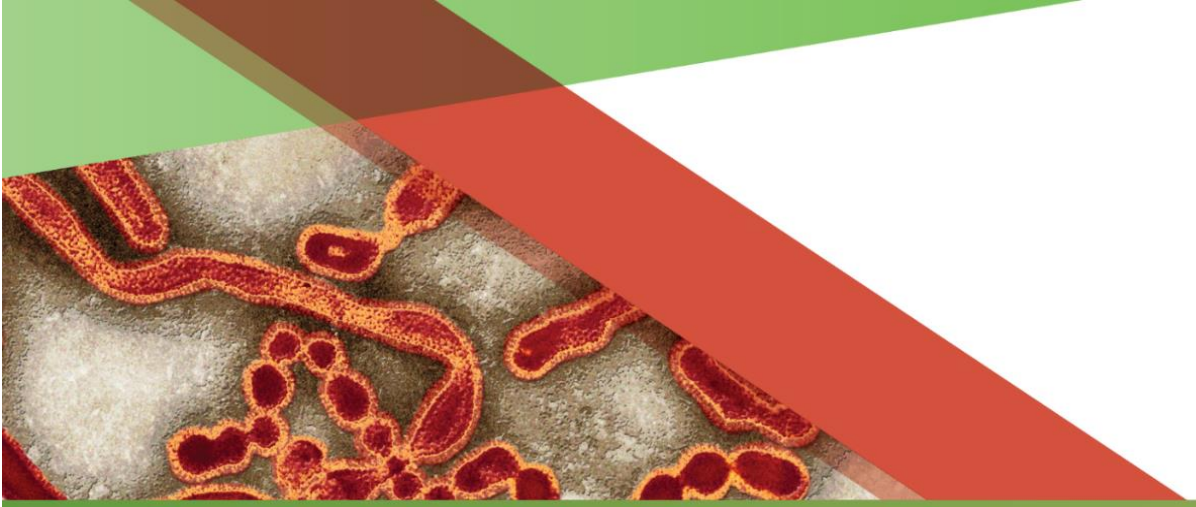

SURVEILLANCE REPORT

Influenza virus characterisation

Summary Europe, July 2020

Summary

This is the ninth report for the 2019–20 influenza season. As of week 30/2020, 164 887 influenza detections had been reported across the WHO European Region; 73% type A viruses, with A(H1N1)pdm09 prevailing over A(H3N2), and 27% type B viruses, with 4 479 (98%) of 4 568 ascribed to a B/Victoria lineage.

Since the June 2020 characterisation report[1], three shipments of influenza-positive specimens from 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), 1 661 virus specimens have been received, with collection dates after 31 August 2019.

Of the 49 A(H1N1)pdm09 viruses from EU/EEA countries characterised antigenically since the June report, 36 were well recognised by antisera raised against the 2019–20 vaccine virus, A/Brisbane/02/2018. The 13 viruses showing poor reactivity generally carried amino acid substitutions (notably N156K) in the HA1 150-loop region. The 468 EU/EEA test viruses with collection dates from week 40/2019 genetically characterised at the WIC have fallen within subclades of clade 6B.1A: 425 6B.1A5A, 30 6B.1A5B, 1 6B.1A6 and 12 6B.1A7.

The majority (39) of the 68 A(H3N2) viruses from EU/EEA countries characterised antigenically in July 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 clade 3C.3a and subgroups 3C.2a1b+T131K and 3C.2a1b+T135K viruses have been detected, but for viruses detected since 1 February 2020, subgroups 3c.2a1b+T135KA/B have prevailed in the USA, while those of clade 3C.3a and subgroup 3C.2a1b+T131K have dominated in Europe. In total, 500 viruses from EU/EEA countries have been characterised genetically at the WIC: 282 were clade 3C.3a, 137 were 3C.2a1b+T131K, 61 were 3C.2a1b+T135K-A and 20 were 3C.2a1b+T135K-B.

Thirty-two B/Victoria-lineage viruses from EU/EEA countries were antigenically characterised in July, all were subclade 1A(Δ3)B. Four viruses were not recognised well by antiserum raised against B/Washington/02/2019, the vaccine virus for the 2020–2021 northern hemisphere influenza season. Poor recognition was associated with HA1 amino acid substitutions of either N126K or T155A. In total, 306 EU/EEA viruses have been characterised genetically at the WIC: 290 were subclade 1A(Δ3)B and 16 were subclade 1A(Δ2).

A single B/Yamagata-lineage virus from France, with a collection date in February 2020, was antigenically characterised in July. As for all recently circulating B/Yamagata-lineage viruses, all eight EU/EEA viruses characterised genetically at the WIC since week 40/2019 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.

[1] European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, June 2020. Stockholm: ECDC; 2020. Available from: https://www.ecdc.europa.eu/sites/default/files/documents/ECDC-Influenza-Characterisation-Report-Jun-2020.pdf

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Table 1 shows a summary of influenza virus detections in the WHO European Region reported to ECDC's TESSy database since the start of the 2019–20 season (weeks 40/2019–30/2020), with a total of 164 887 detections over this period, four of which were detected during weeks 26–30/2020. Of the type B viruses ascribed to a lineage (n = 4 568) B/Victoria-lineage viruses (n = 4 479) have predominated over B/Yamagata-lineage viruses (n = 89) by a large margin, while for type A viruses subtyped (n = 47 195), A(H1N1)pdm09 viruses (56.0%) have predominated over A(H3N2) viruses (44.0%). Overall, in excess of 92 000 more samples have been tested in 2019–20 than in 2018–19 but there have been 41 060 (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, declared a pandemic by WHO 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 but 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 40/2019–30/2020)[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	**11302**	**108950**	**120252**	**72.9**	**2.7:1**	**203564**	**98.8**	**86:1**
A(H1N1)pdm09	6126	20302	26428	56.0		44179	57.2	
A(H3N2)	4174	16593	20767	44.0	0.79:1	33117	42.8	0.7:1
A not subtyped	1002	72055	73057			126271		
Influenza B	**6325**	**38310**	**44635**	**27.1**		**2380**	**1.2**	
Victoria lineage	2449	2030	4479	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	36214	40067			2215		
Total detections (total tested)	**17627 (52452)**	**147260 (>889099)**	**164887 (>941551)**			**205947 (>849439)**		

[a] *Numbers taken from Flu News Europe week 20/2020 and weeks 26–30/2020 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, 64 shipments of specimens (virus isolates and/or clinical specimens) have been received at the Crick Worldwide Influenza Centre (WIC), from 28 EU/EEA countries, three of which were received since the June report (one from Hungary and two from Madrid, Spain). The packages contained 1 661 virus-related samples with collection dates after 31 August 2019 and were made up of 1 176 type A viruses, with 553 and 610 subtyped as A(H1N1)pdm09 and A(H3N2) respectively, and 485 type B viruses, with 378 and 18 ascribed to B/Victoria and B/Yamagata lineages, respectively (Tables 2a/b). Genetic and antigenic characterisation data generated at the WIC up to 21 February 2020, for viruses with collection dates from 31 August 2019 to 31 January 2020, contributed to the WIC virus characterisation report (the deadline for the report was 21 February 2020) that was presented at the WHO influenza vaccine composition meeting (VCM) in February 2020. At this meeting recommendations were made for the northern hemisphere 2020–21 season. Data on viruses with collection dates after 31 January 2020 will contribute to the WIC VCM report in September for recommendations for the southern hemisphere 2021 season. Recommendations for the current 2019–20 northern hemisphere and the subsequent 2020 southern hemisphere, and 2020–21 northern hemisphere seasons have been published [1,2,3].

WIC would like to thank those WHO-recognised national influenza centres (NICs) that have responded to messages requesting the sharing of influenza-positive samples with recent collection dates. We encourage other NICs and laboratories that share influenza-positive samples with the WIC to do so in August and early September to allow virus characterisation in time for the September 2020 WHO VCM. Please note that, to inform the September 2020 southern hemisphere influenza VCM, we focus on samples with collection dates from 1 February 2020 onwards, and more than one shipment from a country is encouraged to ensure that we capture any 'end-of-season' samples from countries in the northern hemisphere.

During the lockdown imposed by the UK Government due to the COVID-19 pandemic, WIC has been operating with a reduced number of staff. 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 re-instated 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 GISAID during the month of July (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.

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 Number received	A Number propagated[1]	H1N1pdm09 Number received	H1N1pdm09 Number propagated[1]	H3N2 Number received	H3N2 Number propagated[2]		B Number received	B Number propagated[1]	B Victoria lineage Number received	B Victoria lineage Number propagated[1]	B Yamagata lineage Number received	B Yamagata lineage Number propagated[1]
2019														
SEPTEMBER														
Czech Republic	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	5			3	3						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		
Czech Republic	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	6			2	2	2	2		1	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	in process				5	in process		
Bulgaria	2			1	0	1	1							
Croatia	6			4	1	1	0	1			1	0		
Cyprus	2					1	0		1	0				
Czech Republic	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	30			12	12	6	0	6			12	12		
United Kingdom	18			4	in process	11	in process				3	in process		

*** 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 characterisation of which will not be used to inform the WHO VCM in September 2020).

As of 2020-08-10

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 Number received	A Number propagated[1]	H1N1pdm09 Number received	H1N1pdm09 Number propagated[1]	H3N2 Number received	H3N2 Number propagated[2]		B Number received	B Number propagated[1]	B Victoria lineage Number received	B Victoria lineage Number propagated[1]	B Yamagata lineage Number received	B Yamagata lineage Number propagated[1]
2020														
JANUARY														
Austria	2	1	0						1	0				
Belgium	52			29	in process	18	in process				5	in process		
Bulgaria	28			14	in process	12	in process				2	0		
Cyprus	27			4	0	22	in process				1	in process		
Czech Republic	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	in process							
Italy	3			1	1	1	1				1	1		
Lithuania	2					2	1	1						
Norway	22			1	0	14	in process				6	in process	1	in process
Poland	9	1	0	4	in process	2	in process		2	in process				
Portugal	7			1	in process	1	in process				5	in process		
Romania	15			4	3	7	1		1	0	3	3		
Slovakia	1					1	in process							
Slovenia	7			4	in process	2	in process				1	1		
Spain	18			13	12				1	0	4	4		
United Kingdom	38			18	in process	11	in process		3	0	6	in process		
FEBRUARY														
Austria	2	1	0						1	0				
Belgium	50			28	28	17	17				5	5		
Bulgaria	26			5	5	12	9	1			9	9		
Cyprus	38			6	5	21	in process				11	in process		
Denmark	9					6	4	2			3	3		
Estonia	12			5	in process	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	2	in process	2	in process	3	in process				2	in process		
Iceland	10			4	4	2	2				4	4		
Ireland	12			1	0				4	in process	7	in process		
Italy	25			7	7	12	12				6	6		
Norway	13			4	in process	5	2	0			3	in process	1	in process
Poland	22			10	4	9	6	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	2	in process	23	in process	2	in process		8	in process				
Sweden	18			8	8	5	3	2			5	5		
United Kingdom	14			1	1	2	2		7	in process	4	4		
MARCH														
Belgium	6			4	4						2	2		
Bulgaria	9			2	2	1	1				6	6		
Cyprus	9			1	1	1	in process				7	in process		
Estonia	5					4	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	in process							
Iceland	13			4	4	6	6				3	3		
Ireland	14			3	3	1	in process		6	in process	4	in process		
Norway	37			5	in process	18	15	0			14	in process		
Poland	4			4	2									
Portugal	4			3	2	1	1							
Slovenia	8					2	2				6	6		
Spain	7			4	in process	1	in process		2	in process				
United Kingdom	19								17	in process	2	in process		
APRIL														
Iceland	1										1	1		
Norway	1										1	in process		
	1661	13	0	553	353	610	259	103	89	0	378	245	18	8
28 Countries		0.78%		33.3%		36.7%			5.4%		22.8%		1.1%	
				70.8%							29.2%			

*** 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 characterisation of which will not be used to inform the WHO VCM in September 2020).

