

Country Report: Kazakhstan

Worldwide Influenza Centre, WHO CC for Reference and Research on Influenza
The Francis Crick Institute, 1 Midland Road, NW1 1AT

September 2023 to January 2024



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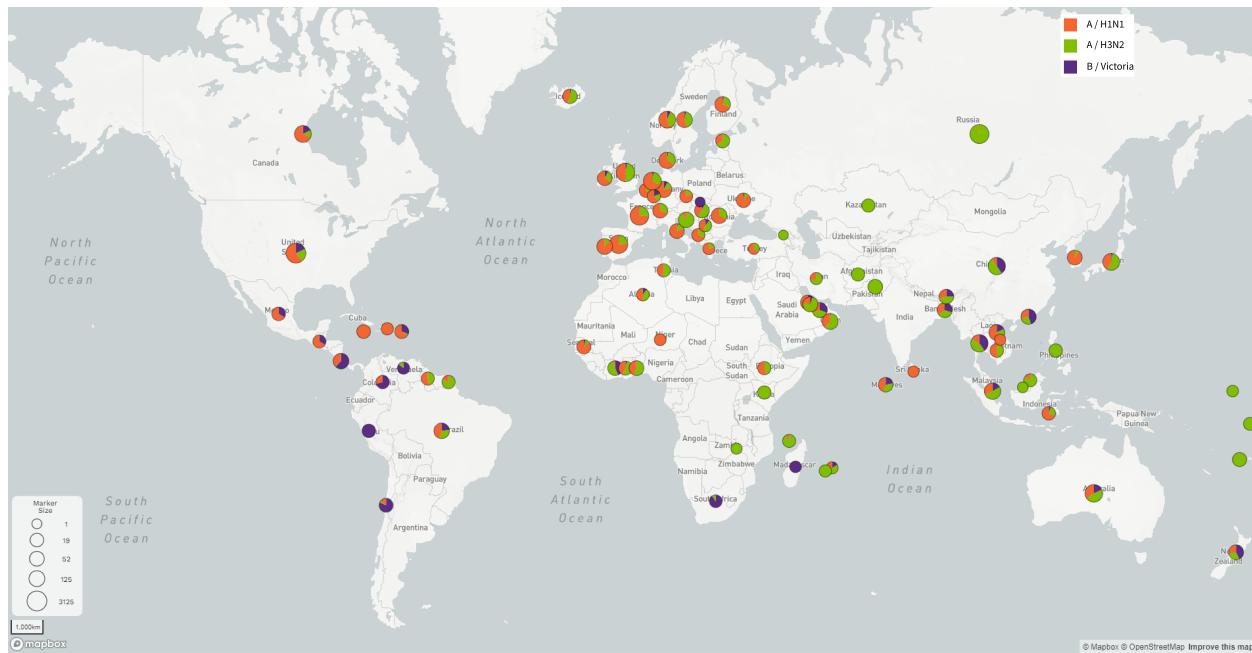
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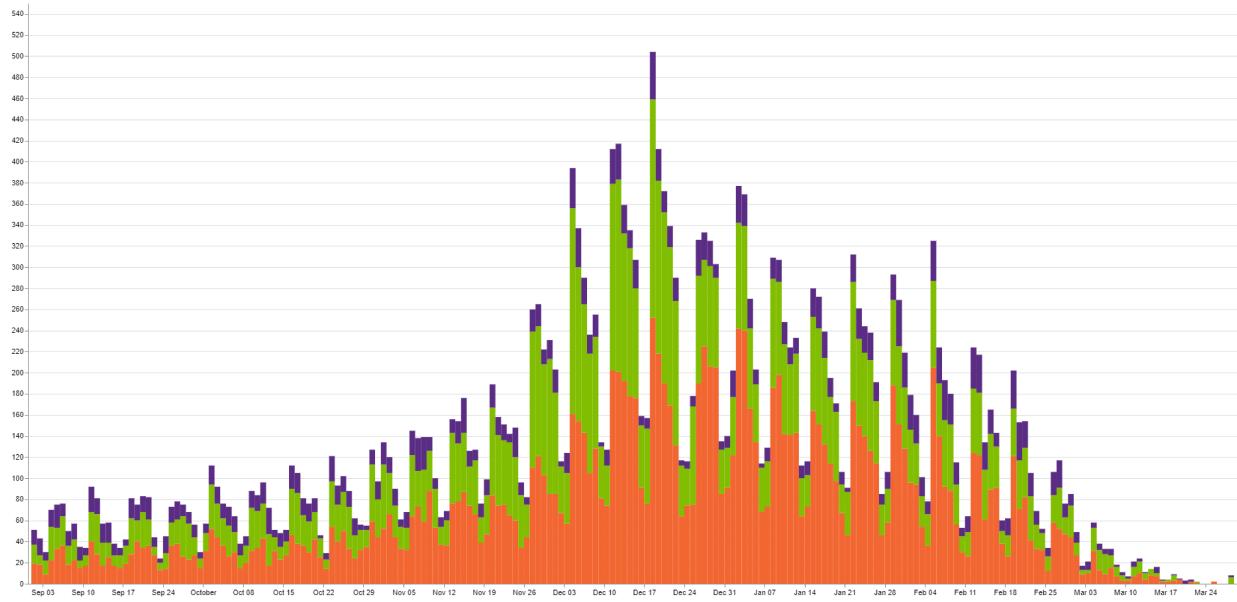
For more information about what we have observed over the last twelve months please see our reports for September 2023 and February 2024. All of our reports since 2003 are available at <https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports>

Influenza by type/subtype:

Geographical distribution of seasonal influenza viruses with collection dates from September 2023 through to February 2024 as deposited in GISAID, coloured by Type/subtype. Geographic markers scaled to detection proportions.

