Influenza virus characterization

Summary report, Europe, February 2023

Document number: WHO/EURO:2023-6189-45954-68789

Corrigendum

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1. Page 36, paragraph 3:

   Delete:

   "Notably, a significant number of viruses (dispersed throughout the phylogeny), detected in Spain (Catalonia), have been reported to carry genes encoding HA with an additional amino acid deletion at HA1 position 165 (del165) (Figure 4b).".

2. Page 39, Figure 4b:

   Replace the phylogenetic tree from Figure 4b with the amended one.

These corrections were incorporated into the electronic file on 21 May 2023.

Acknowledgments

This report was prepared by Rod Daniels, Burcu Ermetal, Aine Rattigan and Nicola Lewis (Crick Worldwide Influenza Centre) for the World Health Organization Regional Office for Europe under WHO contract. Data from The European Surveillance System – TESSy was provided by the respective country and area and released by ECDC.

Summary

The December 2022 characterization report[1], was the third report for the 2022-2023 influenza season. Currently, as of week 08/2023, 231 015 detections have been reported. This represents a 5.2-fold increase in detections compared to the same period of the 2021-2022 season, despite a modest decrease (4%) in the number of samples tested. Of the 2022-2023 detections, 84% were type A viruses, with A(H3N2) and A(H1N1)pdm09 viruses being detected in equal proportions overall, following a rise in the proportion of A(H1N1)pdm09 viruses detected in recent weeks. Since December, the proportion of detections being type B viruses has risen from 6% to 16% and all 3 371 viruses (9% of the total) ascribed to a lineage have been B/Victoria. The epidemic threshold (10% influenza positivity within sentinel specimens) was crossed in week 45/2022 and has remained above this to week 08/2023.

Forty shipments from countries within the WHO European Region were received at the London WHO Collaborating Centre, the Francis Crick Worldwide Influenza Centre (WIC) since the December report. This report focuses on viruses with collection dates after 31 August 2022 for which HA gene sequences were submitted to, and released in, the EpiFlu™ database of the Global Initiative on Sharing All Influenza Data (GISAID) in January and February 2023, together with sequences and antigenic data generated at the WIC.

Globally, the great majority of A(H1N1)pdm09 viruses detected in the first 21 weeks of the 2022-2023 season have HA genes in clade 6B.1A.5a.2 (**5a.2**). Compared to the same period of the 2021-2022 season, as a proportion of type A viruses detected in the WHO European Region, there has been an increase from 7% to 50%. Circulating clade 5a.2 viruses are well recognised by post-infection ferret antisera raised against A/Victoria/2570/2019-like (5a.2) viruses, in vaccines for the northern hemisphere 2022-2023 influenza season, but are recognised less well by post-vaccination sera from humans. As recently circulating viruses carry HA1 K54Q, A186T, Q189E, E224A, R259K and K308R amino acid substitutions compared to A/Victoria/2570/2019, the recommendation was to change the vaccine component to an A/Sydney/5/2021-like (**5a.2a**) virus for the southern hemisphere 2023 season. Following emergence and geographic spread of viruses with additional HA1 amino acid substitutions of P137S, K142R, D260E and T277A, A/Victoria/4897/2022-like (**5a.2a.1**) viruses were recommended for use in the 2023-2024 northern hemisphere season.

In Europe and across the world A(H3N2) viruses have been dominant with the great majority of recently detected viruses, as assessed from sequence deposition in GISAID's EpiFlu™ database, falling in the 'Bangladesh-like' (3C.2a1b.2a.2 (**2**)) HA clade. Viruses with clade 2 HA genes have shown extensive genetic drift with some associated antigenic drift which has necessitated development of a new clade nomenclature system (see main text). While post-infection ferret antisera have shown some viruses to induce clade-specific responses, there are various levels of cross-clade reactivity in HI assays. Sera from humans vaccinated with A/Darwin/9/2021-like (**2a**) viruses has shown significant cross-clade reactivity and has been retained as the vaccine virus recommendation for both 2013 southern hemisphere and 2023-2024 northern hemisphere influenza seasons.

Across the world generally, few B/Victoria-lineage viruses have been detected during first 21 weeks of the 2022-2023 influenza season though numbers of detections have increased in recent weeks in the WHO European Region. The vast majority of viruses with collection dates in 2023, for which sequences have been deposited in GISAID's EpiFlu™ database, have HA genes that fall in the V1A.3a.2 subgroup with defining HA1 A127T, P144L and K203R amino acid substitutions. Post-infection ferret antisera raised against V1A.3a.2 viruses recognise circulating viruses well, despite the emergence of viruses with a variety of HA1 amino acid substitutions. B/Austria/1359417/2021-like (V1A.3a.2) viruses have been retained as the vaccine virus recommendation for both 2023 southern hemisphere and 2023-2024 northern hemisphere influenza seasons.

No cases of infection with circulating B/Yamagata-lineage viruses have been confirmed since March of 2020. All HA gene sequences from the 77 viruses detected in 2020, inclusive of 16 from the WHO European Region, belonged to genetic clade Y3 and had three HA1 amino acid substitutions (L172Q, D229N and M251V) compared to B/Phuket/3073/2013-like viruses which are still recommended for use in quadrivalent influenza vaccines. **There is need to share all B/Yamagata-lineage viruses detected recently for detailed characterization to determine if there are any in circulation that are not related to Live Attenuated Influenza Vaccines.**

[1]Influenza virus characterization: summary report, Europe December 2022. World Health Organization Regional Office for Europe and European Centre for Disease Prevention and Control; Copenhagen and Stockholm; 2022, https://apps.who.int/iris/handle/10665/365632, accessed 20 March 2023).

Table 1 shows a summary of influenza virus detections in the WHO European Region reported to The European Surveillance System (TESSy) database during the 2022-2023 season (weeks 40/2022-08/2023), compared to the same period in the 2021-2022 season. For sentinel surveillance there has been a 2.5-fold increase in number of specimens tested but a 8.3-fold increase in the number of influenza virus detections, while for non-sentinel surveillance there has been a decrease in the reported number of tests (128 562: 7.6%) but a 5.0-fold increase in the number of influenza virus detections for the current season. In the same period of 2020, during the earlier stages of the COVID-19 pandemic, for combined sentinel and non-sentinel surveillance just 450 147 specimens were tested and only 712 influenza virus detections were reported (results not shown). These data probably relate to significant numbers of samples being taken from patients fulfilling ILI and/or ARI criteria who were infected with other agents, possibly SARS-CoV-2 the virus responsible for the COVID-19 pandemic. With large swathes of the human population now carrying a significant level of immunity to SARS-CoV-2, following either infection and/or vaccination, influenza has been able to re-establish itself after nearly two years of low-level circulation.

Table 1. Influenza virus detections in the WHO European Region from the start of reporting for the 2022-2023 season (weeks 40/2022-08/2023)[a]

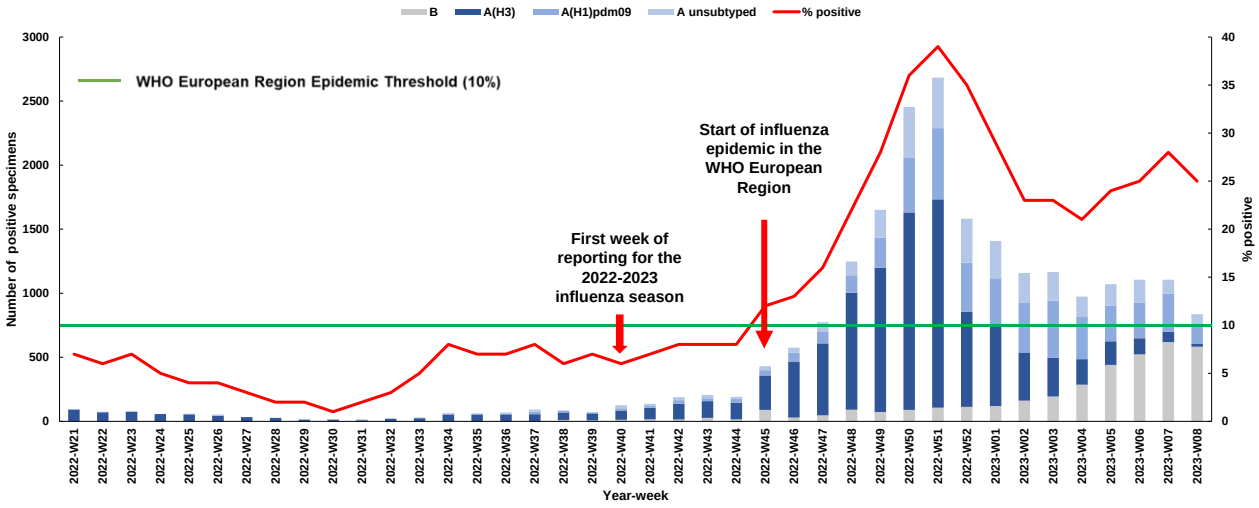
Virus type/subtype/lineage	Cumulative number of detections for weeks 40-48/2022			Totals*		Cumulative number of detections for weeks 40/2021-08/2022			Totals*	
	Sentinel sources	Non-sentinel sources	Totals	%	Ratios	Sentinel sources	Non-sentinel sources	Totals	%	Ratios
Influenza A	**17415**	**176001**	**193416**	**83.7**	**5.1:1**	**2512**	**40633**	**43145**	**96.6**	**28.4:1**
A(H1N1)pdm09	4583	28514	33097	49.6		144	942	1086	6.8	
A(H3N2)	9668	23910	33578	50.4	1.0:1	1662	13313	14975	93.2	13.8:1
A not subtyped	3164	123577	126741			706	26378	27084		
Influenza B	**3649**	**33950**	**37599**	**16.3**		**34**	**1486**	**1520**	**3.4**	
Victoria lineage	1049	2322	3371	100.0		6	13	19	100.0	
Yamagata lineage	0	0	0			0	0	0		
Lineage not ascribed	2601	31628	34229			28	1473	1501		
Total detections (total tested)	**21 064 (89 424)**	**209 951 (>1 559 976)**	**231 015 (>1 649 400)**			**2 546 (36 483)**	**42 119 (>1 688 538)**	**44 665 (>1 725 021)**		

[a] Numbers taken from Flu News Europe week 08 reports for the two most recent influenza seasons

* 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 Victoria:Yamagata lineages.

The rate of influenza positivity in sentinel samples showed a slight rise towards the end of the 2021-2022 season and continued to hover around 7% until week 44/2022 (Figure 1). The epidemic threshold (10%) was crossed in week 45/2022 and rose week-on-week until week 51/2022 (39%) before decreasing to 21% in week 04/2023 and rising again to 28% in week 07/2023 before decreasing to 25% in week 08/2023. These percentage values and fluctuations will reflect issues related to reduced sentinel surveillance consultations during the festive (Christmas/New Year) period and/or timely/irregular reporting to TESSy by some countries.

Figure 1. Influenza positivity in sentinel-source specimens by week (2022-2023) – WHO Europe[a]



[a] Figure adapted from FluNewsEurope weeks 36-39/2022 and 08/2023 reports (https://flunewseurope.org/Archives)

The ratio of type A to type B detections has decreased significantly from 2021-2022 to 2022-2023 (28.4:1 to 5.1:1) as has the dominance of A(H3N2) over A(H1N1)pdm09 (13.8:1 to 1.0:1) (Table 1). While the number of influenza B virus detections has increased from 1 520 to 37 599 (~25-fold), the number of viruses ascribed to a lineage has increased from 1.3% to 9.0% with all being of the B/Victoria lineage. Currently, it appears that measures introduced relating to the COVID-19 pandemic are still having an effect, with greater numbers of respiratory clinical specimens being tested for influenza compared to seasons prior to and during the first year of the COVID-19 pandemic, but influenza detections in the first 21 weeks of the 2022-2023 season have greatly surpassed those reported during the same period of 2021-2022.

Data presented for viruses with collection dates after 31 August 2021 until 31 January 2022 contributed to the WHO influenza vaccine composition meeting (VCM) for the northern hemisphere 2022-2023 season, where it was recommended to change the A(H3N2) and B/Victoria-lineage components of influenza vaccines to match those used in 2022 southern hemisphere vaccination campaigns [1]. At the VCM held in September 2022, which focussed on data from viruses collected after 31 January 2022 until 31 August 2022, it was recommended to change the A(H1N1)pdm09 vaccine component for the 2023 southern hemisphere season [2]. Genetic and antigenic characterisation data generated at the WIC for viruses with collection dates after 31 August 2022 until 31 January 2023 informed the VCM in February 2023 when recommendations were made for the northern hemisphere 2023-2024 influenza season and the A(H1N1)pdm09 vaccine component was further updated compared to that to be used in the 2023 southern hemisphere season [3].

This and recent influenza characterization reports (https://www.ecdc.europa.eu/en/seasonal-influenza/surveillance-and-disease-data/influenza-virus-characterisation) have been based mainly on phylogenetic analyses of complete HA gene sequences submitted to GISAID's EpiFlu™ database, inclusive of sequences generated at the WIC. Here A(H1N1)pdm09, A(H3N2) and B/Victoria-lineage HA gene phylogenies prepared for the December 2022 report are shown (Figures 2a, 3a and 4a). Additional phylogenies (Figures 2b, 3b and 4b) are presented for HA sequences derived from viruses with collection and HA sequence submission dates from the days indicated in Table 2, with a sequence download date of 28 February 2023. The numbers of HA sequences, downloaded from GISAID, numbers remaining after de-duplication and the numbers used in the new representative phylogenies generated for this February report are shown.

Table 2. Summary of the numbers of HA gene sequences available and used in generating the new phylogenies presented in this report

Virus subtype/lineage	Global full length HA sequences available as of 2022-02-28				
	Virus collection date (from)	Sequence submission date (from)	Number Downloaded	Number de-duplicated and aligned	Number used in phylogenies*
A(H1N1)pdm09	2023-01-01	2023-01-01	834	809	132
A(H3N2)	2023-01-01	2023-01-01	743	722	125
B/Victoria	2023-01-01	2023-01-01	498	486	137
B/Yamagata	2022-01-01	2023-01-01	0	0	0

*** Inclusive of sequences generated recently at the WIC, but not including sequences from reference and vaccine viruses**

Fifty-nine shipments containing specimens (n = 2 116: virus isolates and/or clinical specimens) with collection dates after 31 August 2022 were received at the WIC (40 since the December report) from WHO Global Influenza Surveillance and Response System (GISRS) recognised National Influenza Centres (NICs) in 40 WHO European Region Member States (Table 3). Many of the samples contained in the recently received shipments were in the virus characterization process at the time of preparing this report.

A total of 438 viruses from the WHO European Region (173 A(H1N1)pdm09, 209 A(H3N2) and 56 B/Victoria-lineage) were characterized antigenically since the December report (Tables 4, 5 and 6 respectively).

Table 3a. Summary of seasonal influenza clinical samples and virus isolates* with collection dates after 2022-08-31 contained in packages received from WHO European Region Member States

MONTH	TOTAL RECEIVED	A		H1N1pdm09		H3N2		B		B Victoria lineage		B Yamagata lineage	
Country/area	Seasonal viruses	Number received	Number propagated[1]	Number received	Number propagated[1]	Number received	Number propagated[2]	Number received	Number propagated[1]	Number received	Number propagated[1]	Number received	Number propagated[1]
2022													
September													
Albania	3					3	in process						
Belgium	1									1	1		
Croatia	2					2	1						
Cyprus	1					1	in process						
France	15			3	in process	10	in process			2	2		
Germany	6					5	5			1	1		
Netherlands	9			7	in process	2	in process						
Norway	14			12	1	1	1			1	0		
Portugal	2					2	2						
Spain	39			11	in process	28	in process						
Sweden	5			1	in process	4	in process						
UK (England)	7			4	4	3	in process						
October													
Austria	4					4	in process						
Belgium	1									1	1		
Croatia	10			3	3	5	in process			2	1		
Denmark	11			4	3	5	5			2	2		
France	28			9	9	12	11			7	6		
Germany	19			1	in process	18	18						
Greece	1					1	in process						
Iceland	2					2	in process						
Ireland	13	1	0	6	in process	6	in process						
Kazakhstan	10							7	in process	3	in process		
Kyrgyzstan	4									4	4		
Lithuania	4	1	in process			3	in process						
Netherlands	13			6	0	4	in process			3	in process		
Norway	35			18	6	12	11			5	4		
Portugal	33			8	4	25	25						
Romania	2			2	2								
Slovenia	3					3	in process						
Sweden	8			3	in process	4	in process	1	in process				
Spain	199	3	0	22	in process	172	in process			2	in process		
Switzerland	3			1	1	2	2						
UK (England)	6			1	1	5	5						
UK (N. Ireland)	14			13	0	1	0						
November													
Austria	2			1	in process					1	in process		
Belgium	8	1	in process	3	3	1	1			3	2		
Bosnia and Herzegovina	2									2	in process		
Croatia	6			3	3					3	in process		
Denmark	3					2	2			1	1		
Estonia	15			1	in process	14	in process						
France	9					7	in process			2	1		
Georgia	15	9	0	2	0	4	in process						
Germany	15			6	in process	8	in process			1	1		
Greece	7					6	in process			1	0		
Hungary	7			2	2	4	4			1	1		
Iceland	14			7	in process	7	in process						
Ireland	24	1	0	12	in process	10	in process			1	in process		
Israel	8			4	in process	2	2			2	in process		
Italy	26			4	4	22	in process						
Kazakhstan	11			1	0			2	in process	8	in process		
Kyrgyzstan	14	3	in process	3	in process	4	in process	1	0	3	in process		
Lithuania	29			13	13	14		1	0	1	1		
Macedonia	1					1	in process						
Montenegro	1					1	0						
Netherlands	6			3	3	3	in process						
Norway	13			9	6	4	2						
Poland	10			3	in process	7	in process						
Portugal	30			5	in process	23	in process			2	2		
Romania	8			3	3	5	in process						
Slovakia	7	1	in process			6	in process						
Slovenia	9			6	in process	3	in process						
Spain	101	3	in process	8	in process	89	in process			1	0		
Sweden	8			4	in process	3	in process			1	in process		
Switzerland	11			3	3	7	7			1	1		
Tajikistan	7			7	in process								
Turkmenistan	1					1	1						
Ukraine	22			3	2	19	in process						
UK (England)	1			1	1								
UK (Wales)	2							1	0	1	0		

*** 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)
Samples provided in lysis buffer, so only genetic characterisation possible
Some samples were sent as RNA - only genetic characterisation possible
Some samples not cultured because Ct value high (>30), failed sequence, identical sequence, mixed sequence or SARS-COV-2 positive

As of 2023-03-03

Table 3b. Summary of seasonal influenza clinical samples and virus isolates* with collection dates after 2022-08-31 contained in packages received from WHO European Region Member States

MONTH / Country/area	TOTAL RECEIVED Seasonal viruses	A		H1N1pdm09		H3N2		B		B Victoria lineage		B Yamagata lineage	
		Number received	Number propagated[1]	Number received	Number propagated[1]	Number received	Number propagated[2]	Number received	Number propagated[1]	Number received	Number propagated[1]	Number received	Number propagated[1]
December													
Albania	43			23	in process	20	in process						
Armenia	7			7	in process								
Austria	35			5	in process	27	in process	1	0	2	in process		
Belgium	26			3	2	12	12			11	10		
Bosnia and Herzegovina	1							1	in process				
Bulgaria	9			4	in process	5	in process						
Cyprus	25			4	in process	21	in process						
Estonia	55			12	in process	41	in process			2	in process		
Georgia	23			3	1	17	in process	2	0	1	0		
Germany	13			8	in process	3	3			2	in process		
Greece	2			1	in process					1	in process		
Hungary	5			2	2	3	3						
Iceland	29			19	in process	9	in process			1	0		
Ireland	28			19	in process	9	in process						
Israel	42			28	in process	7	in process	1	0	6	in process		
Italy	5			2	2	3	2						
Kazakhstan	6			6	in process								
Kyrgyzstan	22	9	in process	11	in process	1	0	1	0				
Latvia	11			5	in process	4	in process	2	in process				
Macedonia	2			1	in process	1	in process						
Montenegro	6			2	0	3	in process			1	in process		
Netherlands	19			8	in process	6	in process			5	5		
Poland	83			14	in process	62	in process			7	in process		
Portugal	12			4	in process	6	in process			2	2		
Romania	19			9	9	8	7			2	1		
Serbia	12			1	in process	4	in process	1	in process	6	in process		
Slovakia	29			1	in process	27	in process			1	in process		
Slovenia	59	6	in process	17	in process	35	in process			1	in process		
Spain	37			9	in process	20	in process	6	in process	2	2		
Switzerland	26			8	8	15	15			3	3		
Tajikistan	18			13	in process			1	in process	4	in process		
Turkmenistan	5					1	1			4	4		
Ukraine	75	4	0	10	in process	61	in process						
UK (Wales)	12							8	0	4	0		
2023 JANUARY													
Albania	50			34	in process	16	in process						
Armenia	9			5	in process	1	in process	3	in process				
Bosnia and Herzegovina	4			1	0	2	in process	1	0				
Bulgaria	27			15	in process	8	in process			4	0		
Cyprus	3			2	in process	1	0						
Estonia	26			12	in process	12	in process			2	in process		
Georgia	1			1	0								
Germany	15			4	in process	4	in process			7	in process		
Greece	19	1	in process	4	in process	13	in process			1	in process		
Israel	15			12	in process	3	in process						
Latvia	9			2	in process	6	in process	1	in process				
Macedonia	19			7	in process	11	in process			1	in process		
Montenegro	13			6	in process	5	in process			2	in process		
Netherlands	2									2	2		
Portugal	2									2	2		
Romania	11			6	6	3	3	1	0	1	in process		
Serbia	18			9	in process	6	in process	3	in process				
Slovakia	4	2	in process			1	in process			1	in process		
Slovenia	15			8	in process	5	in process	1	in process	1	1		
Spain	21			10	10	7	7	3	in process	1	1		
Tajikistan	5			1	in process			4	in process				
UK (N. Ireland)	30			15	0	13	0	2	0				
UK (Wales)	8							2	0	6	in process		
UK (Wales)	3							3	in process				
FEBRUARY													
Albania	2			2	1								
Armenia	4			1	in process			3	in process				
TOTAL	2116	45	0	668	118	1170	158	64	0	169	65	0	0
40 Countries/areas		2.1%		31.6%		55.3%		3.0%		8.0%		0.0%	
		89.0%								11.0%			

* 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)

Samples provided in lysis buffer, so only genetic characterisation possible
Some samples were sent as RNA - only genetic characterisation possible
Some samples not cultured because Ct value high (>30), failed sequence, identical sequence, mixed sequence or SARS-COV-2 positive

As of 2023-03-03

Influenza A(H1N1)pdm09 virus analyses

All recently circulating viruses have fallen into clade **6B.1A**, defined by the **HA** 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 encoding a range of **HA** amino acid substitutions had emerged, with circulating viruses carrying the substitution **S183P** in **HA1**, although this was not retained in all virus clusters. Subclades with **HA1 S183P** were assigned for the February 2019 WHO VCM, updated for the September 2020 WHO VCM, and a new nomenclature was introduced at the time of the September 2021 WHO VCM (**6B.1A.1 to 6B.1A.7**). HA amino acid substitutions defining the seven subclades have been defined in earlier reports. Subclade **6B.1A.5** viruses carry HA gene mutations encoding **HA1 S183P** and **N260D** amino acid substitutions and had split into two groups designated **6B.1A.5a** represented by **A/Norway/3433/2018** with additional **HA1** amino acid substitutions of **N129D** and **T185A**, and **6B.1A.5b** represented by **A/Switzerland/3330/2017** with additional amino acid substitutions of **HA1 E235D** and **HA2 V193A**. Only subclade **6B.1A.5a** viruses have circulated recently and two subgroups within the **6B.1A.5a** group have been defined based on **HA1** amino acid substitutions of **D187V/A** and **Q189E** (**6B.1A.5a.1**) or **K130N**, **N156K**, **L161I** and **V250A** (**6B.1A.5a.2**). The phylogeny presented in Figure 2a is annotated using the above nomenclature system. The recommended vaccine viruses for the northern hemisphere 2022-2023 (egg-based A/Victoria/5270/2019-like and cell-based A/Wisconsin/588/2019-like) influenza seasons are shown in red [1] as are egg- and cell-based A/Sydney/5/2021, recommended for use in the southern hemisphere 2023 season [2].

