Country Report: Estonia

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

February to August 2024

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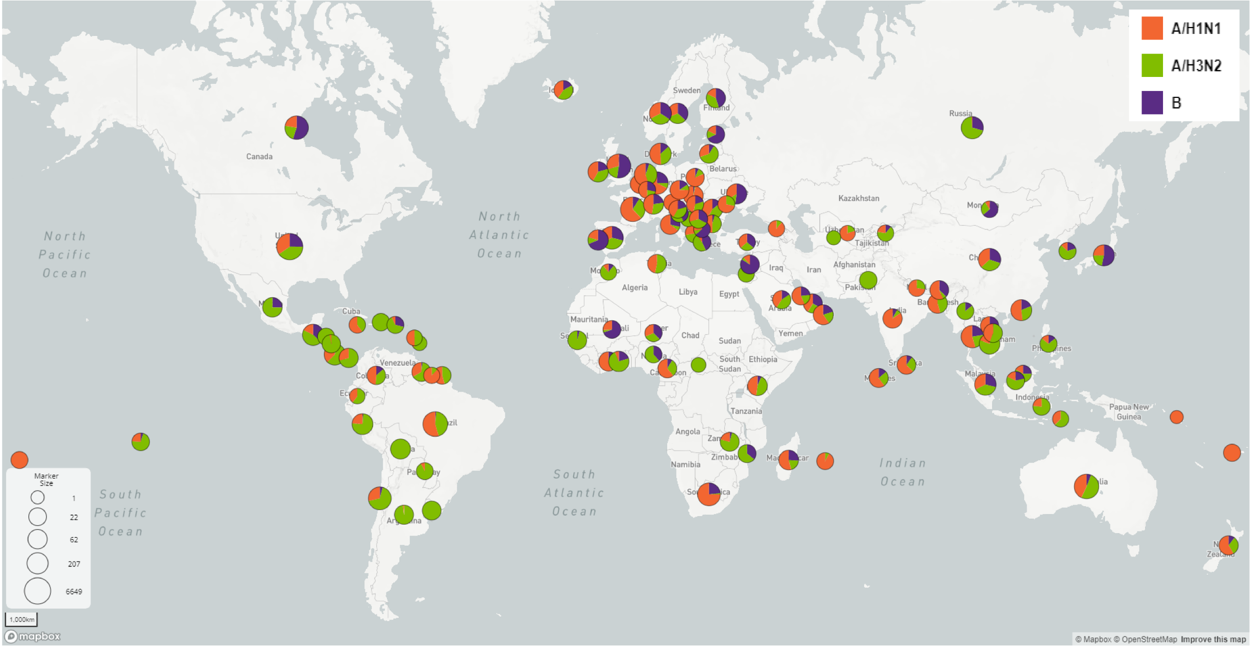
For more information about what we have observed over the last twelve months please see our reports for September 2023 and February 2024. All of our reports since 2003 are available at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports

Influenza by type/subtype:

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



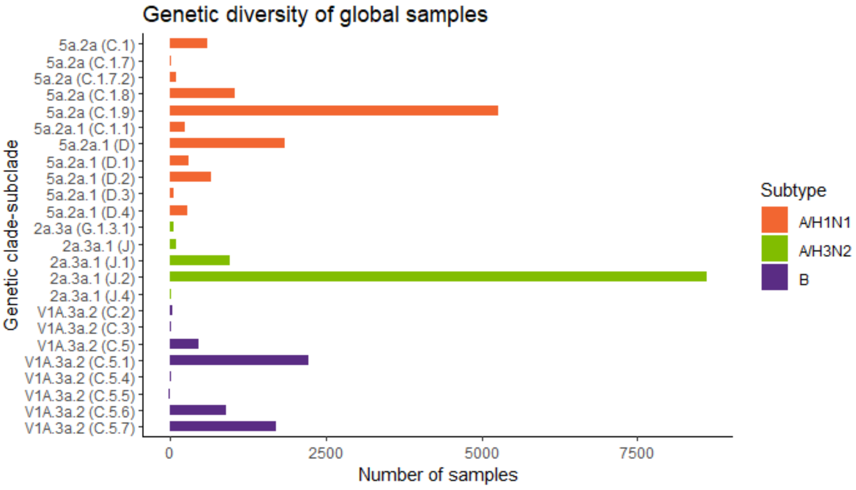
As of September 2024, in the Northern hemisphere influenza activity in temperate countries remained at interepidemic levels. Activity continued to increase in a few countries in Middle Africa.

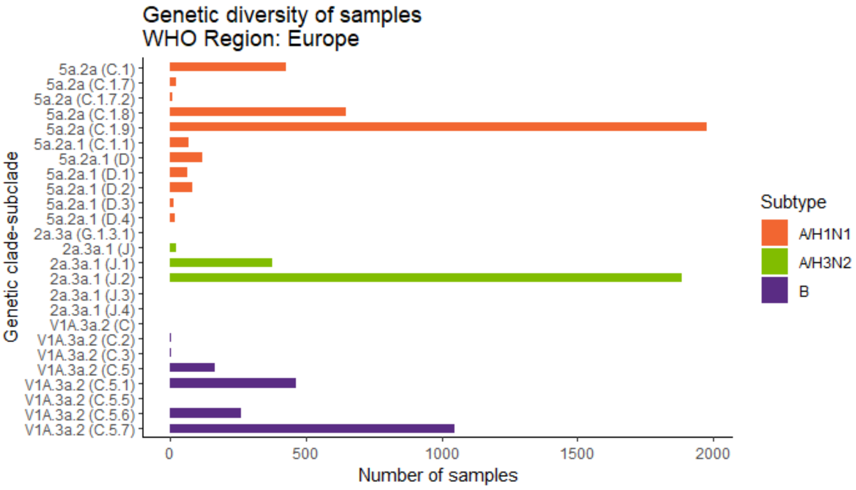
In the Southern hemisphere, influenza activity remained elevated in some countries in South America, Eastern Africa, Southern Africa, and Oceania. Activity declined or was similar compared with the prior report across the Southern hemisphere.

The relative proportions of A/H1N1, A/H3N2 and B/Victoria varied by geographic region, with predominance of A/H3N2 in the Americas, Africa, South East Asia, Western Pacific region and Russian Federation, and some predominance of A/H1N1 in Europe, Middle East, South Africa, Madagascar, India and Brazil. Some countries showed predominance of B/Victoria such as Canada, UK, Portugal, Syria, Ukraine, Mali, Japan and Mongolia, 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 an overall predominance of 5a.2a viruses.

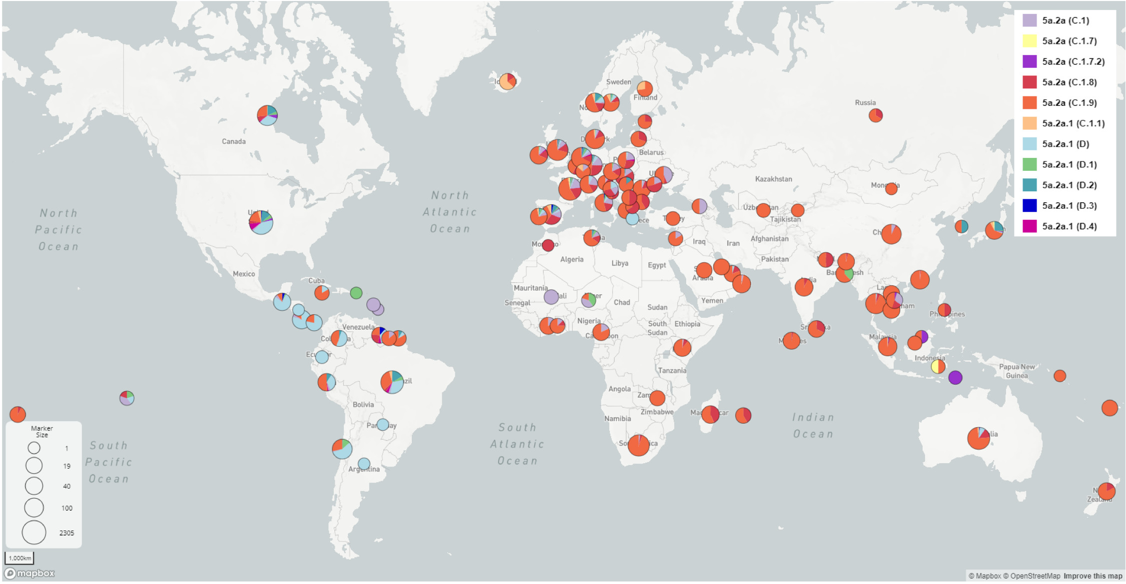
Globally, there is predominance of clade 5a.2a except in the Americas where there is a slight predominance of clade 5a.2a.1. In Europe, viruses from clade 5a.2a were detected with much higher frequency than clade 5a.2a.1.

Within the 5a.2a viruses, characterised by substitutions K54Q, A186T, E224A, R259K and K308R, several subclades were observed: subclade C.1 defined by substitution I418V which split into two further subclades: C.1.8, characterised by V47I with I96T in most sequences, and C.1.9, with substitution K169Q; the majority (>80%) of H1pdm viruses sequenced globally belong to subclade C.1.9, with viruses from C.1.8 as a minority subclade mostly observed in Europe. Minor subclades C.1.7 with substitution I533V and C.1.7.2 with T120A and K142R were circulating in Indonesia in low proportions.

