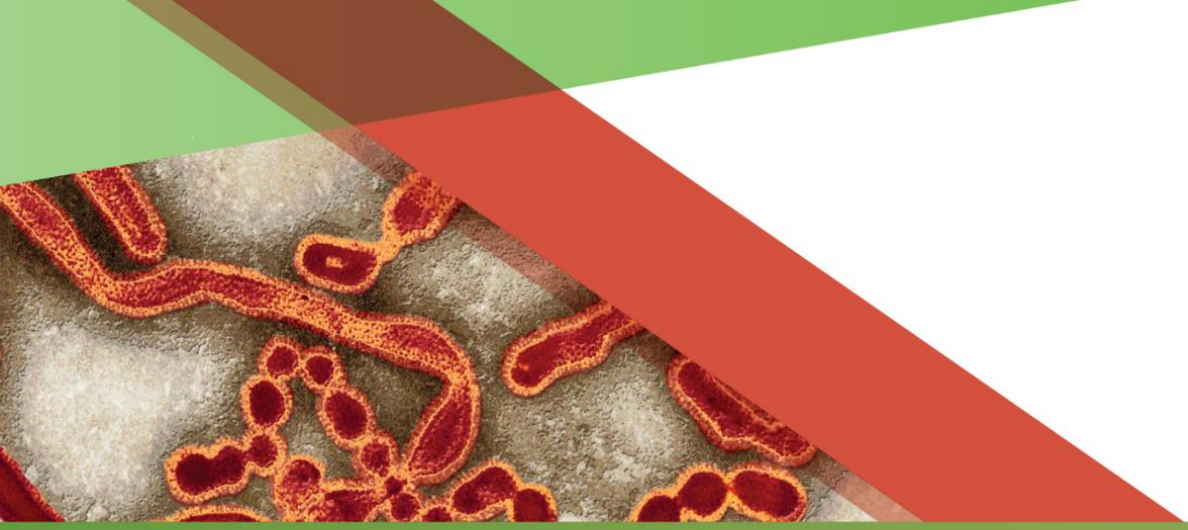

SURVEILLANCE REPORT

Influenza virus characterisation

Summary Europe, February 2020

Summary

This is the fourth report for the 2019–20 influenza season. As of week 8/2020, 127 121 influenza detections across the WHO European Region had been reported; 76% type A viruses, with A(H1N1)pdm09 prevailing over A(H3N2), and 24% type B viruses, with 3 193 (98%) of 3 271 ascribed to a lineage being B/Victoria.

Since the December 2019 characterisation report[1], 25 shipments of influenza-positive specimens from EU/EEA countries have been received at the London WHO CC, the Francis Crick Worldwide Influenza Centre (WIC). In total, 954 virus specimens, with collection dates after 31 August 2019, have been received.

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

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

The great majority of the 104 B/Victoria-lineage viruses characterised in this reporting period gave antigenic profiles characteristic of subgroup 1A(Δ3)B viruses represented by B/Washington/02/2019, the vaccine virus for the 2020 southern hemisphere season, with the minority of viruses giving a profile characteristic of 1A(Δ2) viruses represented by the 2019–20 northern hemisphere vaccine virus B/Colorado/06/2017. In total, 125 viruses have been characterised genetically at the WIC: 118 subgroup 1A(Δ3)B and seven 1A(Δ2).

[1] European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, December 2019. Stockholm: ECDC; 2019. Available from: https://www.ecdc.europa.eu/sites/default/files/documents/influenza-virus-characterisation-december-2019.pdf

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

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 40/2019–8/2020), with a total of 127 121 detections over this period. Since week 1/2020, reported in the December 2019 characterisation report, the proportion of type A viruses had decreased (from 85.5% to 75.9%), with a concomitant rise in the proportion of type B viruses (from 14.6% to 24.1%). Of the type B viruses ascribed to a lineage (n = 3 271) B/Victoria-lineage viruses (n = 3193) have continued to predominate over B/Yamagata-lineage viruses (n = 78) by a large margin. Conversely, of the type A viruses subtyped (n = 37 021) there has been a significant increase in the proportion of A(H1N1)pdm09 viruses (27.9% to 53.6%) and a reduction in the proportion of A(H3N2) viruses (72.1% to 46.4%). Overall, the ratio of type A to type B detections is dramatically reduced compared with the 2018–19 season (86:1 to 3.2:1), 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 40/2019–8/2020)[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	**9632**	**86915**	**96547**	**75.9**	**3.2:1**	**203564**	**98.8**	**86:1**
A(H1N1)pdm09	5341	14487	19828	53.6		44179	57.2	
A(H3N2)	3542	13651	17193	46.4	0.87:1	33117	42.8	0.7:1
A not subtyped	749	58777	59526			126271		
Influenza B	**4971**	**25603**	**30574**	**24.1**		**2380**	**1.2**	
Victoria lineage	1775	1418	3193	97.6		79	47.9	
Yamagata lineage	20	58	78	2.4	0.02:1	86	52.1	1.1:1
Lineage not ascribed	3176	24127	27303			2215		
Total detections (total tested)	**14603 (39424)**	**112518 (>511822)**	**127121 (>551246)**			**205947 (>849439)**		

[a] Numbers taken from Flu News Europe week 8/2020

*** 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, 41 shipments of specimens (virus isolates and/or clinical specimens) have been received at the Crick Worldwide Influenza Centre (WIC) from 26 EU/EEA countries, with 25 of these arriving in 2020 (weeks 1–8/2020). The packages contained 954 virus-related samples with collection dates after 31 August 2019 and were made up of 690 type A viruses, with 298 and 384 subtyped as A(H1N1)pdm09 and A(H3N2), respectively, and 264 type B viruses, with 205 and 14 ascribed to B/Victoria and B/Yamagata lineages, respectively (Table 2), similar to the ratios reported to TESSy (Table 1). Genetic and antigenic characterisation data generated at the WIC for viruses with collection dates after 31 August 2019 until 31 January 2020 were presented at the WHO influenza vaccine composition meeting in February 2020 when recommendations were made for the northern hemisphere 2020–21 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].

Table 2. 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

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]
SEPTEMBER														
Czech Republic	1					1	1							
Finland	1					1	1							
France	6			1	1	3	2	1			2	in process		
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	in process							
OCTOBER														
Denmark	3			2	2	1	1							
Finland	2			1	1	1	1							
France	5			3	3						2	2		
Germany	6			2	2	4	in process							
Greece	1					1	in process							
Iceland	9					8	4	4			1	1		
Ireland	11			1	1	9	in process						1	0
Latvia	3			1	1						2	2		
Lithuania	1										1	1		
Netherlands	3			2	in process	1	0	1						
Norway	28			5	4	19	3	15			3	2	1	0
Poland	1	1	0											
Portugal	7			2	2	2	in process		3	in process				
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	2	1	in process							
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	in process	22	in process		2	0	7	6		
Italy	7			2	2	3	1	2			2	2		
Latvia	10			2	2	3	3				5	5		
Lithuania	2			2	in process									
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	14	in process	3	in process		30	in process	54	in process		
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	in process	52	in process				1	in process		
DECEMBER														
Austria	19			5	in process	9	7	2			5	4		
Belgium	18			5	3	9	in process				4	3		
Bulgaria	2			1	0	1	in process							
Croatia	6			4	1	1	0	1			1	0		
Cyprus	2					1	in process		1	in process				
Czech Republic	2					2	1	1						
Estonia	1			1	1									
France	36			14	1	7	3	4			15	in process		
Germany	13			6	6	6	4	2			1	1		
Greece	6			4	in process	2	in process							
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	in process	12	in process				1	1		
Netherlands	10			1	1	9	7	2						
Norway	15			8	in process	1	in process				1	in process	5	2
Poland	5	2	0	1	0	2	1	0						
Portugal	20			2	2	3	2	1			15	15		
Romania	8										8	in process		
Slovenia	9			5	5	3	3				1	1		
Spain	30			12	in process	6	0	6			12	in process		
United Kingdom	13			3	3	9	9				1	1		
2020 JANUARY														
Austria	2	1	in process						1	in process				
Bulgaria	19			9	in process	8	4				2	0		
Cyprus	20			4	in process	16	in process							
Czech Republic	5			2	2	3	3							
Estonia	14			7	4	3	1	1			4	4		
France	1										1	1		
Germany	24			6	in process	9	in process				8	in process	1	in process
Greece	45			22	in process	20	in process		2	0	1	1		
Italy	3			1	1	1	1				1	in process		
Lithuania	2					2	1	1						
Norway	17			1	in process	11	in process				5	in process		
Poland	4	1	0	2	1	1	1							
Romania	15			4	in process	7	in process		1	in process	3	3		
Slovenia	4			2	2	1	1				1	1		
Spain	18			13	in process				1	in process	4	in process		
United Kingdom	31			15	in process	10	in process		3	in process	3	in process		
FEBRUARY														
Germany	7			5	in process	2	in process							
26 Countries	954	8	0	298	110	384	97	75	45	0	205	81	14	6
		0.84%		31.2%		40.3%			4.7%		21.5%		1.5%	
		72.3%							27.7%					

*** 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 from Northern Ireland and Scotland, in lysis-mix, for which genetic characterisation only can be performed

As of 2020-02-29

Influenza A(H1N1)pdm09 virus analyses

Tables 3-1 to 3-6 show the results of haemagglutination inhibition (HI) assays of A(H1N1)pdm09 viruses performed with a panel of post-infection ferret antisera since the December 2019 report. The 151 test viruses are sorted by date of collection and genetic group/subgroup, where known at the time of writing this report. The results are summarised in Table 3-7.

132/151 (87%) A(H1N1)pdm09 test viruses were antigenically indistinguishable from the A/Michigan/45/2015 northern hemisphere 2018–19 influenza season vaccine virus [4], being recognised at titres within twofold of the titre of the post-infection ferret antiserum with the homologous virus, the number increasing to 140/151 (93%) for titres within fourfold. Somewhat poorer recognition was observed with the ferret antiserum raised against the A/Brisbane/02/2018 northern hemisphere 2019–20 influenza season vaccine virus [1], with 80/151 (53%) and 129/151 (85%) being recognised at titres within twofold and fourfold, respectively. Similar reactivity was observed with antisera raised against egg-propagated A/Slovenia/2903/2015 (clade 6B.1) and A/Switzerland/3330/2017 (genetic subgroup 6B.1A5B) with 133/151 (88%) and 129/151 (85%) test viruses being recognised at titres within fourfold of homologous titres while antiserum raised against egg-propagated A/Switzerland/2656/2017 (clade 6B.1A) recognised only 110/151 (73%) at titres up to fourfold reduced.

Good recognition was observed with antisera raised against four cell culture-propagated viruses (A/Bayern/69/2009, A/Paris/1447/2017, A/Norway/3422/2018 and A/Ireland/84630/2018) with 91–95% of test viruses being recognised at titres within fourfold of the respective homologous titres. The antiserum raised against cell culture-propagated A/Lviv/N6/2009 is an unusual virus/antiserum combination with A/Lviv/N6/2009 encoding **HA1** amino acid polymorphism of **G155G/E**, with E predominating, and **D222G** substitution: this antiserum recognised only 68 test viruses (45%) at a titre within fourfold of the homologous titre.

For test viruses showing low reactivity with antisera raised against the vaccine viruses represented in the panel and some of the reference viruses where HA gene sequencing has been completed, HA1 amino acid substitutions are shown in HI tables (**Tables 3-1, 3-4** and **3-5**). Amino acid substitutions of **G155E** or **N156K** or **N156S** were observed with viruses carrying **HA1 N156K;** these viruses often had additional substitutions with a phylogenetic group being formed by those that carried additional substitutions of **K130N** and **L161I** or **A195E** in genetic subgroup **6B.1A5A** (Figure 1).

A selection of full length HA gene sequences generated at the WIC, with collection dates after 31 August 2019, together with some of those from recently circulating viruses deposited in GISAID were used to generate the phylogeny shown in Figure 1. 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 the most recently circulating viruses carrying the substitution **S183P** in **HA1**, although this is not retained in all genetic groups. Figure 1 is 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), and the recommended vaccine virus, A/Brisbane/02/2018, is shown in red [1]. The seven subclades are defined by the following HA amino acid substitutions:

- 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;
- 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**);
- Subclade **6B.1A3** viruses, represented by **A/Norway/3737/2018**, carry HA gene mutations encoding **HA1 T120A** and **S183P** amino acid substitutions;
- Subclade **6B.1A4** represented by **A/Hungary/20/2018** carries HA gene mutations encoding **HA1 N129D, A144E** and **S183P** amino acid substitutions;
- 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**;
- 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;
- 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 majority of recently circulating viruses have fallen in subgroup **6B.1A5A** which contains a number of virus clusters, two of which have been detected in significant numbers, one defined by **HA1 D187A** and **Q189E** substitutions and the other by **HA2 V193A** substitution. Significant numbers of viruses in subgroup **6B.1A5B** (with additional **HA1** substitutions of **K130N**, **K160M**, **T216K** and **H296N**) and subclade **6B.1A7** (with additional **HA1** substitutions of **E68D**, **T120A**, **S121N** and **L161I**) have also been detected (Figure 1). The great majority of viruses in the various subgroups 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. Recently, an A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus (with **HA1 D187A** and **Q189E** amino acid substitutions), was recommended for use in the northern hemisphere 2020–2021 influenza season [3].

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/Bayern 69/09 MDCK	A/Lviv N6/09 MDCK	A/Mich 45/15 Egg	A/Slov 2903/2015 Egg	A/Paris 1447/17 MDCK	A/Swit 2656/17 Egg	A/Bris 02/18 Egg	A/Norway 3433/18 MDCK	A/Swit 3330/17 Egg	A/Ire 84630/18 MDCK
		Passage history												
		Ferret number			F09/15*1	F13/18*1	F31/16*1	NIB F48/16*1	F03/18*2	F20/18*1	F09/19*1	F04/19*1	F23/18*1	F08/19*1
		Genetic group					6B.1	6B.1	6B.1A	6B.1A	6B.1A1	6B.1A5A	6B.1A5B	6B.1A6
REFERENCE VIRUSES														
A/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	160	160	80	40	160	80	80	320	80	<
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	320	80	320	320	160	640	160	80
A/Michigan/45/2015		6B.1	2015-09-07	E3/E4	320	320	1280	1280	1280	2560	640	2560	640	1280
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	320	320	1280	2560	1280	1280	1280	1280	640	1280
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	160	80	640	1280	1280	1280	1280	2560	640	1280
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	1280	2560	5120	2560	2560	1280	2560	2560	2560
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	160	1280	1280	1280	1280	640	2560	640	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	80	<	320	640	320	320	160	640	320	320
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	320	80	640	640	640	1280	320	1280	1280	640
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	160	80	640	1280	1280	640	640	1280	640	1280
TEST VIRUSES														
A/Czech Republic/1428/2019		6B.1A5A	2019-08-20	MDCK2/MDCK1	320	320	1280	640	1280	640	640	2560	640	1280
A/Denmark/3254/2019		6B.1A5A	2019-10-06	MDCK3/MDCK1	160	80	640	640	1280	640	640	1280	320	640
A/Mougins/1891/2019		6B.1A5A	2019-10-07	MDCK3/MDCK1	160	80	640	640	640	320	320	1280	640	640
A/Latvia/10-025804/2019		6B.1A5A	2019-10-09	MDCK2/MDCK1	320	160	640	1280	1280	640	640	2560	640	1280
A/Le Cannet/1893/2019		6B.1A5A	2019-10-10	MDCK3/MDCK1	320	160	640	640	1280	640	640	1280	640	1280
A/Le Cannet/1892/2019		6B.1A5A	2019-10-11	MDCK3/MDCK1	160	160	640	640	1280	640	640	1280	320	1280
A/Hessen/70/2019		6B.1A5A	2019-10-15	C2/MDCK1	320	160	640	640	640	640	640	1280	320	1280
A/Denmark/3256/2019		6B.1A5A	2019-10-15	MDCK3/MDCK1	160	80	640	640	640	640	640	1280	640	640
A/Hessen/71/2019		6B.1A5A	2019-10-16	C2/MDCK1	160	160	640	640	640	640	640	1280	320	640
A/Finland/133/2019		6B.1A5A	2019-10-30	MDCK1/MDCK1	320	160	1280	640	1280	640	640	2560	640	1280
A/Latvia/11-003941/2019		6B.1A5A	2019-11-02	MDCK2/MDCK1	320	160	640	640	1280	640	320	2560	640	640
A/Latvia/11-003858/2019		6B.1A5A	2019-11-02	MDCK2/MDCK1	160	80	320	640	640	640	320	1280	320	640
A/Finland/132/2019		6B.1A5A	2019-11-03	MDCK1/MDCK1	320	160	640	640	1280	640	640	1280	640	640
A/Denmark/3288/2019		6B.1A5A	2019-11-08	MDCK4/MDCK1	80	80	320	320	640	1280	160	1280	320	320
A/Denmark/3280/2019	N156K, K130N, L161I, V250A	6B.1A5A	2019-11-10	MDCK4/MDCK1	80	40	80	40	40	80	40	320	80	40
A/Berlin/57/2019		6B.1A5A	2019-11-11	C1/MDCK1	160	160	640	640	1280	640	640	1280	640	640
A/Lyon/2003/2019		6B.1A5A	2019-11-12	MDCK2/MDCK1	320	160	1280	640	1280	640	640	2560	640	1280
A/Lyon/2037/2019		6B.1A5A	2019-11-18	MDCK2/MDCK1	320	320	1280	1280	1280	1280	640	1280	320	1280
A/Nordrhein-Westfalen/136/2019		6B.1A5A	2019-11-20	C1/MDCK1	320	160	640	640	1280	640	640	1280	640	640
A/Lyon/CHU/R19.132.13/2019		6B.1A5A	2019-11-23	MDCK2/MDCK1	160	160	640	640	1280	640	640	1280	640	640
A/Niedersachsen/195/2019		6B.1A5A	2019-11-25	C1/MDCK1	320	160	640	640	1280	640	640	2560	640	1280
A/Denmark/3284/2019		6B.1A5B	2019-11-08	MDCK4/MDCK1	80	<	320	320	640	<	320	640	320	640
A/Denmark/3283/2019		6B.1A5B	2019-11-08	MDCK3/MDCK1	320	80	1280	1280	1280	1280	640	2560	640	1280
A/Denmark/3279/2019		6B.1A5B	2019-11-10	MDCK4/MDCK1	80	40	320	640	640	640	320	640	320	640
A/Denmark/3295/2019		6B.1A5B	2019-11-15	MDCK3/MDCK1	320	80	1280	1280	1280	<	1280	2560	640	1280
A/Denmark/3311/2019		6B.1A5B	2019-11-16	MDCK3/MDCK1	160	80	640	640	1280	640	640	1280	640	1280
							Vaccine NH 2018-19 SH 2019				Vaccine NH 2019-20 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 Tree