As of 2020-08-10

Influenza A(H1N1)pdm09 virus analyses

The first A(H1N1)pdm09 HA phylogeny is repeated from the June 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 June 2020 (Figure 1a). The second is again based on viruses with collection dates from 1 February 2020, but with sequences deposited in GISAID during July 2020; a total of 363 sequences were 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]. 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 split 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 into 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 been detected. However, as indicated in previous reports, based on sequences deposited in GISAID for viruses detected from 1 February 2020 onwards, the vast majority fell in subgroup 6B.1A5A, with an approximately equal split between two of the genetic clusters defined above, (i) and (iii), with a minority falling in subgroup **6B.1A5B** (Figures 1a and 1b). This pattern was seen for viruses detected in the USA and EU/EEA countries. Both phylogenies are made up of sequences from viruses detected in February and March, and have very similar profiles.

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 June 2020 report. The 49 test viruses are sorted by date of collection and genetic group/subgroup, if known at the time of writing this report. A total of 40 were subgroup **6B.1A5A** viruses, one each were subgroup **6B.1A5B** and subclade **6B.1A7** viruses and sequene is unknown (pending) for seven. Table 3-4 shows a summary of the results.

The panel of post-infection ferret antisera was raised against 10 individual viruses, three of which were egg-propagated viruses, representing recently recommended vaccine viruses. Antisera raised against nine of the viruses, all but that raised against A/Denmark/3280/2019, showed similar HI reactivity, recognising 19 to 36 (39–74%) test viruses at titres within twofold of respective homologous titres and 33 to 37 (67–76%) at titres within fourfold (Table 3-4). A/Denmark/3280/2019 is representative of a cluster of viruses carrying HA1 amino acid substitutions N156K, K130N, L161I and V250A, and antiserum raised against it recognised only 13 (27%) test viruses at titres within fourfold (all within twofold) of the homologous titre. Where sequence was known, all viruses recognised well by this antiserum carried the N156K substitution with additional HA1 amino acid substitutions (Table 3-2) and sequence is pending for three additional viruses detected in March that show good reactivity with the antiserum (Table 3-3). The viruses with HA1 N156K substitution showed poor reactivity with antisera raised against all three vaccine viruses.

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

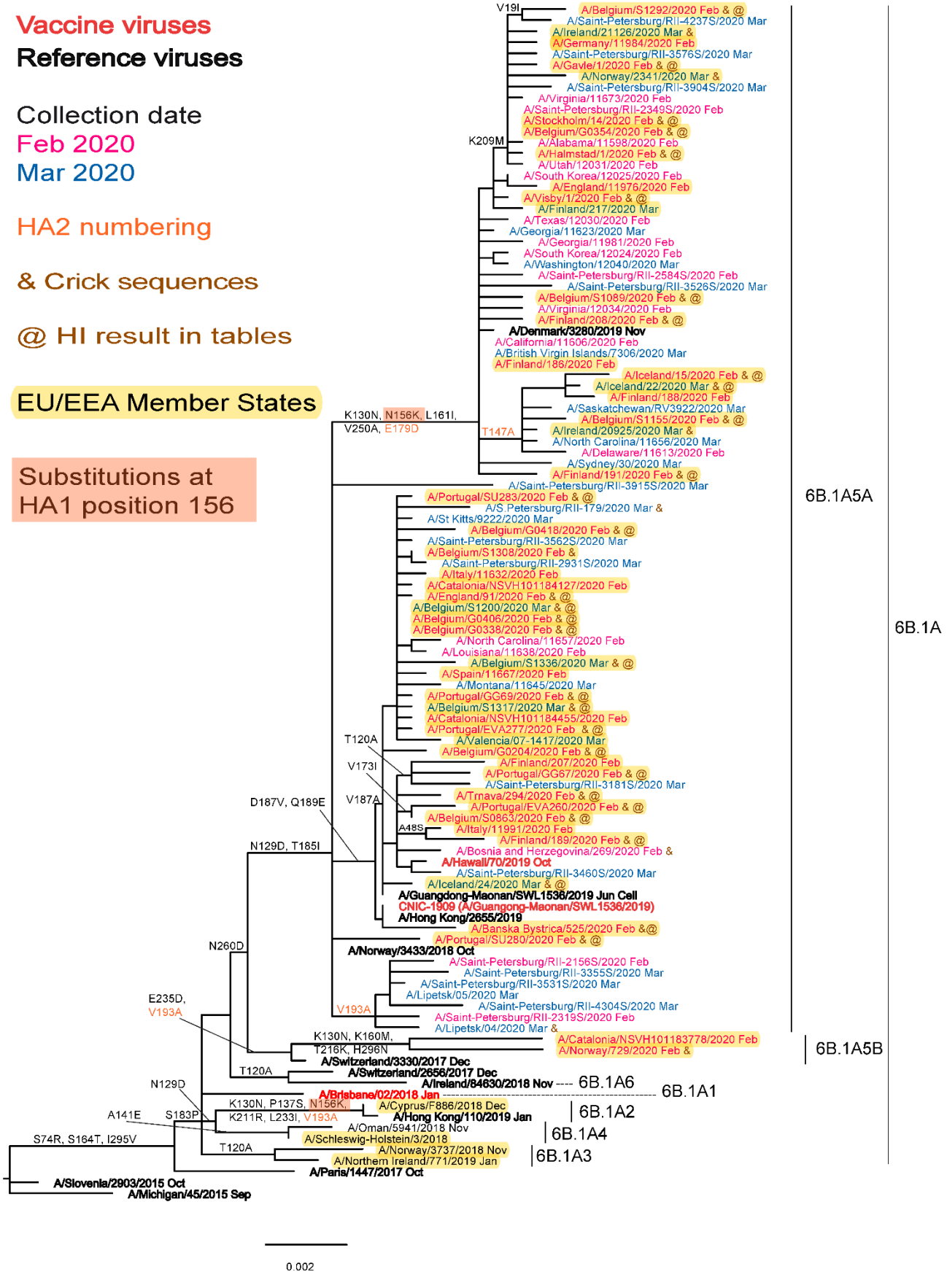

Figure 1b. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes (GISAID, July 2020)