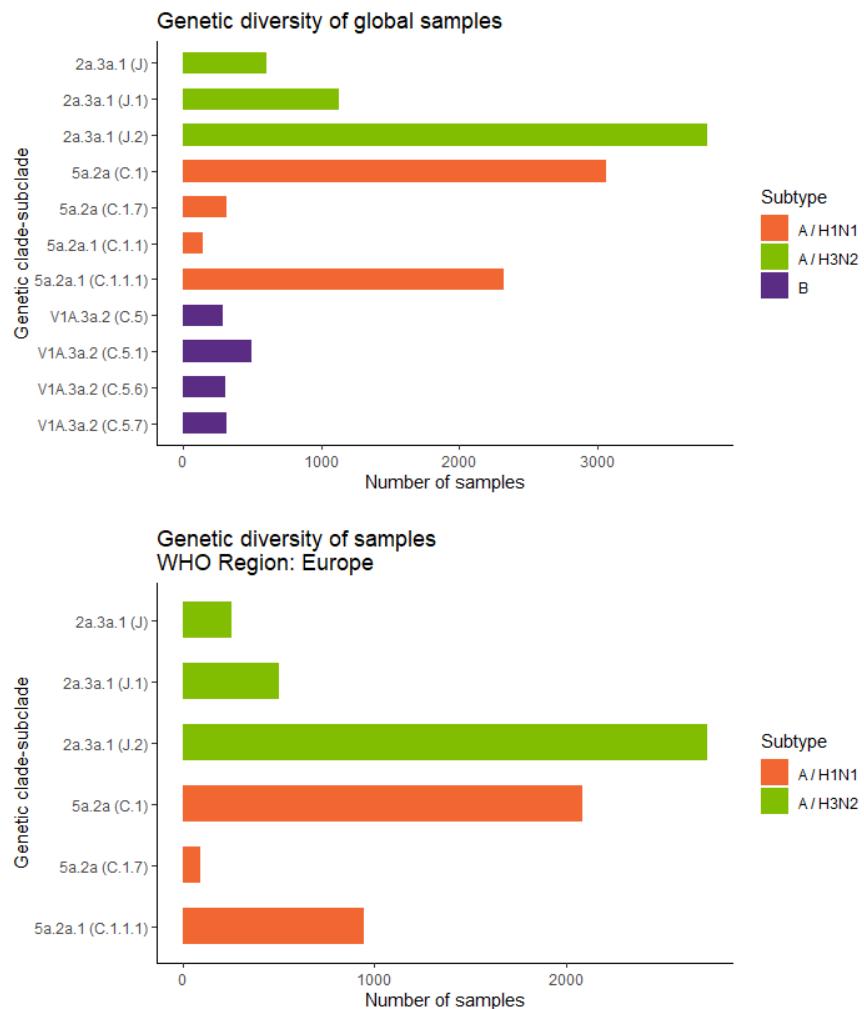


Globally, influenza detections reached a peak in December 2023 and have decreased since then until falling below the epidemic levels in March 2024. The relative proportions of A/H1N1, A/H3N2 and B/Victoria varied by geographic region with predominance of A/H1N1 in Europe and North and Central America and some predominance of A/H3N2 in Asia, Africa and Australia. Some countries in South America showed predominance of B/Victoria, as well as South Africa and Madagascar, as indicated by the different colours in the pie charts by country.



Genetic diversity:

Plots showing genetic diversity of A/H1N1, A/H3N2 and B/Victoria that underwent sequencing during the reporting period. A(global) B(WHO region)



Phylogenetic analyses: A/H1N1

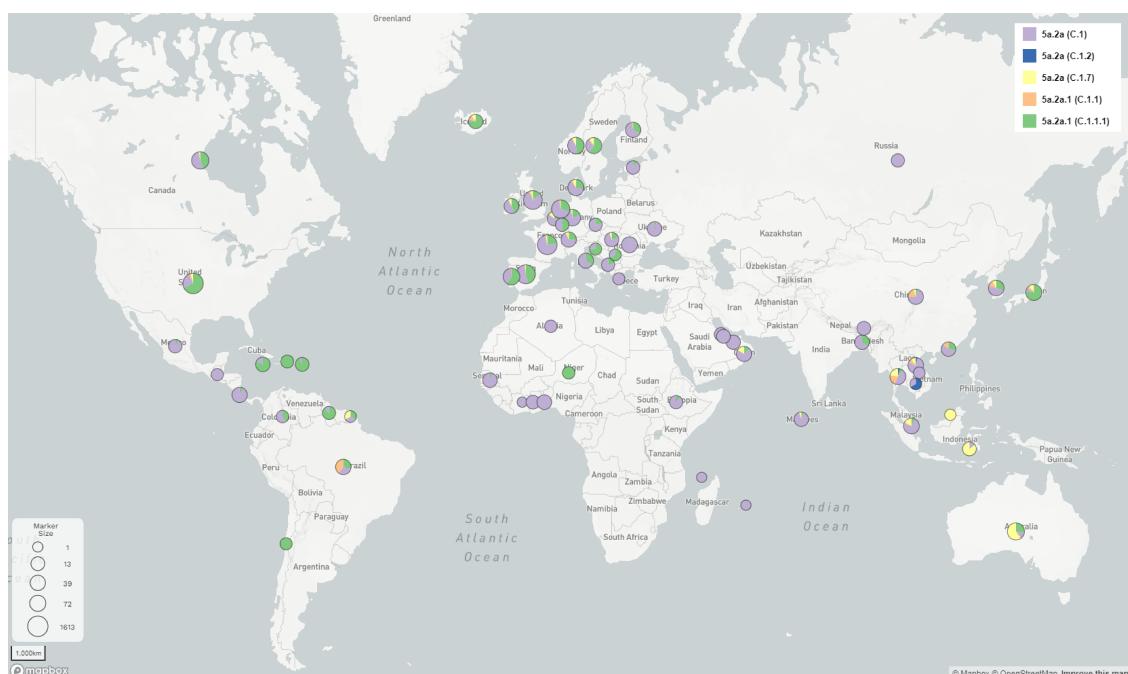
6B.1A.5a.2a and 6B.1A.5a.2a.1 clade viruses both continued to circulate with differing relative proportions depending on region, with a global predominance of 5a.2a viruses.

Within the 5a.2a viruses, characterised by substitutions K54Q, A186T, E224A, R259K and K308R, a major subclade C.1 defined by substitution I418V was observed, which split into two further subclades, one characterised by V47I with I96T in most sequences, and another subclade with substitution K169Q (no references assigned yet); the majority of H1pdm viruses sequenced in Europe, Africa and Asia belong to subclade C.1. A minor subclade C.1.7 with substitution I533V (no reference assigned yet), was observed with viruses predominating in New Zealand and Indonesia, and in minor proportions in Europe and Asia. Another minor subclade C.1.5 was detected in minor proportions in the Middle East, Australia and Madagascar.

Within the 5a.2a.1 viruses, characterised by substitutions P137S, K142R, D260E, T277A, E356D and N451H, there are two main groups of viruses: a major clade with T216A (C.1.1.1) represented by A/Victoria/4897/2022, predominating in the Americas, Japan, Niger and some countries in Europe, showing additional heterogeneity with a subclade characterised by R45K, another subclade with R113K and V427I and a third subclade with T120A ; and a minor subclade represented by A/Wisconsin/67/2022 (C.1.1), circulating in low proportions in Brazil, US, Eastern Europe and South East Asia.

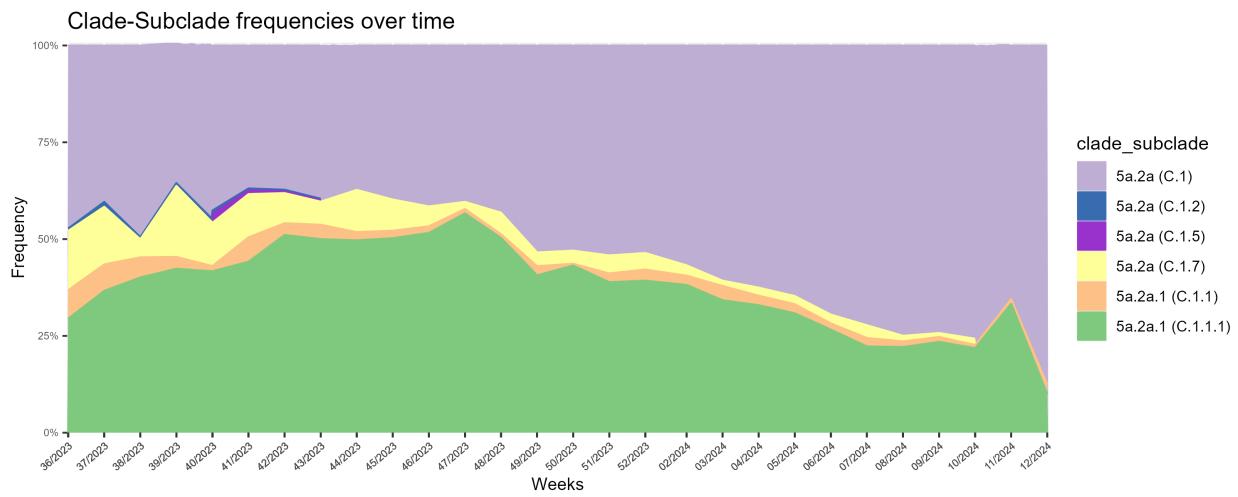
No A/H1N1 viruses from Kazakhstan were received. We include representative figures and a phylogenetic tree as a general overview of the season.