Table 3-2. 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/Bayern 69/09 MDCK	A/Lviv N6/09 MDCK	A/Mich 45/15 Egg	A/Slov 2903/2015 Egg	A/Paris 1447/17 MDCK	A/Swit 2656/17 Egg	A/Bris 02/18 Egg	A/Norway 3433/18 MDCK	A/Swit 3330/17 Egg	A/Ire 84630/18 MDCK
		Ferret number			F09/15[*1]	F13/18[*1]	F31/16[*1]	NIB F48/16[*1]	F03/18[*2]	F20/18[*1]	F09/19[*1]	F04/19[*1]	F23/18[*1]	F08/19[*1]
		Genetic group					6B.1	6B.1	6B.1A	6B.1A	6B.1A1	6B.1A5A	6B.1A5B	6B.1A6
REFERENCE VIRUSES														
A/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	320	320	80	40	160	160	80	320	80	40
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	320	160	320	320	160	640	320	160
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	160	160	640	640	640	1280	640	1280	320	640
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	320	160	1280	1280	1280	1280	640	1280	640	640
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	320	80	640	1280	1280	1280	640	1280	640	1280
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	640	2560	1280	1280	2560	1280	2560	1280	1280
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	320	1280	1280	2560	2560	1280	2560	1280	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	160	80	640	640	640	640	320	1280	640	640
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	160	80	640	640	640	640	320	1280	640	640
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	320	160	1280	1280	1280	1280	640	2560	640	1280
TEST VIRUSES														
A/Orebro/3/2019		6B.1A5A	2019-09-15	MDCK0/MDCK1	320	160	640	640	640	640	640	2560	640	640
A/Falun/4/2019		6B.1A5A	2019-09-17	MDCK0/MDCK1	160	80	640	640	320	640	320	1280	640	640
A/Umea/2/2019		6B.1A5A	2019-11-10	MDCK0/MDCK1	160	80	640	640	320	640	320	1280	320	640
A/Umea/4/2019		6B.1A5A	2019-11-11	MDCK0/MDCK1	160	80	640	640	320	640	320	1280	320	640
A/Umea/3/2019		6B.1A5A	2019-11-11	MDCK0/MDCK1	160	160	640	640	320	640	320	1280	640	640
A/Lulea/1/2019		6B.1A5A	2019-11-18	MDCK0/MDCK1	160	80	640	640	320	640	320	1280	320	640
A/Croatia/8025/2019		6B.1A5A	2019-12-02	MDCKx/MDCK1	320	160	640	1280	1280	1280	640	1280	640	640
A/Iceland/86/2019		6B.1A5A	2019-12-08	MDCK1/MDCK1	160	80	640	640	320	320	320	1280	320	320
A/Karlstad/3/2019		6B.1A5B	2019-11-15	MDCK0/MDCK1	320	80	1280	1280	640	1280	640	1280	640	1280
A/Iceland/85/2019		6B.1A5B	2019-12-01	MDCK1/MDCK1	160	80	640	640	640	640	640	1280	640	640
A/Croatia/7847/2019		6B.1A7	2019-11-20	MDCKx/MDCK1	640	160	1280	1280	2560	1280	1280	2560	1280	1280
A/Croatia/7846/2019		6B.1A7	2019-11-20	MDCKx/MDCK1	320	160	1280	1280	1280	1280	1280	2560	1280	1280
							Vaccine NH 2018-19 SH 2019				Vaccine NH 2019-20 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 Tree

Table 3-3. 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/Bayern 69/09 MDCK F09/15*1	A/Lviv N6/09 MDCK F13/18*1	A/Mich 45/15 Egg F31/16*1	A/Slov 2903/2015 Egg NIB F48/16*1	A/Paris 1447/17 MDCK F03/18*2	A/Swit 2656/17 Egg F20/18*1	A/Bris 02/18 Egg F09/19*1	A/Norway 3433/18 MDCK F04/19*1	A/Swit 3330/17 Egg F23/18*1	A/Ire 84630/18 MDCK F08/19*1
		Genetic group					6B.1	6B.1	6B.1A	6B.1A	6B.1A1	6B.1A5A	6B.1A5B	6B.1A6
REFERENCE VIRUSES														
A/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	640	320	160	40	160	160	160	320	160	40
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	160	160	320	320	320	1280	160	80
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	160	160	640	640	1280	1280	640	1280	640	640
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	320	160	640	640	1280	640	640	1280	640	640
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	320	80	640	640	1280	1280	640	1280	640	640
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	640	1280	1280	1280	1280	1280	2560	1280	1280
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	320	1280	1280	2560	1280	640	2560	1280	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	160	40	320	320	320	320	320	640	320	320
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	320	160	640	1280	1280	1280	640	1280	1280	640
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	320	160	1280	1280	1280	1280	640	2560	640	1280
TEST VIRUSES														
A/Ireland/87362/2019		6B.1A5A	2019-10-30	MDCK1	160	160	640	640	640	640	640	1280	640	640
A/Ireland/87733/2019		6B.1A5A	2019-11-03	MDCK2	160	80	320	320	640	320	320	640	160	320
A/Slovenia/2924/2019		6B.1A5A	2019-11-18	MDCK2/MDCK1	160	160	640	640	640	640	320	1280	320	320
A/Ireland/95067/2019		6B.1A5A	2019-11-26	MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Ireland/95264/2019		6B.1A5A	2019-11-27	MDCK2	160	80	320	640	640	640	320	1280	320	640
A/Ireland/95337/2019		6B.1A5A	2019-11-28	MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Ireland/95766/2019		6B.1A5A	2019-11-29	MDCK2	160	160	640	640	1280	640	640	1280	640	640
A/Alsace/2631/2019		6B.1A5A	2019-12-02	MDCK2/MDCK1	320	80	640	640	640	640	640	1280	320	640
A/Slovenia/3106/2019		6B.1A5A	2019-12-04	MDCK1/MDCK1	320	160	640	640	640	640	640	1280	320	640
A/Slovenia/3139/2019		6B.1A5A	2019-12-06	MDCKx/MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Franche Comte/2784/2019		6B.1A5A	2019-12-09	MDCK1/MDCK1	160	160	640	320	640	640	320	1280	320	320
A/Bretagne/2725/2019		6B.1A5A	2019-12-09	MDCK1/MDCK1	320	320	1280	1280	1280	1280	640	2560	640	1280
A/Slovenia/3222/2019		6B.1A5A	2019-12-12	SIAT2/MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Slovenia/3218/2019		6B.1A5A	2019-12-12	SIAT1/MDCK1	160	80	320	640	640	640	320	1280	320	320
A/Slovenia/3247/2019		6B.1A5A	2019-12-13	MDCK3/MDCK1	80	80	640	640	640	640	320	1280	320	640
A/Paris/2834/2019		6B.1A5A	2019-12-23	MDCK2/MDCK1	160	160	640	640	640	640	640	1280	320	640
A/Pays de Loire/2930/2019		6B.1A5A	2019-12-26	MDCK1/MDCK1	160	80	640	320	80	320	320	1280	320	320
A/Slovenia/161/2020		6B.1A5A	2020-01-08	SIATx/MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Slovenia/148/2020		6B.1A5A	2020-01-08	SIATx/MDCK1	160	80	320	320	320	320	320	640	160	320
A/Centre/2599/2019		6B.1A5B	2019-11-27	MDCK1/MDCK1	160	40	640	1280	1280	640	640	1280	640	1280
A/Alsace/2798/2019		6B.1A5B	2019-12-18	MDCK2/MDCK1	160	80	640	640	1280	640	640	1280	640	640
							Vaccine				Vaccine			
							NH 2018-19				NH 2019-20			
							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 Tree

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

Viruses	Other information	Passage history	Collection date	Passage history	A/Bayern 69/09 MDCK	A/Lviv N6/09 MDCK	A/Mich 45/15 Egg	A/Slov 2903/2015 Egg	A/Paris 1447/17 MDCK	A/Swit 2656/17 Egg	A/Bris 02/18 Egg	A/Norway 3433/18 MDCK	A/Swit 3330/17 Egg	A/Ire 84630/18 MDCK
		Passage history			F09/15[*1]	F13/18[*1]	F31/16[*1]	NIB F48/16[*1]	F03/18[*2]	F20/18[*1]	F09/19[*1]	F04/19[*1]	F23/18[*1]	F08/19[*1]
		Genetic group					6B.1	6B.1	6B.1A	6B.1A	6B.1A1	6B.1A5A	6B.1A5B	6B.1A6
REFERENCE VIRUSES														
A/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	640	160	80	<	160	160	80	160	80	40
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	320	160	640	320	320	640	320	160
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	320	160	640	640	1280	1280	640	1280	640	640
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	320	320	1280	1280	1280	1280	640	1280	640	1280
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	320	80	1280	1280	1280	1280	1280	2560	640	1280
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	640	1280	1280	2560	1280	1280	2560	1280	1280
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	320	1280	1280	2560	1280	1280	2560	1280	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	160	80	640	640	640	640	640	1280	640	640
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	320	160	640	1280	1280	1280	640	2560	1280	1280
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	320	160	1280	1280	1280	1280	640	1280	640	1280
TEST VIRUSES														
A/Netherlands/10258/2019		6B.1A5A	2019-10-31	MDCK-MIX2/MDCK1	160	160	640	640	1280	640	640	2560	640	640
A/Belgium/G0460/2019	N156K, K54E, P137S, A195E	6B.1A5A	2019-11-05	MDCK1	80	80	80	40	80	80	80	640	80	<
A/Austria/1200911/2019		6B.1A5A	2019-11-13	SIAT1/MDCK1	320	160	640	640	1280	640	640	1280	640	640
A/Austria/1200546/2019		6B.1A5A	2019-11-14	SIAT1/MDCK1	160	80	320	320	320	320	160	640	160	320
A/Netherlands/10263/2019		6B.1A5A	2019-11-25	MDCK-MIX2/MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Austria/1206292/2019		6B.1A5A	2019-12-08	SIATx/MDCK1	160	160	640	640	1280	640	320	1280	320	640
A/Austria/1207286/2019	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2019-12-11	SIATx/MDCK2	40	<	<	<	<	<	<	80	<	<
A/Catalonia/3512178NS/2019		6B.1A5A	2019-12-11	P0/MDCK1	160	160	640	640	1280	640	640	1280	320	640
A/Catalonia/3512137NS/2019		6B.1A5A	2019-12-11	P0/MDCK1	320	160	1280	1280	1280	1280	640	2560	640	1280
A/Saint Etienne/2287/2019		6B.1A5A	2019-12-12	MDCK2/MDCK1	160	160	640	640	640	640	640	1280	640	640
A/La Rochelle/2309/2019		6B.1A5A	2019-12-14	MDCK2/MDCK1	160	160	640	320	640	320	320	1280	320	640
A/Austria/1205297/2019		6B.1A5A	2019-12-16	SIAT1/MDCK1	80	80	320	320	640	320	160	640	160	320
A/Belgium/G0526/2019		6B.1A5A	2019-12-17	MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Belgium/G0537/2019	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2019-12-18	MDCK1	80	40	40	<	<	40	<	80	40	<
A/Belgium/G0001/2020		6B.1A5A	2019-12-19	MDCK1	320	160	640	640	1280	640	640	2560	640	640
A/Lyon/2343/2019	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2019-12-19	MDCK2/MDCK1	<	<	<	<	<	<	<	40	<	<
A/Catalonia/3512868NS/2019		6B.1A5A	2019-12-26	P0/MDCK1	320	320	1280	1280	1280	1280	640	2560	640	1280
A/Catalonia/2174495NS/2020		6B.1A5A	2020-01-09	P0/MDCK1	160	80	320	320	640	320	320	1280	320	320
A/Poland/1535/2020		6B.1A5A	2020-01-12	MDCK1/MDCK1	160	160	640	640	1280	640	640	1280	640	640
A/Greece/59/2020		6B.1A5A	2020-01-13	MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Athens.GR/93/2020		6B.1A5A	2020-01-14	MDCK1/MDCK1	160	160	640	640	1280	640	640	1280	640	640
A/Athens.GR/120/2020		6B.1A5A	2020-01-16	Cx/MDCK1	320	160	640	640	640	640	640	1280	640	640
A/Saint Etienne/2362/2019			2019-12-16	MDCK2/MDCK1	80	80	160	320	320	320	160	640	160	320
							Vaccine				Vaccine			
							NH 2018-19				NH 2019-20			
							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 Tree

Table 3-5. 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/Bayern 69/09 MDCK F09/15*1	A/Lviv N6/09 MDCK F13/18*1	A/Mich 45/15 Egg F31/16*1 6B.1	A/Slov 2903/2015 Egg NIB F48/16*1 6B.1	A/Paris 1447/17 MDCK F03/18*2 6B.1A	A/Swit 2656/17 Egg F20/18*1 6B.1A	A/Bris 02/18 Egg F09/19*1 6B.1A1	A/Norway 3433/18 MDCK F04/19*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/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	320	320	80	<	160	160	80	320	80	40
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	320	160	640	320	320	1280	320	160
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	320	160	640	1280	1280	1280	640	1280	640	1280
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	320	320	1280	1280	1280	1280	640	2560	640	1280
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	160	80	640	640	1280	1280	640	1280	640	1280
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	640	2560	2560	2560	2560	1280	2560	1280	2560
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	320	2560	2560	2560	2560	1280	2560	1280	2560
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	80	80	320	320	640	640	320	1280	320	640
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E1	320	160	640	640	1280	1280	640	2560	1280	1280
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	160	80	1280	1280	1280	1280	640	1280	640	1280
TEST VIRUSES														
A/Lisboa/111/2019		6B.1A5A	2019-11-14	SIAT1/MDCK1	160	160	640	640	640	640	640	1280	320	640
A/Lisboa/109/2019		6B.1A5A	2019-11-19	SIAT1/MDCK1	160	160	320	320	320	320	320	1280	160	320
A/Parma/389/2019		6B.1A5A	2019-11-20	MDCK1/MDCK1	80	40	320	160	320	320	160	1280	160	320
A/England/433/2019		6B.1A5A	2019-11-23	SIAT1/MDCK1	160	80	640	320	640	320	320	1280	320	320
A/England/687/2019	K54R, G155E, A187V	6B.1A5A	2019-12-05	SIAT1/MDCK1	160	160	160	80	160	80	160	640	160	80
A/England/690/2019		6B.1A5A	2019-12-06	SIAT1/MDCK1	320	160	1280	1280	1280	640	640	2560	640	640
A/Lisboa/114/2019		6B.1A5A	2019-12-09	MDCK3/MDCK1	80	80	320	320	640	320	320	1280	320	320
A/Palermo/31/2019		6B.1A5A	2019-12-10	MDCK3/MDCK1	160	160	640	640	1280	640	640	2560	640	640
A/Lithuania/MB41308/2019		6B.1A5A	2019-12-12	MDCK2/MDCK1	320	320	1280	1280	1280	1280	640	2560	640	1280
A/England/692/2019		6B.1A5A	2019-12-16	MDCK1/MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Lisboa/115/2019		6B.1A5A	2019-12-18	MDCK3/MDCK1	320	160	640	1280	1280	640	640	2560	640	640
A/Lithuania/MB42127/2019		6B.1A5A	2019-12-21	MDCK1/MDCK1	320	160	1280	640	1280	1280	640	2560	640	1280
A/Parma/390/2019		6B.1A5A	2019-12-24	MDCK1/MDCK1	80	40	320	320	320	320	160	640	160	320
A/Lithuania/MB42385/2019	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2019-12-25	MDCK2/MDCK1	40	<	<	<	<	<	<	80	<	<
A/Lithuania/MB42388/2019		6B.1A5A	2019-12-26	MDCK1/MDCK1	320	160	1280	640	1280	640	640	2560	640	1280
A/Nordrhein-Westfalen/142/2019	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2019-12-28	C1/MDCK3	40	<	<	<	<	<	<	80	<	<
A/Palermo/01/2020		6B.1A5A	2020-01-02	MDCK2/MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Rheinland-Pfalz/2/2020		6B.1A5A	2020-01-04	C1/MDCK1	160	80	320	640	640	320	320	1280	320	320
A/Estonia/125640/2020	N156K, K130N, L161I, V250A, K209M	6B.1A5A	2020-01-08	SIAT1/MDCK2	40	<	40	<	80	40	<	160	40	<
A/Estonia/125685/2020		6B.1A5A	2020-01-09	SIAT1/MDCK1	160	160	640	640	1280	640	320	1280	320	640
A/Palencia/12/2020		6B.1A5A	2020-01-09	MDCK1/MDCK1	320	80	1280	1280	1280	1280	640	2560	640	1280
A/Leon/14/2020		6B.1A5A	2020-01-09	MDCK1/MDCK1	320	160	640	1280	1280	640	640	2560	640	640
A/Leon/10/2020		6B.1A5A	2020-01-09	MDCK1/MDCK1	160	160	640	640	640	640	640	1280	320	640
A/Czech Republic/82/2020		6B.1A5A	2020-01-09	P1/MDCK1	320	80	1280	1280	2560	1280	640	2560	1280	1280
A/Czech Republic/81/2020		6B.1A5A	2020-01-09	P1/MDCK1	160	<	640	640	640	640	320	1280	320	640
A/Bucuresti/256171/2020		6B.1A5A	2020-01-10	SIAT1/MDCK1	320	160	1280	640	1280	1280	640	2560	640	1280
A/Bulgaria/083/2020		6B.1A5A	2020-01-12	MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Bulgaria/092/2020		6B.1A5A	2020-01-13	MDCK2	320	160	640	640	1280	640	640	2560	640	1280
A/Bulgaria/084/2020		6B.1A5A	2020-01-13	MDCK2	160	160	640	640	640	640	320	1280	320	640
A/Bucuresti/256303/2020		6B.1A5A	2020-01-13	MDCK1/MDCK1	80	<	320	160	320	160	160	640	160	320
A/Estonia/125790/2020		6B.1A5A	2020-01-14	SIAT1/MDCK1	160	160	640	640	1280	640	640	2560	640	640
A/Estonia/125789/2020	N156S	6B.1A5A	2020-01-14	SIAT1/MDCK1	40	<	40	<	<	40	<	320	<	<
A/Valladolid/17/2020		6B.1A5B	2020-01-10	MDCK1/MDCK1	320	160	1280	2560	2560	2560	1280	2560	1280	1280
A/Rheinland-Pfalz/1/2020		6B.1A5B		C1/MDCK1	160	40	640	640	1280	640	320	1280	160	640
A/Brandenburg/1/2020		6B.1A7	2020-01-06	C1/MDCK1	160	160	1280	1280	1280	1280	640	2560	640	1280
A/Friuli Venezia Giulia/234/2019			2019-11-26	MDCK1/MDCK1	160	160	640	640	640	640	320	2560	320	640