Prior to the February 2023 VCM the A(H1N1)pdm09 nomenclature system was further updated and shortened:

- **Clade 5a.1** - Signature amino acid substitutions: D187A, Q189E. Former vaccine viruses (NH 2021-2022): A/Guangdong-Maonan/SWL1536/2019 (egg-based) and A/Hawaii/70/2019 (cell culture-based).
- **Clade 5a.2** - Signature amino acid substitutions: N156K, L161I, V250A. Current vaccine viruses (NH 2022-2023): A/Victoria/2570/2019 (egg-based) and A/Wisconsin/588/2019 (cell culture-based).
- **Clade 5a.2a** - Signature amino acid substitutions: K54Q, A186T, Q189E, E224A, R259K, K308R. Current vaccine viruses (SH 2023): A/Sydney/5/2021 (egg- and cell culture-based) which also contain D94N and T216A.
- **Clade 5a.2a.1** - Signature amino acid substitutions: P137S, K142R, D260E. Future vaccine viruses (NH 2023-2024): A/Victoria/4897/2022 (egg-based) and A/Wisconsin/67/2022 (cell culture-based).

This updated nomenclature system is used in the text below and to annotate Figure 2b.

The phylogeny prepared for the December report focused on HA sequences derived from viruses with collection dates after 31 August 2022 for which sequences were submitted to GISAID in December 2022 (Figure 2a). Few clade **5a.1** viruses, detected in September through December, had been reported to GISAID. Recently detected viruses had HA genes in clade **5a.2**, all having clade **5a.2a** defining **HA1 K54Q**, **A186T**, **Q189E**, **E224A**, **R259K** and **K308R** substitutions compared to the vaccine virus A/Victoria/2570/2019 [1]. HA gene clusters had emerged in clade **5a.2a** defined by amino acid substitutions: (i) **HA1 T216A** often with **D94N**, the cluster showing wide geographic distribution and containing the SH2023 vaccine virus A/Sydney/5/2021 [2]; (ii) **HA1 A48P**; and (iii) **HA1 K142R**, **D260E** and **HA2 I91V**, **N124H**, frequently with **HA1 P137S**, **T277A** and **HA2 E29D**. Further diversification had occurred with virus clusters having emerged defined by amino acid substitutions of either **HA1 I185V** or **HA2 I91V** alone. Cluster (iii) viruses dominated and the great majority of these had the additional **HA1 P137S**, **T277A** and **HA2 E29D** amino acid substitutions and are now defined as clade **5a.2a.1**, with a subset of having **HA1 T216A** substitutions. Viruses detected in the WHO European Region were dispersed throughout the phylogeny.

The phylogeny prepared for this February 2023 report focused on HA sequences derived from viruses with collection dates after 31 December 2022 for which sequences were submitted to GISAID up to 28 February 2023 (Table 2 and Figure 2b). The two phylogenies have virtually identical structures with few clade **5a.1** viruses having been detected and clade **5a.2a** viruses predominating over those in cade **5a.2a.1**. Large numbers of viruses in the 'core' amino acid substitution category (having **HA1 K54Q**, **A186T**, **Q189E**, **E224A**, **R259K** and **K308R** substitutions compared to the 2022-2023 northern hemisphere vaccine virus A/Victoria/2570/2019 [1]), represented by the 2023 southern hemisphere vaccine virus A/Sydney/5/2021 [2], have been detected to date in 2023 based on sequences submitted to GISAID. Of note, while clade **5a.2a.1** virus detections have been reported in approximately equal proportions in countries either within or outside the WHO European Region, detections of clade **5a.2a** viruses have been significantly greater in countries within the WHO European Region. Of these clade **5a.2a** detections those with additional HA amino acid substitutions of (i) **HA1 D94N**, (ii) **HA2 I91V** and (iii) **HA1 K142R**, **D260E**, **T270I** and **HA2 I91V**, **N124H** appeared to be largely restricted to WHO European countries.

Since the December report, 173 A(H1N1)pdm09 viruses from the WHO European Region have been characterized antigenically (Tables 4-1 to 4-8) and the results are summarised in Table 4-9. The panel of post-infection ferret antisera used in HI assays, four raised against clade **5a.1** viruses and six against clade **5a.2** viruses (inclusive of, two clade **5a.2a** and two clade **5a.2a.1** viruses), gives clear discrimination of reference viruses in the main clades. This discrimination carried through to the 171 **5a.2** (106 **5a.2a** and 65 **5a.2a.1**) test viruses and the two **5a.1** test viruses (Table 4-9). Greater than 90% of **5a.2a** test viruses were recognised well (within fourfold of the homologous titres, the great majority within twofold) by antisera raised against all **5a.2** reference viruses, which included the vaccine viruses A/Victoria/2570/2019 and A/Sydney/5/2021. The same was generally true for **5a.2a.1** test viruses but for the antisera raised against A/Denmark/3280/2019 (**5a.2**) and cell culture-propagated A/Sydney/5/2021 (**5a.2a**) where only 78.5% and 80% of test viruses, respectively, were recognised within fourfold of the homologous titres.

Antisera induced by clade **5a.1** viruses (e.g., the northern hemisphere 2020-2021 season vaccine viruses, egg-propagated A/Guangdong-Maonan/SWL1536/2019 and cell culture-propagated A/Hawaii/70/2019) in ferrets and humans yielded poor recognition of clade **5a.2** viruses which many humans were unlikely to have been exposed to due to their low-level circulation during the COVID-19 pandemic. This led to recommendation of egg-propagated A/Victoria/2570/2019 and cell culture-propagated A/Wisconsin/588/2019 clade **5a.2** viruses for use in the 2021-2022 and 2022-2023 [1] northern hemisphere influenza seasons. Following emergence of viruses carrying **HA1 K54Q**, **A186T**, **Q189E**, **E224A**, **R259K** and **K308R** substitutions compared to A/Victoria/2570/2019, egg- and cell culture-propagated A/Sydney/5/2021-like viruses (designated clade **5a.2a**) were recommended for vaccine formulations to be used in the 2023 southern hemisphere season [2]. Further diversification of clade **5a.2a** viruses carrying HA substitutions of **HA1 K142R**, **D260E** and **HA2 I91V**, **N124H**, to include **HA1 P137S**, **T277A** and **HA2 E29D**, led to designation of viruses carrying clade **5a.2a.1** HA genes which were poorly recognised by human post-vaccination antisera raised against clade **5a.2** viruses. Clade **5a.2a.1** viruses, egg-propagated A/Victoria/4897/2022 and cell culture-propagated A/Wisconsin/67/2022, were recommended for vaccines to be used in the 2023-2024 northern hemisphere influenza season [3].

Figure 2a. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes (GISAID/WIC, Dec 2022)

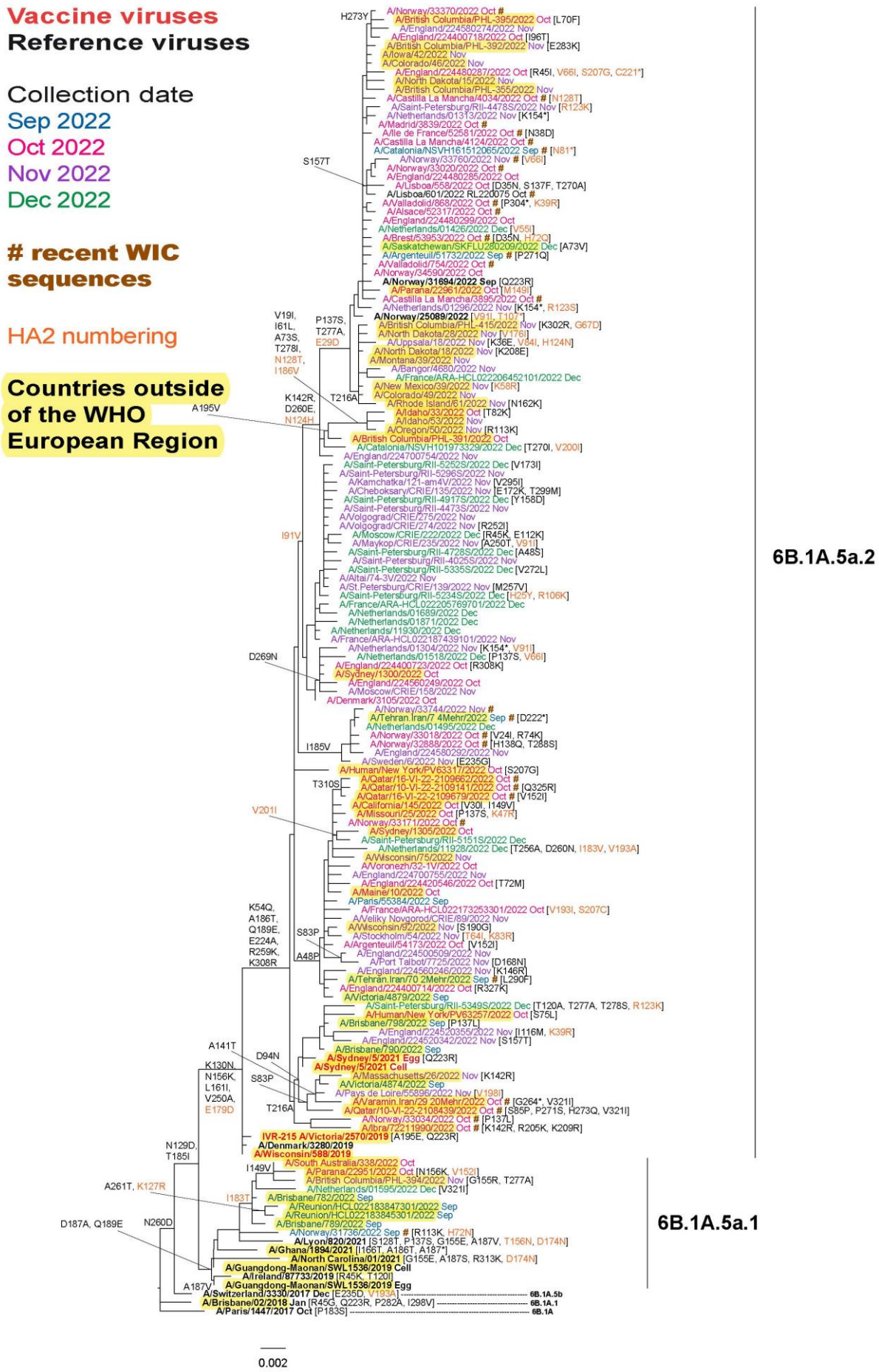


Figure 2b. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes (GISAID/WIC, Feb 2023)

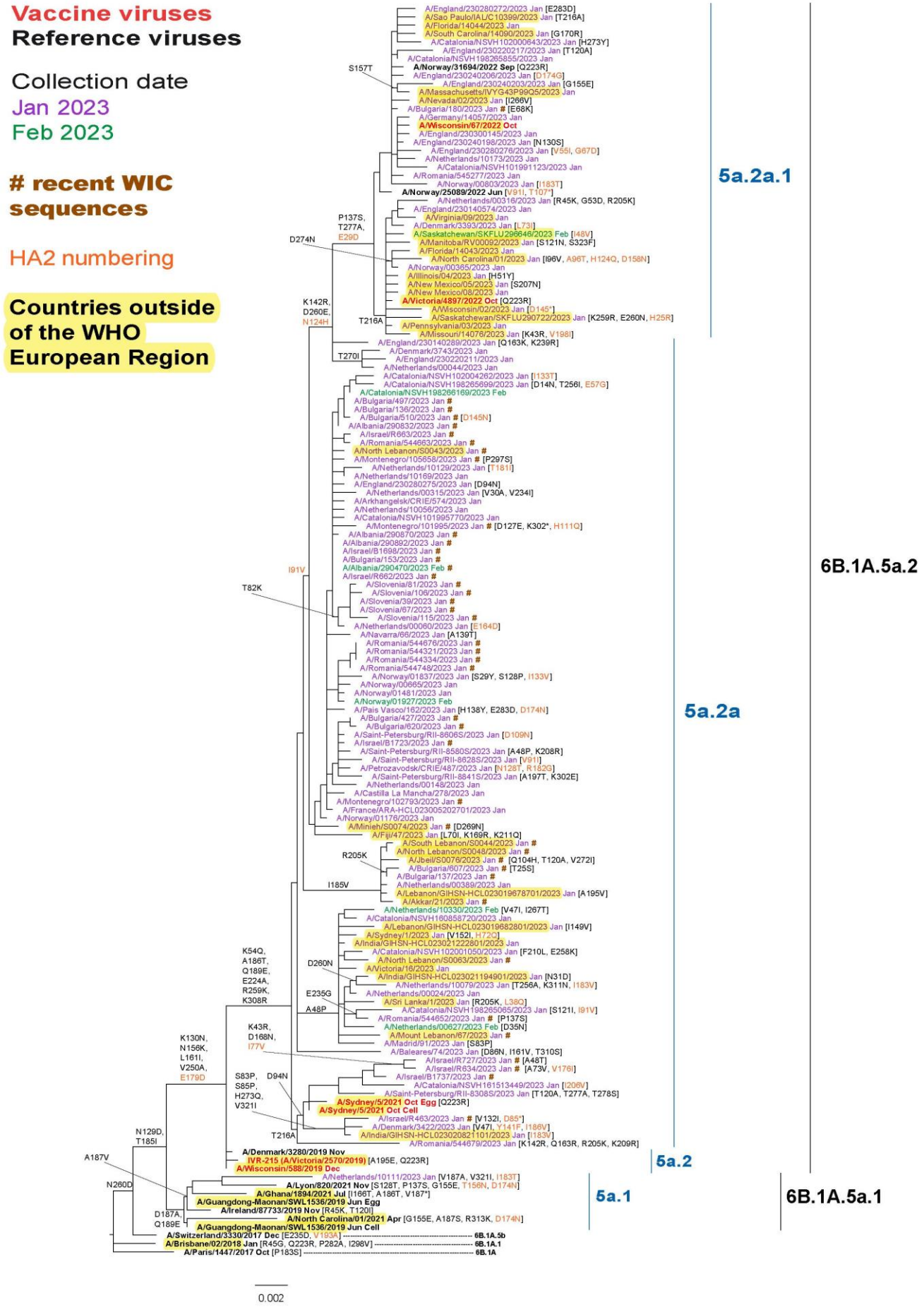


Table 4-1. Antigenic analysis of influenza A(H1N1)pdm09 viruses by HI

Viruses	Other information	Passage history / Ferret number / Genetic group	Collection date	Passage history	Haemagglutination inhibition titre											
					Post-infection ferret antisera											
					A/G-M SWL1536/19 MDCK	A/G-M SWL1536/19 Egg	A/Ghana 1894/21 Egg	A/Lyon 820/21 Egg	A/Denmark 3280/19 MDCK	IVR-215 A/Vic/2570/19 Egg	A/Sydney 5/21 MDCK	A/Sydney 5/21 Egg	A/Norway 25089/22 MDCK	A/Norway 31694/2022 Egg
					F09/20	F12/20	F02/22	F06/22	F28/20	F37/21	F46/22	F04/22	F38/22	F48/22
		Genetic group			5a.1	5a.1	5a.1	5a.1	5a.2	5a.2	5a.2a	5a.2a	5a.2a.1	5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	2560	2560	2560	320	40	80	40	40	40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	1280	640	160	40	80	<40	40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	2560	2560	2560	320	80	160	80	80	40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	320	160	320	320	40	80	40	40	40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	80	<40	40	<40	2560	1280	1280	2560	1280	640
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	80	80	40	80	640	1280	640	640	640	320
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	80	<40	40	<40	1280	2560	2560	2560	2560	1280
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2021-10-16	E3/E2	80	40	40	40	1280	1280	1280	2560	640	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	<40	<40	<40	<40	640	1280	640	1280	1280	640
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10^{-3}	<40	<40	<40	<40	320	640	640	640	640	640
TEST VIRUSES														
A/Georgia/1/2022		5a.2a	not known	MDCK1	40	<40	<40	<40	320	640	640	1280	640	320
A/Denmark/3083/2022		5a.2a	2022-10-02	MDCK4/MDCK1	<40	<40	<40	<40	160	320	160	320	160	40
A/Lyon/CHU/R22.389.14/2022		5a.2a	2022-10-14	MDCK2/MDCK2	40	<40	<40	<40	640	1280	640	1280	640	320
A/Denmark/3097/2022		5a.2a	2022-10-18	MDCK3/MDCK1	40	<40	<40	<40	320	1280	640	640	320	160
A/Denmark/3105/2022		5a.2a	2022-10-26	MDCK4/MDCK1	<40	<40	<40	<40	160	320	160	320	160	80
A/Lithuania/48382/2022		5a.2a	2022-11-20	MDCK1	40	<40	40	<40	640	1280	1280	1280	640	320
A/Lithuania/48777/2022		5a.2a	2022-11-25	MDCK1	<40	<40	<40	<40	640	640	640	640	640	160
A/Georgia/5/2022		5a.2a.1	not known	MDCK1	40	<40	<40	<40	1280	2560	1280	2560	2560	1280
A/Lyon/RU22.1.98/2022		5a.2a.1	2022-10-10	MDCK2/MDCK1	<40	<40	<40	<40	320	640	640	640	640	640
A/Toulon/NOMS22.1.45/2022		5a.2a.1	2022-10-14	MDCK2/MDCK2	40	<40	<40	<40	160	320	320	320	640	320
A/Lyon/CHU/R22.410.47/2022		5a.2a.1	2022-10-31	MDCK2/MDCK2	<40	<40	<40	<40	320	640	640	640	640	320
A/Lithuania/47198/2022		5a.2a.1	2022-11-02	MDCK2/MDCK1	40	<40	<40	40	640	1280	640	1280	1280	640
A/Lithuania/47197/2022		5a.2a.1	2022-11-02	MDCK2/MDCK1	40	<40	<40	40	640	640	640	640	1280	640
A/Lithuania/47196/2022		5a.2a.1	2022-11-02	MDCK2/MDCK1	40	<40	<40	80	640	640	640	1280	640	640
A/Lithuania/47358/2022		5a.2a.1	2022-11-04	MDCK2/MDCK1	40	<40	<40	<40	320	640	320	640	640	640
A/Lithuania/47356/2022		5a.2a.1	2022-11-05	MDCK2/MDCK1	40	<40	<40	40	640	1280	1280	1280	1280	640
A/Lithuania/47359/2022		5a.2a.1	2022-11-06	MDCK2/MDCK1	<40	<40	<40	<40	320	640	320	320	640	320
A/Lithuania/47680/2022		5a.2a.1	2022-11-10	MDCK2/MDCK1	40	<40	<40	<40	640	1280	640	1280	1280	640
A/Lithuania/48385/2022		5a.2a.1	2022-11-20	MDCK1	<40	<40	<40	<40	320	640	640	640	640	320
A/Lithuania/48381/2022		5a.2a.1	2022-11-20	MDCK1	<40	<40	<40	<40	640	1280	640	1280	1280	640
A/Lithuania/48386/2022		5a.2a.1	2022-11-21	MDCK1	<40	<40	<40	<40	640	640	320	640	1280	640
A/Lithuania/48706/2022		5a.2a.1	2022-11-23	MDCK1	40	<40	<40	<40	640	1280	640	1280	1280	640
A/Ireland/74219/2022		5a.2a.1	2022-11-25	MDCK1	40	<40	<40	<40	1280	1280	1280	2560	2560	640
A/Ireland/74223/2022		5a.2a.1	2022-11-27	MDCK1	<40	<40	<40	<40	640	1280	640	1280	1280	640
A/Ireland/74217/2022		5a.2a.1	2022-11-27	MDCK1	40	<40	<40	<40	640	1280	640	1280	1280	640
A/Ireland/74548/2022		5a.2a.1	2022-11-28	MDCK1	<40	<40	<40	<40	640	640	640	640	1280	640
A/Ireland/74537/2022		5a.2a.1	2022-11-28	MDCK1	40	<40	<40	<40	1280	1280	640	1280	1280	640
A/Ireland/74791/2022		5a.2a.1	2022-11-29	MDCK1	40	<40	<40	<40	640	1280	640	640	1280	640

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 4-2. Antigenic analysis of influenza 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/G-M SWL1536/19 MDCK F09/20 5a.1	A/G-M SWL1536/19 Egg F12/20 5a.1	A/Ghana 1894/21 Egg F02/22 5a.1	A/Lyon 820/21 Egg F06/22 5a.1	A/Denmark 3280/19 MDCK F28/20 5a.2	IVR-215 A/Vic/2570/19 Egg F37/21 5a.2	A/Sydney 5/21 MDCK F46/22 5a.2a	A/Sydney 5/21 Egg F04/22 5a.2a	A/Norway 25089/22 MDCK F38/22 5a.2a.1	A/Norway 31694/2022 Egg F48/22 5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	2560	2560	1280	320	40	40	<40	40	<40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	1280	640	320	<40	80	<40	40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	1280	2560	1280	320	40	80	40	40	<40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	320	320	160	320	40	40	40	40	<40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	160	40	<40	40	2560	2560	1280	2560	1280	320
IVR-215 (A/Victorial/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	80	80	40	80	640	1280	640	640	320	320
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	40	40	40	40	1280	2560	2560	2560	1280	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2022-10-31	E3/E2	80	40	40	40	640	1280	1280	1280	640	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	<40	<40	<40	<40	320	640	640	640	640	320
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10-3	<40	40	<40	<40	320	640	320	320	320	640
TEST VIRUSES														
A/Switzerland/95480/2022		5a.2a	2022-10-13	MDCK1/MDCK1	<40	40	<40	<40	320	640	640	1280	640	320
A/Switzerland/74729/2022		5a.2a	2022-11-23	MDCK1/MDCK1	40	40	<40	40	640	640	1280	1280	320	160
A/Switzerland/74639/2022		5a.2a	2022-11-24	MDCK1/MDCK1	40	40	<40	40	640	640	640	640	640	320
A/Switzerland/68182/2022		5a.2a	2022-12-13	MDCK1	40	40	<40	40	1280	1280	1280	1280	1280	320
A/Switzerland/28759/2022		5a.2a	2022-12-19	MDCK1	40	40	<40	40	320	640	640	640	640	320
A/Switzerland/28275/2022		5a.2a	2022-12-19	MDCK1	40	40	<40	<40	320	640	640	640	320	160
A/Switzerland/28469/2022		5a.2a	2022-12-20	MDCK1	<40	40	<40	<40	320	640	640	640	320	160
A/Switzerland/75200/2022		5a.2a	2022-12-23	MDCK1	40	40	<40	40	640	1280	1280	1280	1280	320
A/Ukraine/465/2022		5a.2a.1	2022-11-11	MDCK1	<40	<40	<40	<40	640	640	640	640	640	640
A/Ukraine/464/2022		5a.2a.1	2022-11-14	MDCK1	<40	<40	<40	<40	320	640	320	640	640	320
A/Switzerland/86105/2022		5a.2a.1	2022-11-15	MDCK1/MDCK1	<40	40	<40	40	640	640	640	640	1280	640
A/Hungary/70/2022		5a.2a.1	2022-11-21	MDCK1/MDCK1	<40	<40	<40	<40	320	320	320	320	320	320
A/Hungary/71/2022		5a.2a.1	2022-11-29	MDCK1/MDCK1	<40	<40	<40	<40	320	640	640	640	640	320
A/Ukraine/668/2022		5a.2a.1	2022-12-06	MDCK1	<40	40	<40	<40	640	1280	640	640	1280	640
A/Hungary/86/2022		5a.2a.1	2022-12-07	MDCK1/MDCK1	<40	<40	<40	<40	320	320	320	320	320	160
A/Ukraine/667/2022		5a.2a.1	2022-12-11	MDCK1	<40	<40	<40	<40	320	320	320	320	640	320
A/Ukraine/661/2022		5a.2a.1	2022-12-14	MDCK1	<40	40	<40	<40	640	640	640	640	1280	320
A/Switzerland/69094/2022		5a.2a.1	2022-12-14	MDCK1	<40	<40	<40	<40	320	640	640	320	640	320
A/Ukraine/777/2022		5a.2a.1	2022-12-17	MDCK1	<40	40	<40	<40	320	640	320	640	640	320
A/Ukraine/799/2022		5a.2a.1	2022-12-26	MDCK1	<40	<40	<40	<40	320	640	320	640	640	320
						Vaccine NH 2020-21				Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23		Vaccine SH 2023		