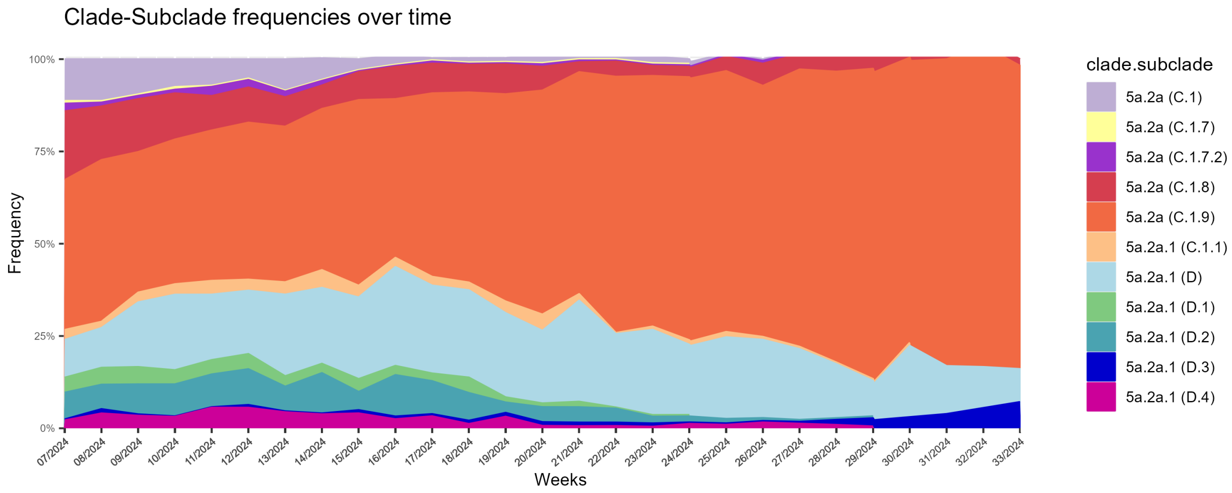
Within the 5a.2a.1 viruses, characterised by substitutions P137S, K142R, D260E, T277A, E356D and N451H, there are two main groups of viruses: major subclade D (former C.1.1.1) with T216A represented by A/Victoria/4897/2022, which has split into four subclades: D.1 with R45K, D.2 with R113K and V427I, D.3 with T120A and I372V and D.4 with T120A. Of these, only subclade D circulates in significant proportions, albeit predominating only in the Americas. Subclade C.1.1 is a minor clade within 5a.2a.1 viruses with no additional substitutions represented by A/Wisconsin/67/2022, which has been detected in significant proportions only in Iceland.

All A/H1N1 viruses from Estonia belong to clade 5a.2a, of which 6 clustered within subclade 5a.2a (C.1.8), 6 within subclade 5a.2a (C.1.9) and 2 within subclade 5a.2a (C.1).

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.

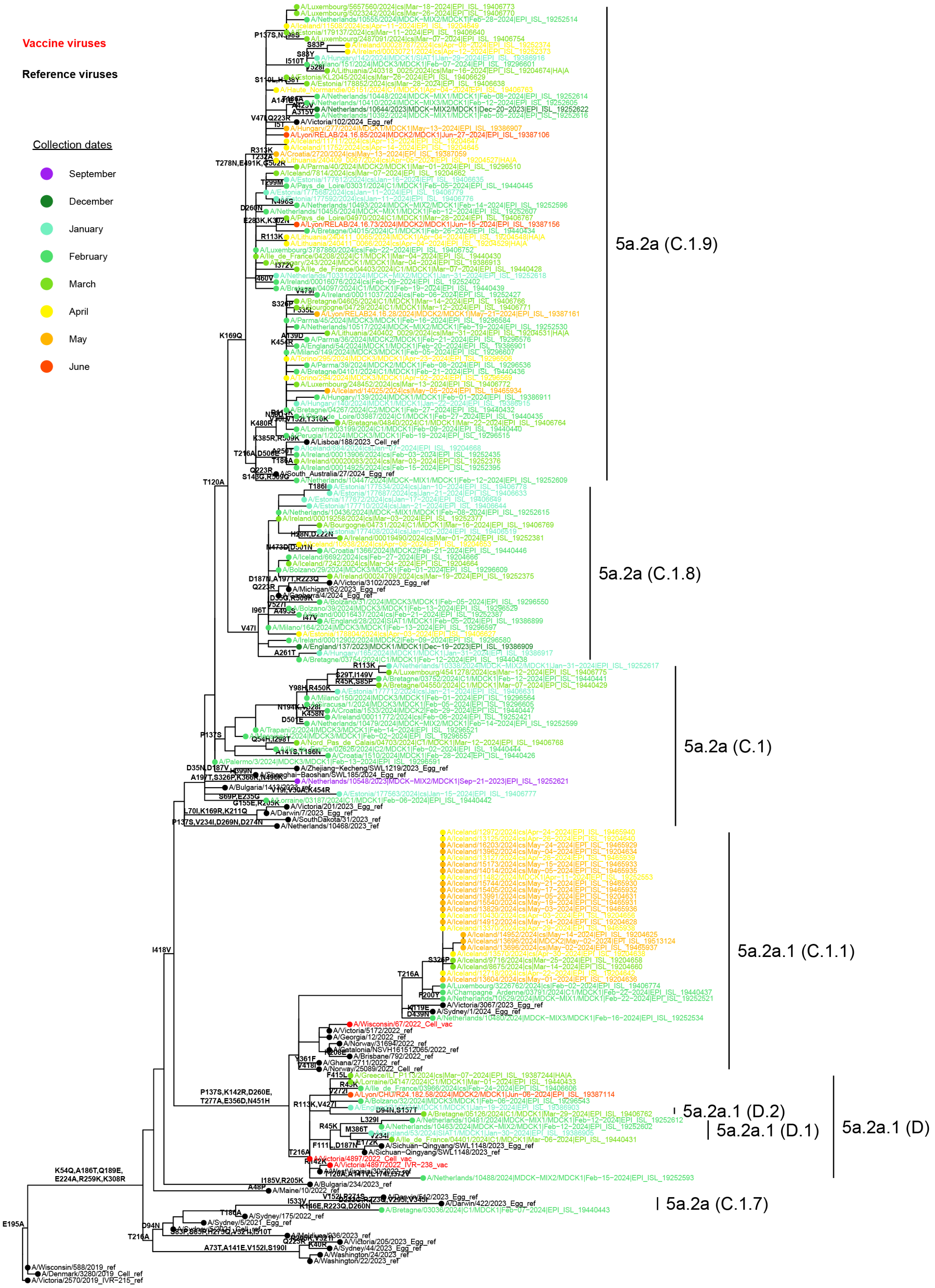


Global time-dependent variation in frequencies of genetic clades-subclades of A/H1N1 viruses collected since 1st February 2024.



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.


Vaccine viruses
Reference viruses
Collection dates
● September
● December
● January
● February
● March
● April
● May
● June
5a.2a (C.1.9)
5a.2a (C.1.8)
5a.2a (C.1)
5a.2a.1 (C.1.1)
5a.2a.1 (D.2)
5a.2a.1 (D.1)
5a.2a.1 (D)
5a.2a (C.1.7)
A/Wisconsin/67/2022_Cell_vac
A/Victoria/4897/2022_Cell_vac
A/Victoria/4897/2022_IVR-238_vac
A/Wisconsin/588/2019_ref
A/Denmark/3280/2019_Cell_ref
A/Victoria/2570/2019_IVR-215_ref

Phylogenetic analyses: H3N2

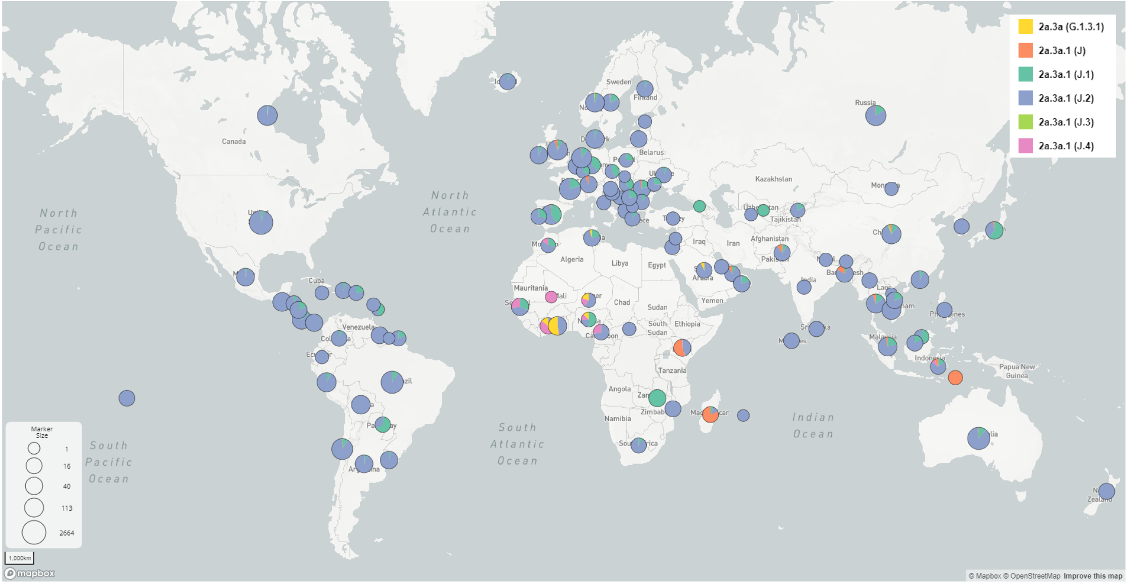
Clade 3C.2a1b.2a.2 (renamed as **2**) predominated since February 2023 in all geographic regions where A/H3N2 circulated.

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, vaccine reference A/Thailand/8/2022). Subclade J split into 4 further subclades: of these, subclade J.2 (reference A/Sydney/878/2023) characterised by N122D (-CHO) and K276E became the dominant subclade, predominating in the majority of continents with >90% frequency. Subclade J.1 (reference A/Sydney/856/2023) characterised by I25V, V347M with additional I418V (in some viruses) was detected in minor frequencies (<10%) in Europe, South-East Asia, Africa and Oceania. Minor subclade J.4 characterised by Q173R, K276E and some viruses with K189R predominated in West Africa earlier during the season.