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

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

Sequences in Phylogenetic Tree

Vaccine NH 2018-19 SH 2019

Vaccine NH 2019-20 SH 2020

Table 3-6. 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/Bayern 69/09 MDCK F09/15[-1]	A/Lviv N6/09 MDCK F13/18[-1]	A/Mich 45/15 Egg F31/16[-1] 6B.1	A/Slov 2903/2015 Egg NIB F48/16[-1] 6B.1	A/Paris 1447/17 MDCK F03/18[-2] 6B.1A	A/Swit 2656/17 Egg F20/18[-1] 6B.1A	A/Bris 02/18 Egg F09/19[-1] 6B.1A1	A/Norway 3433/18 MDCK F04/19[-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/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	160	160	80	40	160	80	80	320	80	40
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	640	640	320	160	640	320	320	640	160	160
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	160	160	640	640	1280	640	640	1280	640	640
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E3	320	320	1280	1280	2560	1280	1280	2560	1280	1280
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	160	80	640	640	1280	640	640	1280	640	640
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	640	640	2560	1280	5120	2560	1280	2560	1280	1280
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	320	320	2560	2560	2560	2560	1280	2560	1280	1280
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	80	40	320	320	640	320	320	1280	320	320
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	160	80	320	320	640	640	320	1280	640	640
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	320	160	1280	1280	2560	1280	1280	2560	1280	1280
TEST VIRUSES														
A/La Reunion/2126/2019			2019-08-22	MDCK2/MDCK2	40	<	40	<	80	<	<	160	40	<
A/La Reunion/2128/2019			2019-09-17	MDCK2/MDCK1	80	80	320	320	640	320	160	1280	320	320
A/Catalonia/2145999NS/2019			2019-10-11	P0/MDCK1	80	80	320	320	640	320	320	1280	320	320
A/Catalonia/3510341NS/2019			2019-10-17	P0/MDCK1	80	80	320	320	320	320	320	640	320	320
A/Catalonia/3510633NS/2019			2019-10-29	P0/MDCK1	80	80	320	320	320	320	320	1280	320	320
A/Lisboa/102/2019			2019-10-31	SIAT3/MDCK1	160	80	320	320	640	320	320	1280	320	320
A/Lisboa/105/2019			2019-11-01	MDCK1/MDCK1	160	160	640	640	640	640	320	1280	320	640
A/Lisboa/103/2019			2019-11-04	SIAT3/MDCK1	160	80	320	640	640	640	320	1280	320	320
A/Lisboa/107/2019			2019-11-10	SIAT2/MDCK1	160	80	320	320	640	320	320	640	320	320
A/Lisboa/106/2019			2019-11-11	SIAT1/MDCK1	160	80	320	640	1280	640	320	1280	320	320
A/Lisboa/110/2019			2019-11-14	SIAT2/MDCK1	40	40	160	160	160	160	80	640	160	160
A/Catalonia/3511346NS/2019			2019-11-20	P0/MDCK1	160	160	640	640	1280	640	320	1280	320	640
A/Netherlands/01659/2019			2019-11-24	hCK1/MDCK1	160	80	640	320	640	640	320	1280	320	640
A/Rennes/2646/2019			2019-11-25	MDCK1/MDCK1	160	80	320	320	640	320	320	1280	160	320
A/Lyon/2067/2019			2019-11-25	MDCK2/MDCK1	80	40	160	160	320	160	160	640	160	160
A/Poitiers/2102/2019			2019-11-26	MDCK2/MDCK1	80	80	320	320	640	320	320	1280	320	320
A/Marseille/2089/2019			2019-11-27	MDCK2/MDCK1	160	160	640	640	1280	640	640	2560	640	640
A/Schleswig-Holstein/6/2019			2019-11-28	C1/MDCK1	160	80	320	320	1280	640	320	1280	320	640
A/Berlin/59/2019			2019-11-29	C1/MDCK1	80	80	320	320	640	320	320	640	160	320
A/Catalonia/3511745NS/2019			2019-11-30	P0/MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Netherlands/10029/2019			2019-12-03	hCK1/MDCK1	160	160	640	640	1280	640	640	2560	640	640
A/Catalonia/12003S/2019			2019-12-05	P0/MDCK1	160	80	640	640	640	640	320	1280	320	640
A/Catalonia/11996S/2019			2019-12-05	P0/MDCK1	160	40	1280	1280	1280	1280	640	2560	640	1280
A/Brandenburg/29/2019			2019-12-11	C2/MDCK1	160	80	320	640	640	640	320	1280	320	320
A/Sachsen/151/2019			2019-12-11	C1/MDCK1	80	80	320	320	640	320	160	1280	160	320
A/Clermont Ferrand/2280/2019			2019-12-11	MDCK3/MDCK1	80	80	320	320	640	320	320	1280	320	320
A/Lyon/2266/2019			2019-12-12	MDCK2/MDCK1	160	80	320	320	640	320	320	1280	320	320
A/Pays de Loire/2796/2019			2019-12-17	MDCK1	160	80	320	320	640	320	320	1280	160	320
A/Hessen/73/2019			2019-12-17	C1/MDCK1	160	80	640	320	640	320	320	1280	320	320
A/Estonia/125382/2019			2019-12-19	SIAT1/MDCK1	160	80	320	320	640	640	320	1280	320	640
A/Bretagne/2804/2019			2019-12-20	MDCK1	160	80	640	320	640	320	320	1280	320	320
A/Mecklenburg-Vorpommern/13/2019			2019-12-23	C1/MDCK1	40	<	40	<	80	40	40	320	40	<
A/Thuringen/125/2019			2019-12-27	C2/MDCK1	160	80	320	320	640	320	320	1280	160	320
							Vaccine NH 2018-19 SH 2019				Vaccine NH 2019-20 SH 2020			

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

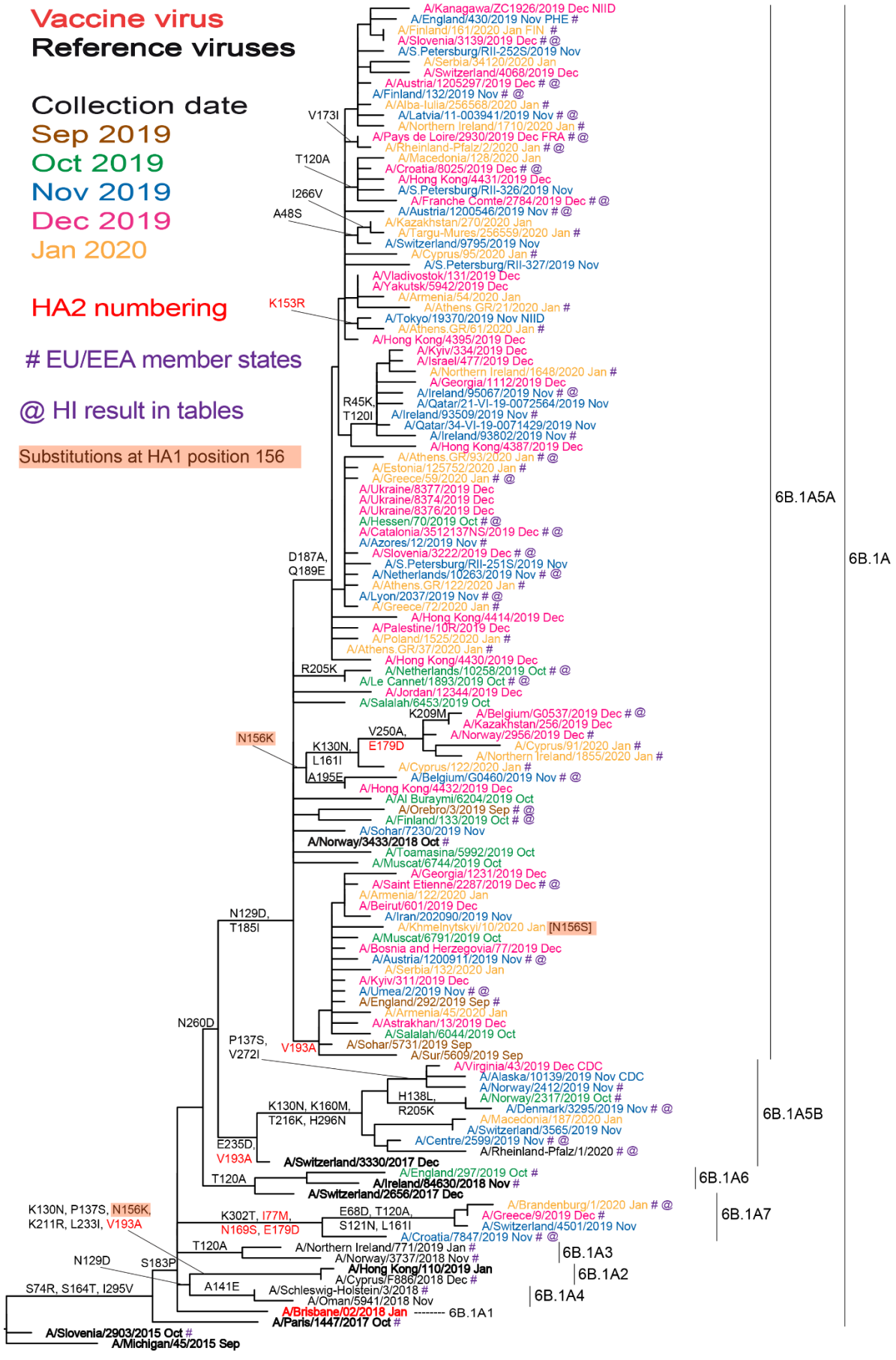
1 < = <40; 2 < = <80; ND =Not Done

Table 3-7. Antigenic analysis of A(H1N1)pdm09 viruses by HI – summary

Viruses	Other information		Haemagglutination inhibition titre									
			Post-infection ferret antisera									
		Passage history	A/Bayern 69/09 MDCK	A/Lviv N6/09 MDCK	A/Mich 45/15 Egg	A/Slov 2903/2015 Egg	A/Paris 1447/17 MDCK	A/Swit 2656/17 Egg	A/Bris 02/18 Egg	A/Norway 3433/18 MDCK	A/Swit 3330/17 Egg	A/Ire 84630/18 MDCK
		Ferret number	F09/15[*1]	F13/18[*1]	F31/16[*1]	NIB F48/16[*1]	F03/18[*2]	F20/18[*1]	F09/19[*1]	F04/19[*1]	F23/18[*1]	F08/19[*1]
		Genetic group			6B.1	6B.1	6B.1A	6B.1A	6B.1A1	6B.1A5A	6B.1A5B	6B.1A6
REFERENCE VIRUSES												
A/Bayern/69/2009	G155E		160	160	80	40	160	80	80	320	80	<
A/Lviv/N6/2009	G155E, D222G		640	640	320	80	320	320	160	640	160	80
A/Michigan/45/2015		6B.1	320	320	1280	1280	1280	2560	640	2560	640	1280
A/Slovenia/2903/2015	clone 37	6B.1	320	320	1280	2560	1280	1280	1280	1280	640	1280
A/Paris/1447/2017		6B.1A	160	80	640	1280	1280	1280	1280	2560	640	1280
A/Switzerland/2656/2017		6B.1A	640	1280	2560	5120	2560	2560	1280	2560	2560	2560
A/Brisbane/02/2018		6B.1A1	320	160	1280	1280	1280	1280	640	2560	640	1280
A/Norway/3433/2018		6B.1A5A	80	<	320	640	320	320	160	640	320	320
A/Switzerland/3330/2017	clone 35	6B.1A5B	320	80	640	640	640	1280	320	1280	1280	640
A/Ireland/84630/2018		6B.1A6	160	80	640	1280	1280	640	640	1280	640	1280
TEST VIRUSES												
Genetic group	*No tested*	*No with*										
All viruses	151	Titre reduced ≤2-fold	104	4	132	86	121	47	80	142	80	99
		%	*68.9*	*2.6*	*87.4*	*57.0*	*80.1*	*31.1*	*53.0*	*94.0*	*53.0*	*65.6*
		Titre reduced =4-fold	36	64	8	47	16	63	49	2	49	38
		%	*23.8*	*42.4*	*5.3*	*31.1*	*10.6*	*41.7*	*32.5*	*1.3*	*32.5*	*25.2*
		Titre reduced ≥8-fold	11	83	11	18	14	41	22	7	22	14
		%	*7.3*	*55.0*	*7.3*	*11.9*	*9.3*	*27.2*	*14.6*	*4.6*	*14.6*	*9.3*
6B.1A5A	102	Titre reduced ≤2-fold	61	4	90	64	79	38	64	95	45	74
		%	*59.8*	*3.9*	*88.2*	*62.7*	*77.5*	*37.3*	*62.7*	*93.1*	*44.1*	*72.5*
		Titre reduced =4-fold	31	55	3	25	12	45	23	1	39	18
		%	*30.4*	*53.9*	*2.9*	*24.5*	*11.8*	*44.1*	*22.5*	*1.0*	*38.2*	*17.6*
		Titre reduced ≥8-fold	10	43	9	13	11	19	15	6	18	10
		%	*9.8*	*42.2*	*8.8*	*12.7*	*10.8*	*18.6*	*14.7*	*5.9*	*17.6*	*9.8*
6B.1A5B	11	Titre reduced ≤2-fold	9		9	8	11	5	10	11	8	11
		%	*81.8*		*81.8*	*72.7*	*100.0*	*45.5*	*90.9*	*100.0*	*72.7*	*100.0*
		Titre reduced =4-fold	2	1	2	2		4	1		2	
		%	*18.2*	*9.1*	*18.2*	*18.2*		*36.4*	*9.1*		*18.2*	
		Titre reduced ≥8-fold		10		1		2			1	
		%		*90.9*		*9.1*		*18.2*			*9.1*	
6B.1A7	3	Titre reduced ≤2-fold	3		3	3	3	3	3	3	3	3
		%	*100.0*		*100.0*	*100.0*	*100.0*	*100.0*	*100.0*	*100.0*	*100.0*	*100.0*
		Titre reduced =4-fold		3								
		%		*100.0*								
		Titre reduced ≥8-fold										
					Vaccine NH 2018-19 SH 2019				Vaccine NH 2019-20 SH 2020			

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

Figure 1. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes



Influenza A(H3N2) virus analyses

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 is a particular problem for most viruses that fall in genetic clade 3C.2a.

Since the December 2019 characterisation report of the viruses recovered, based on positive neuraminidase activity, 122 retained sufficient HA activity to allow antigenic analysis by HI (Tables 4-1 to 4-8). Test viruses are sorted by date of collection and genetic group/subgroup, where known at the time of writing this report, and the results are summarised in Table 4-9.