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 4-3. Antigenic analysis of influenza 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/G-M SWL1536/19 MDCK F09/20 5a.1	A/G-M SWL1536/19 Egg F12/20 5a.1	A/Ghana 1894/21 Egg F02/22 5a.1	A/Lyon 820/21 Egg F06/22 5a.1	A/Denmark 3280/19 MDCK F28/20 5a.2	IVR-215 A/Vic/2570/19 Egg F37/21 5a.2	A/Sydney 5/21 MDCK F46/22 5a.2a	A/Sydney 5/21 Egg F04/22 5a.2a	A/Norway 25089/22 MDCK F38/22 5a.2a.1	A/Norway 31694/2022 Egg F48/22 5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	1280	1280	1280	320	40	40	40	40	40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	2560	1280	320	40	80	40	40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	2560	2560	1280	320	40	80	40	80	40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	640	320	320	640	40	80	40	80	40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	80	40	40	80	2560	2560	1280	2560	1280	320
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	160	160	80	80	640	1280	640	1280	640	320
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	80	80	40	80	1280	2560	2560	2560	1280	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2022-10-31	E3/E2	160	80	40	80	1280	1280	1280	2560	1280	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	40	40	<40	40	640	1280	1280	1280	1280	640
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10^{-3}	40	40	<40	40	640	640	640	320	640	640
TEST VIRUSES														
A/Croatia/114180/2022		5a.2a	2022-10-22	MDCKx/MDCK1	80	80	40	40	1280	2560	1280	2560	1280	640
A/Norway/33620/2022		5a.2a	2022-10-31	MDCK1	80	80	40	80	1280	2560	2560	2560	2560	640
A/Norway/33584/2022		5a.2a	2022-11-07	MDCK1	40	80	40	40	1280	1280	1280	1280	1280	320
A/Norway/33744/2022		5a.2a	2022-11-09	MDCK1	80	80	40	80	1280	2560	2560	1280	1280	640
A/Belgium/G0292/2022		5a.2a	2022-11-21	C1/MDCK1	80	80	40	40	1280	1280	1280	2560	1280	640
A/Croatia/118556/2022		5a.2a	2022-11-22	MDCKx/MDCK1	80	80	40	40	1280	2560	2560	2560	1280	640
A/Croatia/118699/2022		5a.2a	2022-11-23	MDCKx/MDCK1	40	40	<40	<40	640	640	640	640	640	320
A/Belgium/G0302/2022		5a.2a	2022-11-25	C1/MDCK1	80	80	40	40	1280	2560	1280	1280	1280	640
A/Belgium/S2496/2022		5a.2a	2022-11-28	C1/MDCK1	160	80	40	80	1280	2560	2560	2560	1280	640
A/Belgium/S2710/2022		5a.2a	2022-12-01	C1/MDCK1	40	40	<40	40	640	1280	1280	640	640	320
A/Switzerland/32650/2022		5a.2a	2022-12-09	MDCK2	<40	40	<40	<40	640	640	320	640	640	160
A/Belgium/S2691/2022		5a.2a	2022-12-11	C1/MDCK1	40	40	<40	40	1280	1280	1280	1280	1280	320
A/Catalonia/NSVH101922705/2022		5a.2a.1	2022-10-02	SIAT1/MDCK1	80	40	40	40	1280	2560	1280	2560	2560	2560
A/Catalonia/NSVH171764113/2022		5a.2a.1	2022-10-04	SIAT1/MDCK1	40	40	<40	<40	1280	1280	1280	2560	1280	1280
A/Catalonia/NSVH151195412/2022		5a.2a.1	2022-10-18	SIAT1/MDCK1	<40	<40	<40	<40	640	1280	640	1280	1280	640
A/Croatia/115187/2022		5a.2a.1	2022-10-27	MDCKx/MDCK2	40	40	<40	<40	640	1280	640	640	1280	640
A/Norway/33370/2022		5a.2a.1	2022-10-28	MDCK1	40	80	<40	40	1280	2560	1280	1280	1280	1280
A/Norway/33307/2022		5a.2a.1	2022-11-02	MDCK1	40	80	<40	40	1280	1280	640	1280	1280	640
A/Norway/33583/2022		5a.2a.1	2022-11-07	MDCK1	40	40	<40	80	640	1280	640	1280	1280	640
A/Norway/33662/2022		5a.2a.1	2022-11-09	MDCK1	40	40	<40	40	1280	1280	640	640	1280	640
A/Norway/33760/2022		5a.2a.1	2022-11-11	MDCK1	40	40	<40	40	640	640	640	320	1280	640
A/Croatia/118701/2022		5a.2a.1	2022-11-21	MDCKx/MDCK2	40	40	<40	<40	1280	1280	1280	1280	1280	1280
A/Switzerland/32713/2022		5a.2a.1	2022-12-09	MDCK2	40	160	<40	40	1280	2560	1280	1280	1280	1280

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

< relates to the lowest dilution of antiserum used
ND = Not Done

Table 4-4. Antigenic analysis of influenza 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/G-M SWL1536/19 MDCK F09/20 5a.1	A/G-M SWL1536/19 Egg F12/20 5a.1	A/Ghana 1894/21 Egg F02/22 5a.1	A/Lyon 820/21 Egg F06/22 5a.1	A/Denmark 3280/19 MDCK F28/20 5a.2	IVR-215 A/Vic/2570/19 Egg F37/21 5a.2	A/Sydney 5/21 MDCK F46/22 5a.2a	A/Sydney 5/21 Egg F04/22 5a.2a	A/Norway 25089/22 MDCK F38/22 5a.2a.1	A/Norway 31694/2022 Egg F48/22 5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	1280	1280	1280	320	40	40	40	40	40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	2560	1280	320	40	80	40	40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	2560	2560	1280	320	40	80	40	80	40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	640	320	320	640	40	80	40	80	40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	80	40	40	80	2560	2560	1280	2560	1280	320
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	160	160	80	80	640	1280	640	1280	640	320
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	80	80	40	80	1280	2560	2560	2560	1280	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2022-10-31	E3/E2	160	80	80	80	1280	1280	1280	2560	1280	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	40	40	<40	40	640	1280	1280	1280	1280	640
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10^{-3}	40	40	<40	40	640	640	640	320	640	640
TEST VIRUSES														
A/Georgia/k-1124/2022		5a.2a	2022-12-12	MDCK1	80	160	40	80	1280	2560	2560	2560	1280	640
A/Slovenia/11425/2022		5a.2a	2022-12-14	MDCKx/MDCK1	80	80	40	40	1280	1280	2560	1280	1280	640
A/Slovenia/11448/2022		5a.2a	2022-12-15	SIATx/MDCK1	40	40	40	40	640	1280	1280	1280	640	320
A/Slovenia/11411/2022		5a.2a	2022-12-15	SIATx/MDCK1	80	80	80	40	40	1280	2560	2560	1280	640
A/Slovenia/11433/2022		5a.2a	2022-12-16	SIATx/MDCK1	80	80	40	40	1280	1280	1280	1280	1280	640
A/Slovenia/11471/2022		5a.2a	2022-12-19	SIATx/MDCK1	40	40	<40	40	640	1280	1280	1280	640	320
A/Slovenia/11522/2022		5a.2a	2022-12-20	MDCKx/MDCK1	80	40	<40	40	1280	1280	1280	1280	640	640
A/Slovenia/11555/2022		5a.2a	2022-12-21	MDCKx/MDCK1	80	80	40	40	1280	2560	2560	1280	1280	640
A/Israel/R13016/2022		5a.2a	2022-12-25	P1/MDCK1	<40	40	<40	<40	1280	1280	1280	1280	640	320
A/Slovenia/11687/2022		5a.2a	2022-12-27	MDCKx/MDCK1	40	40	<40	40	1280	1280	1280	1280	640	640
A/Slovenia/11685/2022		5a.2a	2022-12-27	SIATx/MDCK1	80	80	40	80	1280	2560	2560	2560	1280	640
A/Slovenia/11643/2022		5a.2a	2022-12-27	SIATx/MDCK1	80	40	40	40	1280	2560	1280	1280	1280	640
A/Israel/R13228/2022		5a.2a	2022-12-27	P1/MDCK1	<40	<40	<40	<40	320	320	640	640	320	160
A/Romania/544334/2023		5a.2a	2023-01-02	SIAT1/MDCK1	80	40	<40	40	1280	1280	1280	1280	1280	640
A/Romania/544321/2023		5a.2a	2023-01-02	SIAT1/MDCK1	80	80	40	40	1280	2560	2560	2560	1280	640
A/Slovenia/39/2023		5a.2a	2023-01-03	MDCKx/MDCK1	40	80	<40	40	640	1280	640	1280	640	320
A/Israel/B1723/2023		5a.2a	2023-01-03	P1/MDCK1	160	80	80	80	1280	2560	2560	2560	2560	640
A/Romania/544748/2023		5a.2a	2023-01-04	SIAT1/MDCK1	160	80	40	80	2560	2560	2560	2560	2560	1280
A/Romania/544676/2023		5a.2a	2023-01-06	SIAT1/MDCK1	80	80	40	80	1280	2560	2560	2560	1280	640
A/Israel/R463/2023		5a.2a	2023-01-06	P1/MDCK1	<40	<40	<40	<40	640	640	640	1280	640	320
A/Romania/544652/2023		5a.2a	2023-01-07	SIAT1/MDCK1	80	40	<40	40	640	1280	1280	640	640	320
A/Romania/544663/2023		5a.2a	2023-01-08	SIAT1/MDCK1	80	80	40	40	2560	2560	2560	2560	2560	640

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

< relates to the lowest dilution of antiserum used
ND = Not Done

Table 4-5. Antigenic analysis of influenza 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/G-M SWL1536/19 MDCK F09/20 5a.1	A/G-M SWL1536/19 Egg F12/20 5a.1	A/Ghana 1894/21 Egg F02/22 5a.1	A/Lyon 820/21 Egg F06/22 5a.1	A/Denmark 3280/19 MDCK F28/20 5a.2	IVR-215 A/Vic/2570/19 Egg F37/21 5a.2	A/Sydney 5/21 MDCK F46/22 5a.2a	A/Sydney 5/21 Egg F04/22 5a.2a	A/Norway 25089/22 MDCK F38/22 5a.2a.1	A/Norway 31694/2022 Egg F48/22 5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	1280	1280	1280	320	40	80	80	40	40	<40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	640	1280	640	160	<40	80	40	40	<40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	1280	2560	2560	320	80	160	80	80	40	<40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	640	320	320	640	40	80	40	40	40	<40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	80	40	<40	40	1280	2560	2560	2560	1280	640	640
IVR-215 (A/Victorial/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	80	80	40	80	640	1280	640	640	640	1280	160
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	80	80	40	80	1280	2560	2560	2560	1280	1280	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2022-10-31	E3/E2	80	40	40	40	640	1280	1280	1280	1280	1280	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	40	40	<40	<40	1280	1280	1280	1280	1280	1280	640
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10-3	<40	40	<40	40	320	640	320	320	320	320	320
TEST VIRUSES														
A/England/79/2022		5a.1	2022-09-15	SIAT1/MDCK1	640	640	640	160	40	80	40	40	40	<40	<40
A/Netherlands/01283/2022		5a.1	2022-11-15	hCK1/MDCK1	1280	1280	1280	640	160	160	80	160	80	40	40
A/Netherlands/01210/2022		5a.2a	2022-09-02	hCK1/MDCK1	<40	40	<40	<40	640	1280	1280	1280	1280	1280	320
A/England/157/2022		5a.2a	2022-09-19	SIAT1/MDCK1	80	80	40	40	640	2560	1280	1280	1280	1280	320
A/England/125/2022		5a.2a	2022-10-24	SIAT1/MDCK1	80	160	80	80	2560	2560	2560	2560	1280	1280	640
A/Milano/242/2022		5a.2a	2022-11-14	MDCK2/MDCK1	40	80	40	40	640	1280	1280	1280	640	640	320
A/Parma/128/2022		5a.2a	2022-11-17	MDCK2/MDCK1	<40	<40	<40	<40	320	320	320	320	160	160	160
A/Bolzano/34/2022		5a.2a	2022-11-23	MDCK3/MDCK1	80	80	40	40	1280	2560	1280	2560	1280	1280	320
A/Parma/101/2022		5a.2a	2022-11-25	MDCK3/MDCK1	40	80	40	40	1280	1280	1280	1280	640	640	640
A/Berlin/195/2022		5a.2a	2022-11-29	P2/MDCK1	40	40	<40	40	640	1280	1280	1280	640	640	320
A/Niedersachsen/106/2022		5a.2a	2022-12-01	P1/MDCK1	80	80	40	40	640	1280	1280	1280	640	640	320
A/Palermo/5/2022		5a.2a	2022-12-01	MDCK3/MDCK1	80	80	40	40	1280	1280	1280	2560	1280	1280	320
A/Hamburg/4/2022		5a.2a	2022-12-02	P1/MDCK1	40	80	<40	40	320	640	640	640	320	640	320
A/Berlin/198/2022		5a.2a	2022-12-02	P1/MDCK1	40	40	<40	<40	1280	2560	1280	2560	1280	1280	640
A/Bolzano/33/2022		5a.2a	2022-12-05	MDCK3/MDCK1	40	40	<40	<40	640	1280	1280	1280	640	640	320
A/Sachsen/30/2022		5a.2a	2022-12-12	P1/MDCK1	40	40	<40	<40	640	1280	1280	1280	640	640	320
A/Netherlands/11985/2022		5a.2a	2022-12-20	MDCK-MIX2/MDCK1	160	160	80	80	2560	>5120	2560	>5120	2560	2560	640
A/Netherlands/11972/2022		5a.2a	2022-12-20	MDCK-MIX2/MDCK1	40	40	<40	40	1280	1280	1280	1280	1280	1280	640
A/Netherlands/11971/2022		5a.2a	2022-12-20	MDCK-MIX2/MDCK1	80	160	80	80	2560	2560	2560	2560	2560	2560	1280
A/Netherlands/11984/2022		5a.2a	2022-12-22	MDCK-MIX2/MDCK1	80	80	40	40	1280	1280	1280	1280	1280	640	320
A/England/160/2022		5a.2a.1	2022-09-12	SIAT1/MDCK1	40	40	<40	<40	640	1280	640	1280	1280	1280	640
A/Netherlands/01285/2022		5a.2a.1	2022-11-10	hCK1/MDCK1	40	40	<40	<40	640	640	640	640	640	640	640
A/Netherlands/11831/2022		5a.2a.1	2022-11-16	MDCK-MIX2/MDCK1	40	40	<40	<40	640	1280	1280	1280	1280	1280	1280
A/Nordrhein-Westfalen/76/2022		5a.2a.1	2022-11-22	P1/MDCK1	<40	<40	<40	<40	320	320	320	320	320	320	320

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 4-6. Antigenic analysis of influenza A(H1N1)pdm09 viruses by HI

Viruses	Other information	Passage history	Collection date	Passage history	Haemagglutination inhibition titre													
											Post-infection ferret antiserum					NEW	NEW	
					A/G-M SWL1536/19 MDCK	A/G-M SWL1536/19 Egg	A/Ghana 1894/21 Egg	A/Lyon 820/21 Egg	A/Denmark 3280/19 MDCK	IVR-215 A/Victoria/2570/19 Egg	A/Sydney 5/21 MDCK	A/Sydney 5/21 Egg	A/Norway 25089/22 MDCK	A/Norway 31694/22 Egg	A/Norway 31694/22 Egg	A/Norway 31694/22 Egg	A/Catalonia/ NSVH-2065/22 Egg
		Ferret number			F09/20	F12/20	F02/22	F06/22	F28/20	F37/21	F46/22	F04/22	F38/22	F48/22	F04/23	F03/23		
		Genetic group			5a.1	5a.1	5a.1	5a.1	5a.2	5a.2	5a.2a	5a.2a	5a.2a.1	5a.2a.1	5a.2a.1	5a.2a.1		
REFERENCE VIRUSES																		
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	1280	2560	1280	320	40	80	40	80	40	<40	<40	<40	40	
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	1280	640	320	<40	80	<40	40	<40	<40	<40	<40	<40	
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	1280	2560	1280	320	80	160	40	80	<40	<40	<40	<40	40	
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	320	320	160	320	40	80	40	40	<40	<40	<40	<40	40	
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	80	80	40	80	1280	2560	1280	2560	1280	640	1280	1280	1280	
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	160	80	80	80	1280	1280	640	640	640	320	640	640	640	
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	80	80	40	80	1280	2560	1280	1280	640	320	640	1280	2560	
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2021-10-31	E3/E2	80	80	40	80	1280	1280	1280	1280	640	320	640	1280	1280	
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	<40	40	<40	40	640	1280	1280	1280	1280	640	1280	1280	1280	
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10^{-5}	<40	<40	<40	<40	320	320	320	320	320	320	320	320	320	
A/Catalonia/NSVH161512065/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-14	E3 (AM1A/2) 10^{-5}	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5120	
TEST VIRUSES																		
A/Valladolid/42/2022		5a.2a	2022-12-15	MDCK1/MDCK1	80	80	80	40	1280	2560	2560	2560	1280	640	1280		2560	
A/Valladolid/1/2022		5a.2a	2022-12-27	MDCK1/MDCK1	40	40	<40	<40	640	640	640	640	640	160	320		640	
A/Valladolid/1/2023		5a.2a	2023-01-01	MDCK1/MDCK1	80	80	40	80	1280	2560	2560	2560	1280	640	1280		2560	
A/Burgos10/2023		5a.2a	2023-01-09	MDCK1/MDCK1	40	40	<40	40	640	1280	1280	1280	640	320	640		1280	
A/Palencia/11/2023		5a.2a	2023-01-10	MDCK1/MDCK1	80	80	40	80	1280	2560	2560	2560	1280	640	1280		1280	
A/Burgos9/2023		5a.2a	2023-01-10	MDCK1/MDCK1	40	40	40	40	1280	1280	1280	1280	1280	320	640		1280	
A/Albania/290763/2023		5a.2a	2023-01-11	MDCK1	80	80	40	80	1280	2560	1280	2560	1280	640	640		1280	
A/Albania/290892/2023		5a.2a	2023-01-12	MDCK1	40	40	40	80	1280	1280	1280	1280	1280	640	640		1280	
A/Albania/290870/2023		5a.2a	2023-01-12	MDCK1	80	80	40	80	1280	2560	2560	2560	1280	640	1280		2560	
A/Albania/290832/2023		5a.2a	2023-01-12	MDCK1	80	80	40	160	1280	2560	2560	2560	1280	640	1280		1280	
A/Valladolid/16/2023		5a.2a	2023-01-12	MDCK1/MDCK1	80	80	40	80	1280	1280	1280	2560	1280	640	1280		1280	
A/Bulgaria/510/2023		5a.2a	2023-01-16	MDCK1	40	80	<40	80	1280	1280	1280	1280	1280	640	1280		1280	
A/Bulgaria/607/2023		5a.2a	2023-01-16	MDCK1	40	40	<40	40	640	1280	1280	1280	640	640	640		640	
A/Valladolid/18/2023		5a.2a	2023-01-17	MDCK1/MDCK1	40	40	40	40	1280	1280	1280	1280	1280	640	640		1280	
A/Albania/290470/2023		5a.2a	2023-02-01	MDCK1	80	160	80	160	2560	2560	2560	2560	2560	1280	2560		2560	
A/Burgos55/2022		5a.2a.1	2022-12-22	MDCK1/MDCK1	<40	<40	<40	<40	320	640	320	320	640	320	320		640	

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 4-7. Antigenic analysis of influenza A(H1N1)pdm09 viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre												
				Post-infection ferret antiserum												
				A/G-M SWL1536/19	A/G-M SWL1536/19	A/Ghana 1894/21	A/Lyon 820/21	A/Denmark 3280/19	IVR-215 A/Vic/2570/19	A/Sydney 5/21	A/Sydney 5/21	A/Sydney 5/21	A/Norway 25089/22	A/Norway 31694/22
	Passage history			MDCK	Egg	Egg	Egg	MDCK	Egg	MDCK	Egg	MDCK	MDCK	Egg
	Ferret number			F09/20	F12/20	F02/22	F06/22	F28/20	F37/21	F46/22	F04/22	F38/22	F38/22	F48/22
	Genetic group			5a.1	5a.1	5a.1	5a.1	5a.2	5a.2	5a.2a	5a.2a	5a.2a.1	5a.2a.1	5a.2a.1
REFERENCE VIRUSES														
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	C2/MDCK1	1280	1280	640	320	40	80	40	40	40	<40	<40	<40
A/Guangdong-Maonan/SWL1536/2019		5a.1	2019-06-17	E3/E2	1280	1280	640	320	<40	80	<40	40	<40	<40	<40	<40
A/Ghana/1894/2021		5a.1	2021-07-21	E2/E1	2560	1280	1280	320	40	160	40	80	<40	<40	<40	<40
A/Lyon/820/2021		5a.1	2021-11-16	E1/E2	320	320	160	320	40	40	<40	40	<40	<40	<40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	5a.2	2019-11-10	MDCK4/MDCK5	40	80	40	80	1280	2560	1280	2560	1280	1280	640	640
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	5a.2	2018-11-22	E4/D7/E2	80	80	40	80	640	1280	640	640	320	320	320	320
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a	2021-10-16	MDCK3/MDCK3	40	40	40	40	1280	2560	2560	2560	1280	1280	640	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	5a.2a	2022-10-31	E3/E2	80	40	40	40	1280	1280	1280	1280	1280	640	640	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	5a.2a.1	2022-06-15	MDCK3	<40	<40	<40	<40	640	1280	640	640	1280	1280	320	320
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	5a.2a.1	2022-09-24	E3/E1 10^{-5}	40	<40	<40	<40	640	640	640	640	320	320	640	640
TEST VIRUSES														
A/Norway/33034/2022		5a.2a	2022-10-23	MDCK1	80	40	<40	40	640	640	640	640	640	640	640	320
A/Norway/33171/2022		5a.2a	2022-10-26	MDCK1	80	40	<40	40	1280	1280	1280	1280	1280	1280	1280	320
A/Slovenia/10959/2022		5a.2a	2022-11-20	MDCKx/MDCK1	80	80	40	80	1280	2560	2560	1280	1280	1280	1280	640
A/Slovenia/10991/2022		5a.2a	2022-11-21	MDCKx/MDCK1	160	80	40	80	2560	2560	2560	2560	1280	1280	1280	640
A/Slovenia/11068/2022		5a.2a	2022-11-28	SIATx/MDCK1	80	80	40	40	1280	2560	1280	2560	1280	1280	1280	640
A/Slovenia/11185/2022		5a.2a	2022-12-03	MDCKx/MDCK1	80	80	40	80	1280	2560	1280	2560	1280	1280	1280	640
A/Slovenia/11320/2022		5a.2a	2022-12-12	SIAT1/MDCK1	40	40	<40	40	1280	1280	1280	1280	640	640	640	320
A/Valladolid/41/2022		5a.2a	2022-12-18	MDCK1/MDCK1	40	40	<40	80	1280	1280	2560	1280	1280	1280	1280	640
A/Valladolid/52/2022		5a.2a	2022-12-31	MDCK1/MDCK1	80	80	40	80	2560	2560	2560	2560	2560	2560	2560	640
A/Slovenia/43/2023		5a.2a	2023-01-04	MDCKx/MDCK1	40	40	<40	40	1280	1280	1280	1280	640	640	640	320
A/Valladolid/13/2023		5a.2a	2023-01-07	SIAT1/SIAT1	40	40	<40	40	640	1280	1280	1280	1280	1280	1280	320
A/Salamanca/12/2023		5a.2a	2023-01-10	SIAT1/SIAT1	80	80	<40	40	1280	2560	1280	1280	1280	1280	1280	640
A/Valladolid/816/2022		5a.2a.1	2022-09-29	MDCK1	40	40	<40	80	1280	2560	1280	1280	1280	2560	2560	1280
A/Lisboa/581/2022		5a.2a.1	2022-10-09	MDCK1	<40	<40	<40	<40	320	640	320	320	320	640	640	320
A/Norway/32627/2022		5a.2a.1	2022-10-18	MDCK1	40	40	<40	40	640	640	640	640	640	640	640	640
A/Lisboa/594/2022		5a.2a.1	2022-10-23	MDCK1	40	40	<40	40	1280	1280	640	640	1280	1280	1280	640
A/Lisboa/602/2022		5a.2a.1	2022-10-23	MDCK1	40	40	<40	<40	1280	2560	1280	1280	1280	2560	2560	1280
A/Salamanca/637/2022		5a.2a.1	2022-10-25	MDCK2	40	40	<40	80	1280	1280	1280	1280	1280	1280	1280	640
A/Lisboa/618/2022		5a.2a.1	2022-10-31	MDCK1	40	40	<40	<40	1280	2560	1280	1280	1280	2560	2560	1280
A/Valladolid/37/2022		5a.2a.1	2022-12-01	MDCK1/MDCK1	<40	<40	<40	40	640	1280	640	640	640	1280	1280	640
A/Valladolid/2/2023		5a.2a.1	2023-01-03	SIAT1/SIAT2	<40	<40	<40	<40	640	1280	640	640	640	1280	1280	640
A/Burgos/6/2023		5a.2a.1	2023-01-04	SIAT1/SIAT2/MDCK1	<40	<40	<40	40	640	1280	640	640	640	1280	1280	640