Global geographical distribution of influenza A/H1N1 genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade. Map prepared with Microreact. Geographic markers scaled to detection proportions.



Global time-dependent variation in frequencies of genetic clades-subclades of A/H1N1 viruses collected since 1st

September 2023.



Maximum likelihood phylogenetic tree of the H1 HA gene

Maximum likelihood phylogenetic tree inferred using IQtree2 from HA sequence data generated at the WIC. Annotation of amino acids substitutions was performed with Treetime ancestral reconstruction. References and CVVs are marked as Cell or Egg. Virus names are colored by collection month.



| 5a.2

Phylogenetic analyses: H3N2

Clade 3C.2a1b.2a.2 (renamed as **2** since February 2023) predominated since 1st February 2023 in all geographic regions where A/H3N2 circulated.

During this reporting period, the great majority of H3 viruses detected belong to clade 2a.3a.1, which share substitution E50K with clade 2a.3a and present additional substitutions I140K and I223V (subclade J, reference A/Thailand/8/2022). Some viruses from subclade J clustered in a separate branch with additional substitution N122D; these viruses predominated in East Africa and South East Asia and circulated in low proportions in several countries. Subclade J split into 4 further subclades: of these, subclade J.2 (reference A/Sydney/878/2023) characterised by N122D and K276E became the dominant subclade, predominating in the majority of continents except Africa. Subclade J.1 (reference A/Sydney/856/2023) characterised by I25V, V347M and I418V (in some viruses) was seen in Europe, South-East Asia and Oceania, whereas minor subclade J.3 with V505I (no reference assigned yet) was seen in the Democratic Republic of the Congo, China and South East Asia. Minor subclade J.4 characterised by Q173R, K276E and some viruses with K189R (no reference assigned yet) predominated in West Africa, Afghanistan and Guyana.

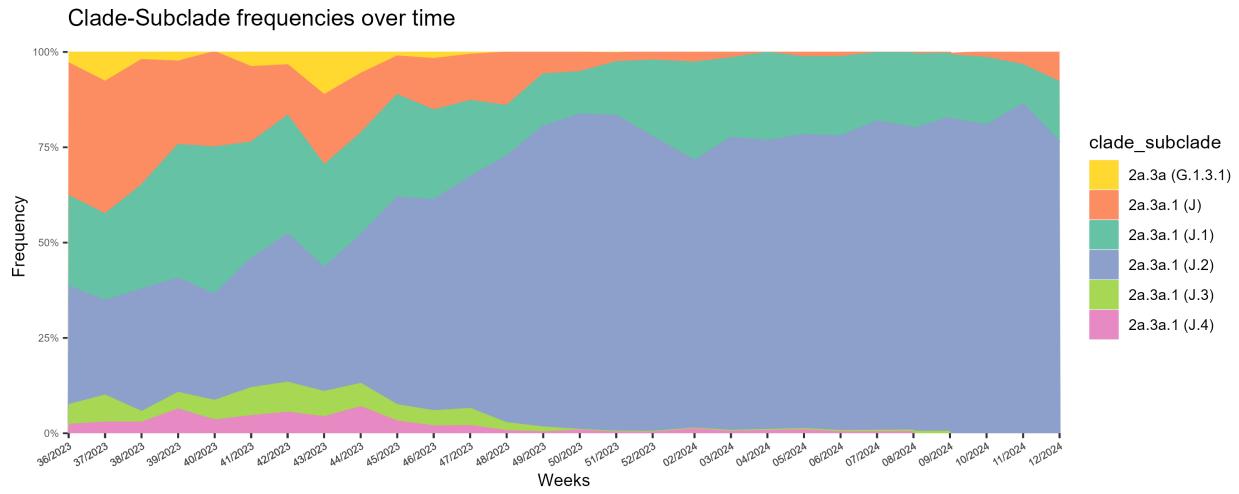
Clade 2a.3a (subclade G.1.3.1, reference A/Finland/402/2023) with substitutions K276E and V347M predominated in West Africa.

All A/H3N2 virus HA sequences from Kazakhstan clustered within clade 2a.3a.1, subclade J.2, except for one sequence which clustered within subclade J.

Global geographical distribution of influenza A/H3N2 genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade.Map prepared with Microreact. Geographic markers scaled to detection proportions.