Test viruses were poorly recognised by antiserum raised against the cell culture-propagated subclade 3C.2a2 viruses, A/Bretagne/1413/2017, and the egg-propagated subgroup 3C.2a1b+T131K viruses A/Norway/2279/2029 and A/South Australia/34/2019, with the latter being the vaccine virus for the southern hemisphere 2020 season [2]. Similarly, antisera raised against two cell culture-propagated subgroup 3C.2a1b viruses, A/La Rioja/2202/2018 (3C.2a1b+T135K) and A/Norway/3275/2018 (3C.2a1b+T131K), for which no homologous titres are given due to the inability of these cell culture-propagated reference viruses to agglutinate RBCs, recognised only 24 (20%) and 35 (29%) test virus, respectively, at titres of ≥160. Test viruses reacted better with antiserum raised against the northern hemisphere 2018–19 vaccine virus [4], egg-propagated A/Singapore/INFOMH-16-0019/2016 (3C.2a1), with 47 (40%) and 105 (86%) test viruses being recognised at titres within twofold and fourfold of the homologous titre, respectively.

Antisera raised against two cell culture-propagated clade 3C.3a viruses, A/England/538/2018 and A/Kansas/14/2017, recognised 77/122 (64%) and 83/122 (69%) test viruses at titres within twofold and 76% and 78% within fourfold of homologous titres, respectively. However, the antiserum raised egg-propagated NYMC X-327 (A/Kansas/14/2017), the vaccine virus for the northern hemisphere 2019–2020 season [1], recognised only 30 (25%) test viruses at titres within fourfold of the homologous titre. Antiserum raised against cell culture-propagated A/Hong Kong/5738/2014 (clade 3C.2a) recognised all but five (96%) test viruses at titres within fourfold of the homologous titre. Antiserum raised against a tissue culture-propagated subgroup 3C.2a1b+T135K-B virus, A/Hong Kong/2669/2019, recognised subgroup 3C.2a1b+T135K-A/B test viruses well, but antiserum raised against the egg-propagated cultivar of A/Hong Kong/2671/2019 did so poorly, something that is often seen with A(H3N2) viruses.

Overall, the HI data show poor recognition of test viruses by post-infection ferret antisera raised against four of five egg-propagated vaccine/reference viruses. The HA genes of the 85 test viruses for which sequencing had been completed fell in four clusters, 49 in clade 3C.3a, 16 in subgroup 3C.2a1b+T131K, 15 in subgroup 3C.2a1b+T135K-A and five in subgroup 3C.2a1b+T135K-B (Tables 4-1 to 4-5), so the HI data indicate: (i) poor cross-reactivity of antisera raised against subclade 3C.2a2 viruses, (ii) significant clade specificity of the antisera raised against cell culture-propagated clade 3C.3a viruses, A/England/538/2018 and A/Kansas/14/2017, and (iii), of the seven antisera raised against cell culture-propagated viruses, the one raised against A/Hong Kong/5738/2014 (clade 3C.2a) gives the broadest cross-clade/subclade reactivity.

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 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

[2] For example, the September 2013 report: European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, September 2013. Stockholm: ECDC; 2014. 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

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.

Figure 2 shows an HA gene-based phylogeny for a representative set of recently circulating A(H3N2) viruses. Globally, based on sequences deposited in GISAID, viruses in the **3C.2a1b** subgroup have circulated recently in great numbers, with a majority falling in the **3C.2a1b+T131K** cluster. Diversification of subgroup **3C.2a1b** viruses with **HA1 T135K** substitution is occurring, notably with significant geographic spread of viruses in the antigenically distinct **3C.2a1b+T135K-B** cluster, a factor that 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 geographic distribution of clade 3C.3a viruses appears more restricted, with the great majority being reported from the WHO European Region, notably by countries in the western part of the Region.

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 Figure 2 in red. The location on the A/Hong Kong/2671/2019 (**3C.2a1b+T135K-B**) virus, recently recommended for vaccines to be used in the 2020–2021 northern hemisphere season [3], is also indicated as a reference virus.

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			MDCK	SIAT	Egg 10^{-4}	SIAT	Egg	SIAT	SIAT	Egg	SIAT
	Ferret number			St Judes F60/17[*1]	F01/18[*1]	F13/19[*1]	F03/19[*1]	F45/19[*1]	F26/18[*1]	F31/18[*1]	F16/19[*1]	F17/19[*1]
	Genetic group			3C.2a	3C.2a2	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	3C.2a1b+T135K-A	3C.3a	3C.3a	3C.3a
REFERENCE VIRUSES				A/HK 5738/14	A/Bretagne 1413/17	A/Singapore 0019/16	A/Norway 3275/18	A/Sth Aus 34/19	A/La Rioja 2202/18	A/Eng 538/18	NYMC X-327 A/Kansas/14	A/Kansas 14/17
A/Hong Kong/5738/2014	3C.2a	2014-04-30	MDCK1/MDCK2/SIAT1	160	160	320	160	160	160	160	160	160
A/Bretagne/1413/2017	3C.2a2	2017-10-09	MDCK1/SIAT4	320	640	320	320	320	160	160	160	160
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	40	320	40	40	160	80	40	40
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	640	320	640	1280	80	80	40	40
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	<	80	40	<	<	640	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	40	<	80	<	<	<	320	1280	320
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	<	40	<	<	<	320	160	320
TEST VIRUSES												
A/Stockholm/22/2019	3C.2a1b+T131K	2019-08-23	MDCK1/SIAT1	80	40	80	160	160	80	80	40	40
A/Iceland/78/2019	3C.2a1b+T131K	2019-10-08	MDCK1/SIAT1	80	40	160	160	160	80	80	80	40
A/Iceland/81/2019	3C.2a1b+T131K	2019-10-15	MDCK1/SIAT1	160	80	160	160	320	80	160	80	80
A/Latvia/11-028714/2019	3C.2a1b+T131K	2019-11-12	MDCK1/SIAT1	80	80	160	160	320	160	80	80	40
A/Latvia/11-068832/2019	3C.2a1b+T131K	2019-11-26	MDCK1/SIAT1	80	40	160	160	160	80	80	40	40
A/Bremen/24/2019	3C.2a1b+T135K-A	2019-10-02	C1/SIAT1	80	40	160	160	160	160	160	80	80
A/Denmark/3264/2019	3C.2a1b+T135K-A	2019-10-25	SIAT3/SIAT1	160	40	160	160	80	160	160	80	80
A/Denmark/3275/2019	3C.2a1b+T135K-B	2019-11-06	SIAT3/SIAT1	80	<	80	160	<	80	40	<	40
A/Denmark/3292/2019	3C.2a1b+T135K-B	2019-11-13	SIAT2/SIAT1	40	<	80	80	<	40	40	<	40
A/Denmark/3331/2019	3C.2a1b+T135K-B	2019-11-21	SIAT2/SIAT1	40	<	80	80	<	40	40	<	40
						Vaccine NH 2018-19		Vaccine SH 2020			Vaccine NH 2019-20	

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

Sequences in Phylogenetic Tree

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										
				A/HK 5738/14 MDCK St Judes F60/17[-1]	A/Bretagne 1413/17 SIAT F01/18[-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]	AHK 2671/19 Egg F44/19[-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]
	Passage history												
	Ferret number												
	Genetic group			3C.2a	3C.2a2	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	3C.2a1b+T135K-A	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	320	160	160	80	<	160	160	80
A/Bretagne/1413/2017	3C.2a2	2017-10-09	MDCK1/SIAT4	160	640	320	160	320	80	<	160	80	80
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	80	320	40	80	160	40	80	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	640	320	1280	1280	80	80	80	40	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8	40	<	80	<	80	40	320	160	320	80
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	40	40	<	40	<	<	640	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	40	40	80	40	80	<	160	320	1280	320
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	80	40	40	<	<	320	160	320
TEST VIRUSES													
A/Cagnes sur Mer/1850/2019	3C.2a1b+T131K	2019-09-11	MDCK3/SIAT1	80	80	160	160	160	80	<	40	<	40
A/Cannes/1846/2019	3C.2a1b+T131K	2019-09-12	MDCK3/SIAT1	80	80	160	160	160	80	<	80	40	40
A/Czech Republic/1454/2019	3C.2a1b+T131K	2019-09-18	MDCK4/SIAT1	80	160	160	320	320	160	40	80	80	40
A/Skovde/8/2019	3C.2a1b+T131K	2019-09-30	MDCK1/SIAT1	80	160	160	320	320	160	40	80	40	40
A/Iceland/77/2019	3C.2a1b+T131K	2019-10-08	MDCK1/SIAT1	40	80	160	160	160	160	<	80	40	<
A/Iceland/79/2019	3C.2a1b+T131K	2019-10-09	MDCK1/SIAT2	40	80	160	160	160	80	<	40	40	<
A/Bayern/113/2019	3C.2a1b+T131K	2019-10-10	C2/SIAT1	80	160	160	640	320	160	<	160	80	80
A/Stockholm/32/2019	3C.2a1b+T131K	2019-10-14	MDCK0/SIAT1	80	80	160	160	320	80	40	80	<	40
A/Stockholm/30/2019	3C.2a1b+T131K	2019-10-14	MDCK0/SIAT1	80	160	160	320	320	160	40	160	80	80
A/Latvia/11-032248/2019	3C.2a1b+T131K	2019-11-12	MDCK2/SIAT2	80	160	160	320	160	160	<	80	80	80
A/Lyon/2017/2019	3C.2a1b+T135K-A	2019-11-07	MDCK2/SIAT1	160	40	160	320	80	160	<	160	80	80
A/Finland/136/2019	3C.2a1b+T135K-B	2019-10-25	SIAT1/SIAT1	40	<	80	160	<	80	40	40	<	40
A/Finland/130/2019	3C.3a	2019-09-13	SIAT1/SIAT1	40	40	80	<	40	<	<	320	160	160
						Vaccine NH 2018-19		Vaccine SH 2020				Vaccine NH 2019-20	

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

Sequences in Phylogenetic Tree

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									
					A/HK 5738/14	A/Bretagne 1413/17	A/Singapore 0019/16	A/Norway 3275/18	A/Sth Aus 34/19	A/La Rioja 2202/18	A/HK 2671/19	A/Eng 538/18	NYMC X-327 A/Kansas/14	A/Kansas 14/17
		Passage history			MDCK	SIAT	Egg 10^{-4}	SIAT	Egg	SIAT	Egg	SIAT	Egg	SIAT
		Ferret number			St Judes F60/17[*1]	F01/18[*1]	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.2a2	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	3C.2a1b+T135K-A	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	80	160	160	160	80	<	160	160	80
A/Bretagne/1413/2017		3C.2a2	2017-10-09	MDCK1/SIAT4	160	640	320	160	160	80	<	160	160	80
A/Singapore/INFIMH-16-0019/2016		3C.2a1	2016-04-14	E5/E2	160	40	320	40	40	160	40	40	40	<
A/South Australia/34/2019		3C.2a1b+T131K	2019-02-06	E6/E1	160	640	320	640	1280	80	80	80	40	40
A/Hong Kong/2671/2019		3C.2a1b+T135K-B	2019-06-17	E8/E1	<	<	80	<	40	40	320	160	320	80
A/England/538/2018		3C.3a	2018-02-26	MDCK1/SIAT4	40	40	40	<	<	<	<	640	160	320
NYMC X-327 (A/Kansas/14/17)		3C.3a	2017-12-14	Ex/E1	40	<	40	<	40	<	160	320	1280	320
A/Kansas/14/2017		3C.3a	2017-12-14	SIAT3/SIAT2	40	40	40	40	<	<	<	320	160	160
TEST VIRUSES														
A/Slovenia/3126/2019		3C.2a1b+T131K	2019-12-05	SIAT2/SIAT1	80	80	160	320	320	160	<	160	80	80
A/Centre/2559/2019		3C.2a1b+T135K-A	2019-11-25	MDCK2/SIAT2	80	40	160	80	160	160	<	80	80	40
A/Slovenia/3251/2019		3C.2a1b+T135K-A	2019-12-13	SIAT1/SIAT1	80	<	80	160	40	160	40	80	80	40
A/Belgium/G0003/2020		3C.2a1b+T135K-A	2019-12-26	SIAT1	160	80	160	320	160	160	40	160	80	80
A/Paris/2560/2019		3C.3a	2019-11-25	SIAT1	40	40	80	<	<	<	<	320	160	320
A/Pays de Loire/2718/2019		3C.3a	2019-12-10	MDCK1/SIAT1	80	80	160	40	40	40	<	640	320	320
A/Lorraine/2777/2019		3C.3a	2019-12-16	SIAT1	80	80	160	40	40	40	40	640	320	320
A/Belgium/G0539/2019		3C.3a	2019-12-23	SIAT1	160	80	160	80	80	80	<	640	320	320
A/Belgium/G0540/2019		3C.3a	2019-12-24	SIAT1	40	80	80	40	40	40	<	640	160	320
A/Belgium/G0538/2019		3C.3a	2019-12-24	SIAT1	40	80	40	40	40	<	<	640	160	320
A/Belgium/G0004/2020		3C.3a	2019-12-30	SIAT1	40	80	80	40	40	40	<	640	160	320
A/Slovenia/3636/2019		3C.3a	2019-12-30	SIATx/SIAT1	40	80	80	40	40	<	40	640	160	320
A/Slovenia/23/2020		3C.3a	2020-01-01	SIATx/SIAT1	160	160	160	40	40	40	<	640	160	320
							Vaccine NH 2018-19		Vaccine SH 2020				Vaccine NH 2019-20	

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

Sequences in Phylogenetic Tree

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												
										NEW						
				A/HK 5738/14 MDCK St Judes F60/17[1]	A/Bretagne 1413/17 SIAT F01/18[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/Norway 2279/19 Egg F03/20[1]	A/La Rioja 2202/18 SIAT F26/18[1]	A/HK 2671/19 Egg F44/19[1]	A/HK 2669/19 SIAT F04/20[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]
	Passage history			3C.2a	3C.2a2	3C.2a1	3C.2a1b+T131K	3C.2a1b+T131K	3C.2a1b+T131K	3C.2a1b+T135K-A	3C.2a1b+T135K-B	3C.2a1b+T135K-B	3C.3a	3C.3a	3C.3a
	Ferret number															
	Genetic group															
REFERENCE VIRUSES																
A/Hong Kong/5738/2014	3C.2a	2014-04-30	MDCK1/MDCK3/SIAT2	160	80	320	160	160	80	160	40	40	160	160	160	160
A/Bretagne/1413/2017	3C.2a2	2017-10-09	MDCK1/SIAT4	160	320	320	160	160	80	160	40	40	160	160	160	80
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	80	320	80	40	80	320	80	160	80	40	40	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	640	320	640	1280	160	80	160	<	80	40	40	40
A/Norway/2279/2019	3C.2a1b+T131K	2019-09-25	E4	ND	ND	640	ND	320	160	ND	640	160	ND	80	ND	ND
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E1	<	<	80	<	40	<	40	320	160	160	320	80	80
A/Hong Kong/2669/2019	3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	160	40	160	160	80	40	320	160	320	80	160	160	80
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	40	40	<	<	<	40	40	<	640	160	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	E4/E1	40	<	40	<	40	40	40	160	40	320	1280	320	320
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	80	40	40	40	40	40	<	640	320	320	320
TEST VIRUSES																
A/Portugal/6/2019	3C.2a1b+T135K-A	2019-10-22	SIAT1/SIAT1	80	40	160	160	80	40	160	160	160	80	40	40	40
A/Ireland/95061/2019	3C.2a1b+T135K-A	2019-11-25	SIAT1/SIAT1	160	80	160	320	160	40	320	80	320	160	160	160	160
A/England/195160658/2019	3C.2a1b+T135K-A	2019-12-10	SIAT1/SIAT1	40	40	80	160	40	<	160	40	160	40	40	40	40
A/Bayern/115/2019	3C.2a1b+T135K-A	2019-12-16	C1/SIAT1	80	40	160	160	160	40	160	40	160	160	160	160	80
A/Portugal/16/2019	3C.2a1b+T135K-A	2019-12-16	SIAT1/SIAT1	80	40	160	160	80	40	160	80	160	80	80	80	40
A/England/195200780/2019	3C.2a1b+T135K-A	2019-12-23	SIAT1/SIAT1	80	40	160	160	80	40	160	40	160	80	80	80	40
A/Athens.GR/25/2020	3C.2a1b+T135K-A	2020-01-07	MDCK1/SIAT1	40	40	80	80	160	40	80	<	40	<	40	40	<
A/Saarland/25/2019	3C.2a1b+T135K-B	2019-12-16	C2/SIAT1	40	<	40	80	<	<	80	40	160	40	<	<	<
A/Ireland/93664/2019	3C.3a	2019-11-22	SIAT3	40	40	80	40	40	<	40	40	<	320	160	160	320
A/Ireland/95068/2019	3C.3a	2019-11-25	SIAT1	80	80	160	40	40	40	40	40	<	640	320	320	320
A/England/670/2019	3C.3a	2019-12-09	SIAT1/SIAT1	40	40	40	<	<	<	40	40	<	320	160	160	320
A/England/652/2019	3C.3a	2019-12-09	SIAT1/SIAT1	40	40	80	40	40	<	40	40	<	320	160	160	320
A/Hessen/72/2019	3C.3a	2019-12-10	C1/SIAT1	80	40	80	<	<	<	40	40	<	640	160	160	320
A/Austria/1207674/2019	3C.3a	2019-12-12	SIATx/SIAT1	40	40	80	<	<	40	40	<	<	640	160	160	320
A/Austria/1208858/2019	3C.3a	2019-12-16	SIATx/SIAT1	80	80	80	40	40	<	80	40	<	640	320	320	320
A/Austria/1208486/2019	3C.3a	2019-12-16	SIATx/SIAT1	40	40	80	40	<	<	40	40	<	320	160	160	320
A/Berlin/62/2019	3C.3a	2019-12-16	C1/SIAT1	40	<	80	<	40	<	<	<	<	320	160	160	160
A/Austria/1209023/2019	3C.3a	2019-12-17	SIATx/SIAT1	<	<	40	<	<	<	<	<	<	640	160	160	160
A/Austria/1208875/2019	3C.3a	2019-12-17	SIATx/SIAT1	40	80	160	40	40	<	40	40	<	640	160	160	320
A/Austria/1209271/2019	3C.3a	2019-12-18	SIATx/SIAT1	80	80	160	40	80	40	80	40	<	640	320	320	320
A/Austria/1209022/2019	3C.3a	2019-12-18	SIATx/SIAT1	80	80	160	40	40	40	40	40	<	640	320	320	320
A/Lyon/2358/2019	3C.3a	2019-12-20	MDCK2/SIAT1	40	40	80	<	<	<	40	<	<	320	160	160	320
A/Netherlands/10282/2019	3C.3a	2019-12-24	MDCK-MIX2/SIAT1	40	40	40	<	<	<	<	<	<	320	80	80	160
A/Lisboa/118/2019	3C.3a	2019-12-25	SIAT1/SIAT1	40	40	80	<	<	<	40	40	<	320	160	160	320
A/Netherlands/10286/2019	3C.3a	2019-12-30	MDCK-MIX2/SIAT1	40	40	80	40	40	40	40	40	<	640	160	160	320
A/Berlin/4/2020	3C.3a	2020-01-03	C1/SIAT1	40	40	80	<	<	<	40	40	<	320	160	160	160
A/Bulgaria/021/2020	3C.3a	2020-01-06	SIAT1	40	40	80	<	<	<	40	40	<	320	160	160	320
A/Thuringen/3/2020	3C.3a	2020-01-06	C1/SIAT1	40	40	80	<	<	<	40	40	<	320	160	160	320
A/Berlin/2/2020	3C.3a	2020-01-09	C1/SIAT1	40	80	80	<	<	<	40	40	<	320	160	160	320
A/Bulgaria/062/2020	3C.3a	2020-01-10	SIAT1	40	80	80	<	<	<	40	40	<	320	160	160	320
A/Bulgaria/061/2020	3C.3a	2020-01-10	SIAT1	40	80	80	<	<	<	<	40	<	320	160	160	320
A/Bulgaria/090/2020	3C.3a	2020-01-13	SIAT1	40	80	80	40	80	<	40	40	<	640	160	160	320
A/Greece/60/2020	3C.3a	2020-01-13	SIAT1	40	40	40	<	<	<	<	<	<	320	160	160	320
A/Estonia/125785/2020	3C.3a	2020-01-13	SIAT1/SIAT1	40	40	40	<	<	<	<	<	<	320	160	160	320
A/Athens.GR/79/2020	3C.3a	2020-01-14	MDCK1/SIAT1	40	40	80	<	<	<	40	40	<	320	160	160	320
A/Athens.GR/128/2020	3C.3a	2020-01-16	Cx/SIAT1	40	40	40	<	<	<	<	<	<	320	160	160	160
						Vaccine NH 2018-19		Vaccine SH 2020						Vaccine NH 2019-20		