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

< relates to the lowest dilution of antiserum used
ND = Not Done

Table 4-8. Antigenic analysis of influenza A(H1N1)pdm09 viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre											
				Post-infection ferret antiserum											
				A/G-M SWL1536/19	A/G-M SWL1536/19	A/Ghana 1894/21	A/Lyon 820/21	A/Denmark 3280/19	IVR-215 A/Victoria/2570/19	A/Sydney 5/21	A/Sydney 5/21	A/Norway 25089/22	A/Norway 31694/2022
				MDCK F09/20	Egg F12/20	Egg F02/22	Egg F06/22	MDCK F28/20	Egg F37/21	MDCK F46/22	Egg F04/22	MDCK F38/22	Egg F48/22
	Passage history			5a.1	5a.1	5a.1	5a.1	5a.2	5a.2	5a.2a	5a.2a	5a.2a.1	5a.2a.1
	Ferret number												
	Genetic group												
REFERENCE VIRUSES													
A/Guangdong-Maonan/SWL1536/2019		2019-06-17	C2/MDCK1	1280	640	640	160	40	80	<40	40	<40	<40
A/Guangdong-Maonan/SWL1536/2019		2019-06-17	E3/E2	640	1280	320	160	<40	40	<40	40	<40	<40
A/Ghana/1894/2021		2021-07-21	E2/E1	1280	1280	1280	320	40	80	<40	40	<40	<40
A/Lyon/820/2021		2021-11-16	E1/E2	320	320	160	320	40	40	<40	40	<40	<40
A/Denmark/3280/2019	K130N, N156K, L161I, V250A, E189Q	2019-11-10	MDCK4/MDCK5	40	80	40	80	1280	1280	1280	2560	1280	640
IVR-215 (A/Victoria/2570/2019)	K130N, N156K, L161I, V250A, E189Q (A195E, Q223R)	2018-11-22	E4/D7/E2	80	80	40	80	320	1280	320	640	320	160
A/Sydney/5/2021 clone 3.4.1	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	2021-10-16	MDCK3/MDCK3	80	80	40	80	640	1280	1280	1280	1280	640
A/Sydney/5/2021 pooled clones 10-10	K54Q, A186T, E224A, R259K, K308R, D94N, T216A (Q223R)	2022-10-31	E3/E2	160	80	80	80	1280	1280	1280	1280	1280	320
A/Norway/25089/2022	P137S, K142R, D260E, T277A	2022-06-15	MDCK3	40	40	<40	<40	640	1280	640	1280	1280	640
A/Norway/31694/2022	P137S, K142R, D260E, T277A (Q223R)	2022-09-24	E3/E1 10^{-3}	40	<40	<40	<40	320	320	640	320	320	320
TEST VIRUSES													
A/Victoria/4897/2022		2022-10-02	SIAT2/MDCK1	<40	40	<40	<40	640	640	640	640	1280	640
A/Victoria/4897/2022	Viruses representative of the vaccine recommendation for the northern hemisphere 2023-2024 [3]	2022-10-02	E3/E1	<40	<40	<40	<40	640	640	320	640	640	320
IVR-238 (A/Victoria/4897/2022)		2022-10-02	E3/D6/E1	40	40	<40	40	640	1280	640	1280	640	320
A/Romania/542287/2022		2022-11-20	SIAT2/MDCK1	80	80	<40	40	640	640	640	640	640	320
A/Castilla La Mancha/4545/2022		2022-11-27	MDCK1	40	80	<40	80	640	1280	640	1280	640	320
A/Romania/542763/2022		2022-11-28	SIAT1/MDCK1	40	40	<40	40	640	640	640	640	640	320
A/Romania/542762/2022		2022-11-28	SIAT1/MDCK1	80	80	40	40	640	1280	1280	640	640	320
A/Romania/544055/2022		2022-12-27	SIAT1/MDCK1	40	80	<40	40	640	640	640	640	640	320
A/Romania/544202/2022		2022-12-28	SIAT1/MDCK1	40	40	<40	40	320	320	320	320	320	160
A/Romania/544178/2022		2022-12-28	SIAT1/MDCK1	80	80	40	80	640	640	1280	1280	640	320
A/Romania/544061/2022		2022-12-28	SIAT1/MDCK1	80	80	<40	40	640	1280	1280	640	640	320
A/Romania/544308/2022		2022-12-29	SIAT1/MDCK1	80	80	40	40	640	1280	1280	1280	640	320
A/Romania/544322/2022		2022-12-30	SIAT1/MDCK1	40	40	<40	40	640	640	640	640	640	320
A/Romania/544307/2022		2022-12-30	SIAT1/MDCK1	40	80	<40	40	640	1280	1280	1280	640	320
A/Romania/544323/2022		2022-12-31	SIAT1/MDCK1	40	40	<40	40	320	640	640	640	320	160
A/Romania/541366/2022		2022-10-31	SIAT1/MDCK1	40	<40	<40	<40	320	640	640	320	640	320
A/Romania/541365/2022		2022-10-31	SIAT1/MDCK1	<40	40	<40	40	320	640	640	640	640	320
A/Castilla La Mancha/4296/2022		2022-11-03	MDCK1	<40	<40	<40	<40	320	320	320	320	640	320
A/Castilla La Mancha/4492/2022		2022-11-19	MDCK1	<40	40	<40	<40	640	640	640	640	640	640
A/Romania/543518/2022		2022-12-12	SIAT1/MDCK1	40	40	<40	<40	640	640	640	640	1280	640
A/Burgos/45/2022		2022-12-25	MDCK1/MDCK4	<40	40	<40	<40	1280	1280	640	1280	1280	640

Vaccine NH 2020-21

Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23

Vaccine SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 4-9. Antigenic analysis of influenza A(H1N1)pdm09 viruses by HI – Summary

Viruses		Haemagglutination inhibition titre									
		Post-infection ferret antisera									
		A/G-M SWL1536/19	A/G-M SWL1536/19	A/Ghana 1894/21	A/Lyon 820/21	A/Denmark 3280/19	IVR-215 A/Vic/2570/19	A/Sydney 5/21	A/Sydney 5/21	A/Norway 25089/22	A/Norway/ 31694/22
Passage history		MDCK	Egg	Egg	Egg	MDCK	Egg	MDCK	Egg	MDCK	Egg
Ferret number		F09/20	F12/20	F02/22	F06/22	F28/20	F37/21	F46/22	F04/22	F38/22	F48/22
Genetic group		5a.1	5a.1	5a.1	5a.1	5a.2	5a.2	5a.2a	5a.2a	5a.2a.1	5a.2a.1
REFERENCE VIRUSES											
A/Guangdong-Maonan/SWL1536/2019	5a.1	1280	1280	1280	320	40	80	40	40	<40	<40
A/Guangdong-Maonan/SWL1536/2019	5a.1	640	1280	640	160	<40	80	40	40	<40	<40
A/Ghana/1894/2021	5a.1	1280	2560	2560	320	80	160	80	80	40	<40
A/Lyon/820/2021	5a.1	640	320	320	640	40	80	40	40	40	<40
A/Denmark/3280/2019	5a.2	80	40	<40	40	1280	2560	2560	2560	1280	640
IVR-215 (A/Victoria/2570/2019)	5a.2	80	80	40	80	640	1280	640	640	640	160
A/Sydney/5/2021 clone 3.4.1	5a.2a	80	80	40	80	1280	2560	2560	2560	1280	640
A/Sydney/5/2021 pooled clones 10-10	5a.2a	80	40	40	40	640	1280	1280	1280	1280	320
A/Norway/25089/2022	5a.2a.1	40	40	<40	<40	1280	1280	1280	1280	1280	640
A/Norway/31694/2022	5a.2a.1	<40	40	<40	40	320	640	320	320	320	320
TEST VIRUSES											
Number tested	5a.1	2	2	2	2	2	2	2	2	2	2
No with titre reduction ≤2-fold		2	2	1	1						
%		*100.0*	*100.0*	*50.0*	*50.0*						
No with titre reduction =4-fold				1	1						
%				*50.0*	*50.0*						
No with titre reduction ≥8-fold						2	2	2	2	2	2
%						*100.0*	*100.0*	*100.0*	*100.0*	*100.0*	*100.0*
Number tested	5a.2a	106	106	106	106	106	106	106	106	106	106
No with titre reduction ≤2-fold					2	79	101	84	95	98	97
%					*1.9*	*74.5*	*95.3*	*79.2*	*89.6*	*92.5*	*91.5*
No with titre reduction =4-fold					14	18	5	18	8	5	7
%					*13.2*	*17.0*	*4.7*	*17.0*	*7.5*	*4.7*	*6.6*
No with titre reduction ≥8-fold		106	106	106	90	9		4	3	3	2
%		*100.0*	*100.0*	*100.0*	*84.9*	*8.5*		*3.8*	*2.9*	*2.8*	*1.9*
Number tested	5a.2a.1	65	65	65	65	65	65	65	65	65	65
No with titre reduction ≤2-fold						25	59	18	43	64	64
%						*38.5*	*90.8*	*27.7*	*66.2*	*98.5*	*98.5*
No with titre reduction =4-fold					1	26	6	34	19	1	1
%					*1.5*	*40.0*	*9.2*	*52.3*	*29.2*	*1.5*	*1.5*
No with titre reduction ≥8-fold		65	65	65	64	14		13	3		
%		*100.0*	*100.0*	*100.0*	*98.5*	*21.5*		*20.00*	*4.6*		
			Vaccine NH 2020-21				Vaccine SH 2021 NH 2021-22 SH 2022 NH 2022-23		Vaccine SH 2023		

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.

Influenza A(H3N2) virus analyses

A(H3N2) viruses with HA sequences in clade **3C.2a** have been dominant since the 2014-15 influenza season with group **3C.2a1b** viruses predominating over the course of the 2019-2020 season in most WHO-defined regions of the world but for the European Region where there was equivalence of clade **3C.3a** viruses. Since 2019-2020 group **3C.2a1b** viruses have dominated and clade **3C.3a** viruses have not been detected after the period February to August 2020.

Group **3C.2a1b** viruses contain HA amino acid substitutions found in subclade **3C.2a1** (those in clade **3C.2a** plus **N171K** in **HA1** and **I77V** and **G155E** in **HA2**, with most carrying **N121K** in **HA1**, e.g. **A/Singapore/INFIMH-16-0019/2016,** a former vaccine virus), plus **E62G, R142G** and **H311Q** in **HA1**, often with additional amino acid substitutions – notably either **HA1 T135K** commonly with **T128A** (both of which result in loss of potential glycosylation sites) yielding the **3C.2a1b.1** subgroup (e.g., **A/La Rioja/2202/2018**) or **HA1 T131K** and **HA2 V200I** producing the **3C.2a1b.2** subgroup (e.g., **A/South Australia/34/2019**). Distinct clusters of viruses within both these subgroups have emerged defined by specific **HA1** and/or **HA2** amino acid substitutions: **3C.2a1b.1a** with additional amino acid substitutions of **HA1 A138S**, **F193S** and **S198P**, many also with **G186D** and **D190N** (e.g., **A/Denmark/3284/2019**); **3C.2a1b.1b** with additional amino acid substitutions of **HA1 S137F, A138S** and **F193S** (e.g., **A/Hong Kong/2671/2019**); **3C.2a1b.2a** with additional amino acid substitutions of **HA1 K83E** and **Y94N** with **HA2 I193M** (e.g., **A/Slovenia/1637/2020**); **3C.2a1b.2b** with **HA2 V18M** substitution, often with additional **HA1** substitutions (e.g., **A/Bretagne/1323/2020)**. Further evolution involving HA subgroup **3C.2a1b.2a** occurred resulting in two additional subgroups being designated: **3C.2a1b.2a.1** with **HA1** substitutions of **K171N**, **G186S** and **S198P**, represented by 'Cambodia-like' viruses and **3C.2a1b.2a.2** with **HA1** substitutions of **Y159N**, **T160I** (loss of a glycosylation site), **L164Q**, **G186D** and **D190N**, represented by 'Bangladesh-like' viruses.

HA genes of subgroup **3C.2a1b.2a.2** (defined by **HA1** substitutions of **K83E**, **Y94N**, **A128T**, **T131K**, **S138A**, **Y159N**, **T160I** (resulting in loss of a glycosylation site) **L164Q**, **G186D**, **D190N** and **Y195F**) have continued to show extensive evolution such that they are now called **clade 2**, with subclades having been designated based on the following **HA1** amino acid substitutions:

Designated subclade	Defining HA1 amino acid substitutions	
	Clade/subclade related	Subclade specific
2a	Clade 2	H156S
2a.1	Subclade 2a	D53G, D104G, K276R
2a.1a	Subclade 2a.1	L157I, K220R
2a.1b	Subclade 2a.1	I140K, R299K
2a.2	Subclade 2a	D53G, R201L, S219Y
2a.3	Subclade 2a	D53N, N96S, I192F
2a.3a	Subclade 2a.3	E50K
2a.3a.1	Subclade 2a.3a	I140K
2a.3b	Subclade 2a.3	I140M
2b	Clade 2	E50K, F79V, I140K
2c	Clade 2	S205F, A212T
2d	Clade 2	G62R, H156Q, S199P

The first phylogeny, based on HA sequences derived from viruses with collection dates after 31 August 2022 made available in GISAID and generated at the WIC during December 2022, was dominated by sequences derived from viruses detected in countries outside of the WHO European Region (Figure 3a). There was a lack of recently submitted sequences from 'Cambodia-like' **3C.2a1b.2a.1** (**1a**) viruses. All recently collected viruses were 'Bangladesh-like' (**3C.2a1b.2a.2** (**2**) with **HA1** substitutions of **Y159N**, **T160I** (loss of a glycosylation site), **L164Q**, **G186D**, **D190N** and **Y195F**). The latter viruses were split into four major subgroups defined by specific **HA1** amino acid substitutions: (i) (**2b**) **E50K** with a range of additional substitutions, e.g., **F79V**, **I140K**, **S262N** and **R33Q**, with the proportion of viruses with **R33Q** and **S262N** substitutions having increased within the WHO European Region; (ii) (**2a.3**) **D53N**, **N96S** (gain a glycosylation site) and **I192F**, many with additional substitutions defining specific virus clusters, with a new cluster of viruses with **T135K** (resulting in loss of a glycosylation site) and **S145N** substitutions having emerged in the Americas ; (iii) (**2a.1**) **D53G** commonly with **D104G** and **K276R**, and additional substitutions (e.g., **T167S**), with viruses carrying **HA1 T135A** (resulting in loss of a glycosylation site) substitution having emerged in the WHO European Region; (iv) (**2a.1b**) **D53G**, **D104G**, **I140K**, **K276R** and **R299K**. Subgroups **2a.3**, **2a.1** and **2a.1b** also shared **HA1 H156S**

amino acid substitution. Sequences derived from samples collected in the WHO European Region were dispersed throughout the 'Bangladesh-like' (**3C.2a1b.2a.2** (2)) portion of the phylogeny with viruses falling into multiple virus clusters defined by specific amino acid substitutions. Overall, clades **2b** and **2a.3** were dominant being mainly populated by sequences derived from viruses detected in countries outside of the WHO European Region. Most of the new sequences falling in clades **2a.1** and **2a.1b** were from viruses detected in the WHO European Region. Further examples of a subgroup that had emerged in South Africa (defined by **HA1** amino acid substitutions **E83K**, **K121E**, **S205F**, **A212T** and **R261Q** - designated clade **2c**) had not been released in GISAID. Sequences for 'Cambodia-like' **3C.2a1b.2a.1** (**1a**) viruses detected in China in September and October of 2022 had been released, all of which contained an additional **HA1 I48T** amino acid substitution, now designated as clade **1a.1**.

The second phylogeny is based on HA sequences derived from viruses with collection dates after 31 December 2022 made available in GISAID and generated at the WIC up to 28 February 2023 (Table 2 and Figure 3b). Based on the old nomenclature the two phylogenies show similar profiles, but with different relevant proportions of the newly designated clades. For HA sequences derived from viruses detected in 2023 it appears that the bulk of circulating viruses have fallen into five clades with **2b** being dominant (**2b** > **2a.1b** > **2a.3a.1** > **2a.1** > **2a.3b**), with small numbers in additional clades (**1a.1**, **2a**, **2a.3**, **2a.3a**, **2c**). Sequences from the WHO European Region are dispersed throughout the 'Bangladesh-like' (**3C.2a1b.2a.2** (**2**)) region of the phylogeny, but there are clearly clusters of viruses in some clades, notably **2b**, **2a.1** and **2a.3a.1**, that are circulating in countries outside of the WHO European Region

In Figure 3b the location of HA sequences for egg- and cell culture-propagated cultivars of a former vaccine virus, A/Cambodia/e0826360/2020 (**3C.2a1b.2a.1** (**1a**)), are indicated as reference viruses. Egg- and cell culture-based 'Bangladesh-like' viruses (**3C.2a1b.2a.2** (**2**) for use in the 2022-2023 and 2023-2024 northern hemisphere and 2023 southern hemisphere seasons [1, 3, 2], A/Darwin/9/2021 (**2a**) and A/Darwin/6/2021 (**2a**) respectively, are indicated in red.

As described in many previous reports[2], influenza A(H3N2) viruses had been difficult to characterize 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 was a significant problem for most viruses that fell in genetic clade **3C.2a**, although there was some alleviation of this during 2019-2020 with continuation into the 2020-2021 influenza season. This issue is now much alleviated for 'Bangladesh-like' **3C.2a1b.2a.2** (**2**) viruses which agglutinate guinea pig RBCs well, allowing HI assays to be performed.

Results for 209 A(H3N2) 'Bangladesh-like' (**3C.2a1b.2a.2** (**2**)) test viruses from the WHO European Region, fully characterized antigenically since the December report, are shown in Tables 5-1 to 5-8 with a summary in Table 5-9. The test viruses fell within six genetic clades (**2b**, n = 103; **2a.1b**, n = 56; **2a.3a.1**, n = 21; **2a.1**, n = 20; **2a.3b**, n = 6; **2a.3a**, n = 3). Greater than 90% of test viruses in clades **2b**, **2a.3a** and **2a.3a.1** were recognised with fourfold of the homologous titre by the antiserum raised against cell culture-propagated A/Thuringen/10/2022 (**2b**), while viruses in clades **2a.1**, **2a.1b** and **2a.3b** were recognised less well. The remaining reference **3C.2a1b.2a.2** (**2**) viruses against which antisera were raised all contained **HA1 H156S** amino acid substitutions. Cell culture-propagated A/Stockholm/5/2021 (**2a**) and egg-propagated A/Darwin/9/2021 (**2a**) represent current vaccine-related viruses. The antiserum raised against A/Stockholm/5/2021 recognised majorities of test viruses in all clades well (at least 57% within fourfold of homologous titres). Similar results were obtained with the antiserum raised against A/Darwin/9/2021 (at least 73% within fourfold of homologous titres) for all but viruses retaining **HAI H156** (clade **2b**) where only 33% of viruses were recognised within fourfold of homologous titres. However, the antiserum raised against A/Darwin/9/2021 gave homologous titres in the range 640-1280 and only one clade **2b** test virus yielded a HI titre of <80, with 'correlates of protection' data having indicated a titre of 40 as being 'protective'. Of the antisera raised against clade **2a.3** reference viruses: that raised against cell culture-propagated A/Norway/24873/2021 (homologous titre 160-320) performed as well as that raised against A/Darwin/9/2021, while; that raised against egg-propagated A/Norway/24873/2021 (homologous titre 640-1280) showed greater fold-drops against the test viruses but gave absolute titres comparable to those seen with the antiserum raised against cell culture-propagated A/Norway/24873/2021. Generally, antisera raised against clade **2a.1** (A/Slovenia/8720/2022 and A/Lille/50053/2022), **2a.1b** (A/Catalonia/NSVH161512067/2022) and **2a.2** (A/Poland/97/2022) viruses recognised those test viruses with **HA1 H156S** substitutions better than those (**2b**) that retained **H156**.

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

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

Results of HI assays with panels of post-infection ferret antisera raised against A(H3N2) vaccine and reference viruses for viruses detected in EU/EEA countries can be seen in previous influenza characterization reports on ECDC's website. Overall, these data show strong clade/subclade-specific recognition of test viruses by post-infection ferret antisera raised against cell culture-propagated reference viruses, with limited cross-clade/subclade recognition and further reductions in recognition of cell culture-propagated recently circulating viruses by antisera raised against A(H3N2) egg-propagated vaccine viruses.

Figure 3a. Phylogenetic comparison of influenza A(H3N2) HA genes (GISAID/WIC, Dec 2022)

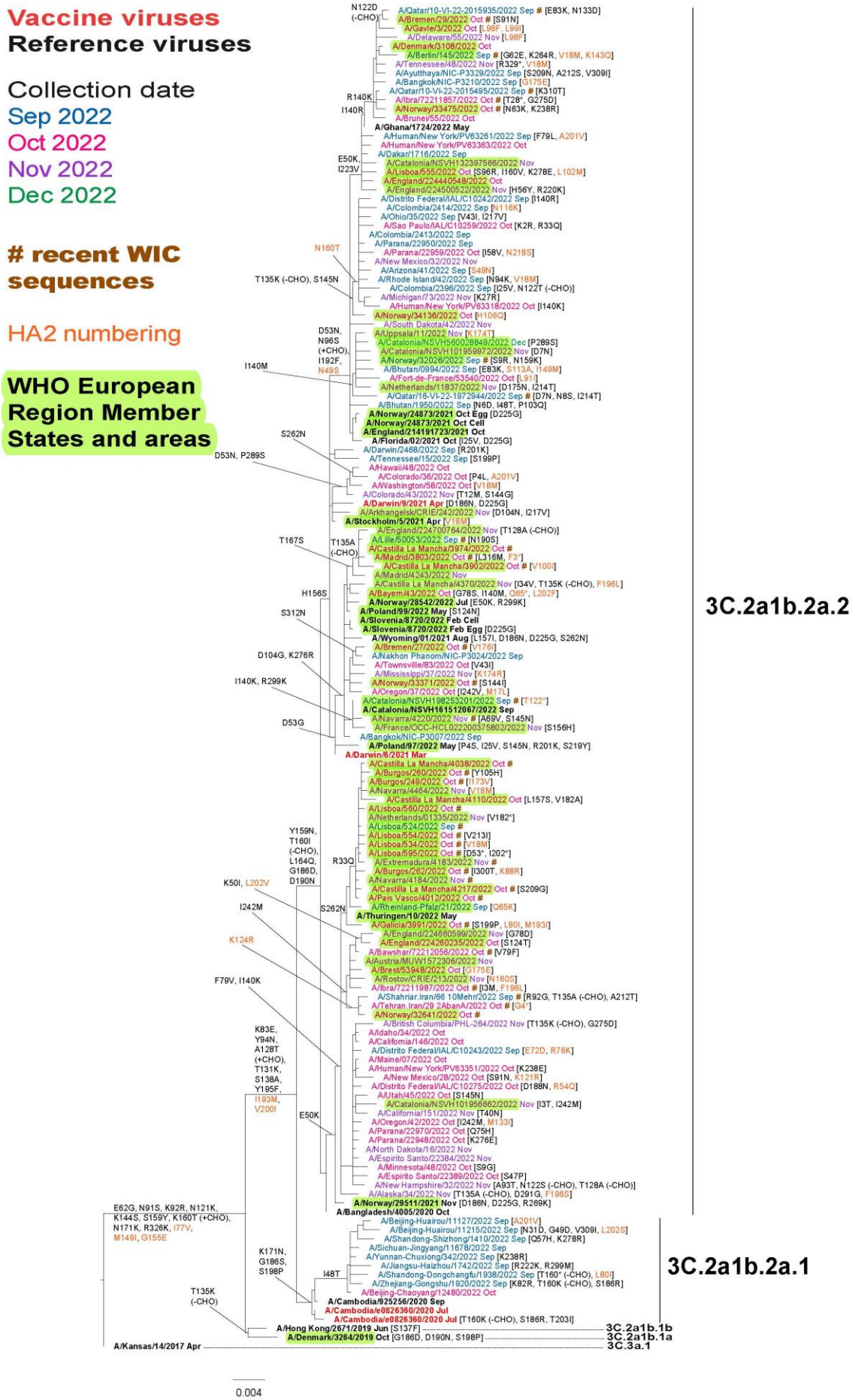


Figure 3b. Phylogenetic comparison of influenza A(H3N2) HA genes (GISAID/WIC, Feb 2023)