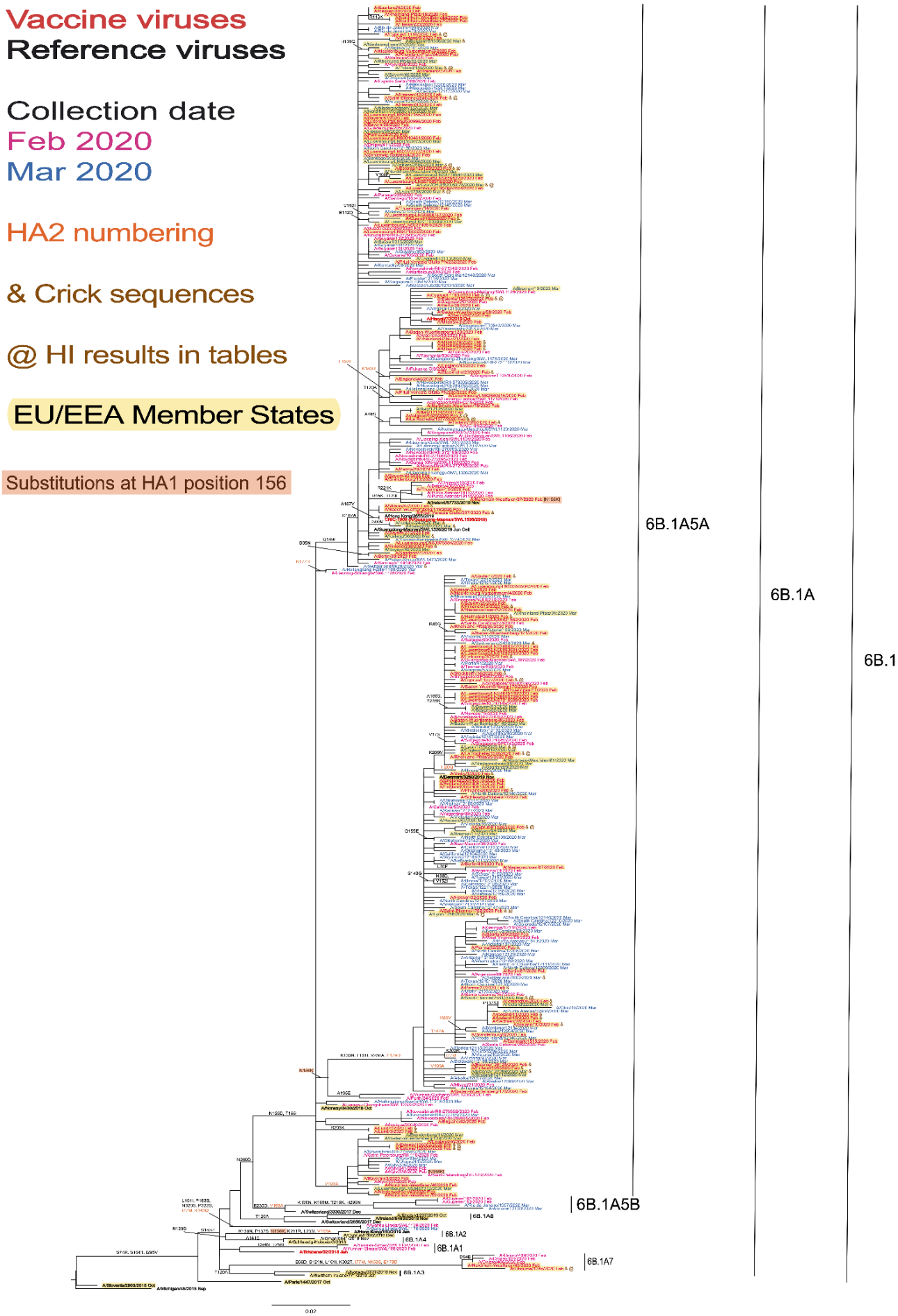

Table 3-1. Antigenic analysis of A(H1N1)pdm09 viruses by HI

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	640	1280	640	1280	40	640	1280	1280	640	1280	
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	1280	2560	1280	2560	<	1280	1280	2560	1280	2560	
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	1280	2560	1280	1280	40	640	1280	1280	1280	1280	
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	320	640	640	1280	<	640	640	640	320	640	
A/Denmark/3280/2019	N156K	6B.1A5A	2019-11-10	MDCK4/MDCK3	80	80	80	160	1280	80	80	160	80	40	
A/Ireland/87733/2019		6B.1A5A	2019-11-03	E4	1280	1280	1280	2560	40	1280	1280	1280	1280	1280	
A/Guangdong-Maonan/SWL1536/2019	D187A, Q189E	6B.1A5A	2019-06-17	E3/E1	640	640	640	2560	<	640	1280	1280	640	640	
A/Guangdong-Maonan/SWL1536/2019	D187A, Q189E	6B.1A5A	2019-06-17	C2/MDCK1	1280	1280	1280	2560	<	640	1280	1280	640	1280	
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	640	1280	1280	2560	<	320	640	640	640	640	
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	640	1280	640	1280	<	640	1280	1280	1280	1280	
TEST VIRUSES															
A/Estonia/126130/2020		6B.1A5A	2020-01-31	SIAT1/MDCK1	640	1280	640	2560	<	640	1280	1280	640	1280	
A/Estonia/126178/2020		6B.1A5A	2020-02-03	SIAT1/MDCK1	640	640	640	1280	<	320	640	640	320	640	
A/Estonia/126128/2020		6B.1A5A	2020-02-04	SIAT1/MDCK1	1280	1280	1280	2560	<	1280	1280	2560	640	1280	
A/Estonia/126062/2020		6B.1A5A	2020-02-04	SIAT1/MDCK1	640	1280	1280	2560	<	640	1280	1280	640	1280	
A/Estonia/126205/2020		6B.1A5A	2020-02-04	SIAT1/MDCK1	1280	640	1280	2560	<	640	1280	1280	640	1280	
					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 trees

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									
		Passage history			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
		Ferret number			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/Michigan/45/2015		6B.1	2015-09-07	E3/E3	640	1280	640	1280	40	640	1280	1280	640	1280
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	1280	2560	1280	2560	<	1280	1280	2560	640	2560
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	1280	2560	1280	1280	40	640	1280	1280	1280	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	320	640	640	1280	<	640	640	640	320	640
A/Denmark/3280/2019	N156K	6B.1A5A	2019-11-10	MDCK4/MDCK3	80	80	80	160	1280	80	80	80	80	40
A/Ireland/87733/2019		6B.1A5A	2019-11-03	E4	1280	1280	1280	2560	40	1280	1280	1280	1280	1280
A/Guangdong-Maonan/SWL1536/2019	D187A, Q189E	6B.1A5A	2019-06-17	E3/E1	640	640	640	2560	<	640	1280	1280	640	1280
A/Guangdong-Maonan/SWL1536/2019	D187A, Q189E	6B.1A5A	2019-06-17	C2/MDCK1	640	640	640	2560	<	640	640	1280	640	640
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	640	1280	1280	1280	<	320	640	640	640	640
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	640	1280	640	1280	<	640	1280	1280	1280	1280
TEST VIRUSES														
A/Paris/1066/2020		6B.1A5A	2020-02-11	MDCK1	640	1280	640	1280	<	320	640	640	320	640
A/Saint-Etienne/2546/2020		6B.1A5A	2020-02-12	MDCK2/MDCK1	640	1280	1280	2560	40	640	1280	1280	640	1280
A/Cyprus/F1116/2020		6B.1A5A	2020-02-16	MDCK1	640	1280	640	2560	40	640	1280	1280	640	1280
A/Champagne-Ardenne/1194/2020		6B.1A5A	2020-02-17	MDCK1	640	640	640	1280	<	320	640	640	320	640
A/Saint-Etienne/1762/2020	N156K, K130N, L161I, V250A	6B.1A5A	2020-02-17	MDCK2/MDCK1	40	<	40	160	640	<	40	40	40	<
A/La Rochelle/1578/2020	N156K, K130N, L161I, K209M, V250A	6B.1A5A	2020-02-17	MDCK2/MDCK1	40	<	40	160	640	<	80	40	40	40
A/Portugal/EVA307/2020		6B.1A5A	2020-02-18	MDCK1	1280	1280	640	2560	40	640	1280	640	320	640
A/Cyprus/F1128/2020	N156K, K130N, L161I, G170E, V250A	6B.1A5A	2020-02-19	MDCK1	80	80	80	320	1280	40	80	80	40	40
A/Cyprus/F1163/2020		6B.1A5A	2020-02-21	MDCK1	320	640	320	640	<	320	640	640	160	640
A/Cyprus/F1180/2020		6B.1A5A	2020-02-23	MDCK1	640	1280	1280	2560	40	640	1280	2560	640	1280
A/Guéret/1628/2020		6B.1A5A	2020-02-23	MDCK2/MDCK1	640	1280	1280	2560	40	640	1280	1280	640	1280
A/Poland/241/2020		6B.1A5A	2020-02-24	MDCK2	640	320	640	1280	<	320	640	640	320	640
A/Portugal/SU315/2020	N156K, K130N, L161I, K209M, V250A	6B.1A5A	2020-02-24	MDCK1	40	80	40	160	640	40	40	40	40	<
A/Portugal/SU314/2020		6B.1A5A	2020-02-24	MDCK1	320	320	320	640	<	160	320	320	160	320
A/Portugal/SU304/2020		6B.1A5A	2020-02-24	MDCK1	640	640	640	1280	40	320	640	640	320	640
A/La Rochelle/1577/2020		6B.1A5A	2020-02-24	MDCK2/MDCK1	1280	1280	1280	2560	40	640	1280	1280	640	1280
A/Poland/103/2020		6B.1A5A	2020-02-25	MDCK2	640	640	640	2560	<	320	1280	1280	640	1280
A/Avignon/1629/2020		6B.1A5A	2020-02-25	MDCK2/MDCK1	640	1280	640	2560	<	640	1280	1280	640	1280
A/Pays de Loire/1652/2020		6B.1A5A	2020-02-26	MDCK1	640	640	640	1280	<	320	1280	1280	320	320
A/Portugal/SU306/2020		6B.1A5A	2020-02-27	MDCK1	640	1280	640	1280	<	320	640	640	320	640
A/Cyprus/F1277/2020	N156K, K130N, L161I, S121N, K209M, V250A	6B.1A5A	2020-02-27	MDCK1	40	<	40	160	640	<	40	40	<	<
A/Portugal/SU317/2020	N156K, K130N, L161I, V250A	6B.1A5A	2020-02-29	MDCK1	40	80	40	160	640	40	40	40	40	<
A/Poland/159/2020		6B.1A5A	2020-03-02	MDCK1	640	640	640	1280	<	320	1280	1280	640	640
A/Portugal/EVA343/2020		6B.1A5A	2020-03-02	MDCK1	1280	1280	640	2560	40	640	1280	1280	320	640
A/Poland/169/2020		6B.1A5A	2020-03-03	MDCK2	320	320	320	1280	<	160	640	640	320	640
A/Cyprus/F1318/2020		6B.1A5A	2020-03-04	MDCK1	320	640	320	1280	<	320	640	640	160	320
A/Portugal/EVA339/2020		6B.1A5A	2020-03-05	MDCK1	640	1280	640	2560	<	640	1280	1280	320	640
A/Poitiers/2589/2020		6B.1A5A	2020-03-05	MDCK3/MDCK1	640	1280	640	2560	<	640	1280	1280	640	1280
A/Paris/2187/2020		6B.1A5A	2020-03-06	MDCK1	640	640	640	2560	40	320	1280	1280	640	640
A/Lyon/1758/2020		6B.1A5A	2020-03-07	MDCK2/MDCK1	640	640	640	1280	<	640	1280	1280	640	640
A/Lyon/CHU-R20.69.78/2020		6B.1A5A	2020-03-09	MDCK2/MDCK1	640	640	640	1280	<	320	640	640	320	640
A/Saint-Etienne/2581/2020	N156K, K130N, L161I, V250A	6B.1A5A	2020-03-09	MDCK3/MDCK1	40	<	40	80	640	40	40	40	40	<
A/Centre/2250/2020		6B.1A5A	2020-03-10	MDCK1	1280	1280	1280	2560	40	640	1280	2560	1280	1280
A/Lyon/1756/2020	N156K, K130N, L161I, V250A	6B.1A5A	2020-03-10	MDCK2/MDCK1	40	<	40	160	640	<	40	40	40	<
A/Lyon/1799/2020	N156K, K130N, L161I, K209M, V250A	6B.1A5A	2020-03-16	MDCK3/MDCK1	40	<	40	160	640	<	40	40	40	<
A/Portugal/MS71/2020		6B.1A5B	2020-02-05	MDCK1	640	1280	640	1280	40	320	640	640	320	640
A/Libourne/1245/2020		6B.1A7	2020-02-15	MDCK2/MDCK1	640	1280	1280	1280	<	320	1280	1280	640	1280
A/Portugal/EVA265/2020		No seq	2020-02-03	MDCK3	40	<	<	80	640	<	<	40	<	<
					Vaccine NH 2018-19		Vaccine NH 2019-20				Vaccine NH 2020-21			
					SH 2019		SH 2020							

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

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

Sequences in phylogenetic trees

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/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
	Ferret number			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/Michigan/45/2015	6B.1	2015-09-07	E3/E3	1280	1280	640	1280	<	640	1280	1280	1280	1280
A/Paris/1447/2017	6B.1A	2017-10-20	MDCK1/MDCK3	1280	2560	1280	2560	<	1280	1280	2560	640	2560
A/Brisbane/02/2018	6B.1A1	2018-01-04	E3/E1	1280	2560	1280	1280	40	640	1280	1280	640	1280
A/Norway/3433/2018	6B.1A5A	2018-10-30	MDCK3	320	640	640	1280	<	640	640	640	320	640
A/Denmark/3280/2019	6B.1A5A N156K	2019-11-10	MDCK4/MDCK3	80	80	80	160	1280	80	80	80	80	40
A/Ireland/87733/2019	6B.1A5A	2019-11-03	E4	1280	1280	1280	2560	40	1280	1280	1280	1280	1280
A/Guangdong-Maonan/SWL1536/2019	6B.1A5A D187A, Q189E	2019-06-17	E3/E1	640	1280	1280	2560	<	640	1280	1280	640	1280
A/Guangdong-Maonan/SWL1536/2019	6B.1A5A D187A, Q189E	2019-06-17	C2/MDCK1	640	640	640	2560	<	640	1280	1280	640	640
A/Switzerland/3330/2017	6B.1A5B clone 35	2017-12-20	E6/E2	640	640	1280	1280	<	320	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
TEST VIRUSES													
A/Bulgaria/1006/2020	pending	2020-02-17	SIAT2/MDCK1	640	1280	1280	1280	<	640	1280	640	320	640
A/Bulgaria/1169/2020	pending	2020-02-29	SIAT2/MDCK1	640	1280	1280	1280	<	640	1280	1280	640	640
A/Ireland/20619/2020	pending	2020-03-03	MDCK3	80	80	40	160	640	40	80	40	40	40
A/Ireland/21126/2020	pending	2020-03-04	MDCK3	40	<	40	80	640	40	40	40	<	<
A/Ireland/20925/2020	pending	2020-03-04	MDCK1	40	80	40	160	640	<	40	40	40	<
A/Bulgaria/1257/2020	pending	2020-03-04	SIAT2/MDCK1	640	1280	1280	1280	<	640	1280	1280	640	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 trees