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

Sequences in Phylogenetic Tree

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

Viruses	Other information		Collection date	Passage history	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 2669/19	A/Eng 538/18	NYMC X-327 A/Kansas/14	A/Kansas 14/17
		Passage history			MDCK	Egg 10^{-4}	SIAT	Egg	SIAT	Egg	SIAT	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]	F04/20[*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	160	320	160	160	160	40	40	320	160	160
A/Singapore/INFIMH-16-0019/2016		3C.2a1	2016-04-14	E5/E2	80	320	80	40	160	40	80	80	40	<
A/South Australia/34/2019		3C.2a1b+T131K	2019-02-06	E6/E1	160	320	640	640	80	80	<	80	40	40
A/Hong Kong/2671/2019		3C.2a1b+T135K-B	2019-06-17	E8/E1	<	80	<	40	40	640	160	160	320	80
A/Hong Kong/2669/2019		3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	80	80	80	40	160	80	320	80	160	40
A/England/538/2018		3C.3a	2018-02-26	MDCK1/SIAT4	40	40	40	<	<	40	<	640	160	320
NYMC X-327 (A/Kansas/14/17)		3C.3a	2017-12-14	Ex/E1	40	80	<	<	<	160	40	320	1280	320
A/Kansas/14/2017		3C.3a	2017-12-14	SIAT3/SIAT2	40	80	<	<	<	40	<	320	160	320
TEST VIRUSES														
A/Palermo/36/2019		3C.2a1b+T135K-A	2019-12-11	SIAT2/SIAT1	80	80	160	80	160	40	320	160	80	80
A/Palermo/02/2020		3C.2a1b+T135K-A	2020-01-02	SIAT2/SIAT1	40	80	160	160	80	<	160	80	40	40
A/Lithuania/MB42384/2019		3C.3a	2019-12-24	SIAT2/SIAT1	40	80	40	<	<	<	<	320	160	160
A/Parma/391/2019		3C.3a	2019-12-27	SIAT1/SIAT1	40	80	40	40	<	<	<	640	160	320
A/Lithuania/MB170/2019		3C.3a	2019-12-31	SIAT1/SIAT1	40	40	<	<	<	<	<	320	160	160
A/Norway/47/2020		3C.3a	2020-01-03	SIAT1/SIAT1	40	80	40	40	40	<	<	320	160	320
A/Poland/1521/2020		3C.3a	2020-01-05	SIAT1	40	80	<	<	<	<	<	640	40	320
A/Lithuania/MB398/2020		3C.3a	2020-01-05	SIAT1/SIAT1	40	40	<	<	<	<	<	320	160	160
A/Norway/108/2020		3C.3a	2020-01-06	SIAT1/SIAT1	40	80	<	<	40	<	<	640	160	320
A/Czech Republic/38/2020		3C.3a	2020-01-07	P2/SIAT1	40	80	<	<	<	<	<	320	160	320
A/Czech Republic/87/2020		3C.3a	2020-01-10	P1/SIAT1	40	80	<	<	<	<	<	320	160	320
A/Czech Republic/101/2020		3C.3a	2020-01-13	P1/SIAT1	40	80	<	<	<	<	<	320	160	320
A/Bucuresti/256299/2020		3C.3a	2020-01-13	MDCK1/SIAT1	40	40	<	<	<	<	<	320	160	160
A/Czech Republic/1691/2019			2019-12-05	P3/SIAT1	<	40	<	<	<	<	<	320	80	160
A/Poland/605/2019			2019-12-10	SIAT1	<	<	<	<	<	<	<	320	80	160
						Vaccine NH 2018-19		Vaccine SH 2020					Vaccine NH 2019-20	

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

Sequences in Phylogenetic Tree

Table 4-6. Antigenic analysis of A(H3N2) viruses by HI

Viruses	Other information		Collection date	Passage history	Haemagglutination inhibition titre									
					Post-infection ferret antisera									
					A/HK	A/Singapore	A/Norway	A/Sth Aus	A/La Rioja	A/HK	A/HK	A/Eng	NYMC X-327	A/Kansas
					5738/14	0019/16	3275/18	34/19	2202/18	2671/19	2669/19	538/18	A/Kansas/14	14/17
		Passage history			MDCK	Egg 10^{-4}	SIAT	Egg	SIAT	Egg	SIAT	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]	F04/20[*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	160	320	160	160	160	40	40	160	160	160
A/Singapore/INFIMH-16-0019/2016		3C.2a1	2016-04-14	E5/E2	160	320	40	40	160	80	80	80	40	40
A/South Australia/34/2019		3C.2a1b+T131K	2019-02-06	E6/E1	160	320	640	1280	80	320	<	80	80	40
A/Hong Kong/2671/2019		3C.2a1b+T135K-B	2019-06-17	E8/E1	40	160	<	80	40	640	160	160	640	80
A/Hong Kong/2669/2019		3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	80	160	160	80	160	160	320	80	80	80
A/England/538/2018		3C.3a	2018-02-26	MDCK1/SIAT4	40	80	<	<	<	80	<	640	320	320
NYMC X-327 (A/Kansas/14/17)		3C.3a	2017-12-14	Ex/E1	<	40	<	<	<	320	40	320	1280	320
A/Kansas/14/2017		3C.3a	2017-12-14	SIAT3/SIAT2	40	80	<	<	<	40	<	640	320	320
TEST VIRUSES														
A/Netherlands/01624/2019			2019-11-27	hCK1/SIAT1	40	80	<	<	<	40	<	640	320	320
A/Netherlands/10267/2019			2019-12-02	MDCK-MIX2/SIAT1	80	160	40	40	40	40	<	640	320	640
A/Netherlands/01672/2019			2019-12-04	hCK1/SIAT1	<	40	<	<	<	80	<	640	320	320
A/Netherlands/10268/2019			2019-12-10	MDCK-MIX3/SIAT1	80	160	40	80	40	80	<	640	320	640
A/Netherlands/10273/2019			2019-12-16	MDCK-MIX2/SIAT1	80	320	160	160	80	160	40	1280	640	640
A/Netherlands/10279/2019			2019-12-20	MDCK-MIX2/SIAT1	40	160	80	80	<	80	<	640	320	320
A/Lithuania/MB42123/2019			2019-12-20	SIAT1/SIAT1	40	80	<	<	<	40	<	640	320	320
						Vaccine NH 2018-19		Vaccine SH 2020					Vaccine NH 2019-20	

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

Table 4-7. 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/Sth Aus 34/19 Egg	A/La Rioja 2202/18 SIAT	A/HK 2671/19 Egg	A/HK 2669/19 SIAT	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	F45/19*1	F26/18*1	F44/19*1	F04/20*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	160	320	160	160	160	40	40	160	160	160
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	320	40	40	160	80	80	80	40	40
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	320	1280	1280	80	320	40	80	80	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	2019-06-17	E8/E1	40	80	<	80	40	640	160	160	640	80
A/Hong Kong/2669/2019	3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	160	160	160	80	320	160	320	160	80	80
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	40	<	40	<	40	<	640	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	<	40	<	<	<	160	<	160	640	160
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	80	<	<	<	40	<	320	160	320
TEST VIRUSES													
A/Czech Republic/1633/2019		2019-11-19	P3/SIAT1	40	80	40	40	<	40	<	320	160	320
A/Catalonia/11962S/2019		2019-11-27	P0/SIAT1	80	80	<	40	<	80	<	320	160	320
A/Catalonia/11960S/2019		2019-11-27	P0/SIAT1	40	80	<	40	<	80	<	160	160	320
A/Friuli Venezia Giulia/233/2019		2019-11-28	SIAT2/SIAT1	160	160	320	160	160	160	80	80	80	80
A/Czech Republic/1670/2019		2019-11-28	P3/SIAT1	40	80	40	40	40	320	<	320	160	320
A/Lithuania/MB41285/2019		2019-12-09	SIAT2/SIAT1	40	80	40	40	<	40	<	320	160	320
A/Lithuania/MB40700/2019		2019-12-09	SIAT2/SIAT1	40	80	40	40	<	40	<	320	160	320
A/Lithuania/MB41185/2019		2019-12-11	SIAT1/SIAT1	40	80	80	<	40	40	160	40	<	40
A/Lithuania/MB41235/2019		2019-12-13	SIAT2/SIAT1	40	40	80	<	40	40	160	40	<	<
A/Lithuania/MB41882/2019		2019-12-18	SIAT1/SIAT1	<	40	<	<	<	40	<	320	160	160
					Vaccine NH 2018-19		Vaccine SH 2020					Vaccine NH 2019-20	

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

Table 4-8. 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/Sth Aus 34/19 Egg	A/La Rioja 2202/18 SIAT	A/HK 2671/19 Egg	A/HK 2669/19 SIAT	A/Eng 538/18 SIAT	NYMC X-327 A/Kansas/14/17 Egg	A/Kansas 14/17 SIAT
	Ferret number			St Judes F60/17[*1]	F13/19[*1]	F03/19[*1]	F45/19[*1]	F26/18[*1]	F44/19[*1]	F04/20[*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	160	320	160	160	160	40	40	320	160	160
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	640	80	80	320	80	80	80	80	<
A/South Australia/34/2019	3C.2a1b+T131K	2019-02-06	E6/E1	160	320	640	1280	80	160	<	80	80	40
A/Hong Kong/2671/2019	3C.2a1b+T135K-A	2019-06-17	E8/E1	40	80	<	40	40	640	160	160	320	80
A/Hong Kong/2669/2019	3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	80	160	160	80	160	160	320	160	80	80
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	40	<	<	<	40	<	640	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	Ex/E1	40	40	<	<	<	160	<	320	1280	320
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	80	<	<	<	40	<	640	160	320
TEST VIRUSES													
A/England/194660616/2019		2019-11-12	SIAT1/SIAT1	40	40	40	<	40	<	80	<	<	<
A/England/599/2019		2019-11-13	SIAT1/SIAT1	80	80	<	<	<	40	<	640	160	320
A/England/387/2019		2019-11-13	MDCK1/SIAT1	40	80	80	<	40	80	40	160	80	40
A/England/194820759/2019		2019-11-17	SIAT2/SIAT1	80	160	160	<	80	80	160	40	<	40
A/England/476/2019		2019-11-20	SIAT1/SIAT1	80	80	<	<	<	40	<	640	320	320
A/England/194840298/2019		2019-11-24	SIAT2/SIAT1	80	160	160	320	160	<	160	160	80	160
A/England/601/2019		2019-11-24	SIAT2/SIAT1	80	160	80	40	40	40	<	640	320	640
A/England/194840192/2019		2019-11-25	SIAT2/SIAT1	160	160	320	320	320	80	160	160	160	160
A/England/531/2019		2019-11-25	SIAT1/SIAT1	80	160	40	40	<	40	<	640	320	320
A/England/513/2019		2019-11-26	SIAT1/SIAT1	80	80	<	<	<	40	<	320	160	320
A/England/612/2019		2019-11-29	SIAT1/SIAT1	80	160	40	80	40	40	<	640	320	320
A/England/551/2019		2019-11-29	SIAT1/SIAT1	80	80	<	<	<	40	<	640	160	320
A/England/521/2019		2019-11-29	SIAT1/SIAT1	80	80	40	40	40	40	<	640	160	320
A/England/530/2019		2019-12-02	SIAT1/SIAT1	80	80	40	<	40	40	<	640	320	320
A/England/651/2019		2019-12-05	SIAT1/SIAT1	80	80	<	40	<	40	<	640	320	320
A/England/645/2019		2019-12-05	SIAT1/SIAT1	80	160	40	<	40	<	<	640	320	640
A/England/648/2019		2019-12-07	SIAT1/SIAT1	80	160	80	80	80	80	<	640	320	640
A/England/675/2019		2019-12-08	SIAT1/SIAT1	80	160	40	40	40	40	<	640	320	640
					Vaccine NH 2018-19		Vaccine SH 2020					Vaccine NH 2019-20	

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

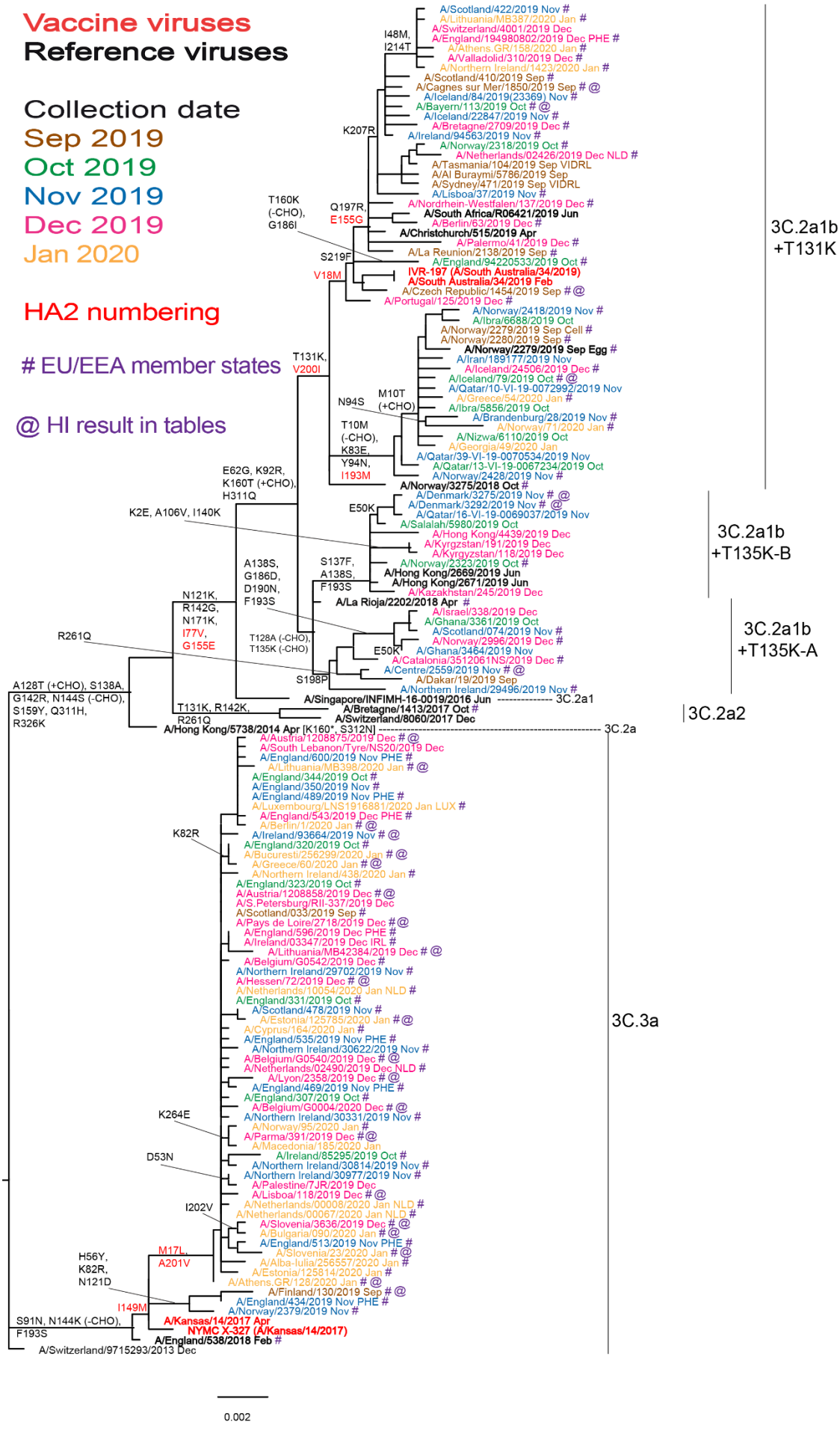
Table 4-9. Antigenic analysis of A(H3N2) viruses by HI – Summary