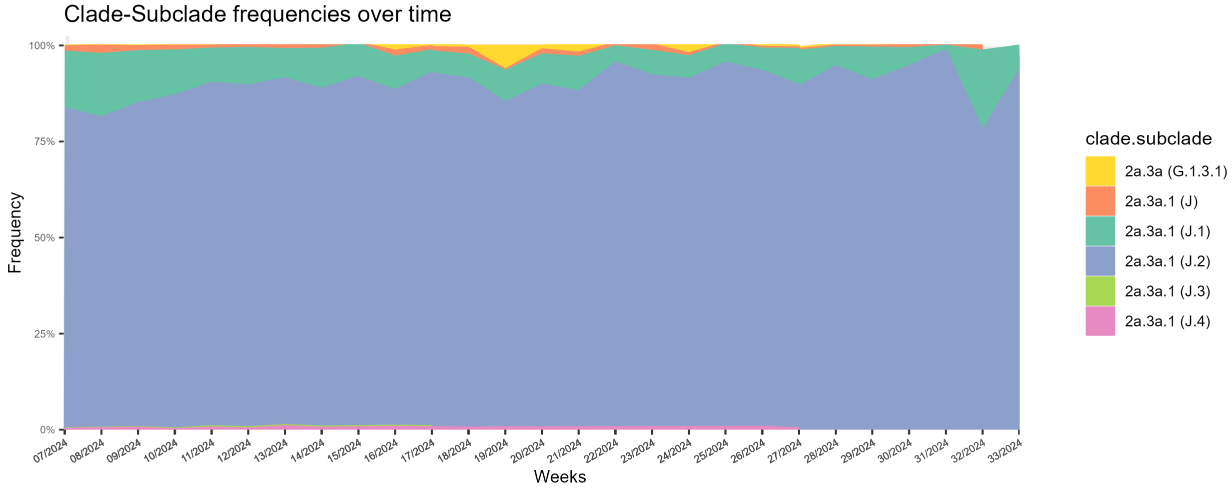
Clade 2a.3a (subclade G.1.3.1, reference A/Finland/402/2023) with substitutions K276E and V347M was detected in West Africa earlier during the season.

All A/H3N2 viruses from Estonia belong to clade 2a.3a.1, of which 9 clustered within subclade 2a.3a.1 (J.2) and 2 within subclade 2a.3a.1 (J.1).

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.

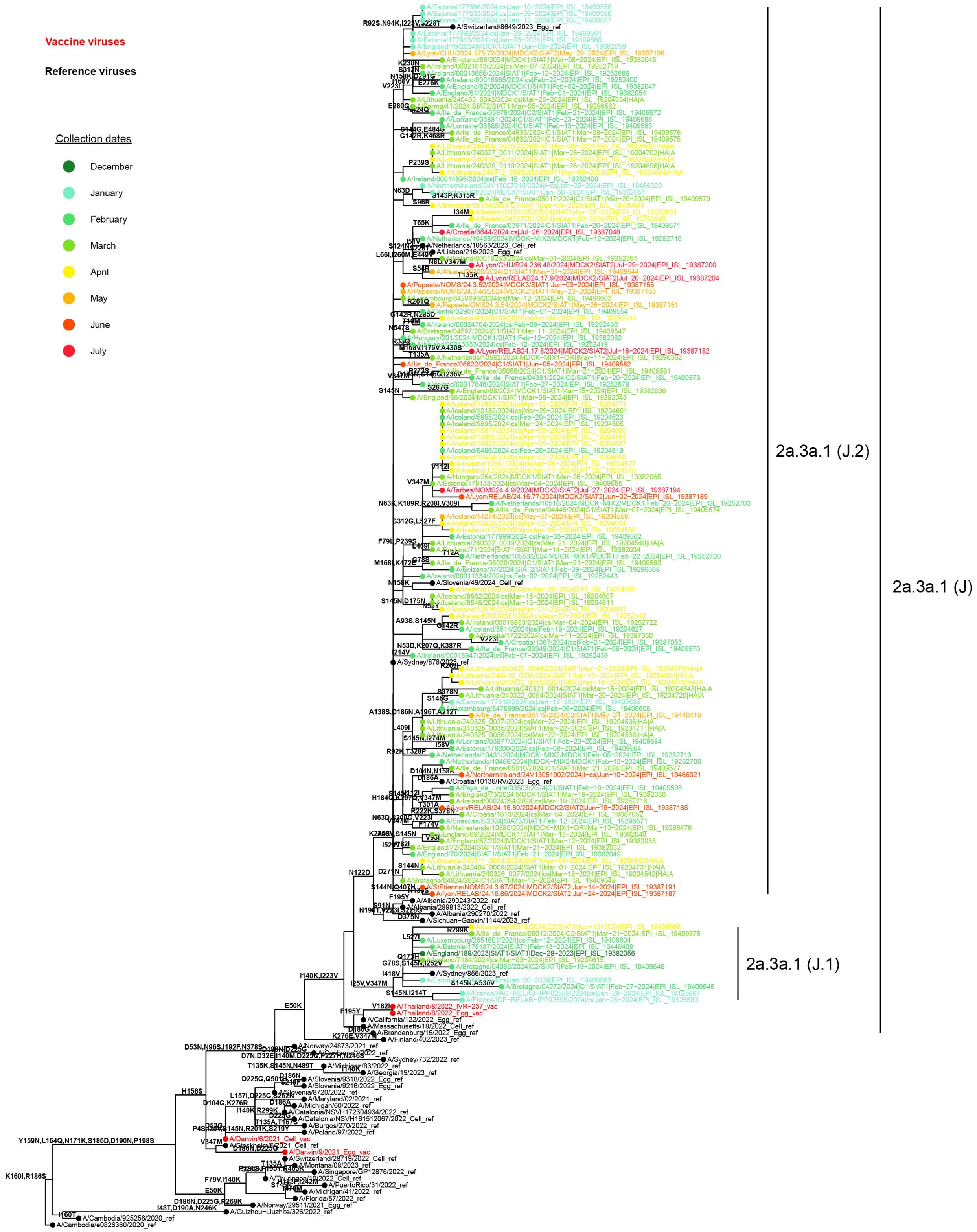


Global time-dependent variation in frequencies of genetic clades-subclades of A/H3N2 viruses collected since 1st February 2024.



Maximum likelihood phylogenetic tree of the H3 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.


Vaccine viruses
Reference viruses
Collection dates
● December
● January
● February
● March
● April
● May
● June
● July
2a.3a.1 (J.2)
2a.3a.1 (J)
2a.3a.1 (J.1)
A/Thailand/8/2022_IVR-237_vac
A/Thailand/8/2022_Egg_vac
A/Darwin/6/2021_Cell_vac
A/Darwin/9/2021_Egg_vac
A/Switzerland/8649/2023_Egg_ref
A/Sydney/878/2023_ref
A/Cambodia/925256/2020_ref
A/Cambodia/e0826360/2020_ref

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 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, subclade C.5 with D197E represents the majority of influenza B viruses characterised during the current influenza season. The most frequent subclades observed within C.5 are: C.5.1 with E183K represented by B/Catalonia/2279261NS/2023, as the dominant subclade predominating in the Americas, Portugal, Ukraine, New Zealand and detected in several other countries in minor proportions; C.5.6 (B/Norway/08717/2023) with D129N predominating in South East Asia, Middle East, South Africa and some European countries; C.5.7 with E183K and E128G predominating in China, Japan, Australia, Russian Federation, Mongolia and some countries in Europe. Minor subclades such as C.5.4 (B/Slovenia/924/2023) with V117I, E128K, A154T and K326R were detected in Chile and the US, and C.5.5 (B/Paraguay/2102/2023) with R80G, E184K were detected in North America in very low proportions.

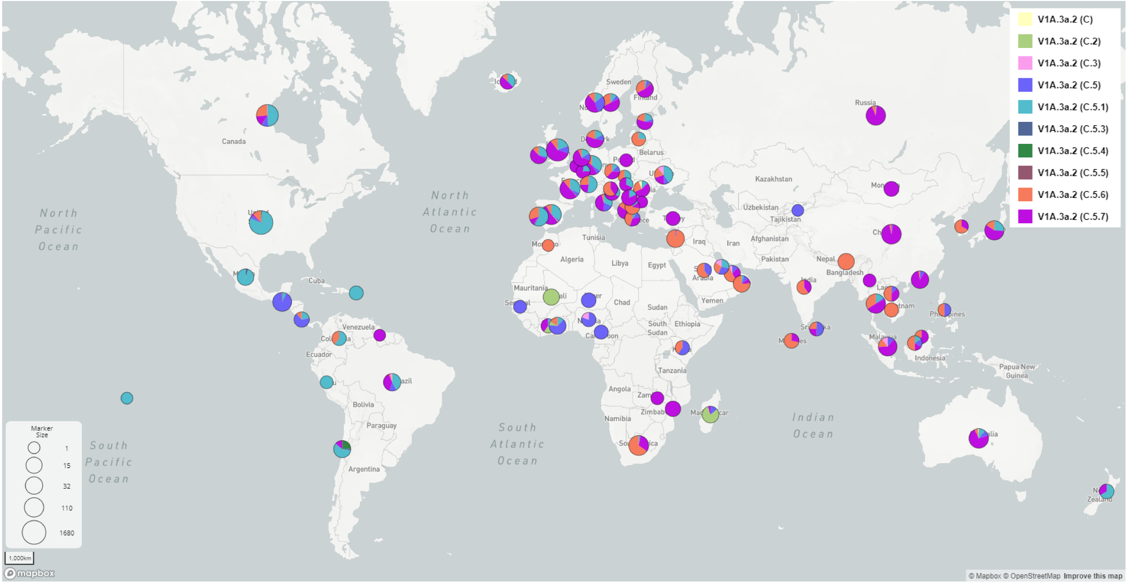
Outside of C.5 viruses, other subclades such as C.2 (T182A, D197E, B/Netherlands/10335/2023) and C.3 (E128K, A154E, S208P, B/Norway/5216/2023) were detected in low frequency in West Africa and Madagascar earlier during the season.

All B/Victoria viruses from Estonia belong to clade V1A.3a.2, of which 9 clustered within subclade V1A.3a.2 (C.5.7), 4 within subclade V1A.3a.2 (C.5.1), 4 within subclade V1A.3a.2 (C.5.6) and 2 within subclade V1A.3a.2 (C.5).