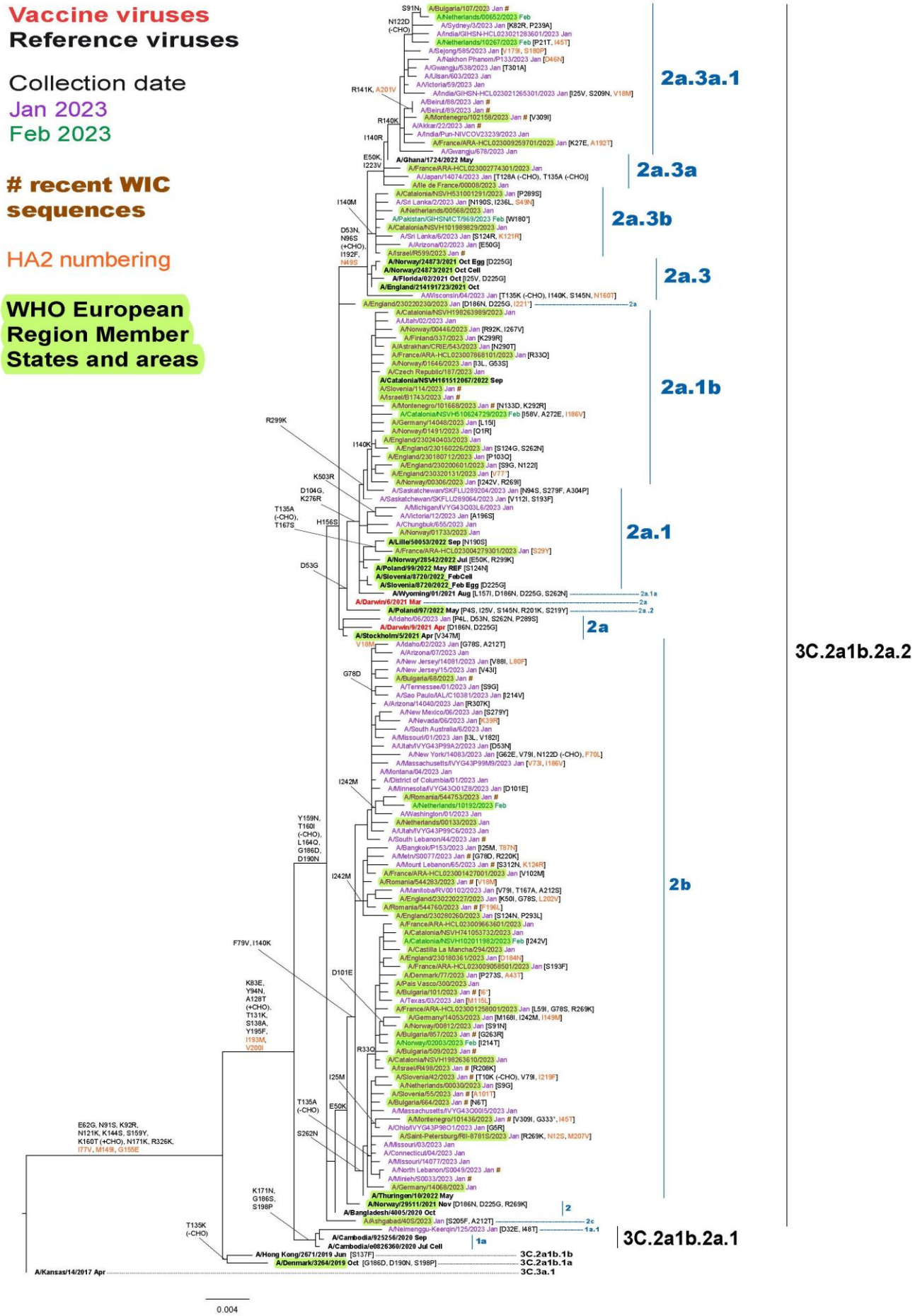


Table 5-1. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera A/Camb 925256/20 SIAT F03/21 1a	A/Camb e0826360/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stockholm 5/21 SIAT F35/21 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 24873/21 SIAT F10/22 2a.3	A/Norway 24873/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 8720/2022 SIAT F24/22 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	640	160	<40	160	320	<40	40	40	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E2	80	640	80	160	160	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	80	160	320	320	160	80	80	80	160	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	80	80	80	640	640	80	160	320	320	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	320	320	640	1280	160	320	320	640	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	80	80	80	320	320	160	320	160	320	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	160	160	640	640	320	640	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	160	160	80	1280	1280	320	640	1280	640	640
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT3	80	80	160	640	640	160	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT2	40	80	80	320	320	80	160	320	640	320
TEST VIRUSES														
A/Denmark/3110/2022	I242M	2b	2022-10-17	SIAT2/SIAT1	80	80	320	320	160	80	160	80	80	40
A/Denmark/3100/2022	I242M	2b	2022-10-17	SIAT2/SIAT1	80	80	320	320	160	80	80	80	80	40
A/Denmark/3101/2022	I242M	2b	2022-10-21	SIAT2/SIAT1	80	80	320	320	160	80	160	80	80	40
A/Denmark/3136/2022	I242M	2b	2022-11-05	SIAT2/SIAT1	80	80	320	320	160	80	160	80	80	40
A/Lyon/NRU22.2.97/2022	R33Q, S262N	2b	2022-10-24	MDCK2/SIAT1	80	80	320	320	160	80	160	80	160	40
A/Denmark/3103/2022	R33Q, S262N	2b	2022-10-25	SIAT3/SIAT1	80	80	320	320	160	80	160	80	80	40
A/Lyon/CHU/R22.415.69/2022	R33Q, S262N	2b	2022-11-05	MDCK2/SIAT1	40	80	320	160	160	80	80	80	160	40
A/Aix/NOMS22.1.44/2022	R33Q, N81D, S262N	2b	2022-10-14	MDCK2/SIAT1	80	80	320	320	160	80	160	80	160	40
A/Navarra/4439/2022	R33Q, F79I, S144G, S262N	2b	2022-11-13	SIAT2/SIAT1	40	80	320	160	160	40	80	80	160	40
A/Navarra/4440/2022	R33Q, K238R, S262N	2b	2022-11-17	SIAT2/SIAT1	80	160	320	320	160	80	160	80	160	40
A/Lyon/NRU22.4.39/2022	T135A(-cho), S262N	2b	2022-11-14	MDCK2/SIAT1	40	160	320	160	160	80	80	80	160	40
A/Navarra/4438/2022	T135A(-cho), S262N	2b	2022-11-18	SIAT2/SIAT1	80	80	160	160	160	80	80	40	160	<40
A/Lyon/CHU/R22.355.53/2022		2a.1	2022-09-05	MDCK2/SIAT1	40	40	80	320	320	80	160	320	640	320
A/Saint-Etienne/NOMS22.1.28/2022		2a.1	2022-09-20	MDCK2/SIAT1	40	40	80	320	640	80	160	640	640	320
A/Melesse/NOMS22.1.23/2022		2a.1	2022-09-26	MDCK2/SIAT1	40	40	80	320	320	80	160	640	320	320
A/Lyon/CHU/R22.372.37/2022	E50K, R299K	2a.1	2022-09-28	MDCK2/SIAT1	<40	40	40	160	320	80	160	320	640	320
A/Lyon/CHU/R22.374.29/2022		2a.1b	2022-10-01	MDCK2/SIAT1	40	40	80	320	320	80	160	320	640	320
A/Lyon/CHU/R22.384.1/2022		2a.1b	2022-10-10	MDCK2/SIAT1	40	80	80	320	320	80	160	320	640	320
A/Denmark/3127/2022	A163X	2a.1b	2022-11-01	SIAT3/SIAT1	40	80	80	320	320	80	160	320	320	320
A/Grenoble/NOMS22.1.42/2022		2a.3a	2022-10-10	MDCK2/SIAT1	80	80	160	320	320	320	640	160	640	160
A/Grenoble/NOMS22.1.57/2022		2a.3a	2022-10-26	MDCK2/SIAT1	40	80	160	320	320	320	640	160	320	160
A/Toulon/NOMS22.1.29/2022		2a.3a.1	2022-08-19	MDCK2/SIAT1	40	160	160	320	320	320	640	160	320	160
A/Toulon/NOMS22.1.33/2022		2a.3a.1	2022-09-15	MDCK2/SIAT1	80	160	160	320	320	320	640	160	160	160
A/Denmark/3108/2022		2a.3a.1	2022-10-27	SIAT3/SIAT1	40	160	160	320	320	320	640	160	160	160
A/Ashabat/1/2022		2a.3b	2022-11-29	MDCKx/SIAT1	80	80	160	320	320	320	640	320	320	160
A/Ashabat/3/2022		2a.3b	2022-12-06	MDCKx/SIAT1	80	80	160	320	320	320	640	320	320	160
						Vaccine NH 2021-22			Vaccine SH 2022 NH 2022-23 SH 2023					

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-2. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera A/Camb 925256/20 SIAT F03/21 2a.1	A/Camb e082636/20 Egg F10/21 2a.1	A/Thuringen 10/22 SIAT F36/22 2a.2	A/Stockholm 5/21 SIAT F35/21 2a.2	A/Darwin 9/21 Egg F39/21 2a.2	A/Norway 24873/21 SIAT F10/22 2a.2	A/Norway 24873/21 Egg F11/22 2a.2	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 87202022 SIAT F24/22 2a.2	A/Catal NSVH-2067/22 SIAT F41/22 2a.2
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	1280	160	40	320	640	<40	80	80	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	160	1280	80	160	320	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	80	320	320	640	320	160	160	160	320	80
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	80	160	80	640	640	160	320	320	640	160
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	640	160	640	1280	160	320	320	640	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	80	80	80	320	640	320	320	160	320	160
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	640	640	320	1280	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	80	160	80	640	640	320	320	640	1280	320
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	80	160	160	640	640	160	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	160	80	640	640	80	320	320	640	320
TEST VIRUSES														
A/Switzerland/24157/2022		2b	2022-12-23	SIAT3/SIAT1	80	160	320	320	320	80	160	80	320	40
A/Switzerland/18284/2022	R33Q, S262N	2b	2022-10-06	SIAT2/SIAT1	80	80	160	160	160	80	80	80	160	40
A/Burgos/257/2022	R33Q, S262N	2b	2022-10-13	SIAT1	80	160	160	160	160	80	80	80	160	40
A/Soria/213/2022	R33Q, S262N	2b	2022-10-13	SIAT1	80	160	320	320	320	80	160	160	320	40
A/Salamanca/198/2022	R33Q, S262N	2b	2022-10-13	SIAT1	80	160	320	320	320	80	160	80	320	80
A/Salamanca/196/2022	R33Q, S262N	2b	2022-10-13	SIAT1	80	160	320	320	320	80	320	80	320	80
A/Switzerland/18694/2022	R33Q, S262N	2b	2022-11-18	MDCK1/SIAT1	80	160	320	320	320	80	160	80	320	40
A/Palencia/118/2022	R33Q, N94S, S262N	2b	2022-10-13	SIAT1	80	160	320	320	320	80	160	80	320	40
A/Switzerland/39985/2022	R33Q, N81D, A163X, S262N	2b	2022-11-21	MDCK1/SIAT1	80	80	320	320	320	80	80	80	320	40
A/Switzerland/07426/2022	T135A(-cho), S262N	2b	2022-11-17	SIAT1/SIAT1	80	160	320	320	320	80	80	80	160	40
A/Ireland/73304/2022	T135A(-cho), S262N	2b	2022-11-23	SIAT1	80	160	320	320	320	80	160	80	160	40
A/Ireland/74535/2022	T128A(-cho), T135A(-cho), S262N	2b	2022-11-28	SIAT2	80	160	160	160	160	80	80	80	160	40
A/Lithuania/48774/2022		2a.1	2022-11-24	SIAT1	40	40	80	320	640	160	160	320	640	320
A/Burgos/82/2022	T135A(-cho), T167S	2a.1	2022-10-13	SIAT1	40	160	40	320	320	80	80	320	640	320
A/Switzerland/54601/2022		2a.1b	2022-11-01	MDCK1/SIAT1	<40	40	40	160	160	40	80	160	320	80
A/Ireland/74250/2022		2a.1b	2022-11-27	SIAT2	40	80	80	320	320	80	160	320	640	320
A/Ireland/74511/2022		2a.1b	2022-11-29	SIAT2	40	80	80	320	320	80	160	320	640	320
A/Switzerland/76550/2022		2a.1b	2022-12-05	SIAT1/SIAT1	40	40	80	320	320	80	160	320	640	160
A/Switzerland/01284/2022		2a.1b	2022-12-05	SIAT1/SIAT1	40	80	80	640	640	160	320	320	1280	320
A/Switzerland/89053/2022		2a.1b	2022-12-06	SIAT1/SIAT1	40	80	80	320	320	80	160	320	640	320
A/Switzerland/12082/2022	R92K	2a.1b	2022-12-08	SIAT1/SIAT1	<40	40	80	160	320	40	80	160	320	160
A/Georgia/2369/2022	N290T	2a.1b	2022-11-24	SIAT1	40	160	80	320	640	80	160	320	640	320
A/Georgia/8/2022	N290T	2a.1b	not known	SIAT1	40	160	80	640	640	160	320	640	640	320
A/Georgia/4/2022	N290T	2a.1b	not known	SIAT1	40	80	160	640	640	80	320	640	1280	320
A/Switzerland/52849/2022	N91	2a.3a.1	2022-11-11	SIAT1/SIAT1	40	80	80	160	320	160	320	160	160	80
A/Switzerland/86247/2022	N91	2a.3a.1	2022-11-14	MDCK1/SIAT1	40	80	160	320	320	160	320	80	160	80
A/Switzerland/85876/2022	N91, V182X	2a.3a.1	2022-11-14	MDCK1/SIAT1	40	80	80	160	320	160	320	160	320	80

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-3. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera A/Camb 925256/20 SIAT F03/21 1a	A/Camb e0826360/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stock 5/21 SIAT F35/21 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 24873/21 SIAT F10/22 2a.3	A/Norway 24873/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 8720/2022 SIAT F24/22 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	640	160	<40	160	320	40	40	80	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	640	80	160	160	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	80	160	320	320	320	80	160	80	320	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	80	80	80	640	640	160	160	320	640	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	160	640	160	640	1280	160	320	640	1280	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	80	80	320	320	320	320	160	160	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	320	640	320	640	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	80	80	320	640	160	320	640	640	320
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	80	80	160	640	640	160	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	80	80	640	320	80	160	320	640	320
TEST VIRUSES														
A/Croatia/101024/2022	I242M	2b	2022-09-01	MDCKx/SIAT1	80	80	320	320	160	80	160	80	160	40
A/Norway/32641/2022	I224M	2b	2022-10-17	SIAT1	40	80	320	320	160	80	80	80	160	40
A/Castilla La Mancha/4112/2022	R33Q, S262N	2b	2022-10-15	SIAT1	80	160	320	320	320	40	80	80	160	40
A/Castilla La Mancha/4057/2022	R33Q, S262N	2b	2022-10-17	SIAT1	80	80	320	160	160	40	80	40	160	40
A/Castilla La Mancha/4107/2022	R33Q, S262N	2b	2022-10-17	SIAT2	40	80	320	160	160	40	80	80	160	40
A/Norway/33623/2022	R33Q, S262N	2b	2022-10-31	SIAT1	80	160	320	320	320	80	160	80	320	40
A/Norway/33536/2022	R33Q, S262N	2b	2022-11-01	SIAT1	40	80	160	160	160	40	80	40	160	<40
A/Castilla La Mancha/4542/2022	R33Q, S262N	2b	2022-11-24	SIAT1	40	80	160	160	160	80	40	40	80	<40
A/Castilla La Mancha/4541/2022	R33Q, S262N	2b	2022-11-24	SIAT1	40	80	160	160	160	80	80	80	160	40
A/Castilla La Mancha/4547/2022	R33Q, S262N	2b	2022-11-26	SIAT1	80	160	320	320	160	80	80	80	160	40
A/Switzerland/68410/2022	R33Q, S262N	2b	2022-12-13	SIAT1	40	80	160	160	160	40	80	40	160	40
A/Switzerland/56875/2022	R33Q, S262N	2b	2022-12-13	SIAT1	40	80	160	160	160	80	80	80	160	40
A/Switzerland/68971/2022	R33Q, N96K, S262N	2b	2022-12-13	SIAT1	40	160	160	160	160	80	80	80	160	40
A/Galicia/3991/2022	R33Q, S199P, S262N	2b	2022-10-16	SIAT1	40	80	160	160	160	40	80	40	160	<40
A/Hungary/73/2022	R33Q, S262N, A272T	2b	2022-11-28	MDCK1/SIAT1	80	80	160	160	160	80	80	40	160	40
A/Hungary/87/2022	R33Q, E41X, D101E, S262N, D291N	2b	2022-12-07	MDCK1/SIAT1	40	80	160	160	160	80	80	40	160	40
A/Hungary/88/2022	T135A(-cho), S262N	2b	2022-12-08	MDCK1/SIAT1	40	80	160	160	160	40	80	40	80	<40
A/Switzerland/12279/2022	T135A(-cho), S262N	2b	2022-12-09	SIAT1	80	160	160	160	160	80	160	80	160	40
A/Switzerland/28719/2022	T135A(-cho), S262N	2b	2022-12-19	SIAT1	80	160	320	160	160	80	160	80	160	40
A/Switzerland/68854/2022	T135A(-cho), S262N	2b	2022-12-23	SIAT1	40	80	160	160	160	80	80	40	80	40
A/Slovenia/11512/2022	T135A(-cho), S144N(+cho), S262N	2b	2022-12-19	MDCKx/SIAT1	40	160	160	160	160	80	80	80	160	40
A/Slovenia/11696/2022	T135A(-cho), S144N(+cho), S262N	2b	2022-12-29	SIATx/SIAT1	40	160	160	320	160	80	80	80	160	<40
A/Slovenia/11516/2022	T10K(-cho), T135A(-cho), S262N	2b	2022-12-19	SIATx/SIAT1	40	160	160	160	160	80	80	80	160	<40
A/Slovenia/11514/2022	T10K(-cho), T135A(-cho), S262N	2b	2022-12-19	SIATx/SIAT1	80	160	160	320	160	80	160	80	160	40
A/Slovenia/11622/2022	T10K(-cho), T135A(-cho), S262N	2b	2022-12-27	MDCKx/SIAT1	40	80	160	160	160	80	80	40	160	<40
A/Slovenia/11517/2022	T10K(-cho), V79I, T135A(-cho), S262N	2b	2022-12-20	MDCKx/SIAT1	80	160	160	160	160	80	80	80	160	40
A/Slovenia/42/2023	T10K(-cho), V79I, T135A(-cho), S262N	2b	2023-01-03	MDCKx/SIAT1	80	160	160	320	320	80	160	80	80	<40
A/Slovenia/11665/2022	T10K(-cho), V79I, T135A(-cho), Q210*, S262N	2b	2022-12-28	SIATx/SIAT1	160	320	320	640	320	80	160	80	320	40

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

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

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera A/Camb 92526/20 SIAT F03/21 1a	A/Camb e0826360/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stock 5/21 SIAT F35/21 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 24873/21 SIAT F10/22 2a.3	A/Norway 24873/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 8720/2022 SIAT F24/22 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	640	160	<40	160	320	40	40	80	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	640	80	160	160	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	80	160	320	320	320	80	160	80	320	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	80	80	80	640	640	160	160	320	640	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	160	640	160	640	1280	160	320	640	1280	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	80	80	320	320	320	320	160	160	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	320	640	320	640	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	80	80	320	640	160	320	640	640	320
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	80	80	160	640	640	160	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	80	80	640	320	80	160	320	640	320
TEST VIRUSES														
A/Norway/33317/2022		2a.1	2022-10-24	SIAT1	40	80	80	320	640	80	160	320	640	320
A/Norway/33060/2022		2a.1	2022-10-27	SIAT1	40	40	80	320	320	80	160	320	640	160
A/Norway/33371/2022	S144I	2a.1	2022-10-27	SIAT1	40	40	40	320	320	80	80	320	640	320
A/Norway/33404/2022	E50K, N94H, R299K	2a.1	2022-11-05	SIAT1	40	80	80	320	640	80	160	320	1280	320
A/Galicia/3994/2022		2a.1b	2022-10-17	SIAT1	<40	40	80	160	160	40	80	160	320	160
A/Norway/33402/2022		2a.1b	2022-10-31	SIAT1	<40	40	40	80	160	40	80	160	320	160
A/Hungary/69/2022		2a.1b	2022-11-11	MDCK1/SIAT1	40	160	80	320	640	80	160	320	640	320
A/Ireland/74222/2022		2a.1b	2022-11-27	SIAT1	<40	80	80	160	320	80	80	160	320	320
A/Hungary/85/2022		2a.1b	2022-12-02	MDCK1/SIAT1	40	80	80	160	320	80	160	320	640	320
A/Switzerland/28394/2022		2a.1b	2022-12-19	SIAT1	40	80	40	160	160	40	80	160	320	160
A/Ukraine/775/2022	T10M (-cho)	2a.1b	2022-12-21	SIAT1	40	80	80	160	320	80	80	320	640	640
A/Ukraine/773/2022	T10M (-cho)	2a.1b	2022-12-21	SIAT1	<40	40	40	160	160	40	80	160	320	160
A/Ukraine/779/2022	T10M (-cho)	2a.1b	2022-12-22	SIAT1	40	80	80	160	320	80	80	320	320	320
A/Ukraine/804/2022	T10M (-cho)	2a.1b	2022-12-26	SIAT1	<40	80	80	160	160	80	80	160	320	160
A/Ukraine/774/2022	G53S	2a.1b	2022-12-21	SIAT1	<40	40	40	160	160	80	80	160	320	160
A/Slovenia/11481/2022	N133D(-cho)	2a.1b	2022-12-19	SIATx/SIAT1	40	40	80	160	320	80	80	320	640	320
A/Hungary/68/2022	N165X(-cho)	2a.1b	2022-11-15	MDCK1/SIAT1	40	160	80	160	320	80	160	320	640	160
A/Croatia/111538/2022	S198T	2a.1b	2022-10-11	MDCKx/SIAT1	40	80	80	160	320	80	160	320	320	320
A/Hungary/75/2022	N290S	2a.1b	2022-11-28	MDCK1/SIAT1	40	40	80	160	160	80	80	160	640	160
A/Norway/32883/2022		2a.3a.1	2022-10-27	SIAT1	40	160	160	320	320	320	640	160	320	80
A/Switzerland/68546/2022		2a.3a.1	2022-12-13	SIAT1	40	80	80	160	160	160	320	80	160	80
A/Switzerland/28577/2022		2a.3a.1	2022-12-19	SIAT1	<40	80	80	160	160	160	320	80	160	80
A/Norway/32603/2022	V309X	2a.3a.1	2022-10-18	SIAT1	40	80	160	160	160	320	320	80	160	80
A/Norway/33475/2022	N63K(-cho), K238R	2a.3a.1	2022-10-27	SIAT1	40	80	80	160	160	160	320	80	160	40
A/Switzerland/68912/2022	E50, I223	2a.3b	2022-12-14	SIAT1	40	80	80	160	320	160	640	160	320	80
A/Norway/32026/2022	S9R, E50, N159K, I223	2a.3b	2022-09-29	SIAT1	<40	80	80	160	320	160	160	80	160	80