Viruses		Haemagglutination inhibition titre											
		Post-infection ferret antisera											
		A/HK 5738/14	A/Bretagne 1413/17	A/Singapore 0019/16	A/Norway 3275/18	A/Sth Aus 34/19	A/Norway 2279/19	A/La Rioja 2202/18	A/HK 2671/19	A/HK 2669/19	A/Eng 538/18	NYMC X-327 A/Kansas/14	A/Kansas 14/17
	Passage history	MDCK	SIAT	Egg 10^{-4}	SIAT	Egg	Egg	SIAT	Egg	SIAT	SIAT	Egg	SIAT
	Ferret number	St Judes F60/17[*1]	F01/18[*1]	F13/19[*1]	F03/19[*1]	F45/19[*1]	F03/20[*1]	F26/18[*1]	F44/19[*1]	F04/20[*1]	F31/18[*1]	F16/19[*1]	F17/19[*1]
	Genetic group	3C.2a	3C.2a2	3C.2a1	3C.2a1b+T131K	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	160	80	320	160	160	80	160	40	40	160	160	160
A/Bretagne/1413/2017	3C.2a2	160	320	320	160	160	80	160	40	40	160	160	80
A/Singapore/INFIMH-16-0019/2016	3C.2a1	160	80	320	80	40	80	320	80	160	80	40	<
A/South Australia/34/2019	3C.2a1b+T131K	160	640	320	640	1280	160	80	160	<	80	40	40
A/Norway/2279/2019	3C.2a1b+T131K	ND	ND	640	ND	320	160	ND	160	160	ND	80	ND
A/Hong Kong/2671/2019	3C.2a1b+T135K-B	<	<	80	<	40	<	40	640	160	160	320	80
A/Hong Kong/2669/2019	3C.2a1b+T135K-B	160	40	160	160	80	40	320	160	320	80	160	80
A/England/538/2018	3C.3a	40	40	40	<	<	<	40	40	<	640	160	320
NYMC X-327 (A/Kansas/14/17)	3C.3a	40	<	40	<	40	40	40	160	40	320	1280	320
A/Kansas/14/2017	3C.3a	40	40	80	40	40	40	40	40	<	640	320	320
TEST VIRUSES													
Number of viruses tested		122	72	122	122*	122	86	122*	110	86	122	122	122
No with titre reduction ≤2-fold		57		47	35		7	24	2	14	77	1	83
%		*46.7*		*40.2*	*28.7*		*9.6*	*19.7*	*2.1*	*19.2*	*63.6*	*0.9*	*68.6*
No with titre reduction =4-fold		60	14	58		11	13		2	3	16	29	12
%		*49.2*	*19.4*	*49.6*		*10.2*	*17.8*		*2.1*	*4.1*	*13.2*	*27.1*	*9.9*
No with titre reduction ≥8-fold		5	58	12		97	53		91	56	28	77	26
%		*4.1*	*80.6*	*10.3*		*89.8*	*72.6*		*95.8*	*76.7*	*23.1*	*72*	*21.5*
Subgroup 3C.2a1b+T131K viruses													
Number of viruses tested		16	16	16	16*	16		16*	11		16	16	16
No with titre reduction ≤2-fold		14		15	16			8	1.0				1
%		*87.5*		*93.8*	*100.0*			*50.0*	*9.1*				*6.3*
No with titre reduction =4-fold		2	5	1		8					4		4
%		*12.5*	*31.3*	*6.3*		*50.0*					*25.0*		*25.0*
No with titre reduction ≥8-fold			11			8			10		12	16	11
%			*68.8*			*50.0*			*90.9*		*75.0*	*100.0*	*68.8*
Subgroup 3C.2a1b+T135K-A viruses													
Number of viruses tested		15	13	15	15*	15	9	15*	11	9	15	15	15
No with titre reduction ≤2-fold		12		10	13		2	13		8			2
%		*80.0*		*66.7*	*86.7*		*22.2*	*86.7*		*88.9*			*13.3*
No with titre reduction =4-fold		3	1	5		1	6			1	8		7
%		*20.0*	*7.7*	*33.3*		*6.7*	*66.7*			*11.1*	*53.3*		*46.7*
No with titre reduction ≥8-fold			12			14	1		11		7	15	6
%			*92.3*			*93.3*	*11.1*		*100.0*		*46.7*	*100.0*	*40.0*
Subgroup 3C.2a1b+T135K-B viruses													
Number of viruses tested		5	5	5	5*	5	1	5*	2	1	5	5	5
No with titre reduction ≤2-fold		1			1					1			
%		*20.0*			*20.0*					*100.0*			
No with titre reduction =4-fold		4		4									
%		*80.0*		*80.0*									
No with titre reduction ≥8-fold			5	1		5	1		2		5	5	5
%			*100.0*	*20.00*		*100.0*	*100.0*		*100.0*		*100.0*	*100.0*	*100.0*
Clade 3C.3a viruses													
Number of viruses tested		49	38	49	49*	49	39	49*	49	39	49	49	49
No with titre reduction ≤2-fold		9		8							49		49
%		*18.4*		*16.3*							*100.0*		*100.0*
No with titre reduction =4-fold		39	8	31			5					7	
%		*79.6*	*21.1*	*63.3*			*12.8*					*14.3*	
No with titre reduction ≥8-fold		1	30	10		49	34		49	39		42	
%		*2.0*	*78.9*	*20.4*		*100.0*	*87.2*		*100.0*	*100.0*		*85.7*	
				Vaccine NH 2018-19		Vaccine SH 2020						Vaccine NH 2019-20	

* 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.

Figure 2. Phylogenetic comparison of influenza A(H3N2) HA genes



Influenza B virus analyses

A total of 264 influenza type B viruses with collection dates after 31 August 2019 have been received at the WIC (Table 2). Of these, 219 were sent with pre-assignment to a lineage: 205 B/Victoria and 14 B/Yamagata.

Influenza B/Victoria-lineage

Of the B/Victoria-lineage viruses from EU/EEA countries received, 104 were assessed by HI assay since the December 2019 report (Tables 5-1 to 5-6). Test viruses are sorted by date of collection and genetic group/subgroup, where known at the time of writing this report, and the results are summarised in Table 5-7.

Poor reactivity with ferret antisera raised against four viruses in **clade 1A** (n=4) was observed for all 104 test viruses, antisera raised against three **subclade 1A(△2)** viruses recognised between 10% and 17% of test viruses at titres within fourfold of their respective homologous titres, and antisera raised against two **subclade 1A(△3)B** viruses recognised 78% and 77% of test viruses at titres within fourfold of their respective homologous titres. Overall, two patterns of reactivity were observed reflecting the subclade of the test virus with **subclade 1A(△2)** viruses reacting well with antisera raised against tissue culture-propagated B/Norway/2409/2017 and egg- and tissue culture-propagated B/Colorado/06/2017, while **subclade 1A(△3)B** viruses reacted well with antisera raised against egg- and tissue culture-cultivars of B/Washington/02/2019. Approximately 22% of the **subclade 1A(△3)B** test viruses showed eightfold or greater reductions in titre with antisera raised against B/Washington/02/2019 compared to homologous titres: those viruses with sequences available at the time of writing this report, carried unusual amino acid substitutions in HA1 (e.g. N126K or E128K or N150K or T155A, sometimes with additional substitutions) (Tables 5-1, 5-3 and 5-4, Figure 3).

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 A/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 A/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 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 in recent months and is represented by the recently recommended vaccine virus **B/Washington/02/2019**.

The HA phylogeny (Figure 3) was constructed using sequences available in GISAID for a set of recently circulating viruses. Over the last five months, viruses in **subclade 1A(△3)B** have dominated, with the great majority having **HA1 K136E,** often with **G133R** substitution, and a number of virus clusters have emerged defined by specific amino acid substitutions, e.g. **HA1 N126K, E128K** or **N150K** with **G184E**, **N197D** (loss of a glycosylation site) and **R279K**. Relatively few **subclade 1A(△2)** viruses have been detected.

Following the spread of **1A(Δ2)** viruses, a representative, B/Colorado/06/2017, was recommended for use in trivalent influenza vaccines for the 2018–19 and 2019–20 northern hemisphere [4, 1] and 2019 southern hemisphere [5] seasons. 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 southern hemisphere and northern hemisphere 2020–2021 seasons [2, 3].

Influenza B/Yamagata-lineage

Five B/Yamagata-lineage viruses were assessed by HI assay since the December 2019 report (Table 6). All test viruses fell in genetic clade 3 and gave similar reactivity profiles with the panel of post-infection ferret antisera used in the HI assay. Notably, all reacted within twofold of the homologous titre of the antiserum raised against the vaccine virus, egg-propagated B/Phuket/3073/2013, and within fourfold for the antiserum raised against the cell culture-propagated cultivar.

[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

The HA phylogeny (Figure 4) was constructed using the most recently submitted sequences to GISAID, for viruses with collection dates after 31 August 2019, together with sequences from a selection of viruses with earlier collection dates. All recently collected viruses have HA genes that continue to 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 D229N** or **D232N** [introducing a potential N-linked glycosylation site] with **R48K**), is occurring. It has been noted in previous characterisation reports for 2018 that 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 2018–2019, 2019–2020 and 2020-2021 [4, 1, 3] northern hemisphere and the 2019 and 2020 [5, 2] southern hemisphere seasons.

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	B/Bris 60/08	B/Sth Aus 81/12	B/Ireland 3154/16	B/Nord-West 1/16	B/Norway 2409/17	B/Colorado 06/17	B/Colorado 06/17	B/Wash'ton 02/19	B/Wash'ton 02/19
		Passage history			Egg	Egg	Egg	MDCK	MDCK	MDCK	MDCK	Egg	MDCK	Egg
		Ferret number			Sh 539, 540, 543, 544, 570, 571, 574[*1,3]	F44/17[*2]	F25/16[*4]	F15/16[*2]	F38/17[*2]	F40/17[*2]	F09/18[*4]	F11/18[*2]	F37/19[*4]	F38/19[*4]
		Genetic group			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES														
B/Brisbane/60/2008		1A	2008-08-04	E4/E4	2560	640	640	40	160	<	20	80	<	320
B/South Australia/81/2012		1A	2012-11-28	E4/E2	2560	640	640	80	160	<	40	80	<	320
B/Ireland/3154/2016		1A	2016-01-14	MDCK1/MDCK4	2560	80	<	80	160	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016		1A	2016-01-04	C2/MDCK2	2560	80	<	80	160	<	<	<	<	<
B/Norway/2409/2017		1A(Δ2)	2017-04-27	MDCK1/MDCK3	160	20	<	<	<	40	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	MDCK1/MDCK2	160	20	<	<	<	40	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	E5/E2	1280	160	40	<	<	20	80	320	<	160
B/Cote D'Ivoire/1662/2018		1A(Δ3)B	2018-07-25	P0/MDCK3	640	80	<	<	<	<	<	<	10	80
B/Washington/02/2019		1A(Δ3)B	2019-01-19	C2/MDCK2	640	160	<	<	<	<	<	160	80	640
B/Washington/02/2019		1A(Δ3)B	2019-01-19	E3/E2	640	80	40	<	<	<	10	160	20	320
TEST VIRUSES														
B/Lyon/1861/2019		1A(Δ2)	2019-10-04	MDCK3/MDCK1	320	40	<	<	<	<	20	160	<	<
B/Iceland/83/2019		1A(Δ2)	2019-11-13	MDCK1/MDCK1	320	20	<	<	<	40	20	80	<	<
B/Lulea/1/2019	E128K, T155A	1A(Δ3)B	2019-08-01	MDCK0/MDCK1	80	20	<	<	<	<	<	<	10	10
B/Finland/124/2019		1A(Δ3)B	2019-08-14	MDCK1/MDCK1	320	80	<	<	<	<	<	<	40	640
B/Latvia/10-010670/2019		1A(Δ3)B	2019-10-03	MDCK2/MDCK1	640	80	<	<	<	<	<	<	80	640
B/Latvia/10-010619/2019		1A(Δ3)B	2019-10-03	MDCK1/MDCK1	320	40	<	<	<	<	<	<	40	320
B/Stockholm/5/2019		1A(Δ3)B	2019-10-05	MDCK0/MDCK1	160	40	<	<	<	<	<	<	80	320
B/Lyon/CHU/ R19.116.25/2019		1A(Δ3)B	2019-10-08	MDCK2/MDCK1	640	40	<	<	<	<	<	<	80	640
B/Denmark/14/2019		1A(Δ3)B	2019-11-02	SIAT2/MDCK1	640	80	<	<	<	<	<	<	80	320
B/Croatia/7789/2019	N150K, G184E, N197D (-CHO), R279K	1A(Δ3)B	2019-11-11	MDCKx/MDCK1	1280	320	160	<	<	<	20	160	10	320
B/Latvia/11-034083/2019		1A(Δ3)B	2019-11-12	MDCK1/MDCK1	320	40	<	<	<	<	<	<	80	640
B/Latvia/11-034080/2019		1A(Δ3)B	2019-11-12	MDCK1/MDCK1	320	40	<	<	<	<	<	<	80	320
B/Latvia/11-034075/2019		1A(Δ3)B	2019-11-12	MDCKx/MDCK1	160	40	<	<	<	<	<	<	40	320
B/Latvia/11-034069/2019		1A(Δ3)B	2019-11-12	MDCK2/MDCK1	320	40	<	<	<	<	<	<	80	320
B/Latvia/11-031992/2019		1A(Δ3)B	2019-11-13	MDCKx/MDCK1	320	80	<	<	<	<	<	<	80	640
B/Lulea/2/2019		1A(Δ3)B	2019-11-21	MDCK0/MDCK1	160	40	<	<	<	<	<	<	40	320
B/Stockholm/9/2019		1A(Δ3)B	2019-11-21	MDCK0/MDCK1	160	20	<	<	<	<	<	<	40	320
B/Denmark/17/2019		1A(Δ3)B	2019-11-23	SIAT2/MDCK1	640	160	<	<	80	<	<	<	80	640
B/Denmark/18/2019		1A(Δ3)B	2019-11-25	SIAT2/MDCK1	160	40	<	<	<	<	<	<	40	320
												Vaccine NH 2018-19 SH 2019 NH 2019-20		Vaccine SH 2020

* 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 Phylogenetic Tree

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										
	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
	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]	F09/18[*4]	F11/18[*4]	F37/19[*4]	F38/19[*4]
	Genetic group			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES													
B/Brisbane/60/2008	1A	2008-08-04	E4/E4	1280	640	640	40	160	<	20	40	<	160
B/South Australia/81/2012	1A	2012-11-28	E4/E2	2560	640	640	40	160	<	20	40	<	160
B/Ireland/3154/2016	1A	2016-01-14	MDCK1/MDCK4	1280	80	40	80	320	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016	1A	2016-01-04	C2/MDCK2	1280	80	40	40	160	<	<	<	<	<
B/Norway/2409/2017	1A(Δ2)	2017-04-27	MDCK1/MDCK3	80	10	10	<	<	80	20	40	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	MDCK1/MDCK2	160	40	20	<	<	80	40	80	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	E5/E2	640	160	80	<	<	20	40	160	<	80
B/Washington/02/2019	1A(Δ3)B	2019-01-19	C2/MDCK2	320	80	40	<	<	<	<	40	40	320
B/Washington/02/2019	1A(Δ3)B	2019-01-19	E3/E2	640	80	80	<	<	<	<	80	20	320
TEST VIRUSES													
B/Iceland/21277/2019	1A(Δ3)B	2019-10-26	MDCK1	320	40	40	<	<	<	<	<	40	320
B/Coimbra/142/2019	1A(Δ3)B	2019-11-21	MDCK1	160	40	40	<	<	<	<	<	40	320
B/Madeira/66/2019	1A(Δ3)B	2019-11-21	MDCK1	160	40	40	<	<	<	<	<	40	320
B/Lisboa/50/2019	1A(Δ3)B	2019-11-21	MDCK1	160	40	20	<	<	<	<	<	40	320
B/Ireland/95062/2019	1A(Δ3)B	2019-11-26	MDCK1	160	40	40	<	<	<	<	<	40	320
B/Ireland/95248/2019	1A(Δ3)B	2019-11-27	MDCK1	160	40	40	<	<	<	<	<	40	320
B/Iceland/24875/2019	1A(Δ3)B	2019-12-12	MDCK1	160	40	20	<	<	<	<	<	20	160
										Vaccine NH 2018-19 SH 2019			Vaccine SH 2020

