mass 02/12 MDCK F10/16*2 | B/Mass 02/12 Egg F06/17*4 | B/Wis 1/10 Egg F36/15*2 | B/Phuket 3073/13 MDCK F27/15*2 | B/Phuket 3073/13 Egg F25/17*2 | B/Maur I-762/18 MDCK F05/19*2 | B/Nor 2134/19 Egg F48/19*2 |
| | | Passage history | | | 3 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 |
| | | Ferret number | | | | | | | | | | | |
| | | Genetic Group | | | | | | | | | | | |
| *REFERENCE VIRUSES* | | | | | | | | | | | | | |
| B/Estonia/55669/2011 | | 2 | 2011-03-14 | MDCK2/MDCK3 | 320 | 40 | 40 | 80 | 40 | 20 | 20 | < | < |
| B/Massachusetts/02/2012 | | 2 | 2012-03-13 | MDCK1/C2/MDCK4 | 1280 | 160 | 320 | 320 | 320 | 80 | 160 | 80 | < |
| B/Massachusetts/02/2012 | | 2 | 2012-03-13 | E3/E3 | 320 | 10 | < | 160 | 40 | < | 40 | < | < |
| B/Wisconsin/1/2010 | | 3 | 2010-02-20 | E3/E2 | 1280 | < | < | 160 | 80 | 10 | 160 | 40 | < |
| B/Stockholm/12/2011 | | 3 | 2011-03-28 | E4/E2 | 640 | < | < | 80 | 80 | 10 | 80 | < | < |
| B/Phuket/3073/2013 | | 3 | 2013-11-21 | MDCK2/MDCK3 | 2560 | 160 | 160 | 160 | 320 | 160 | 160 | 320 | < |
| B/Phuket/3073/2013 | | 3 | 2013-11-21 | E4/E3 | 1280 | < | < | 80 | 80 | 20 | 80 | < | < |
| B/Mauritius/I-762/2018 | | 3 | 2018-09-02 | MDCK1/MDCK3 | 1280 | < | 20 | 80 | 80 | 20 | 40 | 80 | < |
| B/Norway/2134/2019 | | 3 | 2019-06-06 | E2/E2 | 160 | < | < | < | < | < | < | < | 320 |
| *TEST VIRUSES* | | | | | | | | | | | | | |
| B/Norway/993/2020 | | 3 | 2020-02-11 | MDCK1 | 1280 | < | 40 | 160 | 80 | 40 | 80 | 80 | < |
| | | | | | | | | | | | Vaccine# | | |

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used):
1 < = <40; 2 < = <10; 3 hyperimmune sheep serum

# B/Yamagata-lineage virus recommended for use in quadravalent vaccines SH 2019, NH 2019-20, SH 2020 and NH 2020-21

Sequence in Phylogenetic tree (Fig. 4)

# Summaries of data submitted to TESSy

## Genetic characterisation

For the 2019–20 season, as of week 20/2020, a total of 2 752 viruses were characterised genetically and ascribed to a genetic clade (no additional characterisations were reported during weeks 21–39/2020).

- 982 were A(H1N1)pdm09 viruses, with 945 being subclade 6B.1A5 (904 subgroup 6B.1A5A represented by A/Norway/3433/2018 and 41 subgroup 6B.1A5B represented by A/Switzerland/3330/2018), 19 being subgroup 6B.1A7 represented by A/Slovenia/1489/2019, 11 being subgroup 6B.1A1 represented by A/Brisbane/02/2018 and seven attributed to a known group not listed in the 2019–20 reporting categories
- 1 048 were A(H3N2) viruses, with 342 being subgroup 3C.2a1b+T131K represented by A/South Australia/34/2019, 560 being clade 3C.3a represented by A/Kansas/14/2017, 81 being subgroup 3C.2a1b+T135K-B represented by A/Hong Kong/2675/2019, 64 being subgroup 3C.2a1b+T135K-A represented by A/La Rioja/2202/2018 and one attributed to a known group not listed in the 2019–20 reporting categories
- 26 were B/Yamagata-lineage clade 3 represented by the vaccine virus B/Phuket/3073/2013 with a further two attributed to a known group not listed in the 2019–20 reporting categories
- 694 were B/Victoria-lineage viruses, with 630 being subclade 1A(Δ3)B represented by B/Washington/02/2019, 19 being subclade 1A(Δ2) represented by the vaccine virus B/Colorado/06/2017, five being subclade 1A(Δ3)A represented by B/Hong Kong/269/2017 and 40 attributed to a known group not listed in the 2019–20 reporting categories.

## Antiviral susceptibility

Up to week 39/2020, a total of 2 292 influenza viruses, collected from the 2019–20 season, had been tested for susceptibility to neuraminidase inhibitors (oseltamivir and zanamivir): 942 A(H1N1)pdm09, 794 A(H3N2) and 556 type B viruses. Five A(H1N1)pdm09 viruses showed reduced inhibition (RI) or highly reduced inhibition (HRI) to oseltamivir and/or zanamivir. Of these, three viruses carried amino acid substitution H275Y in NA, with one of them also having H295S substitution, both of which are indicative of HRI by oseltamivir. A further two viruses showed RI by oseltamivir in phenotypic assays, one of which also showed RI by zanamivir. One A(H3N2) virus showed HRI by oseltamivir with RI by zanamivir and carried NA R292K amino acid substitution. One B/Victoria-lineage virus showed HRI by oseltamivir and RI by zanamivir in phenotypic assays.