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

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

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre Post-infection ferret antisera									
					A/Canb 925256/20 SIAT F03/21 1a	A/Canb e082636O/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stockholm 5/21 SIAT F35/21 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 24873/21 SIAT F10/22 2a.3	A/Norway 24873/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 8720/2022 SIAT F24/22 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	640	80	<40	160	160	<40	<40	40	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	1280	40	160	320	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	40	80	320	320	160	80	80	80	160	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	40	80	80	640	640	80	160	320	320	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	320	160	320	640	160	320	320	640	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	40	80	160	320	320	320	80	160	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	320	640	320	640	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	80	80	160	320	80	160	640	640	160
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	40	80	80	320	640	80	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	40	40	320	320	80	160	320	640	320
TEST VIRUSES														
A/Norway/32842/2022		2b	2022-10-23	SIAT2	40	40	160	160	160	40	80	40	80	40
A/Israel/B1644/2022	T12M	2b	2022-12-18	P1/SIAT1	40	40	160	160	80	40	80	40	80	<40
A/Georgia/RUS200/2022	I242M	2b	2022-12-12	SIAT1	40	40	160	160	80	40	40	40	80	40
A/Romania/544194/2022	I242M	2b	2022-12-28	SIAT1/SIAT1	40	80	160	160	80	40	80	40	80	<40
A/Romania/544283/2023	I242M	2b	2023-01-02	SIAT1/SIAT1	<40	40	160	160	80	40	40	40	80	<40
A/Romania/544760/2023	I242M	2b	2023-01-10	SIAT1/SIAT1	<40	40	160	80	<40	40	40	40	80	<40
A/Romania/544753/2023	I242M	2b	2023-01-10	SIAT1/SIAT1	40	40	160	160	80	40	40	40	80	<40
A/Israel/R11447/2022	T24X, S124G(-cho), I242M	2b	2022-11-25	P1/SIAT1	40	40	160	160	160	40	40	80	80	40
A/Netherlands/01867/2022	K50I, D188G, I242M	2b	2022-12-21	Hck1/SIAT1	<40	40	80	80	<40	<40	40	40	40	<40
A/Milano/331/2022	I25V, I242M	2b	2022-11-29	SIAT2/SIAT1	40	40	160	160	160	40	80	80	80	<40
A/Netherlands/01476/2022	K50I, I242M	2b	2022-12-07	Hck1/SIAT1	40	40	160	160	80	40	80	40	80	<40
A/Netherlands/01475/2022	K50I, I242M	2b	2022-12-07	Hck1/SIAT1	<40	40	80	160	80	40	40	40	80	<40
A/Netherlands/01218/2022	R33Q, S262N	2b	2022-09-12	Hck1/SIAT1	40	40	160	160	80	40	40	40	80	<40
A/Catalonia/NSVH101923535/2022	R33Q, S262N	2b	2022-10-03	SIAT1/SIAT1	40	40	160	160	80	40	40	40	80	<40
A/Catalonia/NSVH161512277/2022	R33Q, S262N	2b	2022-10-04	SIAT1/SIAT1	40	40	160	80	80	40	40	40	80	<40
A/Catalonia/NSVH151194989/2022	R33Q, S262N	2b	2022-10-04	SIAT1/SIAT1	<40	40	160	80	80	40	40	40	80	<40
A/Catalonia/NSVH101934050/2022	R33Q, S262N	2b	2022-10-19	SIAT1/SIAT1	<40	40	160	80	80	<40	40	40	80	<40
A/Navarra/4550/2022	R33Q, S262N	2b	2022-11-25	SIAT2	40	80	320	160	160	40	80	40	80	40
A/England/106/2022	R33Q, S262N	2b	2022-10-24	SIAT1/SIAT1	40	80	160	160	160	40	80	40	160	<40
A/Baden-Wuttemberg/88/2022	R33Q, S262N	2b	2022-11-29	P2/SIAT1	40	80	160	160	80	40	80	40	80	<40
A/Lisboa/717/2022	R33Q, S262N	2b	2022-11-29	SIAT1/SIAT1	<40	80	160	<40	160	40	80	40	160	40
A/Lisboa/711/2022	R33Q, S262N	2b	2022-11-29	SIAT1/SIAT1	40	160	320	<40	160	80	160	80	160	40
A/Lisboa/723/2022	R33Q, S262N	2b	2022-11-30	SIAT1/SIAT1	<40	80	160	<40	80	40	80	40	80	<40
A/Lisboa/716/2022	R33Q, S262N	2b	2022-12-04	SIAT1/SIAT1	40	80	160	160	80	40	80	40	160	<40
A/Lisboa/714/2022	K27X, R33Q, S262N	2b	2022-11-29	SIAT1/SIAT1	<40	80	160	<40	80	40	80	40	80	<40
A/Belgium/G0010/2023	R33Q, D101E, S262N	2b	2022-12-19	C1/SIAT1	<40	40	80	160	80	40	40	40	80	<40
A/Belgium/S2699/2022	R33Q, D101E, S262N, P273S	2b	2022-12-18	C1/SIAT1	40	80	160	160	80	40	40	40	80	<40
A/Belgium/G0401/2022	T135A(-cho), S262N	2b	2022-12-19	C1/SIAT1	40	40	80	80	160	<40	<40	40	40	40
A/Romania/544197/2022	T135A(-cho), S262N	2b	2022-12-28	SIAT1/SIAT1	40	80	80	160	80	40	40	40	80	<40
A/Milano/397/2022	T135A(-cho), N190X, S262N	2b	2022-11-30	SIAT2/SIAT1	40	40	80	80	40	40	40	40	80	<40
A/Israel/B1398/2022	I25M, T135A(-cho), S262N	2b	2022-11-28	P1/SIAT1	40	80	80	160	80	40	40	40	80	<40

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-6. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre									
					Post-infection ferret antisera									
					A/Cambodia/925256/20 SIAT F03/21 1a	A/Cambodia/e0826360/20 Egg F10/21 1a	A/Thuringen/10/22 SIAT F36/22 2b	A/Stockholm/5/21 SIAT F35/21 2a	A/Darwin/9/21 Egg F39/21 2a	A/Norway/24873/21 SIAT F10/22 2a.3	A/Norway/24873/21 Egg F-11/22 2a.3	A/Poland/97/22 SIAT F39/22 2a.2	A/Slovenia/8720/2022 SIAT F24/22 2a.1	A/Catalonia/NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES														
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	640	80	<40	160	160	<40	<40	40	<40	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	1280	40	160	320	40	80	40	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	40	80	320	320	160	80	80	80	160	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	40	80	80	640	640	80	160	320	320	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	320	160	320	640	160	320	320	640	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	40	80	160	320	320	320	80	160	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	320	640	320	640	320	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	80	80	160	320	80	160	640	640	160
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	40	80	80	320	640	80	320	640	1280	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	40	40	320	320	80	160	320	640	320
TEST VIRUSES														
A/England/151/2022		2a.1	2022-09-14	MDCK1/SIAT1	<40	40	40	80	160	80	80	160	320	320
A/Netherlands/01232/2022	E50K, R299K	2a.1	2022-10-05	Hck1/SIAT1	<40	40	40	160	320	80	160	320	640	160
A/Norway/32860/2022		2a.1b	2022-10-21	SIAT2	<40	40	40	80	160	40	80	80	320	160
A/England/104/2022		2a.1b	2022-10-24	SIAT1/SIAT1	<40	40	40	80	160	40	80	80	160	80
A/Catalonia/NSVH151029260/2022		2a.1b	2022-11-08	SIAT1/SIAT1	<40	40	40	80	160	40	80	160	320	160
A/Rheinland-Pfalz/35/2022		2a.1b	2022-12-01	P1/SIAT1	<40	40	40	80	320	40	160	160	320	320
A/Thuringen/63/2022		2a.1b	2022-12-05	P1/SIAT1	<40	<40	40	80	80	40	80	160	320	80
A/Romania/544311/2022		2a.1b	2022-12-30	SIAT1/SIAT1	<40	40	40	80	160	40	80	80	160	160
A/Belgium/G0007/2023	V182A	2a.1b	2022-12-19	C1/SIAT1	<40	40	40	80	160	40	80	80	320	80
A/Belgium/G0405/2022	V182A	2a.1b	2022-12-19	C1/SIAT1	<40	40	40	80	160	40	40	80	320	160
A/Croatia/109105/2022	S198T	2a.1b	2022-10-03	MDCKx/SIAT2	<40	40	40	160	160	40	80	160	320	160
A/Georgia/T2/2022	N290T	2a.1b	2022-12-05	SIAT1	<40	40	40	80	80	40	40	160	160	80
A/Georgia/T11-4/2022	N290T	2a.1b	2022-12-12	SIAT1	<40	40	40	80	80	40	40	160	320	160
A/Georgia/T27-25/2022	N31S, N290T	2a.1b	2022-12-05	SIAT2	<40	40	80	160	320	40	80	160	320	320
A/Georgia/k-1153/2022	R33X, N290T	2a.1b	2022-12-19	SIAT1	<40	40	40	80	160	80	160	640	640	640
A/Georgia/K18-57/2022	G53D, N290T	2a.1b	2022-12-12	SIAT1	40	40	40	80	160	40	40	80	80	40
A/Georgia/K20-14/2022	P293L	2a.1b	2022-12-12	SIAT1	40	40	40	80	80	40	40	80	160	80
A/Netherlands/01248/2022		2a.3a	2022-10-14	Hck1/SIAT1	40	80	80	160	160	160	320	80	160	80
A/England/110/2022		2a.3a.1	2022-10-05	SIAT1/SIAT1	<40	80	80	80	160	160	160	80	80	80
A/England/103/2022		2a.3a.1	2022-10-06	SIAT1/SIAT1	<40	80	80	80	160	160	320	80	160	40
A/Israel/B1418/2022		2a.3a.1	2022-12-05	P1/SIAT1	<40	80	80	80	160	160	160	40	80	40
A/Israel/B1503/2022		2a.3a.1	2022-12-13	P1/SIAT1	40	40	40	80	160	80	160	40	80	40
A/Bremen/50/2022	S91N, N122D(-cho)	2a.3a.1	2022-11-24	P1/SIAT1	<40	40	40	40	80	80	160	40	80	40
A/Niedersachsen/105/2022	S91N, N122D(-cho)	2a.3a.1	2022-11-29	P1/SIAT1	<40	80	80	80	160	160	320	80	160	40
A/Mecklenburg-Vorpommern/88/2022	S91N, N122D(-cho)	2a.3a.1	2022-12-01	P1/SIAT1	<40	40	80	80	160	80	320	40	160	40
A/Belgium/G0055/2023	S91N, N122D(-cho)	2a.3a.1	2022-12-21	C1/SIAT1	<40	40	80	80	160	80	160	40	80	40
A/England/105/2022		2a.3b	2022-10-21	SIAT1/SIAT1	<40	40	40	80	160	80	160	80	160	40
A/Israel/R599/2023		2a.3b	2023-01-08	P1/SIAT1	<40	40	40	80	160	40	160	40	80	<40

Vaccine
NH 2021-22

Vaccine
SH 2022
NH 2022-23
SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-7. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history / Ferret number / Genetic group	Collection date	Passage history	Haemagglutination inhibition titre											
					Post-infection ferret antisera											
									NEW					NEW		
					A/Camb 925256/20 SIAT F03/21 1a	A/Camb e0826360/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stockholm 5/21 SIAT F35/21 2a	A/Stockholm 5/21 SIAT F01/23 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 24873/21 SIAT F10/22 2a.3	A/Norway 24873/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.2	A/Slov 8720/2022 SIAT F24/22 2a.1	A/Lille 50053/2022 SIAT F02/23 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES																
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	1280	80	<40	160	160	160	<40	<40	40	<40	80	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	1280	40	160	80	320	40	80	40	160	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	40	80	320	320	80	160	80	80	80	160	160	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	40	80	80	640	640	640	80	160	320	320	320	80
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	320	160	320	320	640	160	320	320	640	320	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	40	80	160	160	320	320	320	80	160	160	80
A/Norway/24873/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	320	640	640	320	1280	320	640	640	160
A/Poland/97/2022	P3S, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	80	80	160	160	320	80	160	1280	640	1280	160
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	40	80	80	320	640	640	80	320	640	640	640	640
A/Lille/50053/2022	T135A(-cho), T167S, N190S	2a.1	2022-09-06	MDCK1/SIAT3	ND	ND	ND	ND	320	ND	ND	ND	ND	ND	2560	ND
A/CataloniaNSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	40	40	320	320	320	80	160	320	640	640	320
TEST VIRUSES																
A/Bolzano/46/2022	T135A(-cho), S262N	2b	2022-12-05	SIAT2/SIAT2	40	80	160	160	40	160	40	80	40	80	320	<40
A/Palermo/6/2022	T135A(-cho), S262N	2b	2022-12-06	SIAT3/SIAT2	40	80	160	160	40	80	40	40	40	80	320	<40
A/Netherlands/11980/2022		2a.1b	2022-12-22	MDCK-MIX2/SIAT1	<40	40	40	80	80	160	40	80	160	320	320	160
A/Netherlands/11968/2022	A272V	2a.1b	2022-12-20	MDCK-MIX2/SIAT1	<40	80	80	160	160	160	40	80	160	320	320	160

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used
ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-8. Antigenic analysis of influenza A(H3N2) viruses by HI

Viruses	HA1 substitutions additional to those defining subclades of 3C.2a1b.2a	Passage history Ferret number Genetic group	Collection date	Passage history	Haemagglutination inhibition titre										
					Post-infection ferret antisera										
					A/Camb 925256/20 SIAT F03/21 1a	A/Camb e0826360/20 Egg F10/21 1a	A/Thuringen 10/22 SIAT F36/22 2b	A/Stockholm 5/21 SIAT F15/22 2a	A/Darwin 9/21 Egg F39/21 2a	A/Norway 2487/21 SIAT F10/22 2a	A/Norway 2487/21 Egg F11/22 2a.3	A/Poland 97/22 SIAT F39/22 2a.3	A/Slov 8720/2022 SIAT F24/22 2a.2	A/Lille 50053/2022 SIAT F02/23 2a.1	A/Catal NSVH-2067/22 SIAT F41/22 2a.1b
REFERENCE VIRUSES															
A/Cambodia/925256/2020		1a	2020-09-25	SIAT5	1280	160	<40	320	320	80	40	80	<40	160	<40
A/Cambodia/e0826360/2020		1a	2020-07-16	E5/E3	80	640	40	160	320	40	80	40	80	160	<40
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT2	40	160	320	320	160	80	160	80	160	320	40
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT3	80	80	80	640	640	80	320	320	320	320	160
A/Darwin/9/2021	D186N, D225G (egg)	2a	2021-04-17	E3/E4	80	640	320	640	1280	160	320	640	640	640	160
A/Norway/24873/2021		2a.3	2021-10-24	SIAT3	40	80	80	160	320	160	320	160	160	160	80
A/Norway/2487/2021	D225G (egg)	2a.3	2021-10-24	E3/E1	80	320	160	640	1280	320	1280	320	1280	640	160
A/Poland/97/2022	P33, I25V, S145N, R201K	2a.2	2022-05-09	SIAT2	40	160	80	640	640	320	320	1280	1280	1280	640
A/Slovenia/8720/2022		2a.1	2022-02-10	SIAT1/MDCK1/SIAT2	40	80	80	320	640	160	320	640	640	1280	640
A/Lille/50053/2022	T135A(-cho), T167S, N190S	2a.1	2022-09-06	MDCK1/SIAT3	40	160	40	320	320	80	160	320	640	640	640
A/Catalonia/NSVH161512067/2022		2a.1b	2022-09-14	SIAT1/SIAT3	40	40	80	160	320	80	160	320	640	640	640
TEST VIRUSES															
A/Albania/290586/2023		2b	2023-01-05	SIAT1	160	160	640	640	320	160	320	160	320	640	80
A/Valladolid/24/2022	R33Q, S262N	2b	2022-10-06	SIAT1/SIAT1	40	80	320	160	160	40	80	80	160	160	<40
A/Valladolid/22/2022	R33Q, S262N	2b	2022-10-06	SIAT1/SIAT1	80	160	320	320	320	80	160	160	160	320	80
A/Castilla La Mancha/3894/2022	R33Q, S262N	2b	2022-10-09	SIAT1	40	80	160	160	160	40	80	40	160	160	40
A/Valladolid/27/2022	R33Q, S262N	2b	2022-10-11	SIAT1/SIAT1	40	160	320	320	320	80	160	160	320	320	40
A/Valladolid/11/2022	R33Q, S262N	2b	2022-10-12	SIAT1/SIAT1	40	80	160	320	160	80	80	80	320	320	40
A/Burgos/29/2022	R33Q, S262N	2b	2022-11-01	SIAT1/SIAT1	40	160	320	320	320	80	80	80	320	320	80
A/Salamanca/33/2022	R33Q, S262N	2b	2022-11-02	SIAT1/SIAT1	80	160	320	320	320	80	160	80	320	640	80
A/Burgos/28/2022	R33Q, S262N	2b	2022-11-02	SIAT1/SIAT1	80	160	320	320	320	80	160	80	160	320	40
A/Ceuta/4232/2022	R33Q, S262N	2b	2022-11-08	SIAT1	40	320	320	320	320	80	160	80	160	160	40
A/Bretagne/55452/2022	R33Q, S262N	2b	2022-11-14	SIAT1	40	80	160	160	160	40	80	40	80	160	40
A/Avila/53/2022	R33Q, S262N	2b	2022-12-29	SIAT1/SIAT1	80	160	320	320	320	80	160	80	320	320	40
A/Bulgaria/509/2023	R33Q, S262N	2b	2023-01-16	SIAT1	40	640	640	320	640	160	160	320	320	640	160
A/Castilla La Mancha/4215/2022	R33Q, A212T, S262N	2b	2022-10-28	SIAT1	80	320	320	320	320	80	80	80	160	320	40
A/Castilla La Mancha/4128/2022	R33Q, T128A(-cho), S262N	2b	2022-10-21	SIAT1	80	160	320	160	320	40	160	80	160	160	40
A/Valladolid/31/2022	R33Q, N165X(-cho), S262N	2b	2022-10-09	SIAT1/SIAT1	40	80	160	160	160	40	40	40	80	160	<40
A/Albania/290567/2023	T135A(-cho), S262N	2b	2023-01-05	SIAT1	160	160	320	320	320	80	80	80	160	640	80
A/Bulgaria/664/2023	N6T, T135A(-cho), S262N	2b	2023-01-12	SIAT1	40	160	160	320	160	40	80	80	320	320	<40
A/Castilla La Mancha/3901/2022	T135A(-cho), T167S	2a.1	2022-10-07	SIAT1	40	80	<40	160	320	40	80	320	320	1280	320
A/Palencia/30/2022	T135A(-cho), T167S	2a.1	2022-10-25	SIAT1/SIAT1	<40	40	<40	80	320	40	80	160	320	1280	320
A/Salamanca/34/2022	T135A(-cho), T167S	2a.1	2022-11-02	SIAT1/SIAT1	80	80	40	160	320	40	80	320	640	1280	640
A/Burgos/4/2023	T135A(-cho), T167S	2a.1	2023-01-08	SIAT1/SIAT1	<40	40	<40	80	160	40	80	160	320	640	320
A/Valladolid/19/2022	T135A(-cho), S143T, T167S	2a.1	2022-10-05	SIAT1/SIAT1	40	80	<40	80	320	40	80	320	320	1280	320
A/Valladolid/32/2022	T135A(-cho), S143T, T167S	2a.1	2022-10-10	SIAT1/SIAT1	<40	40	<40	80	320	40	80	160	320	1280	320
A/Valladolid/12/2022	T135A(-cho), S143T, T167S	2a.1	2022-10-13	SIAT1/SIAT1	40	80	<40	80	320	40	80	160	320	1280	320
A/Burgos/5/2023	T135A(-cho), T167S, L244S	2a.1	2023-01-07	SIAT1/SIAT1	<40	160	40	160	320	40	80	320	640	640	320
A/Valladolid/21/2022		2a.1b	2022-10-07	SIAT1/SIAT1	80	80	160	160	640	80	160	320	1280	640	640
A/Aragon/4051/2022		2a.1b	2022-10-18	SIAT1	<40	40	40	160	160	40	80	160	320	640	160
A/Bretagne/55892/2022		2a.1b	2022-11-17	SIAT1	<40	80	80	80	160	40	80	160	320	640	160
A/Albania/290580/2023		2a.1b	2023-01-05	SIAT1	40	80	80	160	320	80	160	320	640	640	320
A/Valladolid/15/2023		2a.1b	2023-01-05	SIAT1/SIAT1	<40	80	40	160	320	40	160	320	640	640	320
A/Albania/290638/2023		2a.1b	2023-01-06	SIAT1	40	80	160	320	640	160	320	640	1280	1280	640
A/Burgos/8/2023		2a.1b	2023-01-09	SIAT1/SIAT1	<40	80	80	160	320	80	160	160	640	640	320
A/Castilla La Mancha/4044/2022	T130I	2a.1b	2022-10-12	SIAT1	<40	80	80	160	320	40	160	320	640	640	320
A/Albania/290633/2023	P103Q	2a.1b	2023-01-06	SIAT2	40	80	80	160	320	80	160	320	640	640	320
A/Segovia/233/2022	A106T	2a.1b	2022-10-08	SIAT1	<40	80	80	160	160	40	80	320	640	640	160
A/Navarra/4220/2022	A69V, S145N	2a.1b	2022-11-09	SIAT1	<40	40	<40	160	320	40	160	320	640	640	640
A/Valladolid/17/2023		2a.3a.1	2023-01-16	SIAT1/SIAT1	40	80	80	80	320	320	320	80	160	160	80
A/Brandenburg/15/2022		2a.3a.1		Ex/E2	80	320	320	640	640	320	1280	320	640	640	320

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023 NH 2023-24

< relates to the lowest dilution of antiserum used

ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 5-9. Antigenic analysis of influenza A(H3N2) viruses by HI - Summary

Viruses		Haemagglutination inhibition titre										
		Post-infection ferret antisera										
	Passage history	A/Camb 925256/20 SIAT	A/Camb e0826360/20 Egg	A/Thuringen 10/22 SIAT	A/Stockholm 5/21 SIAT	A/Darwin 9/21 Egg	A/Norway 24873/21 SIAT	A/Norway 24873/21 Egg	A/Poland 97/22 SIAT	A/Slov 8720/2022 SIAT	A/Lille 50053/2022 SIAT	A/Catal NSVH-2067/22 SIAT
	Ferret number	F03/21	F10/21	F36/22	F35/21	F39/21	F10/22	F11/22	F39/22	F24/22	F02/23	F41/22
	Genetic group	1a	1a	2b	2a	2a	2a.3	2a.3	2a.2	2a.1	2a.1	2a.1b
REFERENCE VIRUSES												
A/Cambodia/925256/2020	1a	1280	80	<40	160	160	<40	<40	40	<40	160	<40
A/Cambodia/e0826360/2020	1a	80	1280	40	160	320	40	80	40	160	160	<40
A/Thuringen/10/2022	2b	40	80	320	320	160	80	80	80	160	320	40
A/Stockholm/5/2021	2a	40	80	80	640	640	80	160	320	320	320	80
A/Darwin/9/2021	2a	80	320	160	320	640	160	320	320	640	640	160
A/Norway/24873/2021	2a.3	40	40	80	160	320	320	320	80	160	160	80
A/Norway/24873/2021	2a.3	80	320	160	320	640	320	1280	320	640	640	160
A/Poland/97/2022	2a.2	40	80	80	160	320	80	160	1280	640	1280	160
A/Slovenia/8720/2022	2a.1	40	80	80	320	640	80	320	640	640	1280	640
A/Lille/50053/2022	2a.1	40	160	40	320	320	80	160	320	640	2560	640
A/Catalonia/NSVH161512067/2022	2a.1b	40	40	40	320	320	80	160	320	640	640	320
TEST VIRUSES												
Number tested	2a.1	20	20	20	20	20	20	20	20	20	8	20
No with titre reduction ≤2-fold					6	5	5		9	18	6	20
%					*30.0*	*25.0*	*25.0*		*45.0*	*90.0*	*75.0*	*100.0*
No with titre reduction =4-fold			1	7	7	14	15	8	7	2	2	
%			*5.0*	*35.0*	*35.0*	*70.0*	*75.0*	*40.0*	*35.0*	*10.0*	*25.0*	
No with titre reduction ≥8-fold		20	19	13	7	1		12	4			
%		*100*	*95.0*	*65.0*	*35.0*	*5.0*		*60.0*	*20.0*			
Number tested	2a.1b	56	56	56	56	56	56	56	56	56	13	56
No with titre reduction ≤2-fold				3	13	9	10		17	30	1	46
%				*5.3*	*23.2*	*16.1*	*17.8*		*30.4*	*53.6*	*7.7*	*82.1*
No with titre reduction =4-fold			2	30	27	32	24	13	27	21	10	9
%			*5.6*	*53.6*	*48.2*	*57.1*	*42.9*	*23.2*	*48.2*	*37.5*	*76.9*	*16.1*
No with titre reduction ≥8-fold		56	54	23	16	15	22	43	12	5	2	1
%		*100.0*	*96.4*	*41.1*	*28.6*	*26.8*	*39.3*	*76.8*	*21.4*	*8.9*	*15.4*	*1.8*
Number tested	2a.3a	3	3	3	3	3	3	3	3	3	0	3
No with titre reduction ≤2-fold				2	2		3	3		1		2
%				*66.7*	*66.7*		*100.0*	*100.0*		*33.3*		*66.7*
No with titre reduction =4-fold				1	1	3				1		1
%				*33.3*	*33.3*	*100.0*				*33.3*		*33.3*
No with titre reduction ≥8-fold		3	3						3	1		
%		*100.0*	*100.0*						*100.0*	*33.3*		
Number tested	2a.3a.1	21	21	21	21	21	21	21	21	21	2	21
No with titre reduction ≤2-fold			1	7	6	1	17	12		1		4
%			*4.8*	*33.3*	*28.6*	*4.8*	*81.0*	*57.1*		*4.8*		*19.0*
No with titre reduction =4-fold			4	12	6	15	4	9	4	4	1	8
%			*19.0*	*57.1*	*28.6*	*71.4*	*19.0*	*42.9*	*19.0*	*19.0*	*50.0*	*38.1*
No with titre reduction ≥8-fold		21	16	2	9	5			17	16	1	9
%		*100.0*	*76.2*	*9.6*	*42.8*	*23.8*			*81.0*	*76.2*	*50.0*	*42.9*
Number tested	2a.3b	6	6	6	6	6	6	6	6	6	0	6
No with titre reduction ≤2-fold				2	2		4	3				2
%				*33.3*	*33.3*		*66.6*	*50.0*				*33.3*
No with titre reduction =4-fold				2	2	6	1	3	3	3		2
%				*33.3*	*33.3*	*100.0*	*16.7*	*50.0*	*50.0*	*50.0*		*33.3*
No with titre reduction ≥8-fold		6	6	2	2		1		3	3		2
%		*100.0*	*100.0*	*33.3*	*33.3*		*16.7*		*50.0*	*50.0*		*33.3*
Number tested	2b	103	103	103	103	103	103	103	103	103	20	103
No with titre reduction ≤2-fold			4	96	39	1	23			6		
%			*3.9*	*93.2*	*37.9*	*1.0*	*22.4*			*5.8*		
No with titre reduction =4-fold		1	24	7	53	33	40	17	2	18	4	1
%		*1.0*	*23.3*	*6.8*	*51.5*	*32.0*	*38.8*	*16.5*	*1.9*	*17.5*	*20.0*	*1.0*
No with titre reduction ≥8-fold		102	75		11	69	40	86	101	79	16	102
%		*99.0*	*72.8*		*10.6*	*67.0*	*38.8*	*83.5*	*98.1*	*76.7*	*80.0*	*99.0*
			Vaccine NH 2021-22			Vaccine SH 2022 NH 2022-23 SH 2023						

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.