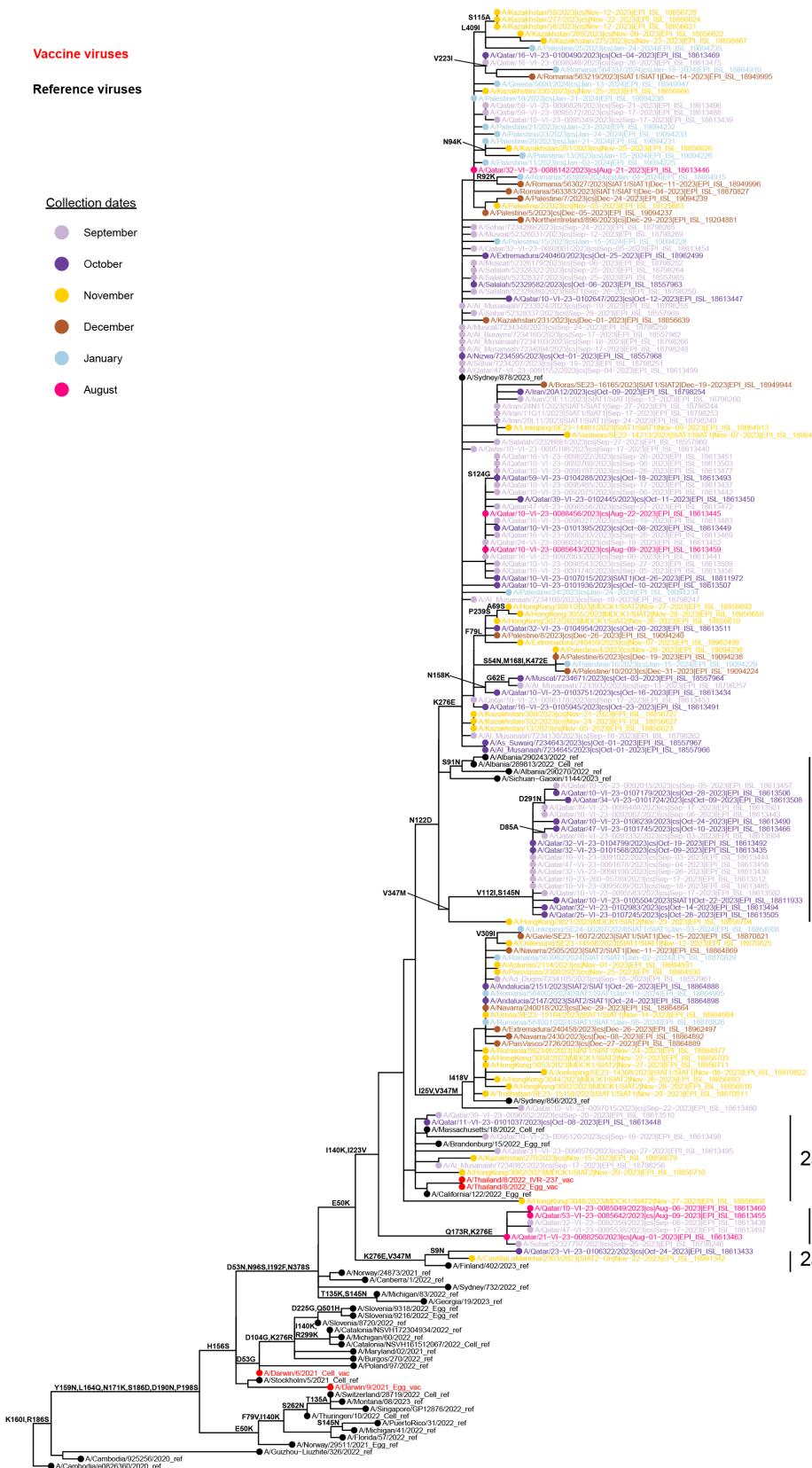


Global time-dependent variation in frequencies of genetic clades-subclades of A/H3N2 viruses collected since 1st September 2023.



Maximum likelihood phylogenetic tree of the H3 HA gene.

Maximum likelihood phylogenetic tree inferred using *lqtree2* from HA sequence data generated at the WIC. Annotation of amino acids substitutions was performed with *Treetime* ancestral reconstruction. References and CVVs are marked as Cell or Egg. Virus names are colored by collection month.



2a.3a.1 (J.2)

2a.3a.1 (J)

2a.3a.1 (J.1)

2a.3a.1 (J)

2a.3a.1 (J.4)

2a.3a

Phylogenetic analyses:

Influenza B viruses

B/Victoria lineage

Clade V1A.3a.2 viruses characterised by substitutions A127T, P144L, N150K, G184E, N197D (-CHO), K203R and R279K (B/Austria/1359417/2021, subclade C) predominated since 1st February 2023 in geographic regions where B/Victoria-lineage viruses were detected.

During this reporting period, only a minority of B/Victoria viruses were detected and characterised in Europe. Within V1A.3a.2, the most recent viruses are characterised by additional substitution D197E, represented by B/Connecticut/01/2021 (subclade C.5). Subclades observed within V1A.3a.2 (C.5) are: C.5.1 with E183K represented by B/Catalonia/2279261NS/2023, detected in Central America, Brazil, Peru, the US, Thailand and Europe; C.5.4 (B/Catalonia/3514402NS/2023) with V117I, E128K, A154T and K326R detected in the Americas; C.5.5 (B/Paraguay/2102/2023) with R80G, E184K detected in US and Central/South America; C.5.6 (B/Brisbane/145/2023) with D129N predominating in Australia, South East Asia, Middle East, Africa and Europe; C.5.7 (no reference assigned yet) with E183K and E128G seen in South East Asia, Europe, Middle East and South Africa.

Other C.5 viruses were detected in variable proportions across the globe. Since 1st September 2023, subclades C.5.1 and c.5.7 have increased their frequency until becoming the dominant subclades, followed by C.5.6.

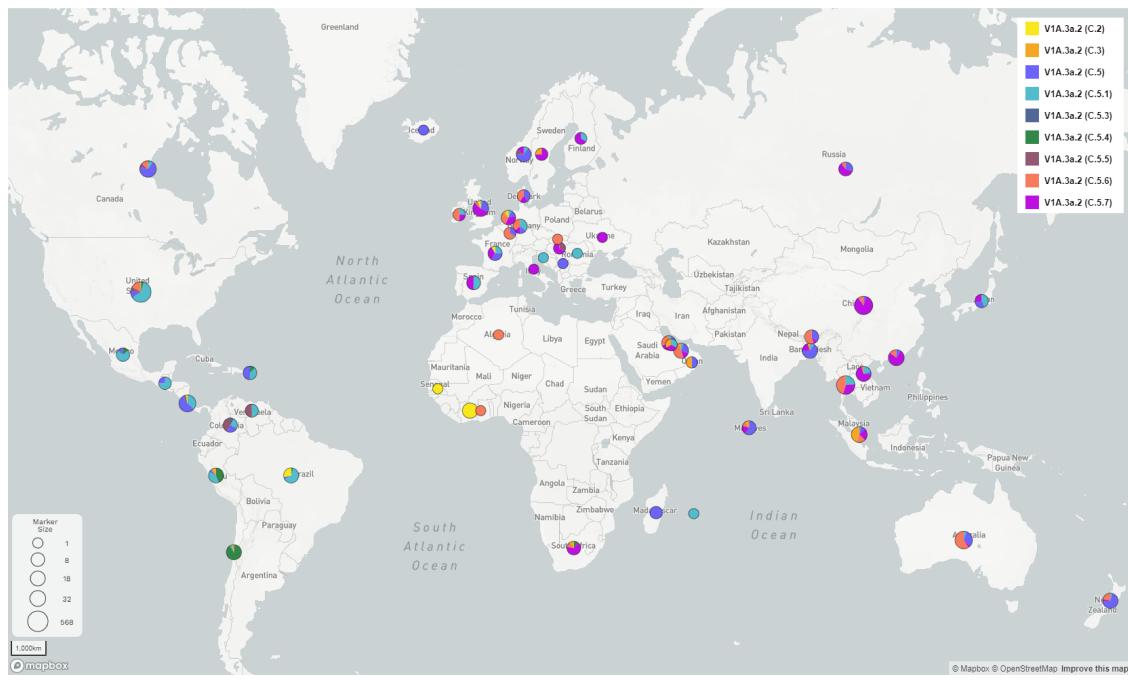
No Clade V1A.3 viruses were detected since 1st February 2023.

No B/Victoria viruses from Kazakhstan were received. We include representative figures and a phylogenetic tree as a general overview of the season.

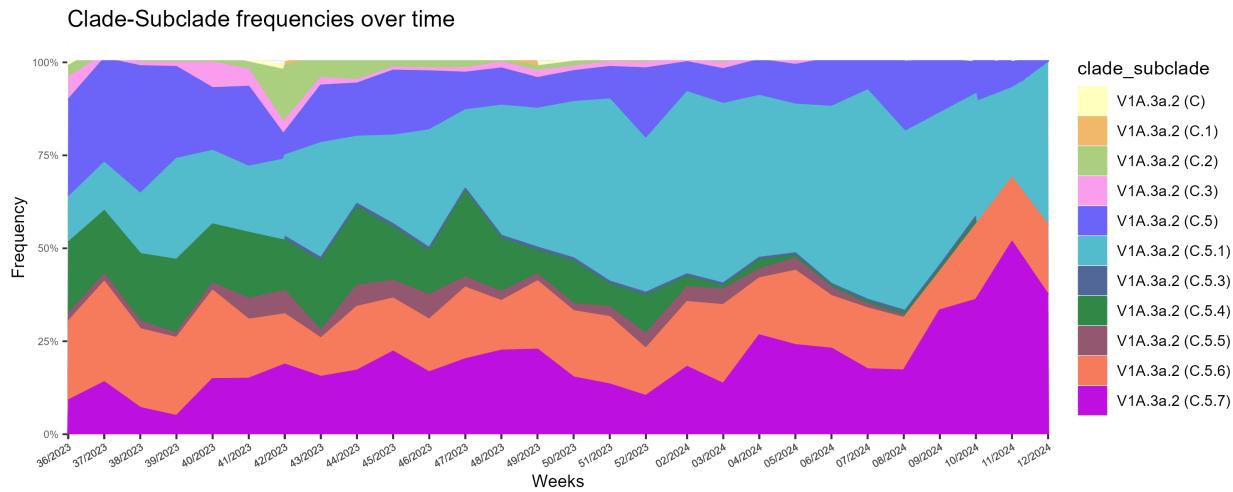
B/Yamagata lineage

No B/Yamagata lineage viruses have been detected since March 2020.