Table 3-4. Antigenic analysis of A(H1N1)pdm09 viruses by HI - Summary

Viruses	Other information	Haemagglutination inhibition titre – Post-infection ferret antisera										
		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
	Passage history	Egg	MDCK	Egg	MDCK	MDCK	Egg	Egg	MDCK	Egg	MDCK
	Ferret number	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/Michigan/45/2015	6B.1	1280	1280	640	1280	<	640	1280	1280	1280	1280
A/Paris/1447/2017	6B.1A	1280	2560	1280	2560	<	1280	1280	2560	640	2560
A/Brisbane/02/2018	6B.1A1	1280	2560	1280	1280	40	640	1280	1280	640	1280
A/Norway/3433/2018	6B.1A5A	320	640	640	1280	<	640	640	640	320	640
A/Denmark/3280/2019	6B.1A5A N156K	80	80	80	160	1280	80	80	80	80	40
A/Ireland/87733/2019	6B.1A5A	1280	1280	1280	2560	40	1280	1280	1280	1280	1280
A/Guangdong-Maonan/SWL1536/2019	6B.1A5A D187A, Q189E	640	1280	1280	2560	<	640	1280	1280	640	1280
A/Guangdong-Maonan/SWL1536/2019	6B.1A5A D187A, Q189E	640	640	640	2560	<	640	1280	1280	640	640
A/Switzerland/3330/2017	6B.1A5B clone 35	640	640	1280	1280	<	320	640	640	640	640
A/Ireland/84630/2018	6B.1A6	640	1280	640	2560	40	640	1280	1280	1280	1280
TEST VIRUSES											
Number of viruses tested[$]		49	49	49	49	49	49	49	49	49	49
Fold reduction in HI titre	2	36	21	32	36	13	19	35	35	33	33
	%	73.5	42.9	65.3	73.5	26.5	38.8	71.4	71.4	67.3	67.3
	4		12	4	1		15	1	1	3	3
	%		24.5	8.2	2.1		30.6	2.1	2.1	6.2	6.2
	8	13	16	13	12	36	15	13	13	13	13
	%	26.5	32.6	26.5	24.4	73.5	30.6	26.5	26.5	26.5	26.5
		Vaccine NH 2018-19 SH 2019		Vaccine NH 2019-20 SH 2020				Vaccine NH 2020-21			

[$] Of the viruses tested 42 were genetically characterised and fell in the following clades/subclades: 6B.1A5A n = 40 (95.2%), 6B.1A5B n = 1 (2.4%), 6B.1A7 n = 1 (2.4%)
Reference virus results are taken from individual tables as examples. Summaries for each antiserum are based on fold-reductions observed on the days that HI assays were performed.

Influenza A(H3N2) virus analyses

The first A(H3N2) HA phylogeny is repeated from the June 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 June 2020 (Figure 2a). The second is again based on viruses with collection dates from 1 February 2020, but with sequences deposited in GISAID during July 2020; a total of 289 sequences (Figure 2b).

Viruses in clade 3C.2a have been dominant since the 2014–15 influenza season, and subgroup 3C.2a1b viruses predominated during 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 June report, based on sequences recently deposited in GISAID, showed viruses in the **3C.2a1b** subgroup to have circulated in the greatest numbers, with approximately equal distribution between the **3C.2a1b+T131K**, **3C.2a1b+T135K-A** and **3C.2a1b+T135K-B** clusters (Figure 2a). The significant geographical 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 influenza season [3]. The geographical 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 July is mainly made up of sequences from viruses detected in North America and Europe during February and March, with some from Asia, South America and the Middle East (Figure 2b). The two phylogenies are very similar with regard 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 season [3], 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 initially highlighted in the November 2014 report[3], this is a particular problem for most viruses that fall into the genetic clade **3C.2a**.

Since the June 2020 characterisation report of the viruses recovered, based on positive neuraminidase activity, 68 retained sufficient HA activity to allow antigenic analysis by HI (Tables 4-1 to 4-4). Test viruses are sorted by date of collection and genetic group/subgroup, if known at the time of writing this report; 39 were clade **3C.3a** viruses, 27 were subgroup **3C.2a1b** viruses (14, 12 and one in clusters **T131K**, **T135K-A** and **T135K-B**, respectively) and two have not been sequenced. Results are summarised in Table 4-5.

The panel of antisera were raised against seven individual clade **3C.2a** viruses and three clade **3C.3a** viruses (Table 4-5). Those raised against tissue culture-propagated A/Hong Kong/5738/2014 (**3C.2a**) and A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) recognised 38 (56%) and 21 (31%) test viruses, respectively, at titres within fourfold of their

[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 from: 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 from: https://www.ecdc.europa.eu/sites/default/files/media/en/publications/Publications/ERLI-Net%20report%20November%202014.pdf

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 21 (31%) and 24 (35%) test viruses respectively at titres of 160 or above. Antisera raised against two previous egg-propagated vaccine viruses, A/Singapore/INFIMH-16-0019/2016 (**3C.2a1**) and A/South Australia/34/2019 (**3C.2a1b+T131K**), recognised 65 (96%) and nine (13%) test viruses, respectively, at titres within fourfold of their homologous titres. The antiserum raised against egg-propagated A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**), the vaccine virus for the northern hemisphere 2020-21 influenza season, recognised only six (9%) test viruses at titre 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, recognised 60 (88%) and 44 (65%) test viruses, respectively, 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 21 (31%) 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 66 test viruses genetically characterised fell in the following clades/subclades: **3C.3a** n = 39 (59.1%), **3C.2a1b+T131K** n = 14 (21.2%), **3C.2a1b+T135K-A** n = 12 (18.2%) and **3C.2a1b+T135K-B** n = 1 (1.5%).

Overall, the HI data show strong clade/subclade-specific recognition of test viruses by post-infection ferret antisera raised against cell culture-propagated reference viruses. Antisera raised against the four egg-propagated vaccine viruses and based on test virus recognition fourfold reduced compared to homologous titres: A/South Australia/34/2019 (**3C.2a1b+T131K**) had a consistently high homologous titre (1280) and showed poor recognition of test viruses (13%), with the majority of titres being ≤40. A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) had a homologous titre of 640 and showed poor recognition of test viruses (9%) but with titres of ≥40; NYMC X-327 (A/Kansas/14/2017, **3C.3a**) had a consistently high homologous titre (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 being ≥80.

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

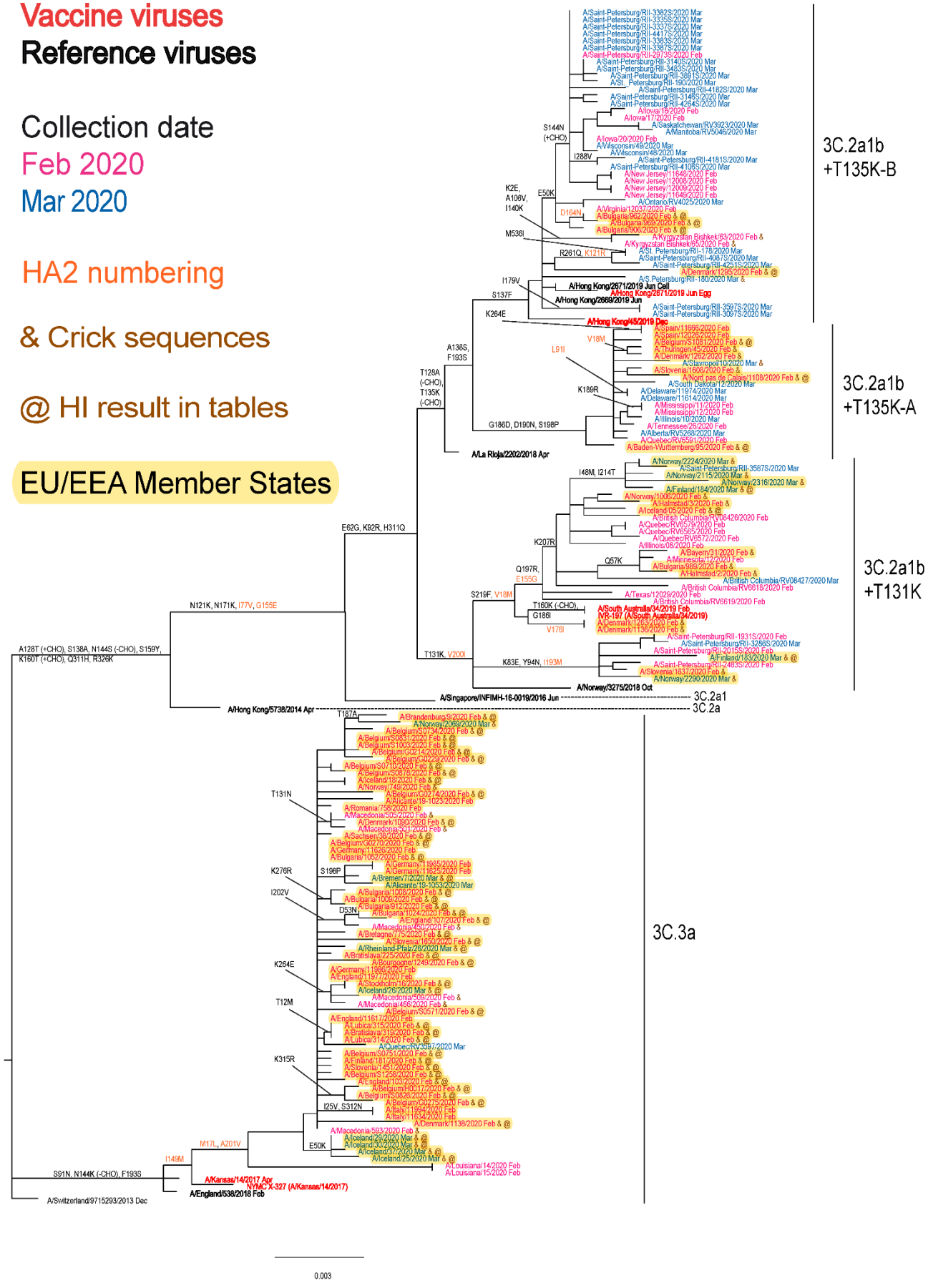

Figure 2b. Phylogenetic comparison of influenza A(H3N2) HA genes (GISAID, July 2020)