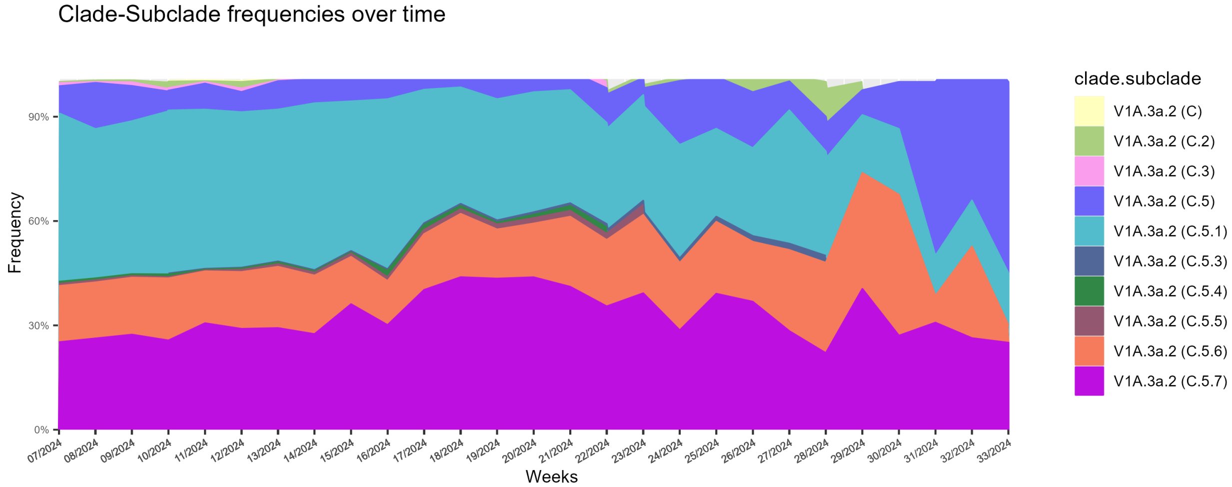
B/Yamagata lineage

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.

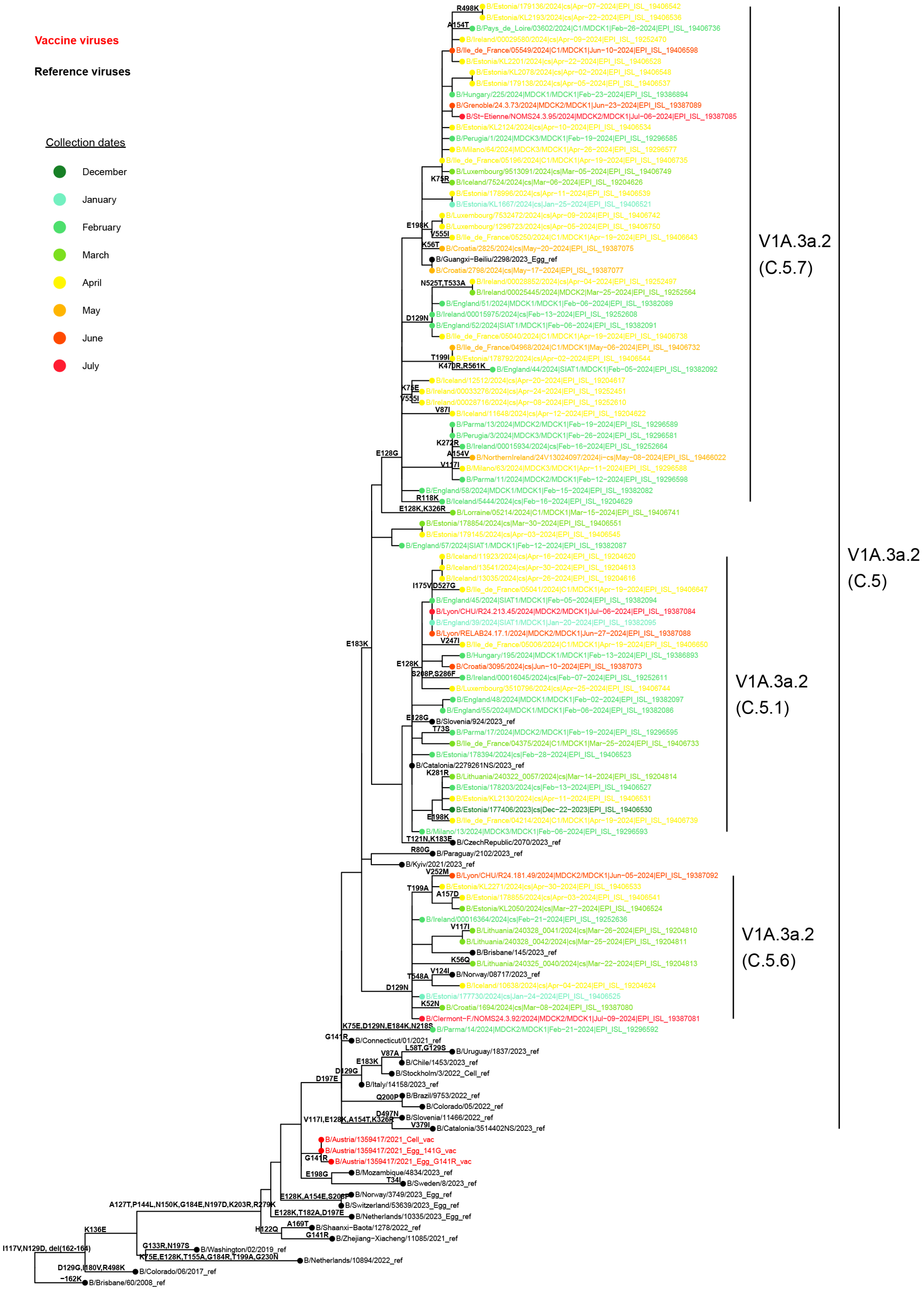


Global time-dependent variation in frequencies of genetic clades-subclades of B/Victoria viruses collected since 1st February 2024.



Maximum likelihood phylogenetic tree of the B/Victoria lineage 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.