Global geographical distribution of influenza B/Victoria genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade.Map prepared with Microreact. Geographic markers scaled to detection proportions.



Global time-dependent variation in frequencies of genetic clades-subclades of B/Victoria viruses collected since 1st September 2023.



Maximum likelihood phylogenetic tree of the B/Victoria lineage HA gene

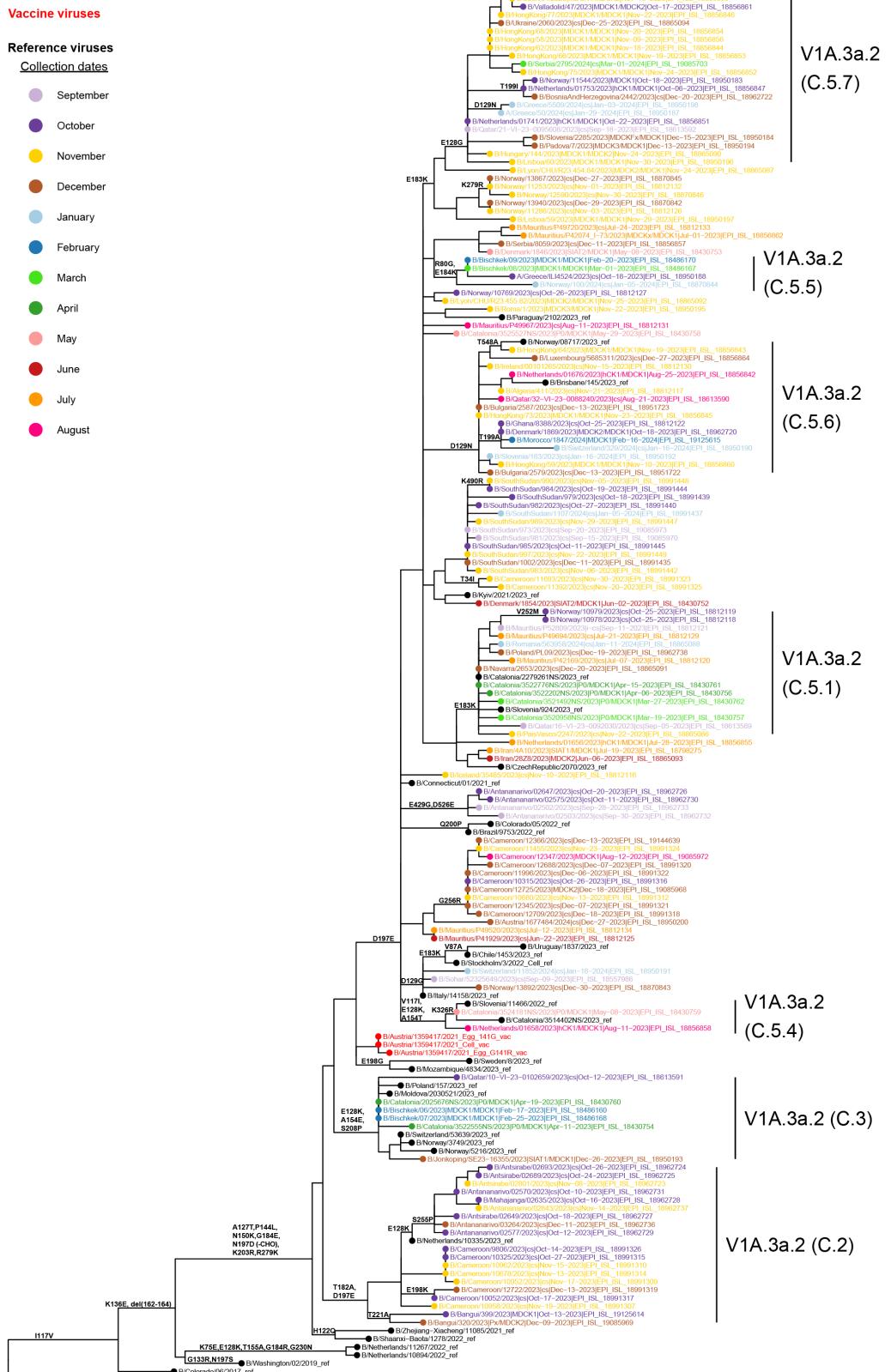
Maximum likelihood phylogenetic tree inferred using *lqtree2* from HA sequence data generated at the WIC. Annotation of amino acids substitutions was performed with *Treetime* ancestral reconstruction. References and CVVs are marked as Cell or Egg. Virus names are colored by collection month.

Vaccine viruses

Reference viruses

Collection dates

- September
- October
- November
- December
- January
- February
- March
- April
- May
- June
- July
- August



Phenotypic analyses

Haemagglutination inhibition (HI) assay data: ferret antisera raised against vaccine recommendations

H1 Summary

HI titres shows that the cell- and egg-based NH 2023-24, 2024-25 and SH 2024 strain A/Victoria/4897/2022 (clade 5a.2a.1 (D)) recognises both 5a.2a and 5a.2a.1 clade viruses well.

No A/H1N1 viruses from Kazakhstan were received. We include a summary comment representing overall antigenic results for the season.

H3 Summary

Generally, HI assays shows variable recognition by current 2a.3a.1 reference and vaccine antisera for a number of 2a.3a.1 viruses that have been analysed since September 2023.

Influenza B summary

All V1A.3a.2 viruses tested were well recognised by antisera raised against the B/Austria/1359417/2021 vaccine virus.

No B/Victoria viruses from Kazakhstan were received. We include a summary comment representing overall antigenic results for the season.

Antiviral susceptibility

All tested viruses were susceptible to neuraminidase inhibitors (NAI) by phenotypic testing and no genetic markers for reduced inhibition by NAIs were identified in NA sequences derived from clinical specimens.

Phenotypic testing for susceptibility to Baloxavir marboxil showed no reduced inhibition among all tested viruses. For all viruses where PA gene sequencing was successful, no markers associated with reduced inhibition by baloxavir marboxil were identified.

HI Tables: H1

No A/H1N1 viruses from Kazakhstan were received.