* 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 Phylogenetic Tree

Table 5-3. 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	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	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[*4]	F11/18[*4]	F37/19[*4]	F38/19[*4]
			Genetic group	1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES													
B/Brisbane/60/2008		1A	2008-08-04	E4/E4	2560	640	320	40	80	<	<	40	<	<	160
B/South Australia/81/2012		1A	2012-11-28	E4/E2	2560	640	640	80	320	<	<	80	<	<	320
B/Ireland/3154/2016		1A	2016-01-14	MDCK1/MDCK4	2560	160	80	160	320	<	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016		1A	2016-01-04	C2/MDCK2	2560	160	80	40	320	<	<	<	<	<	<
B/Norway/2409/2017		1A(Δ2)	2017-04-27	MDCK1/MDCK3	80	20	10	<	<	80	20	80	<	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	MDCK1/MDCK2	320	80	40	<	<	80	40	80	<	<	20
B/Colorado/06/2017		1A(Δ2)	2017-02-05	E5/E2	1280	320	80	<	<	40	20	160	<	40	160
B/Washington/02/2019		1A(Δ3)B	2019-01-19	C2/MDCK2	640	160	80	<	<	<	<	80	40	40	320
B/Washington/02/2019		1A(Δ3)B	2019-01-19	E3/E2	640	160	80	<	<	<	<	160	40	40	320
TEST VIRUSES															
B/Austria/1209211/2019		1A(Δ2)	2019-12-18	SIATx/MDCK1	160	20	20	<	<	40	40	40	<	<	<
B/Austria/1209210/2019		1A(Δ2)	2019-12-18	SIATx/MDCK1	160	10	10	<	<	40	20	40	<	<	<
B/Paris/2931/2019		1A(Δ2)	2019-12-26	MDCK1/MDCK1	320	<	<	<	<	20	10	20	<	<	<
B/Ireland/93804/2019		1A(Δ3)B	2019-11-25	MDCK3	640	80	20	<	<	<	<	<	40	40	320
B/Paris/2643/2019		1A(Δ3)B	2019-12-03	MDCK1/MDCK2	80	20	10	<	<	<	<	<	20	20	160
B/Austria/1206293/2019		1A(Δ3)B	2019-12-07	SIATx/MDCK1	640	80	20	<	<	<	40	<	<	40	320
B/Baden-Wurttemberg/2/2019		1A(Δ3)B	2019-12-09	C2/MDCK1	160	20	10	<	<	<	<	<	<	40	160
B/Pays de Loire/2775/2019		1A(Δ3)B	2019-12-11	MDCK1/MDCK1	160	40	20	<	<	<	<	<	<	40	320
B/Alsace/2705/2019	N126K, D207N, R279K, K345R	1A(Δ3)B	2019-12-11	MDCK1/MDCK1	640	80	40	<	<	<	<	<	<	20	40
B/Nord Pas de Calais/2774/2019	N126K, K345R	1A(Δ3)B	2019-12-16	MDCK1/MDCK1	640	40	40	<	<	<	<	<	<	10	40
B/Alsace/2766/2019		1A(Δ3)B	2019-12-16	MDCK1/MDCK1	320	40	40	<	<	<	<	<	<	40	320
B/Slovenia/3418/2019		1A(Δ3)B	2019-12-19	SIAT1/MDCK1	1280	160	40	<	<	<	80	<	<	80	640
B/Austria/1210344/2019		1A(Δ3)B	2019-12-20	SIATx/MDCK1	160	40	40	<	<	<	<	<	<	20	320
B/Centre/2940/2019		1A(Δ3)B	2019-12-27	MDCK1/MDCK1	1280	160	40	<	<	<	20	<	<	40	320
B/Bayern/1/2020		1A(Δ3)B	2020-01-03	C1/MDCK1	80	40	10	<	<	<	<	<	<	40	160
B/Slovenia/149/2020		1A(Δ3)B	2020-01-08	SIATx/MDCK2	320	80	40	<	<	<	40	<	<	40	320
B/Berlin/1/2020		1A(Δ3)B	2020-01-10	C1/MDCK1	160	40	10	<	<	<	<	<	<	40	160

Vaccine NH 2018-19 SH 2019

Vaccine SH 2020

* 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 Phylogenetic Tree

Table 5-4. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Other information	Passage history	Collection date	Passage history	Haemagglutination inhibition titre									
						Post-infection ferret antisera								
					B/Bris 60/08	B/Bris 60/08	B/Sth Aus 81/12	B/Ireland 3154/16	B/Nord-West 1/16	B/Norway 2409/17	B/Colorado 06/17	B/Colorado 06/17	B/Wash'ton 02/19	B/Wash'ton 02/19
		Passage history			Egg	Egg	Egg	MDCK	MDCK	MDCK	MDCK	Egg	MDCK	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[*4]	F11/18[*4]	F37/19[*4]	F38/19[*4]
		Genetic group			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES														
B/Brisbane/60/2008		1A	2008-08-04	E4/E4	1280	640	320	40	80	<	<	40	<	80
B/South Australia/81/2012		1A	2012-11-28	E4/E2	2560	1280	640	80	160	<	<	80	<	160
B/Ireland/3154/2016		1A	2016-01-14	MDCK1/MDCK4	2560	160	80	80	320	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016		1A	2016-01-04	C2/MDCK2	2560	160	80	80	160	<	<	<	<	<
B/Norway/2409/2017		1A(Δ2)	2017-04-27	MDCK1/MDCK3	160	20	20	<	<	80	20	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	MDCK1/MDCK2	160	40	20	<	<	80	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	E5/E2	640	160	40	<	<	40	20	160	<	80
B/Washington/02/2019		1A(Δ3)B	2019-01-19	C2/MDCK2	640	80	40	<	<	<	<	80	40	320
B/Washington/02/2019		1A(Δ3)B	2019-01-19	E3/E2	1280	160	80	<	<	<	<	160	40	320
TEST VIRUSES														
B/Catalonia/12041S/2020		1A(Δ2)	2019-12-17	P0/MDCK1	80	40	20	<	<	80	40	80	<	10
B/Catalonia/12049S/2020		1A(Δ2)	2019-12-17	P0/MDCK1	40	40	20	<	<	40	20	40	<	<
B/Belgium/G0496/2019		1A(Δ3)B	2019-12-05	MDCK1	160	40	20	<	<	<	<	<	20	320
B/Belgium/G0513/2019		1A(Δ3)B	2019-12-09	MDCK1	160	80	20	<	<	<	<	<	80	320
B/Poitiers/2311/2019	T155A	1A(Δ3)B	2019-12-16	MDCK2/MDCK1	20	20	20	<	<	<	<	<	10	40
B/Catalonia/12038S/2020	N126K, V248A	1A(Δ3)B	2019-12-16	P0/MDCK1	80	40	40	<	<	<	<	<	<	40
B/Catalonia/12044S/2020		1A(Δ3)B	2019-12-17	P0/MDCK1	40	40	20	<	<	<	<	<	20	320
B/Saint Etienne/2361/2019	N126K, R80K, R279K, K345R	1A(Δ3)B	2019-12-19	MDCK2/MDCK1	80	40	40	<	<	<	<	<	<	40
B/Belgium/G0533/2019		1A(Δ3)B	2019-12-20	MDCK1	80	40	10	<	<	<	<	<	40	320
B/Limoges/2376/2019		1A(Δ3)B	2019-12-23	MDCK2/MDCK1	160	40	40	<	<	<	<	<	40	320
B/Estonia/125661/2020		1A(Δ3)B	2020-01-10	SIAT1/MDCK1	160	40	20	<	10	<	<	<	40	320
B/Estonia/125784/2020		1A(Δ3)B	2020-01-13	SIAT1/MDCK1	160	40	20	<	<	<	<	<	40	320
B/Estonia/125783/2020		1A(Δ3)B	2020-01-13	SIAT1/MDCK1	160	40	20	<	10	<	<	<	40	320
B/Estonia/125782/2020	N126K, E198G	1A(Δ3)B	2020-01-13	SIAT1/MDCK1	80	40	40	<	<	<	<	<	<	20
B/Athens.GR/112/2020		1A(Δ3)B	2020-01-16	MDCK1/MDCK1	80	40	20	<	<	<	<	<	80	320
B/Athens.GR/130/2020		1A(Δ3)B		MDCK1/MDCK1	80	20	20	<	<	<	<	<	40	320
B/Lyon/2271/2019			2019-12-12	MDCK2/MDCK1	80	80	40	<	<	<	<	<	<	80
												Vaccine NH 2018-19 SH 2019		Vaccine SH 2020

* 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 Phylogenetic Tree

Table 5-5. 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	B/Bris 60/08 Egg	B/Sth Aus 81/12 Egg	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			Sh 539, 540, 543, 544, 570, 571, 574[*1,3]	F44/17[*4]	F25/16[*4]	F38/17[*2]	F40/17[*2]	F21/18[*4]	F11/18[*4]	F37/19[*4]	F38/19[*4]
	Genetic group			1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES												
B/Brisbane/60/2008	1A	2008-08-04	E4/E4	1280	640	640	80	<	<	160	<	160
B/South Australia/81/2012	1A	2012-11-28	E4/E2	2560	1280	1280	160	<	<	160	<	320
B/Nordrhein-Westfalen/1/2016	1A	2016-01-04	C2/MDCK2	1280	40	<	80	<	<	<	<	<
B/Norway/2409/2017	1A(Δ2)	2017-04-27	MDCK1/MDCK3	80	<	<	<	40	40	80	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	MDCK1/MDCK2	80	<	<	<	40	40	80	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	E5/E2	640	160	<	<	20	40	320	<	160
B/Washington/02/2019	1A(Δ3)B	2019-01-19	C2/MDCK2	160	<	40	<	<	<	80	40	320
B/Washington/02/2019	1A(Δ3)B	2019-01-19	E3/E2	640	80	40	<	<	<	160	40	320
TEST VIRUSES												
B/Palermo/5/2019	1A(Δ2)	2019-12-16	MDCK2/MDCK1	40	<	<	<	40	40	160	<	<
B/Palermo/7/2019	1A(Δ2)	2019-12-23	MDCK2/MDCK1	40	<	<	<	40	40	80	<	<
B/Valladolid/299/2019	1A(Δ3)B	2019-10-23	MDCK1/MDCK1	40	<	<	<	<	<	40	20	320
B/England/695/2019	1A(Δ3)B	2019-12-13	MDCK1/MDCK1	40	<	<	<	<	<	10	40	160
B/Lisboa/37/2019	1A(Δ3)B	2019-12-18	MDCK2/MDCK2	640	80	<	<	<	<	320	<	320
B/Lisboa/32/2019	1A(Δ3)B	2019-12-18	MDCK2/MDCK1	<	<	<	<	<	<	40	40	320
B/Lisboa/55/2019	1A(Δ3)B	2019-12-20	MDCK1/MDCK1	80	<	<	<	<	<	80	40	320
B/Parma/8/2019	1A(Δ3)B	2019-12-23	MDCK1/MDCK1	40	<	<	<	<	<	20	40	320
B/Arges/255788/2019	1A(Δ3)B	2019-12-27	MDCK1/MDCK1	<	<	<	<	<	<	<	40	160
B/Lithuania/MB380/2019	1A(Δ3)B	2019-12-31	MDCK1/MDCK1	40	<	<	<	<	<	20	40	320
B/Parma/1/2020	1A(Δ3)B	2020-01-07	MDCK1/MDCK1	640	40	40	<	<	<	160	20	160
B/Valladolid/15/2020	1A(Δ3)B	2020-01-09	MDCK1/MDCK1	40	<	<	<	<	<	20	40	320
B/Valladolid/11/2020	1A(Δ3)B	2020-01-09	MDCK1/MDCK1	80	<	<	<	<	<	20	40	320
B/Arges/256326/2020	1A(Δ3)B	2020-01-13	MDCK1/MDCK1	320	<	<	<	<	<	20	80	320
B/Bucuresti/256302/2020	1A(Δ3)B	2020-01-13	MDCK1/MDCK1	160	<	<	<	<	<	20	<	40
B/Bucuresti/256301/2020	1A(Δ3)B	2020-01-15	MDCK1/MDCK1	80	<	<	<	<	<	<	<	20
B/Lithuania/MB39700/2019		2019-10-28	MDCK2/MDCK1	160	<	<	<	<	<	40	40	320
										Vaccine NH 2018-19 SH 2019		Vaccine SH 2020

* 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

Table 5-6. 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	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			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[*2]
	Genetic group			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES													
B/Brisbane/60/2008	1A	2008-08-04	E4/E4	1280	640	320	80	80	<	10	160	<	160
B/South Australia/81/2012	1A	2012-11-28	E4/E2	2560	640	640	80	80	<	10	160	<	320
B/Ireland/3154/2016	1A	2016-01-14	MDCK1/MDCK4	2560	160	40	160	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	<	<	<	<	40	80	160	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	MDCK1/MDCK2	80	<	<	<	<	40	40	160	<	<
B/Colorado/06/2017	1A(Δ2)	2017-02-05	E5/E2	640	320	80	<	<	40	40	640	<	160
B/Washington/02/2019	1A(Δ3)B	2019-01-19	C2/MDCK3	640	40	40	<	<	<	<	160	40	160
B/Washington/02/2019	1A(Δ3)B	2019-01-19	E3/E2	640	160	80	<	<	<	20	320	40	640
TEST VIRUSES													
B/Catalonia/2147889NS/2019		2019-10-16	P0/MDCK1	80	<	<	<	<	20	40	80	<	<
B/Ireland/90048/2019		2019-11-12	MDCK1	160	40	10	<	<	<	<	40	40	320
B/Ireland/90739/2019		2019-11-13	MDCK1	80	40	<	<	<	<	<	40	40	320
B/Ireland/92760/2019		2019-11-21	MDCK1	640	40	10	<	<	<	<	80	80	320
B/Catalonia/3511411NS/2019		2019-11-22	P0/MDCK1	640	40	10	<	<	<	<	160	20	80
B/Parma/3/2019		2019-11-25	MDCK1/MDCK1	640	20	20	<	<	<	<	80	<	80
B/Paris/2578/2019		2019-11-26	MDCK1	320	80	10	<	<	<	<	80	40	160
B/Friuli Venezia Giulia/01/2019		2019-11-28	MDCK2/MDCK1	80	<	<	<	<	<	<	20	40	160
B/Parma/5/2019		2019-12-02	MDCK1/MDCK1	320	40	10	<	<	<	<	80	<	40
B/Lisboa/61/2019		2019-12-06	MDCK2/MDCK1	640	40	10	40	<	<	20	40	40	160
B/Paris/2694/2019		2019-12-09	MDCK1	160	<	<	<	<	40	40	160	<	<
B/Catalonia/3512065NS/2019		2019-12-09	P0/MDCK1	40	<	10	<	<	40	80	160	<	<
B/Catalonia/12004S/2020		2019-12-10	P0/MDCK1	320	80	10	<	<	<	<	80	40	320
B/Lisboa/51/2019		2019-12-10	MDCK1/MDCK1	320	40	10	<	<	<	<	40	40	160
B/Lisboa/50/2019		2019-12-10	MDCK1/MDCK1	640	40	10	<	<	<	<	80	40	320
B/Catalonia/12014S/2020		2019-12-11	P0/MDCK1	160	20	10	<	<	<	<	40	40	160
B/Lisboa/44/2019		2019-12-12	MDCK1/MDCK1	320	40	<	<	<	<	<	80	40	160
B/Lisboa/40/2019		2019-12-12	MDCK2/MDCK1	320	<	<	<	<	<	<	10	20	160
B/Lisboa/45/2019		2019-12-14	MDCK1/MDCK1	80	<	<	<	<	<	<	40	40	160
B/Lisboa/56/2019		2019-12-16	MDCK2/MDCK1	<	<	<	<	<	<	<	40	20	160
B/Lisboa/52/2019		2019-12-16	MDCK2/MDCK1	80	<	<	<	<	<	<	20	40	160
B/Lisboa/49/2019		2019-12-16	MDCK3/MDCK1	80	20	<	<	<	<	<	40	40	160
B/Lisboa/35/2019		2019-12-16	MDCK3/MDCK1	160	40	10	<	<	<	<	80	40	160
B/Lisboa/33/2019		2019-12-16	MDCK2/MDCK1	<	<	<	<	<	<	<	20	40	320
B/Lisboa/36/2019		2019-12-17	MDCK3/MDCK1	640	160	80	<	<	<	<	160	10	160
B/Paris/2862/2019		2019-12-24	MDCK1	40	<	10	<	<	<	<	40	40	160
B/Paris/004/2020		2020-01-03	MDCK1	320	80	10	<	<	<	<	40	40	160
											Vaccine NH 2018-19 SH 2019		Vaccine SH 2020

[*] 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

Table 5-7. Antigenic analysis of influenza B/Victoria-lineage viruses by HI - Summary