Influenza B virus analyses

Influenza B/Victoria-lineage

All recently circulating B/Victoria-lineage viruses have fallen in genetic clade **V1A**, represented by **B/Brisbane/60/2008**, a former vaccine virus, but with additional **HA1** amino acid substitutions of **I117V** and **N129D** (e.g., **B/Ireland/3154/2016**). Viruses retaining full-length HAs had remained B/Brisbane/60/2008-like antigenically. However, three genetic groups (described below with amino acid substitutions/deletions relative to B/Brisbane/60/2008 indicated) containing deletions of HA gene codons emerged and displaced viruses with full-length HAs. Viruses in these groups were/are antigenically distinct from B/Brisbane/60/2008 and each other (as noted in the September 2018 characterisation report[4] and earlier ones), such that four antigenically distinguishable groups had been circulating:

- A group with double deletion of **HA1** residues **162** and **163** (subclade **V1A.1**) with amino acid substitutions of **D129G** and **I180V**, and **HA2 R151K** that spread worldwide and is represented by a previous vaccine virus, **B/Colorado/06/2017**. No detections of viruses in this group have been reported recently.
- A group with triple deletion of **HA1** residues **162** to **164** (subclade **V1A.2**) first detected in Asia, with amino acid substitutions of **I180T** and **K209N** that showed limited geographic spread, represented by **B/Hong Kong/269/2017**. No detections of viruses in this group have been reported recently.
- A group with triple deletion of **HA1** residues **162** to **164** (subclade **V1A.3**) first detected in Africa, with amino acid substitution **K136E** often with **G133R** that showed geographic spread and became dominant, represented by **B/Washington/02/2019** the vaccine virus first recommended for use in the 2020 southern hemisphere season and thereafter up to the 2021-2022 northern hemisphere season.

The phylogeny generated for the December report, was based on sequences from viruses with collection dates after 31 August 2022 that were submitted to GISAID in December 2022 (Figure 4a). All viruses were **V1A.3** subclade represented by **B/Washington/02/2019**, falling in the **V1A.3a** group characterized by **HA1 N150K**, **G184E**, **N197D** (resulting in loss of a glycosylation site) and **R279K**, with this group splitting into two subgroups designated **V1A.3a.1** (characterized by **HA1 V220M** and **P241Q** substitutions, with such viruses having been detected in China in the early months of 2022) and **V1A.3a.2** (characterized by **HA1 A127T**, **P144L** and **K203R**, often with additional substitutions, which has spread worldwide and is represented by the **B/Austria/1359417/2021** vaccine virus). While there had been sporadic detections of **V1A.3** subclade viruses in recent months, the vast majority of viruses had HAs that fell in the **V1A.3a.2** subgroup and viruses in this subgroup had continued to evolve leading to emergence of virus clusters defined by specific **HA1** amino acid substitutions, for example: (i) **T182A**, **D197E** and **T221A**; (ii) **E128K**, **A154E** and **S208P**; (iii) **E198G**; (iv) **D129G** and **D197E**; (v) **R80G** and **E184K**; (vi) **E183K;** and (vii) **H122Q** (seemingly restricted to viruses detected in China). Sequences derived from recently detected viruses in WHO European Region countries fell in virus clusters (i), (ii), (iii), (v) and (vi).

The phylogeny generated for this February 2023 report contains HA sequences from viruses with collection dates after 31 December 2022 that were submitted to GISAID up to 28 February 2023 (Figure 4b). The phylogeny has the same structure as that generated for the December report with all the recently detected viruses with HA sequences submitted to and released in GISAID falling in the **V1A.3a.2** subgroup. The great majority of these downloaded HA sequences have come from recently circulating viruses in the WHO European Region and fall in virus HA clusters (i) to (vi) identified above. Further genetic drift can be seen with cluster (i) viruses having additional **HA1 E184K** and **K272R** substitutions, cluster (iv) viruses having additional **HA1 V87A** and **E183K** substitutions and further virus HA clusters having emerged defined by **HA1** amino acid substitutions of either **V117I**, **E128K**, **A154T** and **K326R** or, in viruses from Montenegro, **A154T** with **A202V**.

The WHO Collaborating Centres for Influenza Research and Response have shown the **V.1A.3a.1** group viruses with additional HA1 substitutions to be antigenically distinct from one another. While relatively few B/Victoria-lineage viruses have been available for detailed antigenic characterization, those characterized in the 2021-2022 season were subgroup **V1A.3a.2** viruses which were recognised poorly by post-infection ferret antiserum raised against **B/Washington/02/2019**, the 2021-2022 northern hemisphere vaccine virus. However, the **V1A.3a.2** viruses were recognised well (with HI titres of at least 160 with the antiserum raised against the egg-propagated variant with **HA1 G141R** substitution) by antisera raised against **B/Austria/1359417/2021**, the recommended vaccine virus for 2022-2023 and 2023-2024 northern hemisphere and 2023 southern hemisphere influenza seasons [1, 3, 2].

[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

Fifty-six B/Victoria-lineage test viruses were characterized antigenically at the WIC since the December report (Tables 6-1 and 6-4) and results are summarised in Table 6-5. All test viruses were recognised poorly by antisera raised against former vaccine viruses, B/Colorado/06/2017 (**V1A.1**) and B/Washington/02/2019 (**V1A.3**), as was the case for antisera raised against **V1A.3** viruses that circulated in the Netherlands in 2021-2022. All **V1A.3a.2** test viruses were recognised well, within fourfold of homologous titres (the great majority within twofold), by three of four antisera raised against **V1A.3a.2** reference viruses, while that raised against the egg-propagated cultivar of B/Austria/1359417/2021 with **HA1 G141R** amino acid substitution recognised all but one of the test viruses at a titre of at least 320.

Influenza B/Yamagata-lineage

It is assumed that no B/Yamagata-lineage viruses have been detected after March 2020 as no sequences for such viruses with collection dates after this had been released in GISAID as of 28 February 2023. Figure 5 is repeated from the September 2021 report. All sequences fell in genetic clade **Y3**, 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 which was recommended for inclusion in quadrivalent vaccines for the 2022-2023 northern and 2023 southern hemisphere influenza seasons [1, 2]. Some sub-clustering of sequences, defined by specific amino acid substitutions (e.g., **HA1 N164K, K211R, D229N** or **D232N** [introducing a potential N-linked glycosylation site] sometimes with **R48K**), had occurred. As noted in previous characterization reports, 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.

A concerted effort by all NICs of GISRS is required to identify B/Yamagata-lineage viruses for detailed characterization to determine if there are any in circulation that are not live attenuated influenza vaccine (LAIV)-related.

In relation to the potential 'extinction' of circulating wild-type B/Yamagata-lineage viruses and the need to maintain use of a B/Yamagata-lineage component in quadrivalent influenza vaccines, notably so for LAIV where the attenuated B/Yamagata-lineage component could act as a reassortment partner with circulating wild-type B/Victoria-lineage viruses, vaccine recommendation was modified at the recent VCM related to the northern hemisphere 2023-2024 influenza season [3]. The primary recommendation was for production of trivalent vaccines containing A(H1N1)pdm09, A(H3N2) and B/Victoria-lineage components, with a B/Yamagata-lineage virus being recommended for use by manufacturers continuing to produce quadrivalent vaccines. Surveillance studies will be continued through WHO GISRS, with enhanced influenza type B lineage determination from all countries, to better determine if B/Yamagata-lineage 'extinction' has occurred.

Figure 4a. Phylogenetic comparison of B/Victoria-lineage HA genes (GISAID/WIC, Dec 2022)

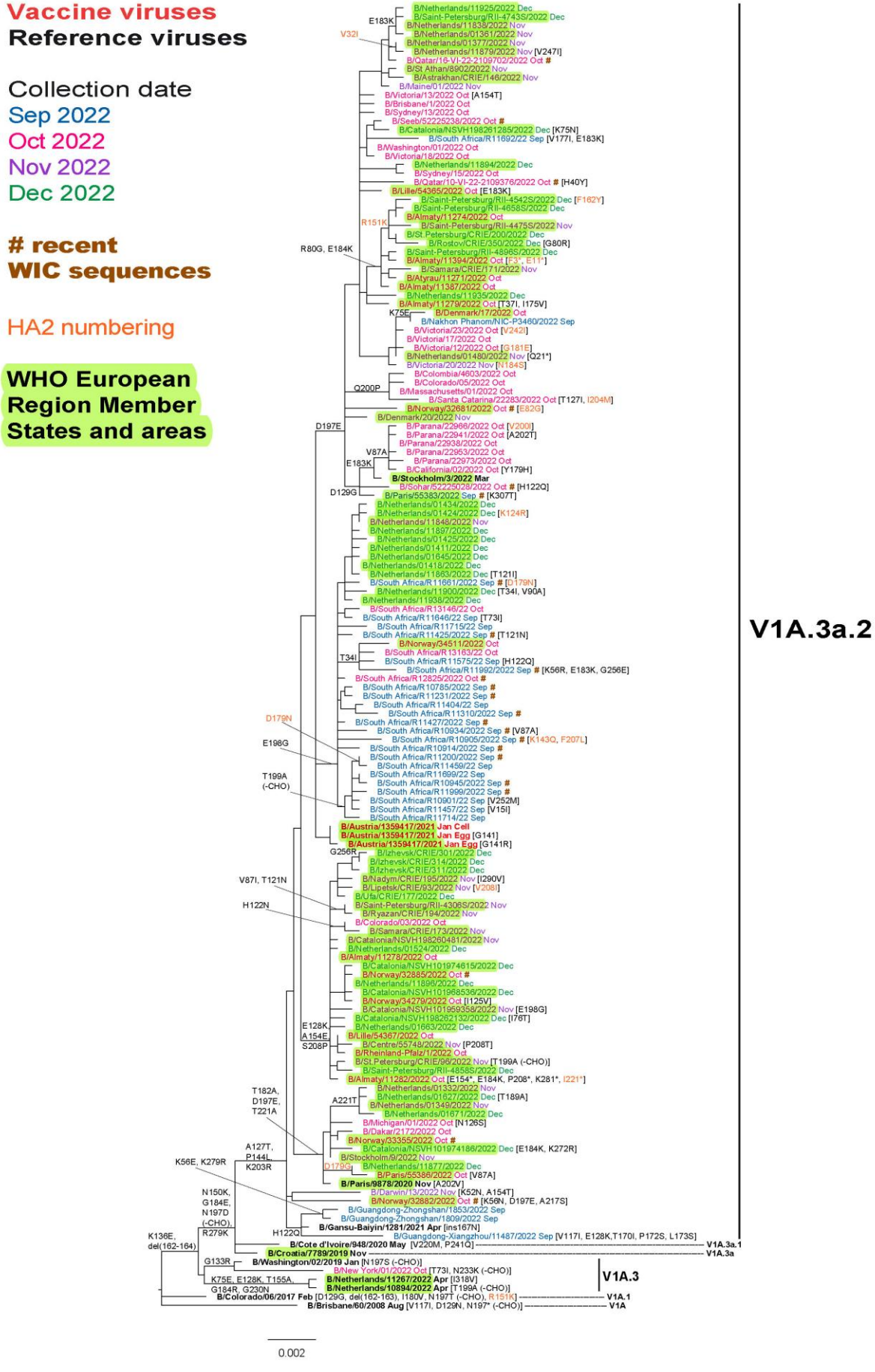


Figure 4b. Phylogenetic comparison of B/Victoria-lineage HA genes (GISAID/WIC, Feb 2023)

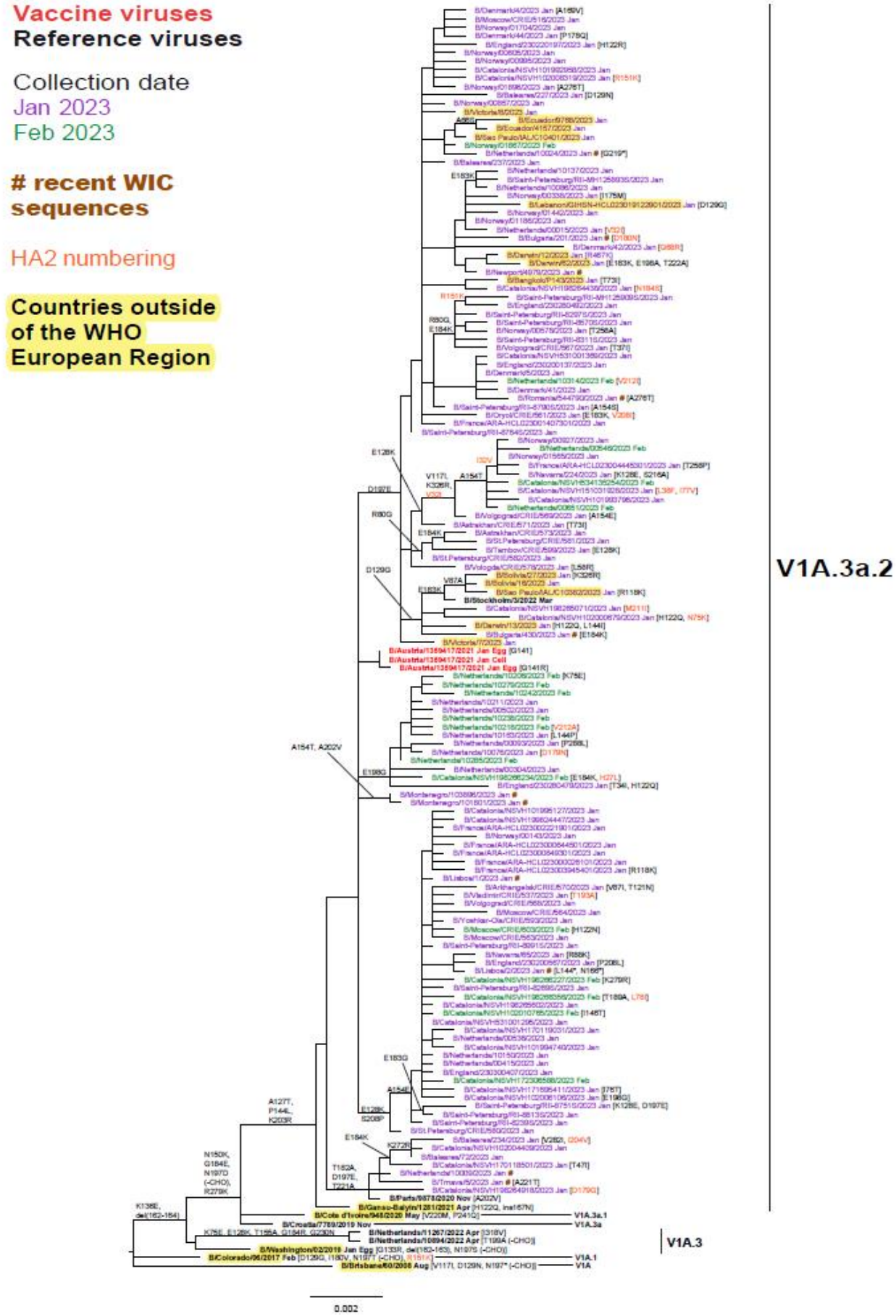


Table 6-1. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre: Post-infection ferret antiserum									
				B/Bris 60/08	B/Colorado 06/17	B/Wash'ton 02/19	B/Neth 11267/22	B/Neth 10894/22	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
			Passage history	Egg Sh 539, 540, 543, 544, 570, 571, 574[1]	Egg F44/18	Egg F20/20	MDCK F29/22	Egg F37/22	MDCK NIB F01/21	Egg G141 F15/21	Egg G141R F44/21		MDCK F28/22
			Genetic group	V1A	V1A.1	V1A.3	V1A.3	V1A.3	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2
REFERENCE VIRUSES													
B/Brisbane/60/2008		V1A	2008-08-04	E4/E4	2560	80	<10	160	<40	<40	<40	<40	<40
B/Colorado/06/2017		V1A.1	2017-02-05	E5/E2	1280	320	80	<10	160	40	<40	<40	<40
B/Washington/02/2019		V1A.3	2019-01-19	E3/E3	320	160	160	20	80	<40	<40	<40	<40
B/Netherlands/11267/2022	G184R	V1A.3	2022-04-14	MDCK-MIX/MDCK2	<40	160	<10	160	40	<40	<40	<40	<40
B/Netherlands/10894/2022	G184R, T199A (-cho), V318I	V1A.3	2022-04-02	E4(Am1AL3)	320	80	20	40	160	<40	<40	<40	<40
B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	SIAT1/MDCK4	320	40	<10	20	<10	1280	1280	320	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	E3/E5	640	20	<10	40	10	2560	1280	640	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141R)	V1A.3a.2	2021-01-09	E3/E5	320	40	<10	40	10	2560	1280	>5120	640
B/Stockholm/3/2022	D129G, E183K, D197E	V1A.3a.2	2022-03-22	SIAT1/MDCK2	320	40	<10	20	<10	1280	640	320	640
TEST VIRUSES													
B/Bishkek/013/2022		V1A.3a.2	2022-10-08	MDCK1/MDCK1	640	40	<10	20	<10	1280	640	320	640
B/Bishkek/014/2022		V1A.3a.2	2022-10-14	MDCK1/MDCK1	640	40	<10	20	<10	1280	1280	320	1280
B/Bishkek/015/2022		V1A.3a.2	2022-10-22	MDCK1/MDCK1	640	40	<10	20	<10	1280	1280	320	640
B/Bishkek/016/2022		V1A.3a.2	2022-10-23	MDCK1/MDCK1	640	40	<10	20	<10	2560	1280	640	640
B/Hungary/72/2022		V1A.3a.2	2022-11-22	MDCK1/MDCK1	320	40	<10	40	<10	1280	1280	640	640
B/Switzerland/19297/2022		V1A.3a.2	2022-11-28	MDCK1	640	80	<10	20	<10	1280	1280	320	640
B/Switzerland/12216/2022		V1A.3a.2	2022-12-09	MDCK1/MDCK1	640	80	<10	20	<10	1280	1280	320	640
B/Switzerland/69064/2022		V1A.3a.2	2022-12-13	MDCK1	640	80	<10	20	<10	1280	1280	320	640
B/Switzerland/28512/2022		V1A.3a.2	2022-12-19	MDCK1	640	80	<10	20	<10	1280	1280	640	640

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 6-2. 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 antiserum								
					B/Bris 60/08	B/Colorado 06/17	B/Wash'ton 02/19	B/Neth 11267/22	B/Neth 10894/22	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
		Passage history			Egg	Egg	Egg	MDCK	Egg	MDCK	Egg G141	Egg G141R	MDCK
		Ferret number			Sh 539, 540, 543, 544, 570, 571, 574[1]	F44/18	F20/20	F29/22	F37/22	NIB F01/21	F15/21	F44/21	F28/22
		Genetic group			V1A	V1A.1	V1A.3	V1A.3	V1A.3	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2
REFERENCE VIRUSES													
B/Brisbane/60/2008		V1A	2008-08-04	E4/E4	1280	160	40	<10	80	<40	<40	<40	<40
B/Colorado/06/2017		V1A.1	2017-02-05	E5/E2	1280	320	80	10	80	<40	<40	<40	<40
B/Washington/02/2019		V1A.3	2019-01-19	E3/E3	640	160	80	20	160	<40	<40	<40	<40
B/Netherlands/11267/2022	G184R	V1A.3	2022-04-14	MDCK-MIX/MDCK2	40	10	<10	160	10	<40	<40	<40	<40
B/Netherlands/10894/2022	G184R, T199A (-cho), V318I	V1A.3	2022-04-02	E4(Am1AL3)	320	40	40	40	80	<40	<40	<40	<40
B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	SIAT1/MDCK4	640	40	<10	40	<10	1280	1280	320	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	E3/E5	320	20	<10	40	<10	1280	1280	320	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141R)	V1A.3a.2	2021-01-09	E3/E5	320	40	10	40	<10	1280	1280	2560	640
B/Stockholm/3/2022	D129G, E183K, D197E	V1A.3a.2	2022-03-22	SIAT1/MDCK2	640	40	<10	40	<10	1280	1280	320	1280
TEST VIRUSES													
B/Norway/32412/2022		V1A.3a.2	2022-10-03	MDCK2	640	40	<10	40	<10	2560	1280	640	640
B/Norway/32681/2022		V1A.3a.2	2022-10-14	MDCK1	1280	80	<10	40	<10	1280	1280	640	1280
B/Catalonia/NSVH161512453/2022		V1A.3a.2	2022-10-18	SIAT1/MDCK1	640	40	<10	20	<10	1280	1280	320	1280
B/Croatia/114021/2022		V1A.3a.2	2022-10-22	MDCKx/MDCK1	640	20	<10	20	<10	1280	1280	640	640
B/Norway/32882/2022		V1A.3a.2	2022-10-25	MDCK1	640	40	<10	40	<10	1280	1280	320	1280
B/Norway/32885/2022		V1A.3a.2	2022-10-29	MDCK1	640	40	<10	40	<10	2560	1280	640	640
B/Croatia/115758/2022		V1A.3a.2	2022-11-02	MDCKx/MDCK2	640	40	<10	20	<10	1280	640	320	1280
B/Israel/B1292/2022		V1A.3a.2	2022-11-20	P1/MDCK1	640	20	<10	20	<10	1280	1280	640	640
B/Israel/B1406/2022		V1A.3a.2	2022-12-01	P1/MDCK1	640	40	<10	20	<10	1280	1280	640	1280
B/Israel/B1417/2022		V1A.3a.2	2022-12-05	P2/MDCK1	640	40	<10	20	<10	640	640	320	1280
B/Israel/B1513/2022		V1A.3a.2	2022-12-09	P1/MDCK1	640	20	<10	20	<10	1280	1280	320	640
B/Belgium/G0012/2023		V1A.3a.2	2022-12-15	C1/MDCK1	640	40	<10	20	<10	2560	1280	640	640
B/Belgium/S2625/2022		V1A.3a.2	2022-12-16	C1/MDCK1	640	20	<10	20	<10	1280	1280	640	640
B/Belgium/G0053/2023		V1A.3a.2	2022-12-19	C1/MDCK1	640	40	<10	20	<10	1280	1280	320	1280
B/Belgium/G0404/2022		V1A.3a.2	2022-12-19	C1/MDCK1	640	80	<10	20	<10	1280	1280	640	1280
B/Belgium/G0403/2022		V1A.3a.2	2022-12-19	C1/MDCK1	640	40	<10	20	<10	640	640	320	640
B/Belgium/S0030/2023		V1A.3a.2	2022-12-21	C1/MDCK1	640	40	<10	20	<10	1280	640	320	1280
B/Israel/R13022/2022		V1A.3a.2	2022-12-25	P1/MDCK1	640	40	<10	20	<10	1280	1280	640	1280
B/Romania/543990/2022		V1A.3a.2	2022-12-26	SIAT1/MDCK1	640	20	<10	20	<10	1280	640	320	640
							Vaccine NH 2021-22				Vaccine SH 2022 NH 2022-23 SH 2023		