HI Tables: H3

Table H3-02. Antigenic analyses of influenza A(H3N2) viruses (Guinea Pig RBC with 20nm Oseltamivir) 2024-03-22

Viruses	Other information	Passage	Haemagglutination inhibition titre											
			A/Thuringen/10/2022 SIAT			VS/Zealand /26719/22 SIAT			A/Stockholm /5/2021 SIAT			A/Darwin /9/21 SVH-2067/22 Egg		
			Ferret number	F36/22	F29/23	F15/22	F39/21	F41/22	F21/23	F36/23	F34/23	F01/24	F06/24	F08/24
Genetic group	Collection Date	Genetic group	2b	2b	2a	2a	2a	2a.1b	2a.3a.1 (J)	2a.3a.1 (J)	2a.3a.1 (J)	2a.3a.1 (J.1)	2a.3a.1 (J.2)	2a.3a.1 (J.2)
REFERENCE VIRUSES														
A/Thuringen/10/2022	S262N	2b	2022-04-01	P1/SIAT3	320	640	320	160	40	80	160	160	40	160
A/Switzerland/28/19/2022	T135A	2b	2022-12-19	SIAT2	160	1280	160	160	40	80	160	160	80	80
A/Stockholm/5/2021		2a	2021-04-16	SIAT0/SIAT5	80	320	320	640	160	160	320	160	320	320
A/Darwin/9/21	D186N, D225G (egg)	2a	2021-04-17	E3/E4	160	640	320	640	160	320	160	160	320	320
A/Stockholm/11/15/2021/2022		2a.1b	2022-09-14	SIAT1/14	80	320	160	320	80	160	320	160	80	80
A/Albania/288/15/2022	N122D	2a.3a.1 (J)	2022-12-13	MDCK/11/SIAT1	80	320	80	320	80	640	320	640	640	320
A/Massachusetts/18/2022		2a.3a.1 (J)		SIAT3/SIAT1	160	640	160	640	160	1280	640	1280	320	640
A/Thailand/08/2022		2a.3a.1 (J)		E3/E1	160	640	320	640	160	640	320	640	320	640
A/Sydney/856/2023		2a.3a.1 (J.1)	2023-09-12	SIAT1/SIAT1	160	640	320	640	160	1280	640	2560	1280	320
240929 A/Croatia/10136/VR/2023		2a.3a.1 (J.2)	2023-12-04	SIAT2	40	160	160	320	80	320	160	320	320	320
241318 A/Netherlands/10553/2023		2a.3a.1 (J.2)	2023-11-10	CK-MX2/SIAT2	160	320	320	640	160	320	640	640	640	640
TEST VIRUSES														
242310 A/Algeria/1/2023		2a.3a.1 (J)	2023-09-03	SIAT2	80	160	80	160	80	640	640	640	1280	320
241449 A/Albania/7/23/2023		2a.3a.1 (J)	2023-09-17	SIAT1	160	320	160	320	160	640	1200	1200	320	320
241038 A/Kazakhstan/27/2023		2a.3a.1 (J)	2023-11-15	SIAT1	80	320	80	320	80	640	320	640	160	320
242485 A/SouthSudan/996/2023		2a.3a.1 (J)	2023-12-07	SIAT2	80	320	80	160	80	640	320	640	160	320
242068 A/Antananarivo/0332/2023		2a.3a.1 (J)	2023-12-14	SIAT1	80	160	80	160	80	320	320	320	160	160
242067 A/Antananarivo/0337/2023		2a.3a.1 (J)	2023-12-15	SIAT1	80	320	160	320	80	640	320	640	160	160
242065 A/Antananarivo/0337/2023		2a.3a.1 (J)	2023-12-20	SIAT1	80	320	80	320	80	320	320	320	160	160
242064 A/Manandona/0346/2023		2a.3a.1 (J)	2023-12-28	SIAT1	80	160	80	160	80	320	320	640	640	80
242063 A/Antananarivo/5000/2024		2a.3a.1 (J)	2024-01-03	SIAT1	80	160	80	160	80	320	320	640	640	160
242505 A/Moldova/36850/2024		2a.3a.1 (J)	2024-01-03	SIAT1	80	160	80	160	80	320	320	320	160	160
241524 A/Albania/52323/2023		2a.3a.1 (J)	2023-12-12	SIAT1	80	320	160	320	80	640	320	640	320	320
241448 A/Albania/7/23/094/2023		2a.3a.1 (J)	2023-09-17	SIAT1	160	320	160	320	80	640	320	640	320	320
240147 A/Albania/7/23/100/2023		2a.3a.1 (J.2)	2023-09-18	SIAT1	80	320	160	320	80	640	160	640	320	320
240144 A/Albania/7/23/130/2023		2a.3a.1 (J.2)	2023-09-18	SIAT1	80	320	160	320	80	320	160	640	640	320
240143 A/Albania/7/23/924/2023		2a.3a.1 (J.2)	2023-09-19	SIAT1	160	320	160	320	80	640	320	640	320	640
240136 A/Indonesia/723434/2023		2a.3a.1 (J.2)	2023-09-24	SIAT1	160	640	160	640	160	640	320	640	640	640
240140 A/Indonesia/727/2023		2a.3a.1 (J.2)	2023-09-24	SIAT1	80	160	80	160	80	640	320	640	320	320
240133 A/Salalah/5232832/2023		2a.3a.1 (J.2)	2023-09-25	SIAT1	160	320	160	320	80	640	160	640	320	640
240132 A/Salalah/5232832/2023		2a.3a.1 (J.2)	2023-09-25	SIAT1	160	320	160	320	80	640	160	640	320	640
240219 A/Qatar/16-VL-23-0098046/2023		2a.3a.1 (J.2)	2023-09-25	SIAT1	160	320	160	320	80	640	160	640	320	640
241045 A/Kazakhstan/27/2023		2a.3a.1 (J.2)	2023-09-25	SIAT1	80	160	80	160	80	320	320	160	160	320
241042 A/Kazakhstan/29/2023		2a.3a.1 (J.2)	2023-11-09	SIAT1	80	160	80	160	80	320	320	160	160	320
241041 A/Kazakhstan/58/2023		2a.3a.1 (J.2)	2023-11-12	SIAT1	80	320	80	320	80	320	160	320	160	320
241040 A/Kazakhstan/59/2023		2a.3a.1 (J.2)	2023-11-12	SIAT1	80	320	80	320	80	320	160	320	160	320
241035 A/Kazakhstan/30/2023		2a.3a.1 (J.2)	2023-11-21	SIAT1	80	320	160	320	80	320	160	640	320	320
241032 A/Kazakhstan/27/2023		2a.3a.1 (J.2)	2023-11-22	SIAT1	80	320	160	320	80	320	160	640	320	640
241031 A/Kazakhstan/32/2023		2a.3a.1 (J.2)	2023-11-23	SIAT1	80	160	80	160	80	320	320	320	320	320
241028 A/Kazakhstan/28/2023		2a.3a.1 (J.2)	2023-11-24	SIAT1	80	160	80	320	80	320	160	320	320	160
241023 A/Kazakhstan/28/2023		2a.3a.1 (J.2)	2023-11-25	SIAT1	80	320	160	320	80	320	160	640	320	640
241023 A/Kazakhstan/33/2023		2a.3a.1 (J.2)	2023-11-25	SIAT1	80	160	80	160	40	320	160	320	320	160
242501 A/Moldova/36881/2024		2a.3a.1 (J.2)	2024-01-30	SIAT1	80	160	80	320	80	320	80	320	320	320
242498 A/Moldova/36829/2024		2a.3a.1 (J.2)	2024-02-07	SIAT1	80	320	160	320	80	640	160	640	640	320
242497 A/Moldova/36860/2024		2a.3a.1 (J.2)	2024-02-08	SIAT1	40	160	80	160	40	160	80	160	320	320
242305 A/Cameroun/9092/2023		2a.3a.1 (J.4)	2023-09-28	SIAT1	80	160	80	320	80	320	160	320	160	320
242303 A/Cameroun/9812/2023		2a.3a.1 (J.4)	2023-10-10	SIAT1	80	160	80	320	80	320	160	320	320	320

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

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

Vaccine SH 2024
NH 2024-25

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

HI tables: Influenza B

No B/Victoria viruses from Kazakhstan were received.