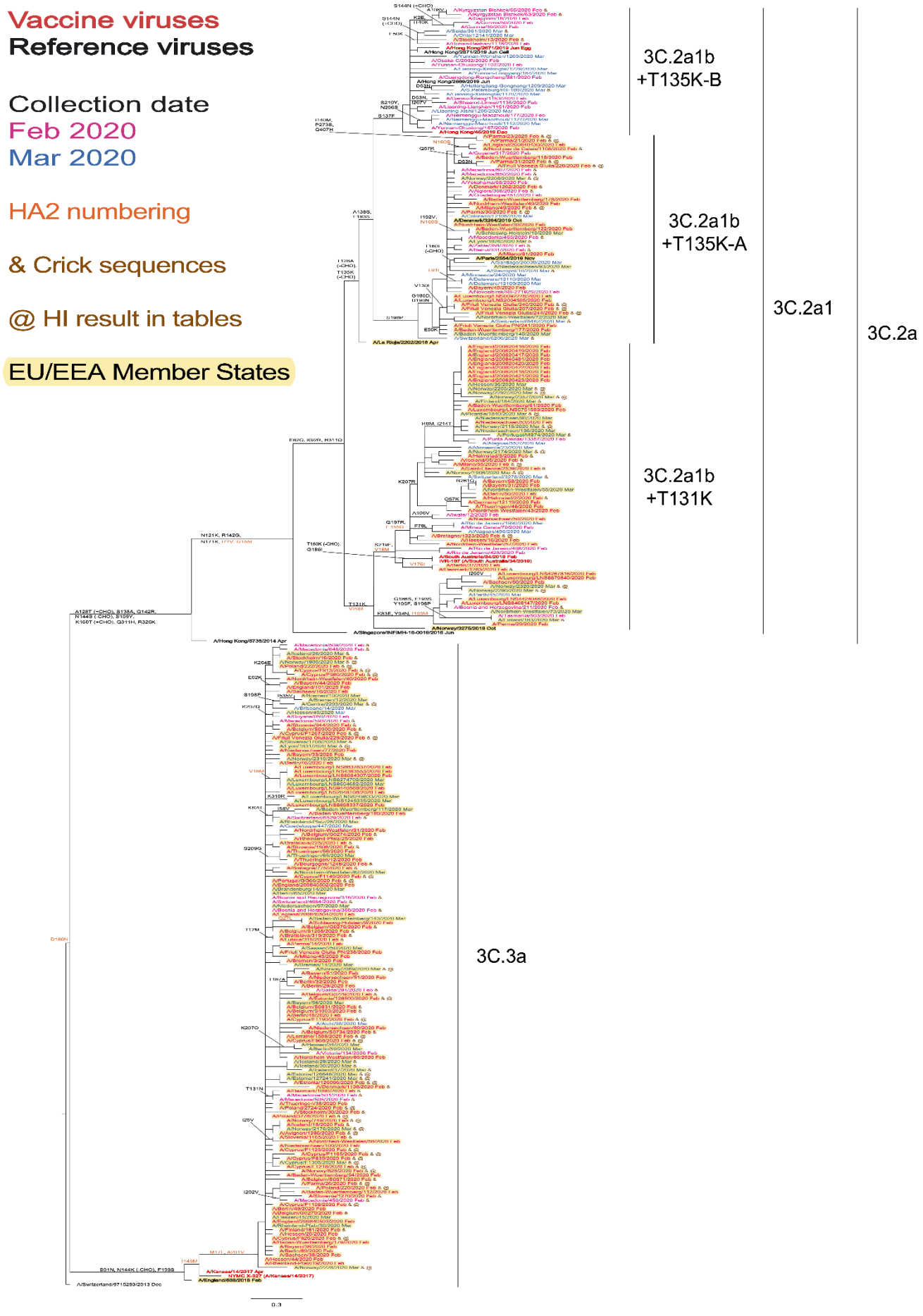

Table 4-1. Antigenic analysis of A(H3N2) viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre											
				Post-infection ferret antisera											
	Passage history			A/HK	A/Singapore	A/Norway	A/Sth Aus	A/La Rioja	A/HK	A/HK	AJEng	NYMC X-327	A/Kansas
				5738/14	0019/16	3275/18	34/19	2202/18	2671/19	2671/19	538/18	A/Kansas/14	14/17
				MDCK	Egg 10^{-4}	SIAT	Egg	SIAT	Egg	Cell	SIAT	Egg	SIAT
	Ferret number			St Judes F60/17[-1]	F13/19[-1]	F03/19[-1]	F45/19[-1]	F26/18[-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+T131K	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	320	320	320	160	160	40	160	320	160	160
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	320	80	40	320	80	40	40	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	320	1280	1280	80	320	40	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E2	40	160	<	80	40	640	160	160	640	80
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	CK1/SIAT4	160	320	320	160	320	320	640	160	160	160
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	80	<	40	<	40	80	320	320	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	80	80	<	40	40	320	160	320	1280	640
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	40	40	40	80	80	320	160	320
TEST VIRUSES													
A/Milano/55/2020	3C.2a1b+T131K	2020-02-10	SIAT2/SIAT1	320	320	320	320	320	40	160	160	160	160
A/Bretagne/1323/2020	3C.2a1b+T131K	2020-02-20	SIAT1	40	160	80	160	160	160	80	40	<	40
A/Picardie/1840/2020	3C.2a1b+T131K	2020-03-02	SIAT1	40	80	80	160	160	40	160	40	40	<
A/Parma/21/2020	3C.2a1b+T135K-A	2020-02-05	SIAT2/SIAT1	80	80	160	80	160	80	320	160	80	40
A/Friuli Venezia Giulia/240/2020	3C.2a1b+T135K-A	2020-02-08	SIAT2/SIAT1	40	80	80	<	80	40	160	40	<	<
A/Milano/49/2020	3C.2a1b+T135K-A	2020-02-10	SIAT2/SIAT1	40	160	80	<	160	160	160	80	80	80
A/Friuli Venezia Giulia/228/2020	3C.2a1b+T135K-A	2020-02-10	SIAT2/SIAT1	40	80	160	40	160	80	320	40	<	<
A/Parma/23/2020	3C.2a1b+T135K-A	2020-02-10	SIAT2/SIAT1	80	160	160	80	160	80	320	80	40	40
A/Friuli Venezia Giulia/257/2020	3C.2a1b+T135K-A	2020-02-11	SIAT2/SIAT1	40	80	80	<	80	40	160	40	<	<
A/Friuli Venezia Giulia/244/2020	3C.2a1b+T135K-A	2020-02-11	SIAT2/SIAT1	40	80	80	<	80	40	80	40	<	<
A/Parma/31/2020	3C.2a1b+T135K-A	2020-02-12	SIAT2/SIAT1	40	160	160	80	160	40	320	40	<	<
A/Parma/30/2020	3C.2a1b+T135K-A	2020-02-17	SIAT2/SIAT1	40	160	80	80	160	80	320	80	40	40
A/Friuli Venezia Giulia/229/2020	3C.3a	2020-02-10	SIAT2/SIAT1	40	80	<	<	<	40	40	320	160	160
A/Parma/26/2020	3C.3a	2020-02-12	SIAT2/SIAT1	40	80	<	<	<	40	40	320	160	320
A/Lorraine/1589/2020	3C.3a	2020-02-24	SIAT1	40	80	<	<	<	40	40	320	160	320
A/Centre/2293/2020	3C.3a	2020-03-09	SIAT1	40	80	<	<	<	40	40	320	160	160
					Vaccine NH 2018-19		Vaccine SH 2020		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 trees

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 St Judes F60/17[-1]	A/Singapore 0019/16 Egg 10^{-4} F13/19[-1]	A/Norway 3275/18 SIAT F03/19[-1]	A/Sth Aus 34/19 Egg F45/19[-1]	A/La Rioja 2202/18 SIAT F26/18[-1]	A/HK 2671/19 Egg F44/19[-1]	A/HK 2671/19 Cell St Judes F21/20[-1]	A/Eng 538/18 SIAT F31/18[-1]	NYMC X-327 A/Kansas/14 Egg F16/19[-1]	A/Kansas 14/17 SIAT F17/19[-1]
	Ferret number												
	Genetic group			3C.2a	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	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	320	320	320	320	160	40	160	320	160	320
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	320	80	80	160	80	40	40	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	320	640	1280	1280	80	320	40	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E2	40	160	<	80	40	640	160	160	640	80
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	CK1/SIAT4	160	320	320	160	320	320	640	160	160	160
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	80	<	40	<	80	80	320	320	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	80	80	<	80	40	320	80	320	1280	640
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	40	80	40	80	80	320	160	640
TEST VIRUSES													
A/Lyon/162/2020	3C.2a1b+T131K	2020-01-16	MDCK2/SIAT1	160	320	640	320	320	160	80	160	80	80
A/Saint-Etienne/2539/2020	3C.2a1b+T131K	2020-02-11	MDCK3/SIAT1	80	160	320	320	80	80	80	40	40	40
A/Portugal/MS74/2020	3C.2a1b+T131K	2020-03-21	SIAT1	160	160	160	80	160	80	320	320	160	160
A/Lyon/86/2020	3C.2a1b+T135K-A	2020-01-09	MDCK2/SIAT1	40	80	80	40	80	80	160	80	40	80
A/Lyon/219/2020	3C.2a1b+T135K-A	2020-01-20	MDCK2/SIAT1	160	320	320	160	320	160	320	320	320	160
A/Lyon/CHU/R19.146.85/2019	3C.2a1b+T135K-B	2019-12-19	MDCK4/SIAT1	80	160	160	80	160	160	160	160	80	80
A/Lyon/CHU/R19.154.50/2019	3C.3a	2019-12-31	MDCK2/SIAT1	80	80	80	80	40	80	80	640	320	320
A/Grenoble/185/2020	3C.3a	2020-01-10	MDCK2/SIAT1	40	80	40	80	40	80	40	640	640	320
A/Cyprus/F835/2020	3C.3a	2020-02-02	SIAT1	40	<	40	80	<	40	40	640	160	320
A/Cyprus/F913/2020	3C.3a	2020-02-04	SIAT1	160	160	80	80	80	80	80	640	320	640
A/Cyprus/F926/2020	3C.3a	2020-02-05	SIAT1	80	80	40	80	40	40	80	640	320	320
A/Cyprus/F960/2020	3C.3a	2020-02-07	SIAT1	80	80	40	80	40	80	80	640	320	320
A/Portugal/GG66/2020	3C.3a	2020-02-08	SIAT1	40	80	40	40	40	80	80	640	320	640
A/Cyprus/F1108/2020	3C.3a	2020-02-16	SIAT1	80	160	40	80	40	80	80	640	320	640
A/Poland/222/2020	3C.3a	2020-02-17	SIAT1	80	160	80	160	80	80	40	160	80	640
A/Poland/220/2020	3C.3a	2020-02-17	SIAT1	80	160	40	80	80	80	40	640	320	640
A/Avignon/1286/2020	3C.3a	2020-02-17	MDCK2/SIAT1	80	160	40	80	40	80	80	640	320	320
A/Poland/2724/2020	3C.3a	2020-02-18	SIAT1	80	160	40	80	40	80	80	640	320	640
A/Poland/3278/2020	3C.3a	2020-02-26	SIAT1	80	160	40	80	40	80	80	640	320	640
A/Lyon/1631/2020	3C.3a	2020-03-01	MDCK3/SIAT1	80	160	40	80	40	80	80	640	320	320
					Vaccine NH 2018-19		Vaccine SH 2020		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 trees