At the WIC this season, 1 030 viruses from EU/EEA countries have been assessed phenotypically against oseltamivir and zanamivir: 380 A(H1N1)pdm09, 361 A(H3N2), 280 B/Victoria-lineage and 9 B/Yamagata-lineage. Two A(H1N1)pdm09 viruses (A/Denmark/3295/2019 and A/Denmark/3311/2019) showed HRI by zanamivir associated with NA Q136K amino acid substitution, one A(H1N1)pdm09 virus (A/Lund/4/2020) showed HRI by oseltamivir with NA H275Y substitution, one A(H3N2) virus (A/Limoges/2326/2019) showed RI by zanamivir associated with NA T148I substitution (resulting in the loss of a potential N-linked glycosylation motif) and one B/Victoria-lineage virus (B/Estonia/125782/2020) showed RI by zanamivir.

# Influenza A(H7N9) virus

On 1 April 2013, WHO's Global Alert and Response [5] reported that the China Health and Family Planning Commission notified WHO of three cases of human infection with influenza A(H7N9). A description of the characteristics of H7N9 viruses can be found on WHO's website [6]. Increased numbers of cases were reported over the course of the following seasons, and cases were reported in 2017, including the fifth (2016–17) and largest wave to date, which included the emergence of highly pathogenic avian influenza (HPAI) strains that have caused some zoonoses, although few human cases were reported during the 2017–18 season [7]. WHO posted an analysis of information on A(H7N9) viruses on 10 February 2017 [8], and ECDC published a rapid risk assessment on the implications of A(H7N9) for public health on 3 July 2017 [9]. Current risk assessments are included in WHO's monthly summary and assessment of influenza at human-animal interface (accessed 7 October 2020). The assessment published on 16 July 2020 indicates that there have been no publicly available reports from animal health authorities in China or other countries on influenza A(H7N9) virus detections in animals in recent months [10]. The most recent human case was detected in mid-March 2019 [11]. The latest overview of avian influenza by ECDC in collaboration with the European Food Safety Authority and the EU Reference Laboratory for Avian Influenza was published on 30 September 2020 and can be found on ECDC's website [12].

# Influenza A(H5) virus

The most recent monthly risk assessment of influenza at the human–animal interface was published by WHO on 16 July 2020. While no new human cases were reported, according to reports received by the World Organisation for Animal Health (OIE), various influenza A(H5) subtypes continue to be detected in birds in Africa, Europe and Asia [10]. No new human cases of A(H5N1) infection have been detected since the case in Nepal in March 2019, the first human case of A(H5N1) infection reported to WHO since 2017. There have, however, been reports of A(H5N1) infection in domestic birds since February 2019 [13]. On 30 September 2020, ECDC published an alert related to outbreaks of avian influenza

viruses in Europe [14] with a link to the latest collaborative report from ECDC and the European Food Safety Authority, which can be found on ECDC's website [12].

# Influenza A(H9N2) virus

Since the previous update on 8 May 2020, two new laboratory-confirmed human cases of influenza A(H9N2) virus infections in China have been reported, both in children with mild disease symptoms and exposure to poultry [10]: one in Shandong province (9 May 2020, disease onset 28 April) and one in Fujian province (13 May 2020, disease onset 4 May). Avian influenza A(H9N2) viruses are enzootic in poultry in Asia and increasingly reported in poultry in Africa.

# Other Influenza zoonotic events

Since the previous update on 8 May 2020, two additional zoonoses with swine viruses have been reported [9]: one A(H1N2)v in Brazil in a 22 year-old female (22 June 2020, onset 12 April) and one A(H1N1)v (clade 1C.2.2) in Germany in a two-year-old male (3 July 2020, onset 9 June). Both patients had swine exposure and recovered well.

# WIC reports for WHO VCMs

A description of results generated by the London WHO Collaborating Centre at the WIC and used at the most recent WHO VCM (held online: 16-24 September 2020 for seasonal influenza viruses), and previous ones, can be found at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports (accessed 7 October 2020).

# Note on the figures

The phylogenetic trees were constructed using RAxML, drawn using FigTree and annotated using Adobe Illustrator. The bars indicate the proportion of nucleotide changes between sequences. Reference strains are viruses to which post-infection ferret antisera have been raised. The colours indicate the month of sample collection. Isolates from WHO NICs in EU/EEA countries are highlighted in yellow. Sequences for most viruses from non-EU/EEA countries were recovered from the GISAID EpiFlu database. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from the GISAID EpiFlu database, which were downloaded for use in the preparation of this report (all submitters of data may be contacted directly via the GISAID website), along with all laboratories who submitted sequences directly to WHO CC London.

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