Vaccine viruses
Reference viruses
Collection dates
December
January
February
March
April
May
June
July
V1A.3a.2 (C.5.7)
V1A.3a.2 (C.5)
V1A.3a.2 (C.5.1)
V1A.3a.2 (C.5.6)
R498K
B/Estonia/179136/2024|cs|Apr-07-2024|EPI_ISL_19406542
B/Estonia/KL2193/2024|cs|Apr-22-2024|EPI_ISL_19406536
A154T
B/Pays_de_Loire/03602/2024|C1/MDCK1|Feb-26-2024|EPI_ISL_19406736
B/Ireland/00029580/2024|cs|Apr-09-2024|EPI_ISL_19252470
B/Ile_de_France/05549/2024|C1/MDCK1|Jun-10-2024|EPI_ISL_19406598
B/Estonia/KL2201/2024|cs|Apr-22-2024|EPI_ISL_19406528
B/Estonia/KL2076/2024|cs|Apr-02-2024|EPI_ISL_19406548
B/Estonia/179138/2024|cs|Apr-05-2024|EPI_ISL_19406537
B/Hungary/225/2024|MDCK1/MDCK1|Feb-23-2024|EPI_ISL_19386894
B/Grenoble/24.3.73/2024|MDCK2/MDCK1|Jun-23-2024|EPI_ISL_19387089
B/St-Etienne/NOMS24.3.95/2024|MDCK2/MDCK1|Jul-06-2024|EPI_ISL_19387085
B/Estonia/KL2124/2024|cs|Apr-10-2024|EPI_ISL_19406534
B/Perugia/1/2024|MDCK3/MDCK1|Feb-19-2024|EPI_ISL_19296585
B/Milano/64/2024|MDCK3/MDCK1|Apr-26-2024|EPI_ISL_19296577
B/Ile_de_France/05196/2024|C1/MDCK1|Apr-19-2024|EPI_ISL_19406735
B/Luxembourg/9513091/2024|cs|Mar-05-2024|EPI_ISL_19406749
K75R
B/Iceland/7524/2024|cs|Mar-06-2024|EPI_ISL_19204626
B/Estonia/178996/2024|cs|Apr-11-2024|EPI_ISL_19406539
B/Estonia/KL1667/2024|cs|Jan-25-2024|EPI_ISL_19406521
B/Luxembourg/7532472/2024|cs|Apr-09-2024|EPI_ISL_19406742
E198K
B/Luxembourg/1296723/2024|cs|Apr-05-2024|EPI_ISL_19406750
V555I
B/Ile_de_France/05250/2024|C1/MDCK1|Apr-19-2024|EPI_ISL_19406643
K56T
B/Croatia/2825/2024|cs|May-20-2024|EPI_ISL_19387075
B/Guangxi-Beiliu/2298/2023_Egg_ref
B/Croatia/2798/2024|cs|May-17-2024|EPI_ISL_19387077
N525T,T533A
B/Ireland/00028852/2024|cs|Apr-04-2024|EPI_ISL_19252497
B/Ireland/00025445/2024|MDCK2|Mar-25-2024|EPI_ISL_19252564
B/England/51/2024|MDCK1/MDCK1|Feb-06-2024|EPI_ISL_19382089
B/Ireland/00015975/2024|cs|Feb-13-2024|EPI_ISL_19252608
D129N
B/England/52/2024|SIAT1/MDCK1|Feb-06-2024|EPI_ISL_19382091
B/Ile_de_France/05040/2024|C1/MDCK1|Apr-19-2024|EPI_ISL_19406738
B/Ile_de_France/04968/2024|C1/MDCK1|May-06-2024|EPI_ISL_19406732
T199I
B/Estonia/178792/2024|cs|Apr-02-2024|EPI_ISL_19406544
K470R,R561K
B/England/44/2024|SIAT1/MDCK1|Feb-05-2024|EPI_ISL_19382092
B/Iceland/12512/2024|cs|Apr-20-2024|EPI_ISL_19204617
K75E
B/Ireland/00033278/2024|cs|Apr-24-2024|EPI_ISL_19252451
V555I
B/Ireland/00028716/2024|cs|Apr-08-2024|EPI_ISL_19252510
V87I
B/Iceland/11848/2024|cs|Apr-12-2024|EPI_ISL_19204622
B/Parma/13/2024|MDCK2/MDCK1|Feb-19-2024|EPI_ISL_19296589
B/Perugia/3/2024|MDCK3/MDCK1|Feb-26-2024|EPI_ISL_19296581
K272R
B/Ireland/00015934/2024|cs|Feb-16-2024|EPI_ISL_19252664
A154V
B/NorthernIreland/24V13024097/2024|i-cs|May-08-2024|EPI_ISL_19468022
V117I
B/Milano/83/2024|MDCK3/MDCK1|Apr-11-2024|EPI_ISL_19296588
B/Parma/11/2024|MDCK2/MDCK1|Feb-12-2024|EPI_ISL_19296598
E128G
B/England/58/2024|MDCK1/MDCK1|Feb-15-2024|EPI_ISL_19382082
R118K
B/Iceland/5444/2024|cs|Feb-16-2024|EPI_ISL_19204629
E128K,K326R
B/Lorraine/05214/2024|C1/MDCK1|Mar-15-2024|EPI_ISL_19406741
B/Estonia/178854/2024|cs|Mar-30-2024|EPI_ISL_19406551
B/Estonia/179145/2024|cs|Apr-03-2024|EPI_ISL_19406545
B/England/57/2024|SIAT1/MDCK1|Feb-12-2024|EPI_ISL_19382087
B/Iceland/11923/2024|cs|Apr-16-2024|EPI_ISL_19204620
B/Iceland/13641/2024|cs|Apr-30-2024|EPI_ISL_19204613
B/Iceland/13036/2024|cs|Apr-26-2024|EPI_ISL_19204616
I175V,D527G
B/Ile_de_France/05041/2024|C1/MDCK1|Apr-19-2024|EPI_ISL_19406647
B/England/45/2024|SIAT1/MDCK1|Feb-05-2024|EPI_ISL_19382094
B/Lyon/CHU/R24.213.45/2024|MDCK2/MDCK1|Jul-06-2024|EPI_ISL_19387084
B/England/39/2024|SIAT1/MDCK1|Jan-20-2024|EPI_ISL_19382095
B/Lyon/RELAB24.17.1/2024|MDCK2/MDCK1|Jun-27-2024|EPI_ISL_19387088
V247I
B/Ile_de_France/05009/2024|C1/MDCK1|Apr-19-2024|EPI_ISL_19406650
B/Hungary/195/2024|MDCK1/MDCK1|Feb-13-2024|EPI_ISL_19386893
E128K
B/Croatia/3095/2024|cs|Jun-10-2024|EPI_ISL_19387073
S208P,S286F
B/Ireland/00016045/2024|cs|Feb-07-2024|EPI_ISL_19252611
B/Luxembourg/3510796/2024|cs|Apr-25-2024|EPI_ISL_19406744
E183K
B/England/48/2024|MDCK1/MDCK1|Feb-02-2024|EPI_ISL_19382097
B/England/55/2024|MDCK1/MDCK1|Feb-06-2024|EPI_ISL_19382086
E128G
B/Slovenia/924/2023_ref
T73S
B/Parma/17/2024|MDCK2/MDCK1|Feb-19-2024|EPI_ISL_19296595
B/Ile_de_France/04375/2024|C1/MDCK1|Mar-25-2024|EPI_ISL_19406733
B/Estonia/178394/2024|cs|Feb-28-2024|EPI_ISL_19406523
B/Catalonia/2279261NS/2023_ref
K281R
B/Lithuania/240322_0057/2024|cs|Mar-14-2024|EPI_ISL_19204814
B/Estonia/178203/2024|cs|Feb-13-2024|EPI_ISL_19406527
B/Estonia/KL2133/2024|cs|Apr-11-2024|EPI_ISL_19406531
B/Estonia/177406/2023|cs|Dec-22-2023|EPI_ISL_19406530
E198K
B/Ile_de_France/04214/2024|C1/MDCK1|Apr-16-2024|EPI_ISL_19406739
B/Milano/13/2024|MDCK3/MDCK1|Feb-06-2024|EPI_ISL_19296593
T121N,K183E
B/CzechRepublic/2070/2023_ref
R80G
B/Paraguay/2102/2023_ref
B/Kyiv/2021/2023_ref
V252M
B/Lyon/CHU/R24.181.49/2024|MDCK2/MDCK1|Jun-05-2024|EPI_ISL_19387092
T199A
B/Estonia/KL2271/2024|cs|Apr-30-2024|EPI_ISL_19406533
A157D
B/Estonia/178865/2024|cs|Apr-03-2024|EPI_ISL_19406541
B/Estonia/KL2050/2024|cs|Mar-27-2024|EPI_ISL_19406524
B/Ireland/00016364/2024|cs|Feb-21-2024|EPI_ISL_19252636
V117I
B/Lithuania/240328_0041/2024|cs|Mar-26-2024|EPI_ISL_19204810
B/Lithuania/240328_0042/2024|cs|Mar-25-2024|EPI_ISL_19204811
B/Brisbane/145/2023_ref
K56Q
B/Lithuania/240325_0040/2024|cs|Mar-22-2024|EPI_ISL_19204813
V124I
T548A
B/Norway/08717/2023_ref
B/Iceland/10638/2024|cs|Apr-04-2024|EPI_ISL_19204624
D129N
B/Estonia/177730/2024|cs|Jan-24-2024|EPI_ISL_19406525
K52N
B/Croatia/1684/2024|cs|Mar-08-2024|EPI_ISL_19387080
B/Clermont-F./NOMS24.3.92/2024|MDCK2/MDCK1|Jul-09-2024|EPI_ISL_19387081
K75E,D129N,E184K,N218S
B/Parma/14/2024|MDCK2/MDCK1|Feb-21-2024|EPI_ISL_19296592
G141R
B/Connecticut/01/2021_ref
L58T,G129S
B/Uruguay/1837/2023_ref
V87A
E183K
B/Chile/1453/2023_ref
D129G
B/Stockholm/3/2022_Cell_ref
D197E
B/Italy/14158/2023_ref
Q200P
B/Brazil/9753/2022_ref
B/Colorado/05/2022_ref
D497N
V117I,E128K,A154T,K326R
B/Slovenia/11466/2022_ref
V379I
B/Catalonia/3514402NS/2023_ref
B/Austria/1359417/2021_Cell_vac
B/Austria/1359417/2021_Egg_141G_vac
G141R
B/Austria/1359417/2021_Egg_G141R_vac
E198G
B/Mozambique/4834/2023_ref
T34I
B/Sweden/8/2023_ref
E128K,A154E,S208P
B/Norway/3749/2023_Egg_ref
B/Switzerland/53639/2022_Egg_ref
E128K,T182A,D197E
B/Netherlands/10335/2023_Egg_ref
A127T,P144L,N150K,G184E,N197D,K203R,R279K
A169T
B/Shaanxi-Baota/1278/2022_ref
H122Q
G141R
B/Zhejiang-Xiacheng/11085/2021_ref
K136E
G133R,N197S
B/Washington/02/2019_ref
I117V,N129D, del(162-164)
K75E,E128K,T155A,G184R,T199A,G230N
B/Netherlands/10894/2022_ref
D129G,I180V,R498K
-162K
B/Colorado/06/2017_ref
B/Brisbane/60/2008_ref

Phenotypic analyses

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

H1 Summary

HI titres show that NH 2023-24, 2024-25 and SH 2024 strains, cell-based A/Wisconsin/67/2022 and egg-based A/Victoria/4897/2022, generally recognised both 5a.2a and 5a.2a.1 clade viruses well. Some four-fold drops were observed with the cell- based A/Wisconsin/67/2022 strain that were not seen with the egg-based A/Victoria/4897/2022.

H3 Summary

HI titres show that the SH 2024 and NH 2024-25 vaccine strains, egg-based A/Thailand/08/2022 (2a.3a.1 (J)) and cell-based A/Massachusetts/18/2022 (2a.3a.1 (J)), demonstrate reduced recognition against a significant number of samples in the J.2 and J.4 subclades. The cell-based SH 2024 and NH 2024-25 vaccine strain, A/Massachusetts/18/2022 (2a.3a.1 (J)) recognised most viruses tested within 2-fold, but showed significant drop in titre to some J.2 and all J.4 viruses tested to date.

Influenza B summary

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

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

Table H1-18. Antigenic analyses of influenza A(H1N1)pdm09 viruses (2024-09-11)

	Viruses	Other information	Genetic group	Collection Date		Haemagglutination inhibition titre				
						Post-infection ferret antiserum				
					Passage	A/Sydney 5/21 MDCK	A/Lisboa/ 188/2023 MDCK	A/Victoria/ 4897/2022 MDCK	IVR-238 A/Vic/4897/22 Egg	A/Wisconsin/ 67/2022 MDCK
					Ferret number	F46/22	F09/24	F05/23	F07/23	F17/23
					Genetic group	5a.2a (C.1)	5a.2a (C.1.9)	5a.2a.1 (D)	5a.2a.1 (D)	5a.2a.1 (C.1.1)
	REFERENCE VIRUSES									
	A/Sydney/5/2021	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a (C.1)	2021-10-16	MDCK3/MDCK4	2560	2560	2560	2560	1280
	A/Lisboa/188/2023	K169Q, T216A, D506E	5a.2a (C.1.9)	2023-11-22	SIAT1/MDCK3	2560	2560	2560	2560	1280
	A/Victoria/4897/2022	P137S, K142R, T216A, D260E, T277A	5a.2a.1 (D)	2022-10-02	SIAT2/MDCK3	2560	2560	5120	2560	2560
	IVR-238 (A/Victoria/4897/2022)	P137S, K142R, T216A, D260E, T277A (R142K, Q223R)	5a.2a.1 (D)	2022-10-02	E3/D6/E1	1280	1280	1280	2560	640
	A/Wisconsin/67/2022		5a.2a.1 (C.1.1)	2022-10-25	MDCK2	1280	1280	2560	1280	1280
	TEST VIRUSES									
244843	A/Estonia/177563/2024		5a.2a (C.1)	2024-01-15	MDCK1	2560	2560	2560	2560	640
244837	A/Estonia/177712/2024		5a.2a (C.1)	2024-01-21	MDCK1	2560	2560	2560	2560	1280
244878	A/Luxembourg/3787860/2024		5a.2a (C.1.9)	2024-02-22	SIAT1	2560	2560	2560	2560	1280
244835	A/Estonia/179137/2024		5a.2a (C.1.9)	2024-03-11	MDCK1	2560	2560	2560	2560	1280
244596	A/HongKong/783/2024		5a.2a (C.1.9)	2024-03-12	MDCK 2/MDCK1	1280	2560	1280	1280	640
244871	A/Luxembourg/248452/2024		5a.2a (C.1.9)	2024-03-13	MDCK1	2560	1280	2560	1280	1280
244869	A/Luxembourg/5023242/2024		5a.2a (C.1.9)	2024-03-26	MDCK1	1280	2560	2560	1280	1280
244873	A/Luxembourg/3226762/2024		5a.2a.1 (C.1.1)	2024-02-02	MDCK1	2560	2560	5120	2560	2560
244630	A/Croatia/1366/2024		no sequence	2024-02-21	MDCK2	1280	1280	1280	1280	640
244628	A/Croatia/1533/2024		no sequence	2024-02-29	MDCK2	640	640	1280	640	640
						Vaccine SH 2023			Vaccine NH 2023-24 SH 2024 NH 2024-25	