Table 4-3. 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 St Judes F60/17[-1]	A/Singapore 0019/16 Egg 10[-4]	A/Norway 3275/18 SIAT	A/Sth Aus 34/19 Egg	A/La Rioja 2202/18 SIAT	A/HK 2671/19 Egg	A/HK 2671/19 Cell St Judes F21/20[-1]	A/Eng 538/18 SIAT	NYMC X-327 A/Kansas/14 Egg	A/Kansas 14/17 SIAT
	Ferret number			F13/19[-1]	F03/19[-1]	F45/19[-1]	F26/18[-1]	F44/19[-1]	F31/18[-1]	F16/19[-1]	F17/19[-1]		
	Genetic group			3C.2a	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	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	320	320	320	320	160	40	160	320	160	320
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	320	80	80	160	80	40	80	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	320	640	1280	1280	80	160	40	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E2	40	160	<	80	40	640	160	160	640	80
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	CK1/SIAT4	160	320	320	160	320	320	640	160	160	160
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	80	<	40	<	80	80	320	320	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	80	80	<	80	40	320	80	320	1280	640
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	40	40	40	80	80	320	160	640
TEST VIRUSES													
A/Norway/1906/2020	3C.2a1b+T131K	2020-03-12	SIAT1	160	320	320	320	160	40	80	160	80	40
A/Norway/2205/2020	3C.2a1b+T131K	2020-03-15	SIAT1	160	160	320	160	160	40	160	160	80	40
A/Norway/2174/2020	3C.2a1b+T131K	2020-03-17	SIAT1	160	160	320	320	160	80	160	160	80	40
A/Norway/2115/2020	3C.2a1b+T131K	2020-03-18	SIAT1	160	160	640	160	160	40	160	160	80	40
A/Norway/2292/2020	3C.2a1b+T131K	2020-03-20	SIAT1	160	160	320	320	160	40	160	160	80	40
A/Norway/2320/2020	3C.2a1b+T131K	2020-03-24	SIAT1	160	160	320	160	160	<	40	160	160	80
A/Norway/2290/2020	3C.2a1b+T131K	2020-03-24	SIAT1	160	160	320	320	160	80	80	320	80	80
A/Norway/2357/2020	3C.2a1b+T131K	2020-03-28	SIAT1	160	320	320	320	320	40	160	320	160	80
A/Norway/2208/2020	3C.2a1b+T135K-A	2020-03-14	SIAT1	80	160	160	80	160	80	160	160	80	40
A/Estonia/126086/2020	3C.3a	2020-01-30	SIAT1/SIAT1	<	40	<	<	<	<	40	320	160	160
A/Estonia/126096/2020	3C.3a	2020-02-01	SIAT1/SIAT1	<	80	<	<	<	40	<	320	160	320
A/Norway/749/2020	3C.3a	2020-02-03	SIAT1	40	80	<	<	<	40	40	320	160	320
A/Norway/828/2020	3C.3a	2020-02-06	SIAT1	40	80	<	<	<	40	40	320	160	320
A/Estonia/126500/2020	3C.3a	2020-02-19	SIAT1/SIAT1	<	40	<	<	<	<	<	320	160	160
A/Estonia/126846/2020	3C.3a	2020-03-02	SIAT1/SIAT1	<	80	<	<	<	40	40	320	160	320
A/Estonia/127241/2020	3C.3a	2020-03-05	SIAT1/SIAT2	40	80	<	80	<	80	40	320	320	320
A/Norway/2069/2020	3C.3a	2020-03-12	SIAT1	<	80	<	<	<	<	<	640	160	160
A/Norway/1900/2020	3C.3a	2020-03-12	SIAT1	<	80	<	<	<	40	40	640	160	320
A/Norway/2228/2020	3C.3a	2020-03-15	SIAT1	80	80	40	80	<	80	40	640	160	320
A/Norway/2176/2020	3C.3a	2020-03-18	SIAT2	40	80	<	<	<	40	40	640	160	320
A/Norway/2310/2020	3C.3a	2020-03-28	SIAT1	40	80	<	40	<	40	40	640	160	160
A/Norway/2231/2020	No seq	2020-03-16	SIAT1	80	160	320	160	160	<	80	160	80	40
					Vaccine NH 2018-19		Vaccine SH 2020		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 trees

Table 4-4. 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 St Judes $F60/17^{-1}$	A/Singapore 0019/16 Egg 10^{-4} $F13/19^{-1}$	A/Norway 3275/18 SIAT $F03/19^{-1}$	A/Sth Aus 34/19 Egg $F45/19^{-1}$	A/La Rioja 2202/18 SIAT $F26/18^{-1}$	A/HK 2671/19 Egg $F44/19^{-1}$	A/HK 2671/19 Cell St Judes $F21/20^{-1}$	A/Eng 538/18 SIAT $F31/18^{-1}$	NYMC X-327 A/Kansas/14 Egg $F16/19^{-1}$	A/Kansas 14/17 SIAT $F17/19^{-1}$
	Ferret number												
	Genetic group			3C.2a	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	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	320	320	320	320	160	40	160	320	160	320
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	320	80	80	160	80	40	40	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	320	640	1280	1280	80	320	40	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E2	40	160	<	80	80	640	160	160	640	80
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	CK1/SIAT4	160	320	320	160	320	320	640	320	160	160
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	80	<	40	<	80	80	320	320	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	40	80	<	40	40	320	40	320	1280	640
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	80	40	40	40	80	80	640	160	640
TEST VIRUSES													
A/Cyprus/F411/2020	3C.3a	2020-01-21	SIAT1	160	160	<	40	<	40	80	1280	640	640
A/Cyprus/F968/2020	3C.3a	2020-02-10	SIAT1	40	160	<	40	<	<	40	640	320	640
A/Cyprus/F1123/2020	3C.3a	2020-02-17	SIAT1	40	160	<	<	<	<	40	640	320	640
A/Cyprus/F1190/2020	3C.3a	2020-02-23	SIAT1	160	320	<	80	40	80	80	1280	640	640
A/Cyprus/F1165/2020	3C.3a	2020-02-23	SIAT1	160	320	<	40	40	80	80	1280	320	640
A/Cyprus/F1149/2020	3C.3a	2020-02-23	SIAT1	80	320	80	160	40	80	40	1280	320	640
A/Cyprus/F1218/2020	3C.3a	2020-02-25	SIAT1	160	320	<	40	80	40	80	640	320	640
A/Cyprus/F1267/2020	3C.3a	2020-02-27	SIAT1	80	160	40	40	40	40	80	640	160	640
A/Cyprus/F1305/2020	3C.3a	2020-03-03	SIAT1	80	160	40	40	40	40	80	640	160	640
A/Ireland/23296/2020	pending	2020-03-09	SIAT1	160	320	320	320	320	160	320	320	80	160
					Vaccine NH 2018-19		Vaccine SH 2020		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 trees

Table 4-5. Antigenic analysis of A(H3N2) viruses by HI – Summary

Viruses	Other information	Haemagglutination inhibition titre											
		Post-infection ferret antisera											
		A/HK 5738/14	A/Singapore 0019/16	A/Norway 3275/18	A/Sth Aus 34/19	A/La Rioja 2202/18	A/HK 2671/19	A/HK 2671/19	A/Eng 538/18	NYMC X-327 A/Kansas/14	A/Kansas 14/17
	Passage history	MDCK	Egg 10^{-4}	SIAT	Egg	SIAT	Egg	Cell	SIAT	Egg	SIAT
	Ferret number	St Jude's F60/17[*1]	F13/19[*1]	F03/19[*1]	F45/19[*1]	F26/18[*1]	F44/19[*1]	St Jude's F21/20[*1]	F31/18[*1]	F16/19[*1]	F17/19[*1]
	Genetic group	3C.2a	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	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	320	320	320	320	160	40	160	320	160	320
A/Singapore/INFIMH-16-0019/2016	3C.2a1	160	320	80	80	160	80	40	40	40	<
A/South Australia/34/2019	3C.2a1b+T131K	320	640	1280	1280	80	320	40	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	40	160	<	80	80	640	160	160	640	80
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	160	320	320	160	320	320	640	160	160	160
A/England/538/2018	3C.3a	40	80	<	40	<	80	80	320	320	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	40	80	<	40	40	320	40	320	1280	640
A/Kansas/14/2017	3C.3a	40	80	40	40	40	80	80	640	160	640
TEST VIRUSES											
Number of viruses tested[$]		68	68	68*	68	68*	68	68	68	68	68
Fold reduction in HI titre											
2		18	39	21		24		8	56	3	36
%		26.5	57.4	30.9		35.3		11.8	82.4	4.4	52.9
4		20	26		9		6	13	4	18	8
%		29.4	38.2		13.2		8.8	19.1	5.8	26.5	11.8
8		30	3		59		62	47	8	47	24
%		44.1	4.4		86.8		91.2	69.1	11.8	69.1	35.3
			Vaccine NH 2018-19		Vaccine SH 2020		Vaccine NH 2020-21			Vaccine NH 2019-20	

[$] Of the viruses tested 66 were genetically characterised and fell in the following clades/subclades: 3C.3a n = 39 (59.1%), 3C.2a1b+T131K n = 14 (21.2%), 3C.2a1b+T135K-A n = 12 (18.2%), 3C.2a1b+T135K-B n = 1 (1.5%)

* Homologous HI titres not available - only results for viruses yielding HI titres of ≥160 with the respective antisera are shown

Reference virus results are taken from individual tables as examples. Summaries for each antiserum are based on fold-reductions observed on the days that HI assays were performed.

Influenza B virus analyses

A total of 485 influenza type B viruses with collection dates after 31 August 2019 have been received at the WIC (Table 2). Of these, 396 were sent with pre-assignment to a lineage: 378 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). This means 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 geographical spread in recent months and is represented by **B/Washington/02/2019**, the vaccine virus recommended in February 2020.

The HA phylogeny generated for the June report showed continued dominance of **subclade 1A(△3)B** viruses having **HA1 K136E,** often with **G133R** substitution, and a number of 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 July is again largely made up of viruses detected in the USA and Europe (with large numbers from Luxembourg and the Russian Federation) during February and March, with just three from April, two detected in Hawaii and one in China (Figure 3b), the phylogeny profile being 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 recommendation of a representative (B/Washington/02/2019) for use in trivalent influenza vaccines for the 2020 southern hemisphere and northern hemisphere 2020–2021 seasons [2, 3].

Of the B/Victoria-lineage viruses from EU/EEA countries received, 32 have been assessed by HI assay since the June 2020 report (Table 5). Test viruses are sorted by date of collection and all were subclade **1A(Δ3)B**.