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

Table 6-3. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre									
				Post-infection ferret antiserum									
				B/Bris 60/08	B/Colorado 06/17	B/Wash'ton 02/19	B/Neth 11267/22	B/Neth 10894/22	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
			Passage history	Egg	Egg	Egg	MDCK	Egg	MDCK	Egg G141	Egg G141R	F44/21	MDCK
			Ferret number	Sh 539, 540, 543, 544, 570, 571, 574[1]	F44/18	F20/20	F29/22	F37/22	NIB F01/21	F15/21	F44/21	F28/22	
			Genetic group	V1A	V1A.1	V1A.3	V1A.3	V1A.3	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2
REFERENCE VIRUSES													
B/Brisbane/60/2008		V1A	2008-08-04	E4/E4	2560	160	40	<10	80	<40	<40	<40	<40
B/Colorado/06/2017		V1A.1	2017-02-05	E5/E2	1280	320	80	<10	160	<40	<40	<40	<40
B/Washington/02/2019		V1A.3	2019-01-19	E3/E3	640	160	160	40	160	<40	<40	<40	<40
B/Netherlands/11267/2022	G184R	V1A.3	2022-04-14	MDCK-MIX/MDCK2	40	20	<20	160	<10	<40	<40	<40	<40
B/Netherlands/10894/2022	G184R, T199A (-cho), V318I	V1A.3	2022-04-02	E4/E1	640	80	40	80	160	<40	<40	<40	<40
B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	SIAT1/MDCK4	640	40	<20	20	<10	1280	1280	640	1280
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141)	V1A.3a.2	2021-01-09	E3/E5	640	40	<20	40	<10	2560	1280	640	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141R)	V1A.3a.2	2021-01-09	E3/E5	320	20	<20	20	<10	1280	640	2560	640
B/Stockholm/3/2022	D129G, E183K, D197E	V1A.3a.2	2022-03-22	SIAT1/MDCK2	640	40	<20	20	<10	1280	1280	320	1280
TEST VIRUSES													
B/Netherlands/01229/2022		V1A.3a.2	2022-10-02	hCK1/MDCK1	640	40	<20	20	<10	1280	640	320	640
B/Berlin/7/2022		V1A.3a.2	2022-11-09	P1/MDCK1	1280	40	<20	20	<10	1280	1280	320	1280
B/Lisboa/3/2022		V1A.3a.2	2022-11-19	MDCK1/MDCK1	640	40	<20	20	<10	640	640	320	640
B/Lisboa/2/2022		V1A.3a.2	2022-11-22	MDCK1/MDCK1	640	20	<20	20	<10	1280	1280	640	640
B/Lisboa/4/2022		V1A.3a.2	2022-12-13	MDCK1/MDCK1	640	40	<20	20	<10	2560	1280	640	640
B/Netherlands/11975/2022		V1A.3a.2	2022-12-20	MDCK-MIX2/MDCK1	320	20	<20	10	<10	1280	640	320	320
B/Netherlands/11970/2022		V1A.3a.2	2022-12-20	MDCK-MIX2/MDCK1	640	40	<20	20	<10	640	1280	320	640
B/Netherlands/11987/2022		V1A.3a.2	2022-12-21	MDCK-MIX2/MDCK1	320	20	<20	20	<10	1280	640	320	640
B/Netherlands/11994/2022		V1A.3a.2	2022-12-23	MDCK-MIX2/MDCK1	640	40	<20	20	<10	1280	1280	320	1280
B/Netherlands/12140/2022		V1A.3a.2	2022-12-27	MDCK-MIX2/MDCK1	640	40	<20	20	<10	1280	640	320	1280
B/Lisboa/11/2022		V1A.3a.2	2022-12-30	MDCK1/MDCK1	640	20	<20	10	<10	640	640	320	1280
B/Netherlands/10009/2023		V1A.3a.2	2023-01-02	MDCK-MIX2/MDCK1	640	40	<20	20	<10	1280	1280	320	1280
B/Lisboa/1/2023		V1A.3a.2	2023-01-04	MDCK1/MDCK1	320	20	<20	10	<10	1280	640	320	320
B/Netherlands/10024/2023		V1A.3a.2	2023-01-04	MDCK-MIX2/MDCK1	640	40	<20	20	<10	1280	1280	640	1280
B/Lisboa/2/2023		V1A.3a.2	2023-01-09	MDCK1/MDCK1	320	<10	<20	<10	<10	640	640	320	320

Vaccine NH 2021-22

Vaccine SH 2022 NH 2022-23 SH 2023

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND = Not Done

Table 6-4. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre									
				Post-infection ferret antiserum									
				B/Bris 60/08	B/Colorado 06/17	B/Wash'ton 02/19	B/Neth 11267/22	B/Neth 10894/22	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
		Passage history		Egg Sh 539, 540, 543, 544, 570, 571, 574[1]	Egg	Egg	MDCK	Egg	MDCK	Egg G141	Egg G141R	MDCK
		Ferret number		V1A	F44/18	F20/20	F29/22	F37/22	NIB F01/21	F15/21	F44/21	F28/22
		Genetic group		V1A	V1A.1	V1A.3	V1A.3	V1A.3	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2
REFERENCE VIRUSES												
B/Brisbane/60/2008		V1A	E4/E4	2560	160	40	<10	80	<40	<40	<40	<40
B/Colorado/06/2017		V1A.1	E5/E2	640	320	40	<10	80	<40	<40	<40	<40
B/Washington/02/2019		V1A.3	E3/E3	640	160	80	10	160	<40	<40	<40	<40
B/Netherlands/11267/2022	G184R	V1A.3	MDCK-MIX/MDCK2	<40	10	<20	80	<10	<40	<40	<40	<40
B/Netherlands/10894/2022	G184R, T199A (-cho), V318I	V1A.3	E4/E1	320	40	<20	40	160	<40	<40	<40	<40
B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2	SIAT1/MDCK4	320	20	<20	<10	<10	1280	1280	320	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141)	V1A.3a.2	E3/E4	320	20	<20	40	<10	1280	1280	640	640
B/Austria/1359417/2021 Isolate 2	A127T, P144L, K302R (G141R)	V1A.3a.2	E3/E5	160	10	<20	20	<10	1280	640	2560	640
B/Stockholm/3/2022	D129G, E183K, D197E	V1A.3a.2	SIAT1/MDCK3	320	20	<20	<10	<10	1280	640	320	640
TEST VIRUSES												
B/Belgium/S1989/2022		V1A.3a.2	2022-09-30	C1/MDCK1	640	20	<20	<10	<10	1280	640	320	640
B/Belgium/G0240/2022		V1A.3a.2	2022-10-24	C1/MDCK1	640	<10	<20	<10	<10	1280	640	640	320
B/Belgium/G0306/2022		V1A.3a.2	2022-11-28	C1/MDCK1	640	40	<20	<10	<10	1280	1280	320	640
B/Belgium/G0304/2022		V1A.3a.2	2022-11-28	C1/MDCK1	320	<10	<20	<10	<10	1280	640	320	1280
B/Belgium/G0334/2022		V1A.3a.2	2022-12-05	C1/MDCK1	640	20	<20	<10	<10	1280	640	640	640
B/Belgium/G0370/2022		V1A.3a.2	2022-12-12	C1/MDCK1	640	20	<20	<10	<10	640	640	320	640
B/Belgium/S2629/2022		V1A.3a.2	2022-12-13	C1/MDCK1	640	40	<20	<10	<10	1280	1280	640	640
B/Belgium/G0384/2022		V1A.3a.2	2022-12-13	C1/MDCK1	640	40	<20	<10	<10	1280	1280	640	640
B/Salamanca/47/2022		V1A.3a.2	2022-12-30	SIAT1/SIAT1	640	80	<20	<10	<10	640	640	320	640
B/Leon/48/2022		V1A.3a.2	2022-12-30	SIAT1/SIAT1	640	80	<20	<10	<10	640	640	320	640
B/Slovenia/18/2023		V1A.3a.2	2023-01-03	MDCKx/MDCK1	320	20	<20	<10	<10	640	320	160	640
B/Segovia/3/2023		V1A.3a.2	2023-01-07	MDCK1/MDCK1	640	40	<20	<10	<10	1280	640	320	640
B/Belgium/S2470/2022		V1A.3a.2		C1/MDCK1	640	40	<20	<10	<10	640	640	320	640

Vaccine
NH 2021-22

Vaccine
SH 2022
NH 2022-23
SH 2023
NH 2023-24

< relates to the lowest dilution of antiserum used
[1] hyperimmune sheep serum; ND = Not Done

< 4-fold | 4-fold | 8-fold | > 8-fold | < not recognised by the antiserum | ≥ 160 (when homologous titre ≥ 2560) | ≥ 160 (no homologous titre)

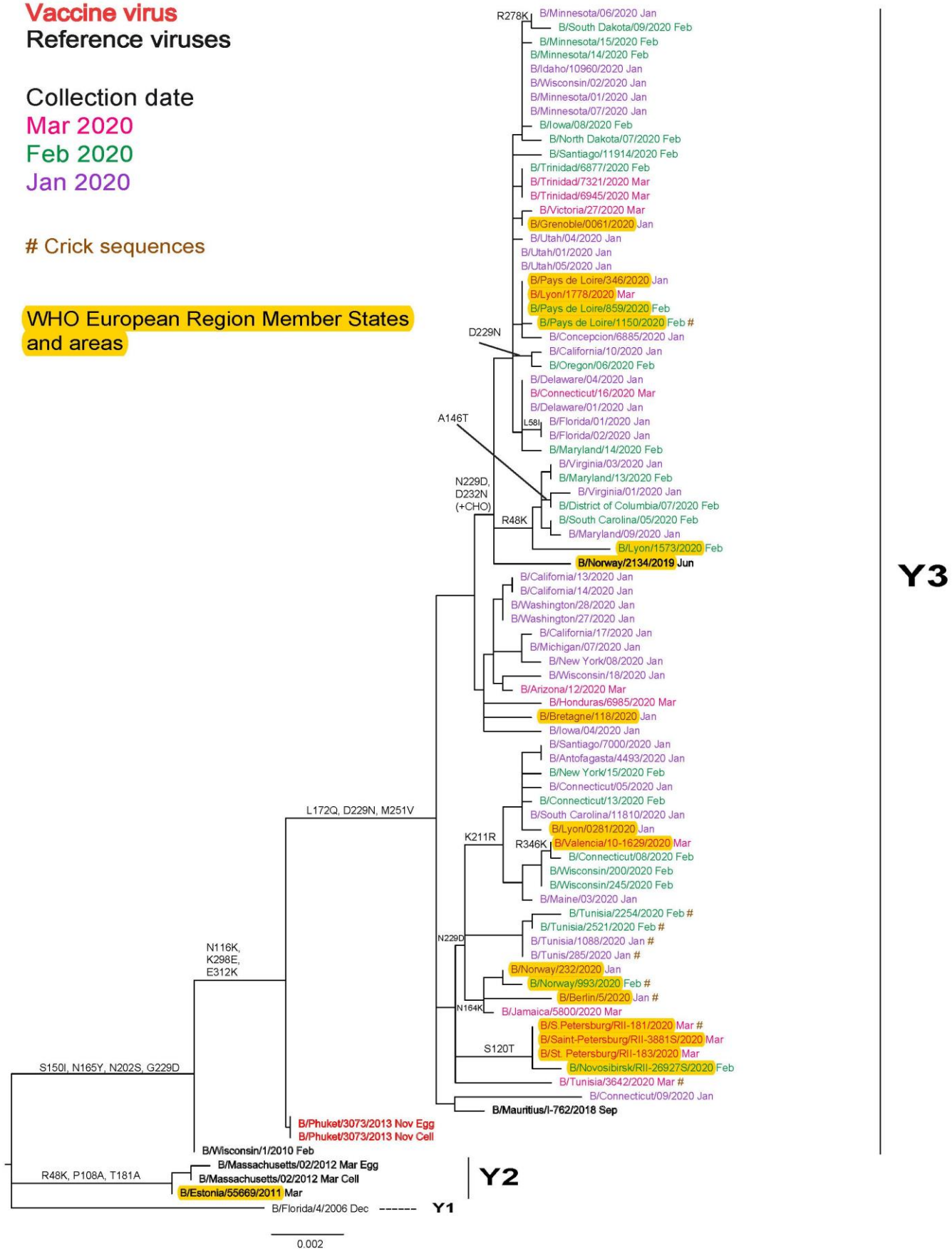
Table 6-5. Antigenic analysis of influenza B/Victoria-lineage viruses by HI - Summary

Viruses		B/Colorado 06/17	B/Wash'ton 02/19	B/Neth 11267/22	B/Neth 10894/22	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
	Passage history	Egg	Egg	MDCK	Egg	MDCK	Egg G141	Egg G141R	MDCK
	Ferret number	F44/18	F20/20	F29/22	F37/22	NIB F01/21	F15/21	F44/21	F28/22
	Genetic group	V1A.1	V1A.3	V1A.3	V1A.3	V1A.3a.2	V1A.3a.2	V1A.3a.2	V1A.3a.2
REFERENCE VIRUSES									
B/Brisbane/60/2008	V1A	160	40	<10	80	<40	<40	<40	<40
B/Colorado/06/2017	V1A.1	320	80	<10	160	<40	<40	<40	<40
B/Washington/02/2019	V1A.3	160	160	40	160	<40	<40	<40	<40
B/Netherlands/11267/2022	V1A.3	20	<20	160	<10	<40	<40	<40	<40
B/Netherlands/10894/2022	V1A.3	80	40	80	160	<40	<40	<40	<40
B/Austria/1359417/2021	V1A.3a.2	40	<20	20	<10	1280	1280	640	1280
B/Austria/1359417/2021 Isolate 2	V1A.3a.2	40	<20	40	<10	2560	1280	640	640
B/Austria/1359417/2021 Isolate 2	V1A.3a.2	20	<20	20	<10	1280	640	2560	640
B/Stockholm/3/2022	V1A.3a.2	40	<20	20	<10	1280	1280	320	1280
TEST VIRUSES									
Number tested	V1A.3a.2	56	56	56	56	56	56	56*	56
No with titre reduction ≤2-fold						56	55		53
%						*100.0*	*98.2*		*94.6*
No with titre reduction =4-fold		8		5			1	17	3
%		*14.3*		*8.9*			*1.8*	*30.4*	*5.4*
No with titre reduction ≥8-fold		48	56	51	56			39	
%		*85.7*	*100.0*	*91.1*	*100.0*			*69.6*	
			Vaccine NH 2021-22				Vaccine SH 2022 NH 2022-23 SH 2023 NH 2023-24		

* All test viruses gave a titre of at least 160 with this antiserum.

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 5. Phylogenetic comparison of B/Yamagata-lineage HA genes (GISAID, September 2021)



Summaries of data submitted to TESSy

Genetic characterization

4 066 viruses detected over the course of the 2022-2023 season (weeks 40/2022-08/2023) were genetically characterized:

- Of 1 087 A(H1N1)pdm09 viruses, all but four belonged to clade 6B.1A.5a.2 with 515 represented by A/Norway/25089/2022 (**5a.2a.1**), 337 by A/Sydney/5/2021 (**5a.2a**) and 33 by A/Victoria/2570/2019 (**5a.2**), while 918 were allocated to the 'Subgroup Not Listed' category (in the guidance produced for TESSy reporting at the beginning of the 2022-2023 influenza season). Four were clade 6B.1A.5a.1 viruses represented by A/Guangdong-Maonan/SWL1536/2019.
- Of 1 789 A(H3N2) viruses, 1 692 belonged to the 'Bangladesh-like' clade (3C.2a1b.2a.2) with 1 065 represented by A/Bangladesh/4005/2020 (**2**), 114 represented by A/Darwin/9/2021 (**2a**) and 513 represented by A/Slovenia/8720/2022 (**2a.1**). Three viruses carried HA genes belonging to clade 3C.2a1b.1a represented by A/Denmark/3264/2019. Ninety-four viruses were allocated to the 'Subgroup Not Listed' category (in the guidance produced for TESSy reporting at the beginning of the 2022-2023 influenza season).
- Of 470 B/Victoria-lineage viruses, 229 were clade V1A.3a.2 represented by B/Austria/1359417/2021. The remaining 241 viruses were allocated to the 'Subgroup Not Listed' category (in the guidance produced for TESSy reporting at the beginning of the 2022-2023 influenza season).

Antiviral susceptibility

Up to week 08/2023, 2 690 viruses were assessed for susceptibility to neuraminidase (NA) inhibitors (NAIs): 1 030 A(H3), 832 A(H1)pdm09 and 352 B virus were assessed genotypically, and 261 A(H3), 166 A(H1)pdm09 and 48 B viruses were assessed phenotypically. Genotypically, two (H1)pdm09 viruses were found to carry the NA H275Y marker, indicative of highly reduced inhibition (HRI) by NAIs oseltamivir and peramivir, and phenotypically no viruses with reduced inhibition (RI) were identified.

Susceptibility to the PA inhibitor baloxavir marboxil (BXM) was assessed genotypically for 2 067 viruses: 1 150 A(H3), 561 A(H1)pdm09 and 356 B viruses. No markers of reduced susceptibility to BXM were detected.

At the WIC, 504 influenza viruses detected within the WHO EURO Region during the 2022-2023 season were assessed phenotypically against oseltamivir and zanamivir: 169 A(H1N1)pdm09, 278 A(H3N2) and 57 B/Victoria-lineage. All but one virus showed Normal Inhibition (NI) by both NAIs : A/Salamanca/637/2022 (A(H1N1)pdm09) showed HRI by oseltamivir and carried NA H275Y amino acid substitution. From sequencing of influenza-positive (types A and B viruses) clinical specimens a further A(H1N1)pdm09 virus (A/Salamanca/1221/2022) was found to have the NA H275Y HRI marker; virus isolation was not successful. No other NA sequences had markers associated with reduced susceptibility to NAIs.

For viruses where PA gene sequencing was successful, no markers associated with reduced inhibition by BXM were identified.

Animal influenza and zoonotic events

Influenza A(H7N9) virus

On 1 April 2013, the WHO Global Alert and Response System [4] reported that the China Health and Family Planning Commission had notified WHO of three cases of human infection with influenza A(H7N9). 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 caused some zoonoses, although few human cases were reported during the 2017-18 season [5]. Current risk assessments for influenza at the human-animal interface can be found on WHO's website https://www.who.int/teams/global-influenza-programme/avian-influenza/monthly-risk-assessment-summary (accessed 10 March 2023). The assessment published on 15 March 2023 contains a link to WHO information on A(H7N9) viruses after there being no publicly available reports from animal health authorities in China or other countries on influenza A(H7N9) virus detections in animals for an increasing time [6]. On 01 June 2022 the Food and Agricultural Organization of the United Nations announced that it was discontinuing monthly A(H7N9) updates as there had been no notifications of avian infections since October 2020. The most recent human case was detected in mid-March 2019 [7]. 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 approved on 15 December 2022 and can be found on ECDC's website [8].

Influenza A(H5) virus

The most recent monthly risk assessment of influenza at the human-animal interface was published by WHO on 15 March 2023. Since the previous risk assessment on 26 January 2023, three cases of human infection with influenza A(H5NX) viruses were reported to WHO [6]. Cambodia reported two cases of human A(H5N1) infection in an 11-year-old girl and her father who both developed disease symptoms on 14 February 2023 following exposure to sick and dead poultry. While the father had mild influenza-like illness (ILI), the girl developed severe disease, was hospitalized, and died on 22 February. Eleven close contacts of the infected individuals were sampled and tested, all were negative for influenza and SARS-CoV-2. Virus sequencing showed that the A(H5N1) viruses from the cases were related to A(H5) genetic clade 2.3.2.1c viruses circulating in poultry in southeast Asia since 2014. China reported a case of A(H5N6) infection in a 53-year-old female who was hospitalized with severe pneumonia on 04 February. The woman had exposure to backyard poultry, but at the time of reporting (24 February), no indication was given of infection outcome and no further cases were suspected among family members.

The latest collaborative report from ECDC and the European Food Safety Authority (EFSA), reported 1 162 HPAI A(H5) detections between 10 September and 02 December 2022, 398 in poultry, 613 in wild birds and 151 in captive birds [8]. Detections occurred in 27 European countries but with a decrease in colony-breeding seabird species and an increase in the number of detections in waterfowl compared to earlier periods. It is suspected that waterfowl might be more involved than seabirds in the incursion of HPAI virus into poultry establishments. The viruses detected since the September 2022 report (clade 2.3.4.4b) have fallen into 11 genotypes, three of which circulated in summer months while eight represented emergent genotypes. Overall, the HPAI epidemic season in 2021-2022 is the largest so far observed in Europe with 2 520 outbreaks in poultry and 50 million birds dead/culled, 227 outbreaks in captive birds, and 3 867 detections in wild birds. The risk of human infection was assessed as low for the general population in EU/EEA countries, and low to medium for occupationally exposed persons.

According to reports compiled by the Food and Agricultural Organization of the United Nations (FAO) as of 23 February 2023, various HPAI subtypes continued to be detected in wild and/or domestic birds in Africa, Americas, Asia and Europe. Since 26 January 2023, a total of 1 131 HPAI outbreaks (33 H5Nx, 1 073 H5N1, five H5N2, one H5N5 and 19 HPAI not confirmed as H5) and four low pathogenic avian influenza (LPAI) outbreak had been reported [9].

HPAI A(H5) viruses have also been detected in wild mammal species in Europe and North America and on mink farms in Europe, with some viruses showing genetic markers of adaptation to replication in mammals.

Influenza A(H9N2) virus

Since the previous WHO risk assessment on 26 January 2023, two zoonotic cases of A(H9N2) infection in China had been reported to WHO [6]. The cases were picked up through ILI surveillance and involved a 6-year-old female who became symptomatic on 23 October 2022, and a 9-month-old female who became symptomatic on 15 November 2022. Both cases had been exposed to poultry, disease symptoms were mild and made complete recoveries. No evidence of human-to-human transmission was found. Avian influenza A(H9N2) viruses are enzootic in poultry in Asia and increasingly reported in poultry in Africa.

Public Health England published an updated risk assessment for avian influenza A(H9N2) in August 2021 [10].

Other influenza zoonotic events

Since the previous WHO update on 26 January 2023 two cases of human infection with swine viruses were reported [6]. The cases of infection with influenza A(H1N1)v viruses were detected in China according to information received during the WHO Consultation and Information Meeting on the Composition of Influenza Virus Vaccines for Use in the 2023-2024 Northern Hemisphere Influenza Season held in February 2023 [11].

WHO Collaborating Centre reports

A description of results generated by the London WHO Collaborating Centre at the WIC and used at the February 2023 WHO VCM (20-23 February 2023 for seasonal influenza viruses), and previous ones, can be found at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports (accessed 20 March 2023).

Note on the figures

The phylogenetic trees were constructed using RAxML, drawn using FigTree, and annotated using Adobe Illustrator. Treemmer was used for down-sampling larger phylogenies to retain a representative tree topology of 150 sequences. 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(s) of sample collection. Sequences for many viruses from non-WHO Europe 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.

References[5]

1. Recommended composition of influenza virus vaccines for use in the 2022-2023 northern hemisphere influenza season. Weekly Epidemiological Record 25 March 2022, vol. 97(12):109-132. Geneva: World Health Organization; 2022 (https://apps.who.int/iris/bitstream/handle/10665/352602/WER9712-eng-fre.pdf).

2. Recommended composition of influenza virus vaccines for use in the 2023 southern hemisphere influenza season. Weekly Epidemiological Record 28 October 2022, vol. 97(43):537-566. Geneva: World Health Organization; 2022 (https://apps.who.int/iris/bitstream/handle/10665/363864/WER9743-eng-fre.pdf).

3. Recommended composition of influenza virus vaccines for use in the 2023-2024 northern hemisphere influenza season. Geneva: World Health Organization; 2023 (https://www.who.int/publications/m/item/recommended-composition-of-influenza-virus-vaccines-for-use-in-the-2023-2024-northern-hemisphere-influenza-season).

[5] All references accessed 20 March 2023.

4. Human infection with influenza A(H7N9) virus in China. 2013 – China, 1 April 2013 [website]. In: World Health Organization, disease outbreak news. Geneva: World Health Organization; 2013 (https://www.who.int/emergencies/disease-outbreak-news/item/2013_04_01-en).

5. Human infection with avian influenza A(H7N9) virus – China, 2017 – China, 26 October 2017 [website]. In: World Health Organization, disease outbreak news. Geneva: World Health Organization; 2017 (https://www.who.int/emergencies/disease-outbreak-news/item/26-october-2017-ah7n9-china-en).

6. Influenza at the human-animal interface. Summary and assessment, 27 January to 3 March 2023. Geneva: World Health Organization; 2023 (https://cdn.who.int/media/docs/default-source/global-influenza-programme/influenza-at-the-human-animal-interface-summary-and-assessment--from-27-january-to-3-march-2023.pdf).

7. Influenza at the human–animal interface. Summary and assessment, 13 February to 9 April 2019. Geneva: World Health Organization; 2019 (https://cdn.who.int/media/docs/default-source/influenza/human-animal-interface-risk-assessments/influenza_summary_ira_ha_interface_09_04_2019.pdf).

8. European Centre for Disease Prevention and Control, European Food Safety Authority, European Union Reference Laboratory for Avian Influenza. Avian influenza overview September - December 2022. Parma and Stockholm: EFSA, ECDC; 2022 (https://www.ecdc.europa.eu/sites/default/files/documents/Avian%20Influenza%20Overview%20Sep-Dec%202022.pdf).

9. Global AIV with zoonotic potential situation update, 23 February 2023. Rome: Food and Agricultural Organization of the United Nations; 2023 (https://mcusercontent.com/dc0b96ca6646c8eedf16a2216/files/f4d1a15d-8fb8-ece1-d4f1-450ff31b41c9/2023_02_23_Global_update_zoonotic_AI.pdf).

10. Public Health England. Guidance, risk assessment of avian influenza A(H9N2) update, 9 August 2021. UK.gov: PHE; 2021 (https://www.gov.uk/government/publications/risk-assessment-of-avian-influenza-ah9n2/risk-assessment-of-avian-influenza-ah9n2).

11. Genetic and antigenic characteristics of zoonotic influenza A viruses and development of candidate vaccine viruses for pandemic preparedness, February 2023. Geneva: World Health Organization; 2023 (https://cdn.who.int/media/docs/default-source/influenza/who-influenza-recommendations/vcm-northern-hemisphere-recommendation-2023-2024/20230224_zoonotic_recommendations.pdf).