< 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 (no homologous titre)

Table H1-35. Antigenic analyses of influenza A(H1N1)pdm09 viruses (2024-09-18)

	Viruses	Other information	Genetic group	Collection Date	Passage	Haemagglutination inhibition titre Post-infection ferret antiserum A/Sydney 5/21	A/Lisboa/ 188/2023	A/Victoria/ 4897/2022	IVR-238 A/Vic/4897/22	A/Wisconsin/ 67/2022
					Passage	MDCK	MDCK	MDCK	Egg	MDCK
					Ferret number	F46/22	F09/24	F05/23	F07/23	F17/23
					Genetic group	5a.2a (C.1)	5a.2a (C.1)	5a.2a.1 (D)	5a.2a.1 (D)	5a.2a.1 (C.1.1)
	REFERENCE VIRUSES									
	A/Sydney/5/2021	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a (C.1)	2021-10-16	MDCK3/MDCK4	2560	1280	1280	2560	1280
	A/Lisboa/188/2023	K169Q, T216A, D506E	5a.2a (C.1)	2023-11-22	SIAT1/MDCK3	2560	2560	2560	2560	2560
	A/Victoria/4897/2022	P137S, K142R, T216A, D260E, T277A	5a.2a.1 (D)	2022-10-02	SIAT2/MDCK3	2560	2560	5120	2560	2560
	IVR-238 (A/Victoria/4897/2022)	P137S, K142R, T216A, D260E, T277A (R142K, Q223R)	5a.2a.1 (D)	2022-10-02	E3/D6/E1	1280	1280	2560	2560	1280
	A/Wisconsin/67/2022		5a.2a.1 (C.1.1)	2022-10-25	MDCK2	2560	2560	2560	2560	2560
	TEST VIRUSES									
244391	A/Spain/2606/2023		5a.2a (C.1)	2023-12-29	MDCK1	2560	2560	2560	2560	2560
244387	A/Spain/1780/2024		5a.2a (C.1)	2024-02-04	MDCK1	2560	2560	2560	1280	1280
244389	A/Spain/2201/2024		5a.2a (C.1.8)	2024-02-01	MDCK1	2560	2560	2560	2560	1280
244386	A/Spain/1814/2024		5a.2a (C.1.8)	2024-02-04	MDCK1	1280	1280	1280	1280	640
244832	A/Estonia/178804/2024		5a.2a (C.1.8)	2024-04-03	MDCK2	5120	5120	2560	2560	1280
244388	A/Spain/1810/2024		5a.2a (C.1.9)	2024-02-02	MDCK1	2560	2560	2560	2560	1280
244384	A/Spain/1720/2024		5a.2a (C.1.9)	2024-02-06	MDCK1	2560	1280	1280	1280	640
244382	A/Spain/1828/2024		5a.2a (C.1.9)	2024-02-10	MDCK1	2560	2560	2560	2560	1280
244938	A/CAT/2167458NS/2024		5a.2a (C.1.9)	2024-03-05	C1/MDCK1	5120	2560	2560	2560	2560
244937	A/CAT/3546125NS/2024		5a.2a (C.1.9)	2024-03-11	C1/MDCK1	2560	2560	2560	2560	1280
244934	A/CAT/3547217NS/2024		5a.2a (C.1.9)	2024-03-25	C1/MDCK1	2560	1280	2560	2560	1280
244383	A/Spain/1817/2024		5a.2a.1 (D)	2024-02-06	MDCK1	2560	1280	2560	1280	1280
244936	A/CAT/3546363NS/2024		5a.2a.1 (D)	2024-03-13	C1/MDCK1	2560	1280	2560	1280	2560
244935	A/CAT/2174846NS/2024		5a.2a.1 (D)	2024-03-21	C1/MDCK1	2560	1280	5120	2560	2560
244933	A/CAT/3549595NS/2024		5a.2a.1 (D)	2024-04-30	C1/MDCK1	2560	2560	5120	2560	2560
244939	A/CAT/3545504NS/2024		5a.2a.1 (D.2)	2024-03-04	C1/MDCK1	2560	2560	2560	2560	2560
						Vaccine SH 2023			Vaccine NH 2023-24 SH 2024 NH 2024-25	

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND =

☐ < 4-fold 🟨 4-fold 🟧 8-fold 🟥 > 8-fold < not recognised by the antiserum 🟦 ≥ 160 (no homologous titre)

Table H1-36. Antigenic analyses of influenza A(H1N1)pdm09 viruses (2024-09-24)

						Haemagglutination inhibition titre				
						Post-infection ferret antiserum				
	Viruses	Other information				A/Sydney 5/21	A/Lisboa/ 188/2023	A/Victoria/ 4897/2022	IVR-238 A/Vic/4897/22	A/Wisconsin/ 67/2022
					Passage	MDCK	MDCK	MDCK	Egg	MDCK
					Ferret number	F46/22	F09/24	F05/23	F07/23	F17/23
			Genetic group	Collection Date	Genetic group	5a.2a (C.1)	5a.2a (C.1)	5a.2a.1 (D)	5a.2a.1 (D)	5a.2a.1 (C.1.1)
	REFERENCE VIRUSES									
	A/Sydney/5/2021	K54Q, A186T, E224A, R259K, K308R, D94N, T216A	5a.2a (C.1)	2021-10-16	MDCK3/MDCK4	2560	1280	1280	2560	1280
	A/Lisboa/188/2023	K169Q, T216A, D506E	5a.2a (C.1)	2023-11-22	SIAT1/MDCK3	2560	2560	2560	2560	2560
	A/Victoria/4897/2022	P137S, K142R, T216A, D260E, T277A	5a.2a.1 (D)	2022-10-02	SIAT2/MDCK3	2560	2560	5120	2560	2560
	IVR-238 (A/Victoria/4897/2022)	P137S, K142R, T216A, D260E, T277A (R142K, Q223R)	5a.2a.1 (D)	2022-10-02	E3/D6/E1	2560	1280	2560	2560	1280
	A/Wisconsin/67/2022		5a.2a.1 (C.1.1)	2022-10-25	MDCK2	2560	2560	2560	2560	2560
	TEST VIRUSES									
244846	A/Estonia/177568/2024		5a.2a (C.1.9)	2024-01-11	MDCK1	2560	2560	2560	2560	1280
244884	A/SouthSudan/1041/2024		5a.2a (C.1.9)	2024-05-29	MDCK2	5120	2560	2560	2560	1280
244882	A/SouthSudan/1023/2024		5a.2a (C.1.9)	2024-06-05	MDCK2	2560	2560	2560	2560	2560
244880	A/SouthSudan/1039/2024		5a.2a (C.1.9)	2024-06-07	MDCK1	2560	2560	2560	2560	1280
						Vaccine SH 2023			Vaccine NH 2023-24 SH 2024 NH 2024-25	

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND =

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

HI Tables: H3

Table H3-22. Antigenic analyses of influenza A(H3N2) viruses (Guinea Pig RBC with 20nm Oseltamivir) 2024-09-10