Poor test virus reactivity with ferret antisera raised against viruses in **clade 1A** (n=4) was observed. 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 0 (0%), 14 (44%) and two (6%) 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 all and 28 (88%) test viruses, respectively, at titres within fourfold of their corresponding homologous titres. The 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 unusual amino acid substitutions in HA1 (i.e. N126K or T155A or N126K with R279K and K345R (Table 5).

Influenza B/Yamagata-lineage

One B/Yamagata-lineage virus has been characterised antigenically (Table 6) and genetically at the WIC since the June report. The HA phylogeny, for viruses with collection dates from 1 January 2020, has been updated from the June report to contain five sequences submitted to GISAID in June, one each from France and the Russian Federation, and three from Chile for viruses detected in January and February (Figure 4). As for other recently detected B/Yamagata-lineage viruses, the HA genes fall into 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] sometimes with **R48K**), has occurred. Three of the sequences recently deposited in GISAID, from Chile and France, 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 [2] southern hemisphere seasons. This remains the case for the virus, B/Pays de Loire/1150/2020, which was antigenically characterised in July (Table 6).

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

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

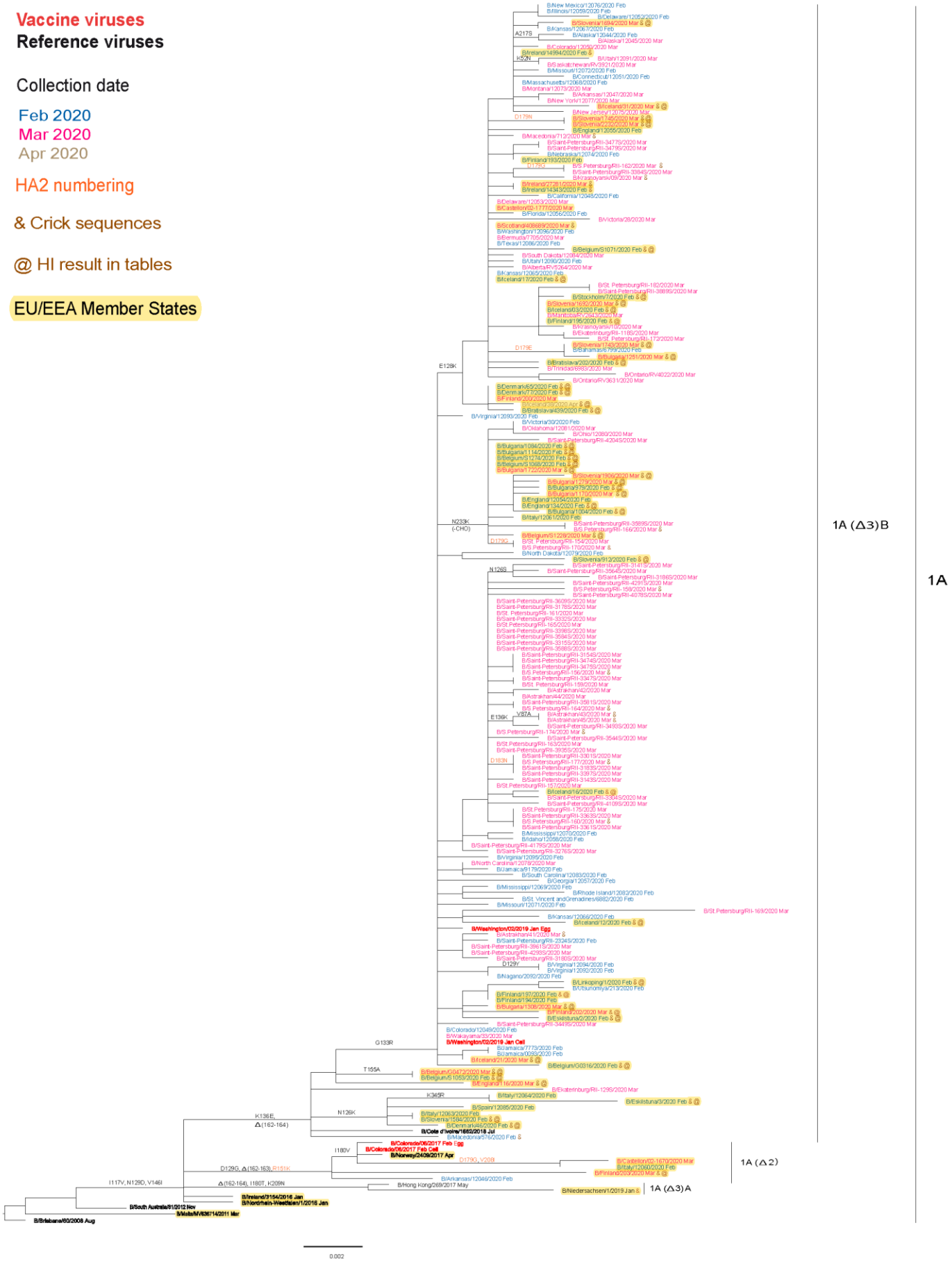

Figure 3b. Phylogenetic comparison of influenza B/Victoria-lineage HA genes (GISAID, July 2020)