Viruses	Other information		Haemagglutination inhibition titre: Post-infection ferret antisera								
			B/Bris 60/08	B/Sth Aus 81/12	B/Ireland 3154/16	B/Nord-West 1/16	B/Norway 2409/17	B/Colorado 06/17	B/Colorado 06/17	B/Wash'ton 02/19	B/Wash'ton 02/19
		Passage history	Egg	Egg	MDCK	MDCK	MDCK	MDCK	Egg	MDCK	Egg
		Ferret number	F44/17[*2]	F25/16[*4]	F38/17[*2]	F16/16[*2]	F40/17[*2]	F09/18[*4]	F11/18[*2]	F37/19[*4]	F38/19[*4]
		Genetic group	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)B	1A(Δ3)B
REFERENCE VIRUSES											
B/Brisbane/60/2008		1A	640	640	40	160	<	20	80	<	320
B/South Australia/81/2012		1A	640	640	80	160	<	40	80	<	320
B/Ireland/3154/2016		1A	80	<	80	160	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016		1A	80	<	80	160	<	<	<	<	<
B/Norway/2409/2017		1A(Δ2)	20	<	<	<	40	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	20	<	<	<	40	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	160	40	<	<	20	80	320	<	160
B/Cote D'Ivoire/1662/2018		1A(Δ3)B	80	<	<	<	<	<	<	10	80
B/Washington/02/2019		1A(Δ3)B	160	<	<	<	<	<	160	80	640
B/Washington/02/2019		1A(Δ3)B	80	40	<	<	<	10	160	20	320
TEST VIRUSES											
Genetic group	No tested	*No with*	104	104	87	104	104	104	104	104	104
All viruses		Titre reduced ≤2-fold	1			1	10	17	6	78	64
		%	*1.0*			*1.0*	*9.6*	*16.3*	*5.8*	*75.0*	*61.5*
		Titre reduced =4-fold	4	1	1		1	1	10	3	16
		%	*3.8*	*1.0*	*1.1*		*1.0*	*1.0*	*9.6*	*2.9*	*15.4*
		Titre reduced ≥8-fold	99	103	86	103	93	86	88	23	24
		%	*95.2*	*99.0*	*98.9*	*99.0*	*89.4*	*82.7*	*84.6*	*22.1*	*23.1*
	No tested	*No with*	66	66	52	66	66	66	66	66	66
1A(Δ3)B		Titre reduced ≤2-fold	1					5	3	56	57
		%	*1.6*					*7.6*	*4.5*	*84.8*	*86.4*
		Titre reduced =4-fold	3	1		1			1	2	
		%	*4.5*	*1.6*		*1.6*			*1.6*	*3.1*	
		Titre reduced ≥8-fold	62	65	52	65	66	61	62	8	9
		%	*93.9*	*98.4*	*100.0*	*98.4*	*100.0*	*92.4*	*93.9*	*12.1*	*13.6*
	No tested	*No with*	9	9	7	9	9	9	9	9	9
1A(Δ2)		Titre reduced ≤2-fold					7	8	3		
		%					*77.8*	*88.9*	*33.3*		
		Titre reduced =4-fold					1	1	5		
		%					*11.1*	*11.1*	*55.6*		
		Titre reduced ≥8-fold	9	9	7	9	1		1	9	9
		%	*100.0*	*100.0*	*100.0*	*100.0*	*11.1*		*11.1*	*100.0*	*100.0*
									Vaccine NH 2018-19 SH 2019 NH 2019-20		Vaccine SH 2020

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.

Figure 3. Phylogenetic comparison of influenza B/Victoria-lineage HA genes

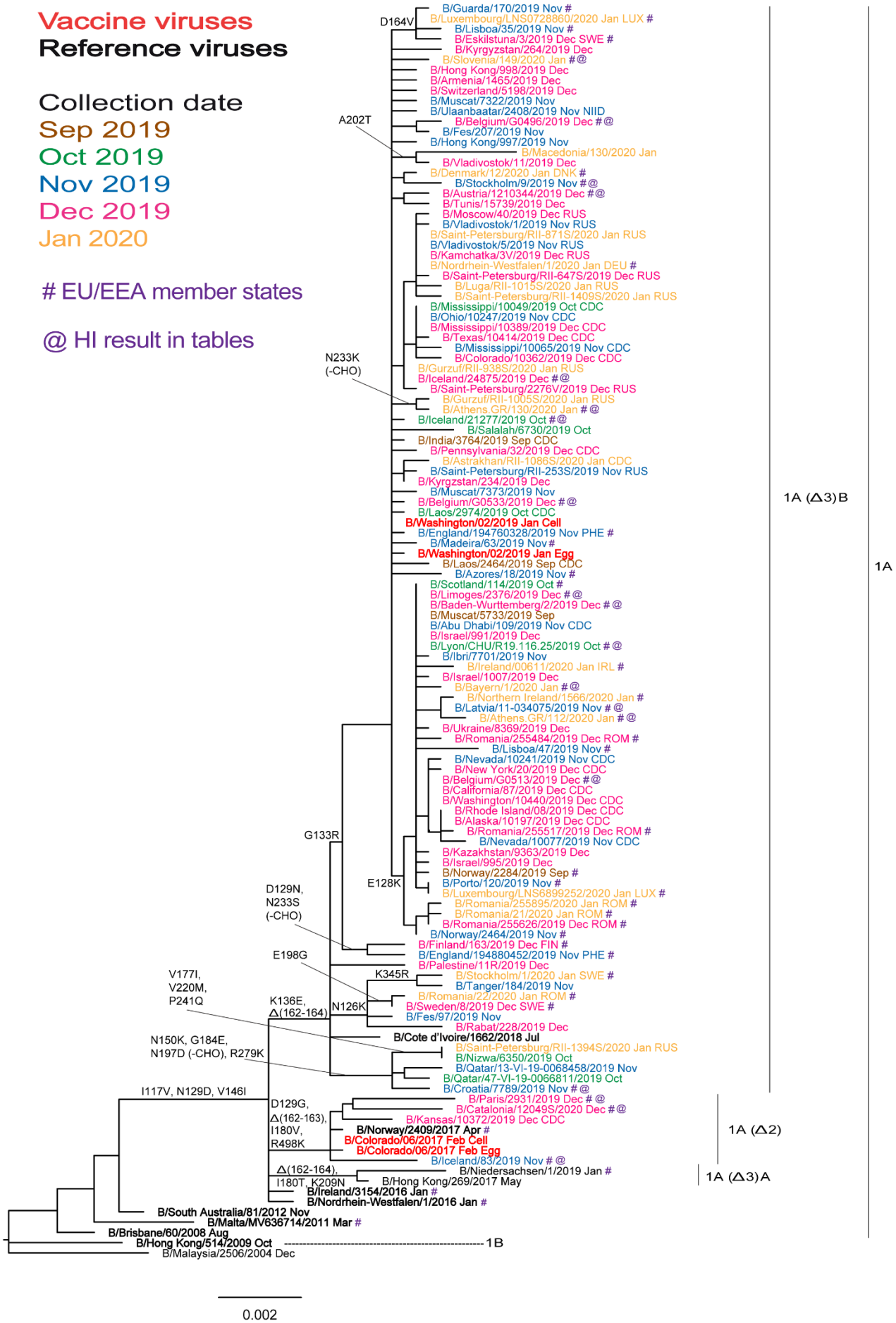


Table 6. Antigenic analysis of influenza B/Yamagata-lineage viruses by HI

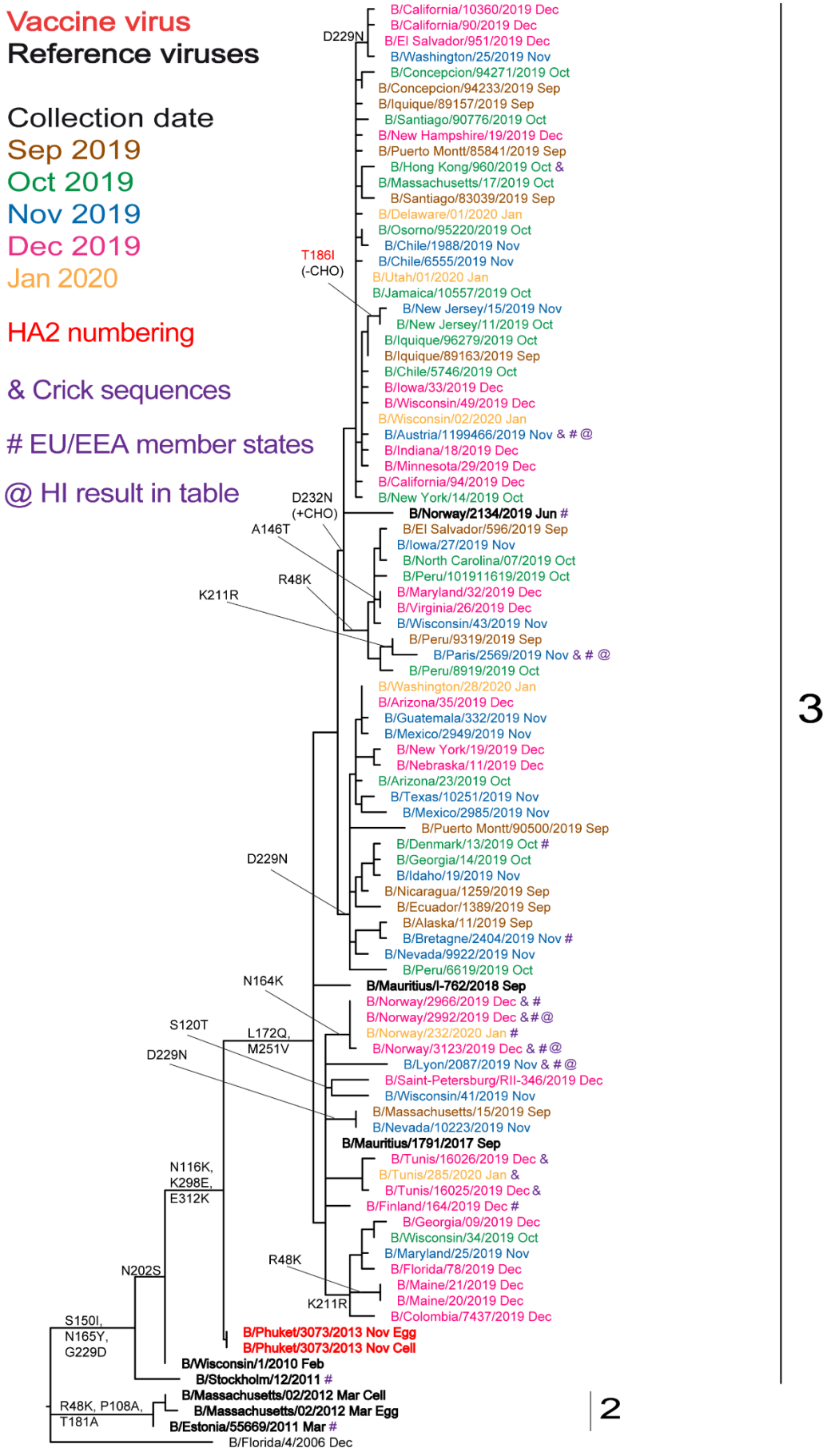
Viruses	Other information	Passage history Ferret number Genetic Group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera B/Phuket 3073/13 Egg SH614[*1,3] 3	B/Estonia 55669/11 MDCK F39/17[*2] 2	B/Mass 02/12 MDCK F10/16[*2] 2	B/Mass 02/12 Egg F06/17[*4] 2	B/Wis 1/10 Egg F36/15[*2] 3	B/Stock 12/11 Egg F05/17[*2] 3	B/Phuket 3073/13 MDCK F27/15[*2] 3	B/Phuket 3073/13 Egg F25/17[*2] 3	B/Maur 1791/17 MDCK F04/18[*2] 3	B/Maur I-762 MDCK F05/19[*2] 3	B/Nor 2134/19 Egg F48/19[*2] 3
REFERENCE VIRUSES															
B/Estonia/55669/2011		2	2011-03-14	MDCK2/MDCK3	640	40	40	80	40	40	40	40	20	40	<
B/Massachusetts/02/2012		2	2012-03-13	MDCK1/C2/MDCK4	1280	160	320	320	320	160	160	160	160	320	10
B/Massachusetts/02/2012		2	2012-03-13	E3/E3	320	10	<	160	40	40	10	40	<	10	20
B/Wisconsin/1/2010		3	2010-02-20	E3/E2	1280	<	<	160	80	160	40	320	40	40	40
B/Stockholm/12/2011		3	2011-03-28	E4/E2	640	<	<	80	80	160	40	80	20	40	20
B/Phuket/3073/2013		3	2013-11-21	MDCK2/MDCK3	2560	160	320	160	320	160	160	160	320	640	20
B/Phuket/3073/2013		3	2013-11-21	E4/E3	1280	<	<	80	80	80	20	80	20	40	20
B/Mauritius/1791/2017		3	2017-09-20	MDCK1/MDCK4	1280	<	20	40	40	80	40	80	80	80	<
B/Mauritius/I-762/2018		3	2018-09-02	MDCK1/MDCK3	1280	<	20	80	80	80	80	80	80	160	<
B/Norway/2134/2019		3	2019-06-06	E2/E2	160	<	<	<	<	10	<	<	<	<	640
TEST VIRUSES															
B/Austria/1199466/2019		3	2019-11-09	SIAT1/MDCK1	1280	<	<	80	80	80	80	160	80	160	10
B/Lyon/2087/2019		3	2019-11-25	MDCK2/MDCK1	1280	<	10	40	40	40	40	80	40	80	10
B/Paris/2569/2019		3	2019-11-26	MDCK1	640	<	<	40	40	40	40	40	40	80	<
B/Norway/2992/2019		3	2019-12-30	MDCK1/MDCK1	320	<	10	40	40	40	40	40	40	80	<
B/Norway/3123/2019		3	2019-12-30	MDCK1/MDCK1	640	<	20	40	40	40	40	80	40	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 and SH 2020

Sequences in Phylogenetic Tree

Figure 4. Phylogenetic comparison of influenza B/Yamagata-lineage HA genes



Summaries of data submitted to TESSy

Genetic characterisation

For the 2019–20 season, as of week 8/2020, 2 198 viruses had been characterised genetically and ascribed to a genetic clade:

- 769 were A(H1N1)pdm09 viruses, with 734 being subclade 6B.1A5 (697 subgroup 6B.1A5A represented by A/Norway/3433/2018 and 37 subgroup 6B.1A5B represented by A/Switzerland/3330/2018), 17 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;
- 829 were A(H3N2) viruses, with 261 being subgroup 3C.2a1b+T131K represented by A/South Australia/34/2019, 435 being clade 3C.3a represented by A/Kansas/14/2017, 77 being subgroup 3C.2a1b+T135K-B represented by A/Hong Kong/2675/2019, 55 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;
- 572 were B/Victoria-lineage viruses, with 511 being subclade 1A(Δ3)B represented by B/Washington/02/2019, 18 being subclade 1A(Δ2) represented by the vaccine virus B/Colorado/06/2017, three 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 8/2020, a total of 879 viruses (365 A(H3N2), 336 A(H1N1)pdm09 and 178 type B) collected in the course of the 2019–20 season had been tested for susceptibility to neuraminidase inhibitors, oseltamivir and zanamivir. One A(H3N2) virus showed highly reduced inhibition (HRI) by oseltamivir and reduced inhibition by zanamivir (RI) and carried NA R292K amino acid substitution. One A(H1N1)pdm09 virus carried NA H275Y substitution indicative of HRI by oseltamivir. One type B virus showed evidence of RI by oseltamivir.

At the WIC this season, 460 viruses from EU/EEA countries have been assessed phenotypically against oseltamivir and zanamivir: 147 A(H1N1)pdm09, 178 A(H3N2), 129 B/Victoria-lineage and 6 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(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 [6] reported that the China Health and Family Planning Commission notified the WHO of three cases of human infection with influenza A(H7N9). A description of the characteristics of H7N9 viruses can be found on the WHO website [7]. 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 [8]. WHO posted an analysis of information on A(H7N9) viruses on 10 February 2017 [9], and ECDC published a rapid risk assessment on the implications of A(H7N9) for public health on 3 July 2017 [10]. A summary and assessment of influenza viruses at the human–animal interface on 20 January 2020 reports that no new cases of human infection had been detected since the 25 November 2019 report and indicates that there have been no publicly available reports on A(H7N9) from animal health authorities in China in recent months on A(H7N9) detections in animals [11]. The most recent human case was detected in mid-March 2019 [12]. 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 20 December 2019 and can be found on the ECDC website [13].

Influenza A(H5) virus

The most recent monthly risk assessment of influenza at the human–animal interface was published by WHO on 20 January 2020. While no new human cases were reported, detections of various A(H5Nx) subtypes have continued in birds in Africa, Europe and Asia [11]. No new human cases of A(H5N1) infection have been detected since the case in Nepal in March 2019, where there have been reports of A(H5N1) infection in domestic birds since February 2019. This was the first human case of A(H5N1) infection reported to WHO since 2017 [14]. On 18 November 2016, ECDC published a rapid risk assessment related to outbreaks of highly pathogenic avian influenza H5N8 viruses in Europe [15]. As described above, the EU Reference Laboratory for Avian Influenza, in

collaboration with ECDC and the European Food Standards Agency, published the latest overview of avian influenza on 20 December 2019, which can be found on the ECDC website [13].

WHO CC reports

A description of results generated by the London WHO CC at the WIC and used at the most recent WHO vaccine composition meeting (held in Geneva, Switzerland 24–28 February 2020), and previous ones, can be found at: https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports

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 marked (#). 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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