Summary of sample characterisation

We follow a sequencing-first approach where we sequence all the clinical samples, with further selection of samples for isolation in cell culture and antigenic characterisation based on representative genetic diversity. Samples with identical sequences may not be selected for further characterisation.

Virus name	Original passage sent	Collection date	Type/Subtype	Date received	HI table date	HI comments	WIC Passage history	Antigenic characterisation			Genetic characterisation			Antiviral susceptibility phenotypic testing			
											Genetic clade	Submitted to GISAID	EPI Accession	Sequencing comments	Oseltamivir	Zanamivir	Baloxavir marboxil
A/Kazakhstan/246/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/245/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/244/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/242/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/238/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/231/2023	cs	2023-12-01	H3	2024-01-18		Virus not recovered	cs	2a.3a.1 (J.2)	2024-02-02	18856639							
A/Kazakhstan/228/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/227/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/226/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/223/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/220/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/217/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/216/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/215/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/208/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/204/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/202/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/201/2023	cs	2023-12-01	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/346/2023	cs	2023-11-27	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/336/2023	cs	2023-11-25	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856666					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/336/2023	cs	2023-11-25	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085724					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/282/2023	cs	2023-11-25	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/281/2023	cs	2023-11-25	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856626					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/281/2023	cs	2023-11-25	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085726					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/332/2023	cs	2023-11-24	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856627					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/332/2023	cs	2023-11-24	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085727					Normal inhibition	Normal inhibition	Normal inhibition
A/Kazakhstan/276/2023	cs	2023-11-24	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/275/2023	cs	2023-11-23	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856667							
A/Kazakhstan/275/2023	cs	2023-11-23	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085728							
A/Kazakhstan/273/2023	cs	2023-11-23	H3	2024-01-18		Virus not recovered	cs								no sequence		
A/Kazakhstan/317/2023	cs	2023-11-22	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/316/2023	cs	2023-11-22	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/277/2023	cs	2023-11-22	H3	2024-01-18	2024-03-22		Failed sequence - not cultured	cs	2a.3a.1 (J.2)	2024-02-02	18856624						
A/Kazakhstan/277/2023	cs	2023-11-22	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085730							
A/Kazakhstan/272/2023	cs	2023-11-22	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/312/2023	cs	2023-11-21	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/309/2023	cs	2023-11-21	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856727							
A/Kazakhstan/309/2023	cs	2023-11-21	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085731							
A/Kazakhstan/308/2023	cs	2023-11-21	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/307/2023	cs	2023-11-20	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/270/2023	cs	2023-11-15	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J)	2024-02-02	18856679							
A/Kazakhstan/270/2023	cs	2023-11-15	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J)	2024-04-16	19085732							
A/Kazakhstan/94/2023	cs	2023-11-12	H3	2024-01-18		Failed sequence - not cultured	cs								no sequence		
A/Kazakhstan/59/2023	cs	2023-11-12	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856728							
A/Kazakhstan/59/2023	cs	2023-11-12	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085733							
A/Kazakhstan/58/2023	cs	2023-11-12	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856621							
A/Kazakhstan/58/2023	cs	2023-11-12	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085734							
A/Kazakhstan/289/2023	cs	2023-11-09	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856622					Insufficient Titre	Insufficient Titre	Insufficient Titre
A/Kazakhstan/289/2023	cs	2023-11-09	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085735					Insufficient Titre	Insufficient Titre	Insufficient Titre
A/Kazakhstan/13/2023	cs	2023-11-05	H3	2024-01-18	2024-03-22		cs	2a.3a.1 (J.2)	2024-02-02	18856623							
A/Kazakhstan/13/2023	cs	2023-11-05	H3	2024-01-18	2024-03-22		SIAT1	2a.3a.1 (J.2)	2024-04-16	19085712							

Summary of the latest WHO Influenza Vaccine Composition meetings

Genetic and antigenic characterization data generated at the Worldwide Influenza Centre for viruses with collection dates after 31 August 2023 until 31 January 2024 informed the WHO influenza vaccine composition meeting (VCM) in February 2024 when recommendations were made for the Northern hemisphere (NH) 2024–2025 influenza season. At the February 2024 VCM it was recommended to change the A(H3N2) vaccine components for the 2024–2025 NH season. Previously, at the September 2023 VCM, which focused on data from viruses collected after 31 January 2023 until 31 August 2023, it was recommended to change the A(H1N1)pdm09 and A(H3N2) vaccine components for the 2024 SH season.

It is recommended that vaccines for use in the 2024-2025 NH influenza season contain the following:

Trivalent: Egg-based Vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Thailand/8/2022 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Trivalent: Cell- or recombinant-based Vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/Massachusetts/18/2022 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Quadrivalent (egg- or cell culture- or recombinant-based vaccines): Above 3 components; and a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Influenza B/Yamagata-lineage

No B/Yamagata-lineage viruses with collection dates after March 2020 have been detected or sequences released in GISAID as of 31st January 2024.

The absence of confirmed detection of naturally occurring B/Yamagata lineage viruses is indicative of very low risk of infection by B/Yamagata lineage viruses. Therefore, it is the opinion of the WHO influenza vaccine composition advisory committee that inclusion of a B/Yamagata lineage antigen in quadrivalent influenza vaccines is no longer warranted, and every effort should be made to exclude this component as soon as possible. A continued 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.

Annex

Updated genetic (clade-subclade) classification of seasonal influenza viruses

Note: During the September 2022 VCM, virus genetic clade/group nomenclature for seasonal influenza viruses was reviewed by the WHO Collaborating Centres. The main text of this Technical Note employs this new nomenclature.

In addition, some of the most recent clade definitions are combined with Nextstrain / Nextclade subclade classification (shown within parentheses) which provides a more detailed resolution to describe genetic diversity.

Influenza type A viruses

A(H1N1)pdm09

- All A(H1N1)pdm09 viruses detected recently descend from **6B.1A.5a**. The new nomenclature drops the prefix 6B.1A. Clade **5a** has split into two antigenically distinct clusters: Clade 5a.1 (no longer circulating) and Clade 5a.2, represented by former vaccine virus: A/Victoria/2570/2019. Signature amino acid substitutions are described against A/Victoria/2570/2019 from here onwards.
- **Clade 5a.2**
 - signature amino acid substitutions K130N, N156K, A187D, L161I and V250A
 - Vaccine virus: A/Victoria/2570/2019
 - **Clade 5a.2a (C.1)**
 - signature amino acid substitutions Clade 5a.2 + K54Q, A186T, E224A, R259K and K308R.
 - Vaccine virus: A/Sydney/5/2021.
 - **Clade 5a.2a (C.1) + I418V**
 - Reference virus: A/Netherlands/10468/2023
 - **Clade 5a.2a.1 (C.1.1)**
 - signature amino acid substitutions Clade 5a.2a + P137S, K142R, D260E, T277A
 - Vaccine virus: A/Wisconsin/67/2022
 - **Clade 5a.2a.1 (C.1.1.1)**
 - signature amino acid substitutions Clade 5a.2a.1 (C.1.1) + T216A
 - Vaccine virus: A/Victoria/4897/2022
 - **Clade 5a.2a (C.1.2)**
 - signature amino acid substitutions Clade 5a.2a + A48P
 - Reference virus: A/Maine/10/2022
 - **Clade 5a.2a (C.1.3)**
 - signature amino acid substitutions Clade 5a.2a + A73T, A141E, V152I, S190I, T216A
 - Reference virus: A/Washington/22/2023
 - **Clade 5a.2a (C.1.4)**
 - signature amino acid substitutions Clade 5a.2a + S85P, H273Q, V321I