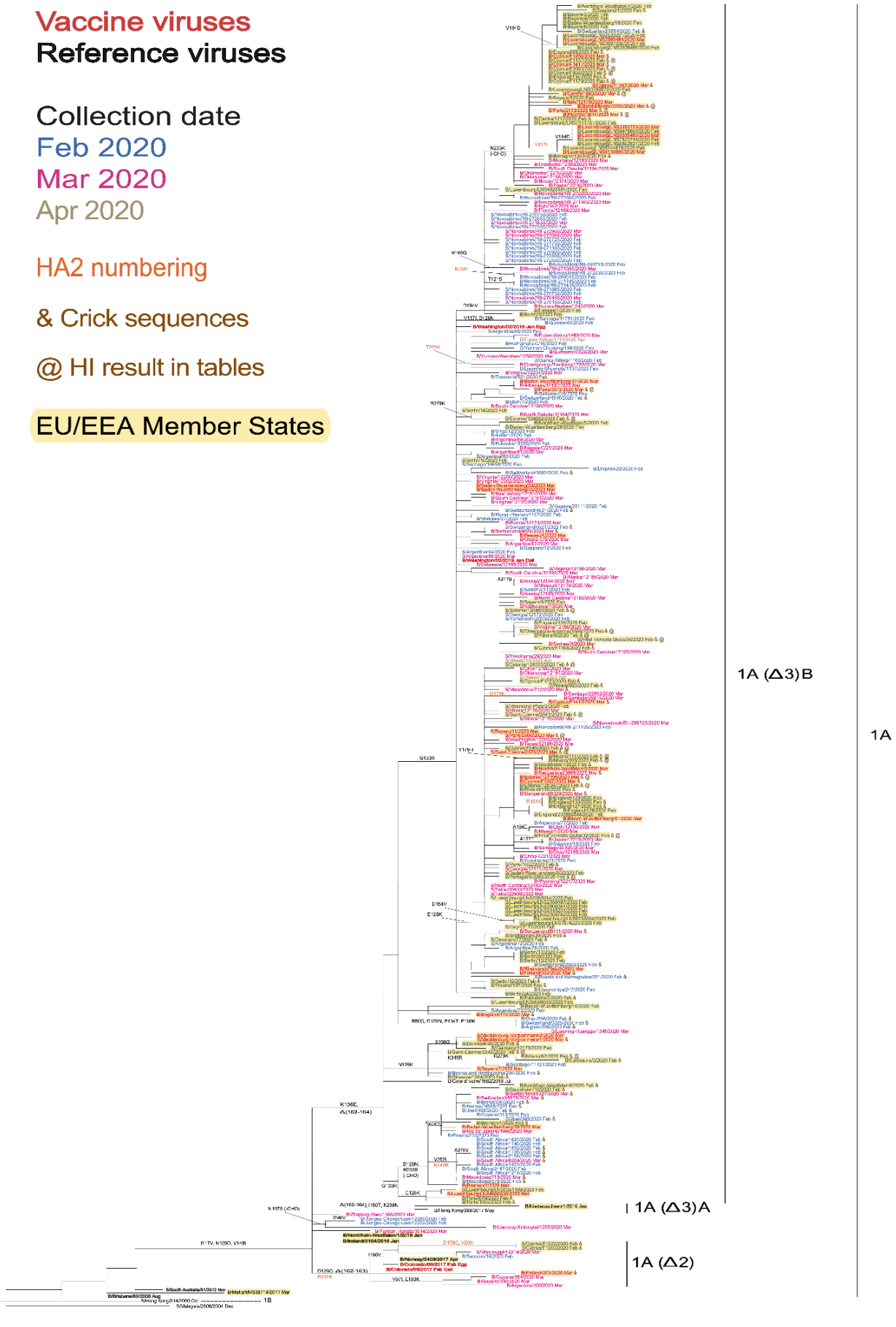

Table 5. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre											
				Post-infection ferret antisera											
	Passage history			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
	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			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)	1A(Δ3)
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	2560	1280	1280	80	160	<	20	160	<	320
B/Ireland/3154/2016	1A	2016-01-14	MDCK1/MDCK4	2560	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	80	<	<	<	<	80	80	160	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	MDCK1/MDCK2	80	<	<	<	<	80	80	160	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	E5/E2	1280	160	40	<	<	40	40	320	<	160
B/Washington/02/2019	1A(Δ3) B	2019-01-19	C2/MDCK3	1280	80	40	<	<	<	10	160	20	320
B/Washington/02/2019	1A(Δ3) B	2019-01-19	E3/E2	640	160	80	<	<	<	20	160	40	320
TEST VIRUSES													
B/Clermont-Ferrand/2411/2019	1A(Δ3) B	2019-12-28	MDCK2/MDCK1	40	20	10	<	<	<	10	10	40	160
B/Lyon/CHU-R20.2.98/2020	T155A 1A(Δ3) B	2020-01-04	MDCK2/MDCK1	160	20	20	<	<	<	10	20	20	20
B/Lyon/156/2020	T155A 1A(Δ3) B	2020-01-16	MDCK2/MDCK1	320	40	40	<	<	<	10	20	20	40
B/Lyon/225/2020	1A(Δ3) B	2020-01-20	MDCK2/MDCK1	80	20	20	<	<	<	10	20	20	160
B/Estonia/126087/2020	1A(Δ3) B	2020-01-30	SIAT1/MDCK1	80	40	10	<	<	10	10	20	40	320
B/Milano/62/2020	N126K, R279K, K345R 1A(Δ3) B	2020-02-04	MDCK2/MDCK1	<	10	10	<	<	<	10	10	20	10
B/Cyprus/F938/2020	1A(Δ3) B	2020-02-06	MDCK1	160	40	40	<	<	<	10	40	40	80
B/Cyprus/F949/2020	1A(Δ3) B	2020-02-07	MDCK1	160	40	20	<	<	<	10	20	40	320
B/Portugal/SU282/2020	1A(Δ3) B	2020-02-08	MDCK1	160	40	20	<	<	10	20	40	40	320
B/Friuli Venezia Giulia/32/2020	1A(Δ3) B	2020-02-10	MDCK2/MDCK1	160	20	20	<	<	<	10	20	40	160
B/Estonia/126333/2020	1A(Δ3) B	2020-02-11	SIAT1/MDCK1	80	40	20	<	<	10	20	40	40	320
B/Friuli Venezia Giulia/36/2020	1A(Δ3) B	2020-02-12	MDCK2/MDCK1	160	40	20	<	<	10	20	40	40	320
B/Parma/9/2020	1A(Δ3) B	2020-02-12	MDCK2/MDCK1	160	40	20	<	10	<	20	20	40	320
B/Cyprus/F1093/2020	1A(Δ3) B	2020-02-14	MDCK1	640	80	40	<	10	10	10	40	40	320
B/Estonia/126397/2020	1A(Δ3) B	2020-02-14	SIAT1/MDCK1	80	40	10	<	<	10	20	40	40	160
B/Cyprus/F1137/2020	1A(Δ3) B	2020-02-18	MDCK1	80	40	20	<	<	<	10	20	20	320
B/Estonia/126489/2020	1A(Δ3) B	2020-02-18	SIAT1/MDCK1	80	40	10	<	<	10	20	40	40	320
B/Saint-Etienne/2541/2020	1A(Δ3) B	2020-02-20	MDCK3/MDCK1	160	20	20	<	<	10	20	20	40	160
B/Cyprus/F1179/2020	1A(Δ3) B	2020-02-23	MDCK1	80	40	20	<	<	<	10	40	40	320
B/Champagne-Ardenne/1586/2020	1A(Δ3) B	2020-02-24	MDCK1	160	40	20	<	<	10	20	40	40	320
B/Milano/111/2020	1A(Δ3) B	2020-02-26	MDCK3/MDCK1	160	40	20	<	10	10	20	20	40	320
B/Milano/105/2020	1A(Δ3) B	2020-02-26	MDCK3/MDCK1	80	20	20	<	<	10	20	40	40	320
B/Saint-Etienne/2543/2020	N126K 1A(Δ3) B	2020-02-26	MDCK2/MDCK1	80	20	10	<	<	<	10	<	10	10
B/Estonia/126682/2020	1A(Δ3) B	2020-02-27	SIAT1/MDCK1	160	40	10	<	10	10	20	80	40	320
B/Saint-Etienne/2578/2020	1A(Δ3) B	2020-03-01	MDCK2/MDCK1	80	20	10	<	<	<	10	20	40	160
B/Centre/1963/2020	1A(Δ3) B	2020-03-02	MDCK1	160	40	40	<	10	10	20	40	40	320
B/Paris/2113/2020	1A(Δ3) B	2020-03-03	MDCK2	160	40	20	<	<	<	10	40	40	320
B/Saint-Etienne/2550/2020	1A(Δ3) B	2020-03-04	MDCK3/MDCK1	320	40	20	<	<	10	40	40	40	320
B/Estonia/127199/2020	1A(Δ3) B	2020-03-09	SIAT1/MDCK1	160	40	20	<	10	10	20	40	40	160
B/Paris/2560/2020	1A(Δ3) B	2020-03-13	MDCK1	80	40	20	<	<	10	10	40	40	320
B/Paris/3072/2020	1A(Δ3) B	2020-03-18	MDCK2	320	80	40	<	10	10	10	80	40	320
B/Picardie/3414/2020	1A(Δ3) B	2020-03-23	MDCK1	80	20	20	<	<	<	10	20	40	320
Sequences in phylogenetic trees											Vaccine SH 2019 NH 2019-20		Vaccine SH 2020 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

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

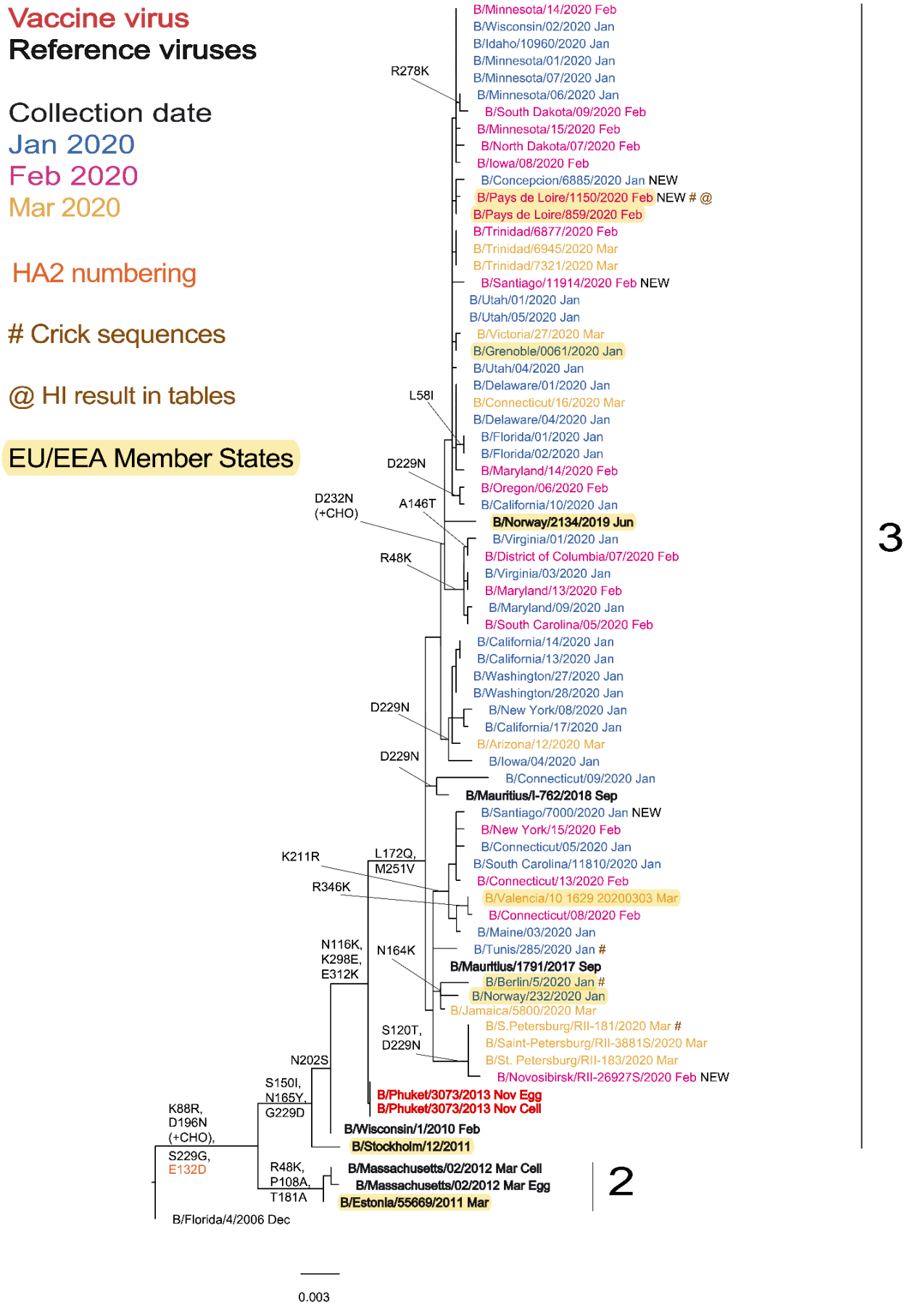

Table 6. Antigenic analysis of influenza B/Yamagata-lineage viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre									
				Post-infection ferret antisera									
	Passage history			B/Phuket 3073/13	B/Estonia 55669/11	B/Mass 02/12	B/Mass 02/12	B/Wis 1/10	B/Phuket 3073/13	B/Phuket 3073/13	B/Maur I-762	B/Nor 2134/19
	Ferret number			Egg	MDCK	MDCK	Egg	Egg	MDCK	Egg	MDCK	Egg
	Genetic Group			SH614[*1,3]	F39/17[*2]	F10/16[*2]	F06/17[*4]	F36/15[*2]	F27/15[*2]	F25/17[*2]	F05/19[*2]	F48/19[*2]
				3	2	2	2	3	3	3	3	3
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/1791/2017	3	2017-09-20	MDCK1/MDCK4	1280	<	20	40	40	20	40	40	<
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/Pays de Loire/1150/2020	3	2020-02-12	MDCK1/MDCK1	1280	<	10	<	40	20	40	40	<

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

Sequences in phylogenetic trees

Summaries of data submitted to TESSy

Genetic characterisation

For the 2019–20 season, as of week 20/2020, 2 752 viruses were characterised genetically and ascribed to a genetic clade (no additional characterisations were reported during weeks 21–30/2020).

- In total, 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.
- There were 1 048 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.
- A total of 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.
- There were 694 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 30/2020, a total of 2 179 influenza viruses, collected from the 2019–20 season, had been tested for susceptibility to neuraminidase inhibitors (oseltamivir and zanamivir): 924 A(H1N1)pdm09, 729 A(H3N2) and 526 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, 960 viruses from EU/EEA countries have been assessed phenotypically against oseltamivir and zanamivir: 358 A(H1N1)pdm09, 350 A(H3N2), 244 B/Victoria-lineage and eight 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, the World Health Organization (WHO) Global Alert and Response [4] reported that the China Health and Family Planning Commission had 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 [5]. 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, though few human cases were reported during the 2017–18 season [6]. WHO posted an analysis of information on A(H7N9) viruses on 10 February 2017 [7], and ECDC published a rapid risk assessment on the implications of A(H7N9) for public health on 3 July 2017 [8]. Current risk assessments are included in the WHO monthly summary and assessment of influenza at human-animal interface (accessed 13 August 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 [9]. The most recent human case was detected in mid-March 2019 [10]. 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 June 2020 and can be found on ECDC's website [11].

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 [9]. 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 [12]. On 18 November 2016, ECDC published a rapid risk assessment related to outbreaks of highly pathogenic avian influenza H5N8 viruses in Europe [13]. As described above, on 30 June 2020 the EU Reference Laboratory for Avian Influenza, in collaboration with ECDC and the European Food Safety Authority, published the latest overview of avian influenza, which can be found on ECDC's website [11].

Influenza A(H9N2) virus

Since the last update on 8 May 2020, two new laboratory-confirmed human cases of influenza A(H9N2) virus infections in China, both in children with mild disease symptoms and exposure to poultry, have been reported [9]: 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 are increasingly being reported in poultry in Africa.

Other influenza zoonotic events

Since the last 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 2-year-old male (3 July 2020, onset 9 June). Both patients had swine exposure and recovered well.

WHO Collaborating Centre reports

A description of results generated by the London WHO Collaborating Centre at the WIC and used at the most recent WHO vaccine composition meeting (held in Geneva, Switzerland on 24–28 February 2020) can be found, along with previous descriptions, at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports (accessed 13 August 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 National Influenza Centres 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 the WHO Collaborating Centre, London.

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