	Viruses	Other information	Genetic group	Collection Date		Haemagglutination inhibition titre											
						Post-infection ferret antiserum											
					Passage	A/Albania /289813/2022 SIAT	assachusetts /18/2022 SIAT	A/Thailand /08/2022 Egg	A/Sydney /856/2023 SIAT	A/Croatia/)136/RV/2023 SIAT	A/Croatia/)136/RV/2023 Egg	/Netherlands /10563/2023 SIAT	A/Slovenia /49/2024 SIAT	A/Lisboa/ 216/2023 Egg	\/France/IDF- P29542/2023 Cell	A/Norway /12374/2023 Cell	'BurkinaFaso /3131/2023 Cell
					Ferret number	F21/23	F36/23	F34/23	F01/24	F06/24	F16/24	F08/24	F11/24	F15/24	F22/24	F21/24	F32/24
					Genetic group	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)	2a.3a.1 (J.2)	2a.3a.1 (J.2)	2a.3a.1 (J.2)	2a.3a.1 (J.4)	2a.3a.1 (J.4)	2a.3a.1 (J.4)
	REFERENCE VIRUSES																
	A/Albania/289813/2022	N122D	2a.3a.1 (J)	2022-12-13	IDCK1/SIAT2	1280	320	1280	640	160	160	320	80	320	160	80	40
	A/Massachusetts/18/2022		2a.3a.1 (J)		SIAT3/SIAT1	1280	640	1280	1280	160	160	320	80	320	320	160	80
	A/Thailand/08/2022		2a.3a.1 (J)		E3/E1	1280	320	1280	640	320	640	640	320	640	640	160	160
	A/Sydney/856/2023		2a.3a.1 (J.1)	2023-09-12	SIAT1/SIAT2	1280	320	640	640	160	160	320	160	320	160	80	80
	A/Croatia/10136/RV/2023	S145N	2a.3a.1 (J.2)	2023-12-04	SIAT3	160	80	160	160	160	160	320	320	320	320	80	40
	A/Croatia/10136/RV/2023	S145N	2a.3a.1 (J.2)		E3 (Am1Al2)	640	320	640	640	640	640	640	640	640	320	320	80
	A/Netherlands/10563/2023	S124N	2a.3a.1 (J.2)	2023-11-10	(-MIX2/SIAT3	320	160	320	320	160	320	320	160	320	320	160	40
	A/Slovenia/49/2024	N158K	2a.3a.1 (J.2)	2024-01-08	IDCKx/SIAT3	40	<40	160	<40	80	40	40	1280	160	<40	40	<40
	A/Lisboa/216/2023	S124N	2a.3a.1 (J.2)	2023-12-15	E3 (Am1Al2)	640	320	640	640	320	320	640	320	640	320	160	80
	A/France/IDF-IPP29542/2023	R142G, K189R	2a.3a.1 (J.4)	2023-11-30	IDCK1/SIAT2	<40	<40	40	40	40	80	80	<40	40	80	40	40
	A/Norway/12374/2023		2a.3a.1 (J.4)	2023-11-28	SIAT4	160	80	160	160	160	160	320	80	160	160	80	80
	A/BurkinaFaso/3131/2023	R142G, K189R	2a.3a.1 (J.4)	2023-11-20	SIAT3	80	40	80	<40	80	80	80	<40	80	80	80	80
	TEST VIRUSES																
244854	A/Estonia/178001/2024		2a.3a.1 (J.1)	2024-01-30	SIAT1	640	320	640	640	160	160	320	80	320	160	80	80
244850	A/Estonia/178187/2024		2a.3a.1 (J.1)	2024-02-13	SIAT1	640	640	640	640	160	160	320	80	320	160	80	40
244860	A/Estonia/177566/2024		2a.3a.1 (J.2)	2024-01-10	SIAT1	320	160	320	160	160	160	320	160	160	160	80	40
244858	A/Estonia/177562/2024		2a.3a.1 (J.2)	2024-01-12	SIAT1	320	80	160	160	160	160	160	80	160	160	80	40
244857	A/Estonia/177610/2024		2a.3a.1 (J.2)	2024-01-15	SIAT1	160	80	320	160	320	160	320	160	160	160	160	80
244855	A/Estonia/177892/2024		2a.3a.1 (J.2)	2024-01-26	SIAT1	320	80	320	160	160	160	320	160	320	320	80	40
244876	A/Luxembourg/6475699/2024		2a.3a.1 (J.2)	2024-02-06	SIAT1	320	160	320	160	160	160	320	160	320	160	80	40
244852	A/Estonia/178200/2024		2a.3a.1 (J.2)	2024-02-08	SIAT1	320	160	320	160	160	160	320	160	320	160	80	40
244633	A/Croatia/1613/2024		2a.3a.1 (J.2)	2024-03-04	SIAT2	160	40	160	80	80	160	160	80	160	80	40	<40
244849	A/Estonia/179133/2024		2a.3a.1 (J.2)	2024-03-04	SIAT1	320	160	320	160	320	160	320	160	320	160	160	40
244716	A/Ile_de_France/06119/2024		2a.3a.1 (J.2)	2024-05-24	C2/SIAT2	640	160	320	80	320	160	320	160	640	160	80	<40
244798	A/Bangui/172/2024		2a.3a.1 (J.2)	2024-07-11	SIAT1	640	160	640	320	320	320	320	160	320	160	160	40

< relates to the lowest dilution of antiserum used

[1] hyperimmune sheep serum; ND = Not Done

Vaccine
SH 2024
NH 2024-25

☐ < 4-fold 🟨 4-fold 🟧 8-fold 🟥 > 8-fold < not recognised by the antiserum 🟦 ≥ 160 (no homologous titre)

Table H3-36. Antigenic analyses of influenza A(H3N2) viruses (Guinea Pig RBC with 20nm Oseltamivir) 2024-09-19

	Viruses	Other information	Genetic group	Collection Date		Haemagglutination inhibition titre											
						Post-infection ferret antiserum											
						A/Albania /289813/2022	lassachusetts /18/2022	A/Thailand /08/2022	A/Sydney /856/2023	A/Croatia/ 0136/RV/2023	A/Croatia/ 0136/RV/2023	/Netherlands /10563/2023	A/Slovenia /49/2024	A/Lisboa/ 216/2023	/France/IDF- P29542/2023	A/Norway /12374/2023	/BurkinaFaso /3131/2023
					Passage	SIAT	SIAT	Egg	SIAT	SIAT	Egg	SIAT	SIAT	Egg	Cell	Cell	Cell
					Ferret number	F21/23	F36/23	F34/23	F01/24	F06/24	F16/24	F08/24	F11/24	F15/24	F22/24	F21/24	F32/24
					Genetic group	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)	2a.3a.1 (J.2)	2a.3a.1 (J.2)	2a.3a.1 (J.2)	2a.3a.1 (J.4)	2a.3a.1 (J.4)	2a.3a.1 (J.4)
	REFERENCE VIRUSES																
	A/Albania/289813/2022	N122D	2a.3a.1 (J)	2022-12-13	MDCK1/SIAT2	1280	640	1280	1280	160	160	320	160	320	320	160	80
	A/Massachusetts/18/2022		2a.3a.1 (J)		SIAT3/SIAT1	1280	640	1280	1280	160	160	320	80	320	320	80	80
	A/Thailand/08/2022		2a.3a.1 (J)		E3/E1	1280	320	640	640	320	320	640	320	640	320	160	160
	A/Sydney/856/2023		2a.3a.1 (J.1)	2023-09-12	SIAT1/SIAT2	640	320	640	640	160	160	320	80	320	160	80	80
	A/Croatia/10136/RV/2023		2a.3a.1 (J.2)	2023-12-04	SIAT3	160	80	160	160	160	160	320	160	160	160	80	40
	A/Croatia/10136/RV/2023		2a.3a.1 (J.2)		E3 (Am1Al2)	640	160	640	640	640	640	640	320	640	640	160	80
	A/Netherlands/10563/2023		2a.3a.1 (J.2)	2023-11-10	MDCK-MIX2/SIAT3	320	160	320	320	160	320	320	160	320	320	160	40
	A/Slovenia/49/2024	N158K	2a.3a.1 (J.2)	2024-01-08	MDCKx/SIAT3	<40	<40	80	<40	80	40	80	1280	160	<40	40	<40
	A/Lisboa/216/2023	S124N	2a.3a.1 (J.2)	2023-12-15	E3 (Am1Al2)	320	160	640	640	160	320	320	320	640	320	160	80
	A/France/IDF-IPP29542/2023	R142G, K189R	2a.3a.1 (J.4)	2023-11-30	MDCK1/SIAT2	<40	<40	40	<40	40	40	40	<40	40	40	40	80
	A/Norway/12374/2023		2a.3a.1 (J.4)	2023-11-28	SIAT4	160	80	160	80	80	160	320	80	160	160	80	80
	A/BurkinaFaso/3131/2023	R142G, K189R	2a.3a.1 (J.4)	2023-11-20	SIAT3	40	<40	80	<40	80	40	80	<40	40	80	40	80
	TEST VIRUSES																
244218	A/Catalonia/NSVH102359047/2024		2a.3a.1 (J)	2024-06-07	SIAT2/MDCK1	320	160	320	320	160	160	160	80	80	80	40	<40
244875	A/Luxembourg/2651601/2024		2a.3a.1 (J.1)	2024-02-12	SIAT1	640	320	640	640	160	160	160	80	320	160	80	40
244947	A/CAT/3545207NS/2024		2a.3a.1 (J.1)	2024-02-26	C1/SIAT1	640	320	640	640	160	160	320	80	160	320	80	80
244944	A/CAT/3545572NS/2024		2a.3a.1 (J.1)	2024-03-04	C1/SIAT1	320	160	320	320	80	160	160	80	80	160	40	40
244853	A/Estonia/177999/2024		2a.3a.1 (J.2)	2024-02-03	SIAT2	320	160	320	320	160	320	320	160	320	320	160	40
244945	A/CAT/3545505NS/2024		2a.3a.1 (J.2)	2024-03-04	C1/SIAT1	320	80	320	160	160	160	320	160	320	160	80	40
244946	A/CAT/3545411NS/2024		2a.3a.1 (J.2)	2024-03-04	C1/SIAT1	320	160	320	160	160	160	320	160	320	160	80	40
244943	A/CAT/3545938NS/2024		2a.3a.1 (J.2)	2024-03-11	C1/SIAT1	320	80	160	160	160	160	320	160	320	160	80	40
244942	A/CAT/2175033NS/2024		2a.3a.1 (J.2)	2024-03-21	C1/SIAT1	320	160	320	320	160	160	320	160	320	160	80	40
244941	A/CAT/3549065NS/2024		2a.3a.1 (J.2)	2024-04-21	C1/SIAT1	320	80	320	160	160	160	320	160	160	160	80	40
244940	A/CAT/2194631NS/2024		2a.3a.1 (J.2)	2024-05-02	C1/SIAT1	160	80	320	160	160	160	320	160	320	160	80	40
244904	A/SouthSudan/1069/2024		2a.3a.1 (J.2)	2024-07-12	SIAT1	160	80	160	160	160	160	320	160	320	160	80	40
244899	A/SouthSudan/1064/2024		2a.3a.1 (J.2)	2024-07-17	SIAT1	160	80	160	160	160	160	160	160	320	160	80	40
244901	A/SouthSudan/1062/2024		2a.3a.1 (J.2)	2024-07-17	SIAT1	640	320	640	640	320	320	640	320	640	640	320	80
244887	A/SouthSudan/1045/2024		2a.3a.1 (J.2)	2024-07-29	SIAT1	160	80	160	160	160	160	320	160	320	160	80	40
244886	A/SouthSudan/1044/2024		2a.3a.1 (J.2)	2024-07-31	SIAT1	320	160	160	160	160	160	320	160	320	160	80	40

Vaccine
SH 2024
NH 2024-25

< 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 (no homologous titre)

HI tables: Influenza B

Table BV-13. Antigenic analyses of influenza B viruses (Victoria lineage) 2024-09-11