- Reference virus: A/Maldives/936/2023
- **Clade 5a.2a (C.1.5)**
 - signature amino acid substitutions Clade 5a.2a + I185V
 - Reference virus: A/Bulgaria/234/2023
- **Clade 5a.2a (C.1.6)**
 - signature amino acid substitutions Clade 5a.2a with I418V + L70I, K169R, K211Q
 - Reference virus: A/South Dakota/31/2023
- **Clade 5a.2a (C.1.7)**
 - signature amino acid substitutions Clade 5a.2a + I533V
 - Reference virus: not assigned yet

A(H3N2)

All viruses detected recently belong to clade **3C.2a1b.2a** which has split into two clades, 3C.2a1b.2a.1 and 3C.2a1b.2a.2. The new nomenclature drops the prefix 3C.2a1b.2a, renaming these clades as **1** and **2**. Gain/Loss of glycosylation is represented by +CHO/-CHO.

- **Clade 1**
 - Signature amino acid substitutions G186S, S198P
 - Reference virus: A/Tasmania/503/2020
 - **Clade 1a**
 - Signature amino acid substitutions Clade 1 + K171N
 - Vaccine virus: A/Cambodia/e0826360/2020

[Signature amino acid substitutions are described against A/Cambodia/e0826360/2020 from here onwards](#)

- **Clade 1a.1**
 - Signature amino acid substitutions Clade 1a + I48T
 - Reference virus: A/Guizhou-Liuzhite/326/2022
- **Clade 2**
 - Signature amino acid substitutions Y159N, T160I (-CHO), L164Q, N171K, S186D, D190N, P198S
 - Reference virus: A/Norway/29511/2021
 - **Clade 2a**
 - Signature amino acid substitutions Clade 2 + H156S
 - Vaccine virus: A/Darwin/9/2021
 - **Clade 2a.1**
 - Signature amino acid substitutions Clade 2a + D53G, D104G, K276R
 - Reference virus: A/Slovenia/8720/2022
 - **Clade 2a.1a**
 - Signature amino acid substitutions Clade 2a.1 + L157I
 - Reference virus: A/Maryland/02/2021
 - **Clade 2a.1b**
 - Signature amino acid substitutions Clade 2a.1 + I140K, R299K
 - Reference virus: A/Catalonia/NSVH161512067/2022
 - **Clade 2a.2**
 - Signature amino acid substitutions Clade 2a + D53G, R201K, S219Y
 - Reference virus: A/Poland/97/2022
 - **Clade 2a.3**
 - Signature amino acid substitutions Clade 2a + D53N, N96S (+CHO), I192F
 - Reference virus: A/Norway/24873/2021
 - **Clade 2a.3a**

- Signature amino acid substitutions Clade 2a.3 + E50K
- Reference virus: A/Finland/402/2023
- **Clade 2a.3a.1 (J)**
 - Signature amino acid substitutions Clade 2a.3a + I140K, I223V
 - Vaccine virus: A/Thailand/8/2022
 - **Clade 2a.3a.1 (J.1)**
 - Signature amino acid substitutions Clade 2a.3a.1 + I25V, V347M
 - Reference virus: A/Sydney/856/2023
 - **Clade 2a.3a.1 (J.2)**
 - Signature amino acid substitutions Clade 2a.3a.1 + N122D, K276E
 - Reference virus: A/Sydney/878/2023
 - **Clade 2a.3a.1 (J.3)**
 - Signature amino acid substitutions Clade 2a.3a.1 + V50I
 - Reference virus: not assigned yet
 - **Clade 2a.3a.1 (J.4)**
 - Signature amino acid substitutions Clade 2a.3a.1 + Q173R, K276E
 - Reference virus: not assigned yet
- **Clade 2a.3b**
 - Signature amino acid substitutions Clade 2a.3 + I140M
 - Reference virus: A/Sydney/732/2022
- **Clade 2b**
 - Signature amino acid substitutions Clade 2 + E50K, F79V, I140K
 - Reference virus: A/Thuringen/10/2022

Influenza type B viruses

B/Victoria/2/87 lineage

Signature amino acid substitutions are described against B/Brisbane/60/2008.

In recent months, only viruses derived from **clade V1A.3a.2** have circulated.

- **Clade V1A.3**
 - Signature amino acid substitutions I117V, N129D, K136E, del(162-164)
 - Vaccine virus: B/Washington/02/2019
 - **Clade V1A.3a**
 - Signature amino acid substitutions Clade V1A.3 + N150K, G184E, N197D (+CHO) and R279K
 - Reference virus: B/Croatia/7789/2019
 - **Clade V1A.3a.1**
 - Signature amino acid substitutions Clade V1A.3a + V220M, P241Q
 - Reference virus: B/Cote d'Ivoire/948/2020
 - **Clade V1A.3a.2 (C)**
 - Signature amino acid substitutions Clade V1A.3a + A127T, P144L, N150K, G184E, N197D(-CHO), K203R, R279K
 - Vaccine virus: B/Austria/1359417/2021
 - **Clade V1A.3a.2 (C.1)**
 - Signature amino acid substitutions Clade V1A.3a.2 + H122Q
 - Reference virus: B/Shaanxi-Baota/1278/2022

- **Clade V1A.3a.2 (C.2)**
 - Signature amino acid substitutions Clade V1A.3a.2 + T182A, D197E
 - Reference virus: B/Netherlands/10335/2023
- **Clade V1A.3a.2 (C.3)**
 - Signature amino acid substitutions Clade V1A.3a.2 + E128K, A154E, S208P
 - Reference virus: B/Norway/5216/2023
- **Clade V1A.3a.2 (C.4)**
 - Signature amino acid substitutions Clade V1A.3a.2 + E198G
 - Reference virus: B/Sweden/8/2023
- **Clade V1A.3a.2 (C.5)**
 - Signature amino acid substitutions Clade V1A.3a.2 + D197E
 - Reference virus: B/Connecticut/01/2021
 - **Clade V1A.3a.2 (C.5.1)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + E183K
 - Reference virus: B/Catalonia/2279261NS/2023
 - **Clade V1A.3a.2 (C.5.2)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + Q200P
 - Reference virus: B/Colorado/05/2022
 - **Clade V1A.3a.2 (C.5.3)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + V87A, D129G, E183K
 - Reference virus: B/Uruguay/1837/2023
 - **Clade V1A.3a.2 (C.5.4)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + V117I, E128K, A154T
 - Reference virus: B/Catalonia/3514402NS/2023
 - **Clade V1A.3a.2 (C.5.5)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + R80G
 - Reference virus: B/Paraguay/2102/2023
 - **Clade V1A.3a.2 (C.5.6)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + D129N
 - Reference virus: B/Brisbane/145/2023
 - **Clade V1A.3a.2 (C.5.7)**
 - Signature amino acid substitutions Clade V1A.3a.2 with D197E + E183K, E128G
 - Reference virus: not assigned yet