	Viruses	Other information	Genetic group	Collection Date	Haemagglutination inhibition titre Post-infection ferret antiserum					
						B/Bris 60/08	B/Austria 1359417/21	B/Austria 1359417/21	B/Austria 1359417/21	B/Stock 3/22
					Passage	Egg	MDCK	Egg G141	Egg G141R	MDCK
					Ferret number	Sh 539, 540, 543, 544, 570, 571, 5741	NIB F01/21	F40/21	F44/21	F28/22
					Genetic group	V1A	V1A.3a.2 (C)	V1A.3a.2 (C)	V1A.3a.2 (C)	V1A.3a.2 (C.5)
	REFERENCE VIRUSES									
	B/Brisbane/60/2008		V1A	2008-08-04	E4/E3	2560	40	<40	<40	<40
	B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2 (C)	2021-01-09	SIAT1/MDCK4	640	1280	640	320	640
	B/Austria/1359417/2021	A127T, P144L, K302R (G141)	V1A.3a.2 (C)	2021-01-09	E3/E4	320	1280	640	320	640
	B/Austria/1359417/2021	A127T, P144L, K302R (G141R)	V1A.3a.2 (C)	2021-01-09	E3/E5	320	1280	640	2560	640
	B/Stockholm/3/2022	D129G, E183K, D197E	V1A.3a.2 (C.5)	2022-03-22	SIAT1/MDCK3	320	640	640	320	640
	TEST VIRUSES									
244813	B/Estonia/179145/2024		V1A.3a.2 (C.5)	2024-04-03	MDCK1	320	640	320	160	640
244580	B/HongKong/190/2024		V1A.3a.2 (C.5)	2024-06-14	MDCK 1/MDCK1	640	640	320	160	640
244574	B/HongKong/192/2024		V1A.3a.2 (C.5)	2024-06-21	MDCK 1/MDCK1	640	1280	640	320	640
244864	B/Luxembourg/3510796/2024		V1A.3a.2 (C.5.1)	2024-04-25	MDCK1	320	640	320	320	640
244622	B/Croatia/3095/2024		V1A.3a.2 (C.5.1)	2024-06-10	MDCK1	640	640	320	320	640
244625	B/Croatia/1694/2024		V1A.3a.2 (C.5.6)	2024-03-08	MDCK1	640	640	320	320	1280
244867	B/Luxembourg/9513091/2024		V1A.3a.2 (C.5.7)	2024-03-05	MDCK1	320	640	320	320	640
244812	B/Estonia/179138/2024		V1A.3a.2 (C.5.7)	2024-04-05	MDCK1	320	640	320	320	640
244811	B/Estonia/179136/2024		V1A.3a.2 (C.5.7)	2024-04-07	MDCK1	320	640	320	320	640
244809	B/Estonia/178996/2024		V1A.3a.2 (C.5.7)	2024-04-11	MDCK1	640	640	320	320	640
244624	B/Croatia/2798/2024		V1A.3a.2 (C.5.7)	2024-05-17	MDCK1	320	640	320	160	640
244623	B/Croatia/2825/2024		V1A.3a.2 (C.5.7)	2024-05-20	MDCK1	640	1280	640	320	1280
244578	B/HongKong/191/2024		V1A.3a.2 (C.5.7)	2024-06-15	MDCK 1/MDCK1	640	640	320	320	640
244576	B/HongKong/194/2024		V1A.3a.2 (C.5.7)	2024-06-20	MDCK 1/MDCK1	640	1280	640	640	1280
							Vaccine SH 2022 NH 2022-23 SH 2023 NH 2023-24 SH 2024 NH 2024-25		Vaccine SH 2022 NH 2022-23 SH 2023 NH 2023-24 SH 2024 NH 2024-25	

< 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 (no homologous titre)

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.

					Antigenic characterisation			Genetic characterisation				Antiviral susceptibility phenotypic testing		
Virus name	Original passage sent	Collection date	Type/Subtype	Date received	HI table date	HI comments	WIC Passage history	Genetic clade	Submitted to GISAID	EPI Accession	Sequencing comments	Oseltamivir	Zanamivir	Baloxavir marboxil
B/Estonia/KL2271/2024	cs	2024-04-30	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.6)	2024-09-11	19406533				
B/Estonia/179115/2024	cs	2024-04-25	BV	2024-08-30		Virus not recovered	cs				no sequence			
B/Estonia/KL2201/2024	cs	2024-04-22	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.7)	2024-09-11	19406528				
B/Estonia/KL2193/2024	cs	2024-04-22	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.7)	2024-09-11	19406536				
B/Estonia/179024/2024	cs	2024-04-19	BV	2024-08-30		Virus not recovered	cs				no sequence			
B/Estonia/KL2130/2024	cs	2024-04-11	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.1)	2024-09-11	19406531				
B/Estonia/178996/2024	cs	2024-04-11	BV	2024-08-30	2024-09-11		cs	V1A.3a.2 (C.5.7)	2024-09-11	19406539		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/178996/2024	cs	2024-04-11	BV	2024-08-30	2024-09-11		MDCK1	V1A.3a.2 (C.5.7)	2024-09-26	19440460		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/KL2124/2024	cs	2024-04-10	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.7)	2024-09-11	19406534				
B/Estonia/179136/2024	cs	2024-04-07	BV	2024-08-30	2024-09-11		cs	V1A.3a.2 (C.5.7)	2024-09-11	19406542		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/179136/2024	cs	2024-04-07	BV	2024-08-30	2024-09-11		MDCK1	V1A.3a.2 (C.5.7)	2024-09-26	19440461		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/179138/2024	cs	2024-04-05	BV	2024-08-30	2024-09-11		cs	V1A.3a.2 (C.5.7)	2024-09-11	19406537		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/179138/2024	cs	2024-04-05	BV	2024-08-30	2024-09-11		MDCK1	V1A.3a.2 (C.5.7)	2024-09-26	19440462		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/179145/2024	cs	2024-04-03	BV	2024-08-30	2024-09-11		cs	V1A.3a.2 (C.5)	2024-09-11	19406545		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/179145/2024	cs	2024-04-03	BV	2024-08-30	2024-09-11		MDCK1	V1A.3a.2 (C.5)	2024-09-26	19440463		Normal inhibition	Normal inhibition	Normal inhibition
B/Estonia/178855/2024	cs	2024-04-03	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.6)	2024-09-11	19406541				
B/Estonia/KL2078/2024	cs	2024-04-02	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.7)	2024-09-11	19406548				
B/Estonia/178792/2024	cs	2024-04-02	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.7)	2024-09-11	19406544				
B/Estonia/178789/2024	cs	2024-04-02	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178854/2024	cs	2024-03-30	BV	2024-08-30	2024-09-24		cs	V1A.3a.2 (C.5)	2024-09-11	19406551				
B/Estonia/178854/2024	cs	2024-03-30	BV	2024-08-30	2024-09-24		MDCK1	V1A.3a.2 (C.5)	2024-10-08	19465941				
B/Estonia/178853/2024	cs	2024-03-29	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/KL2050/2024	cs	2024-03-27	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.6)	2024-09-11	19406524				
B/Estonia/KL2055/2024	cs	2024-03-26	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178758/2024	cs	2024-03-26	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178645/2024	cs	2024-03-20	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/KL1912/2024	cs	2024-02-28	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178397/2024	cs	2024-02-28	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178394/2024	cs	2024-02-28	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.1)	2024-09-11	19406523				
B/Estonia/178321/2024	cs	2024-02-25	BV	2024-08-30		Failed sequence – not cultured	cs				no sequence			
B/Estonia/178203/2024	cs	2024-02-13	BV	2024-08-30	2024-09-24		cs	V1A.3a.2 (C.5.1)	2024-09-11	19406527				
B/Estonia/178203/2024	cs	2024-02-13	BV	2024-08-30	2024-09-24		MDCK1	V1A.3a.2 (C.5.1)	2024-10-08	19465942				
B/Estonia/KL1667/2024	cs	2024-01-25	BV	2024-08-30	2024-09-24		cs	V1A.3a.2 (C.5.7)	2024-09-11	19406521				
B/Estonia/KL1667/2024	cs	2024-01-25	BV	2024-08-30	2024-09-24		MDCK1	V1A.3a.2 (C.5.7)	2024-10-08	19465943				
B/Estonia/177730/2024	cs	2024-01-24	BV	2024-08-30		Virus not recovered	cs	V1A.3a.2 (C.5.6)	2024-09-11	19406525				
B/Estonia/177406/2023	cs	2023-12-22	BV	2024-08-30	2024-09-24		cs	V1A.3a.2 (C.5.1)	2024-09-11	19406530				
B/Estonia/177406/2023	cs	2023-12-22	BV	2024-08-30	2024-09-24		MDCK1	V1A.3a.2 (C.5.1)	2024-10-08	19465944				
A/Estonia/178804/2024	cs	2024-04-03	H1pdm	2024-08-30	2024-09-18		cs	5a.2a (C.1.8)	2024-09-11	19406627		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/178804/2024	cs	2024-04-03	H1pdm	2024-08-30	2024-09-18		MDCK2	5a.2a (C.1.8)	2024-09-26	19440499		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/178852/2024	cs	2024-03-28	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.9)	2024-09-11	19406638				
A/Estonia/KL2045/2024	cs	2024-03-26	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.9)	2024-09-11	19406629				
A/Estonia/179137/2024	cs	2024-03-11	H1pdm	2024-08-30	2024-09-11		cs	5a.2a (C.1.9)	2024-09-11	19406640		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/179137/2024	cs	2024-03-11	H1pdm	2024-08-30	2024-09-11		MDCK1	5a.2a (C.1.9)	2024-09-26	19440451		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/178398/2024	cs	2024-02-29	H1pdm	2024-08-30		Virus not recovered	cs				no sequence			
A/Estonia/177712/2024	cs	2024-01-21	H1pdm	2024-08-30	2024-09-11		cs	5a.2a (C.1)	2024-09-11	19406631		Normal inhibition	Normal inhibition	Failed
A/Estonia/177712/2024	cs	2024-01-21	H1pdm	2024-08-30	2024-09-11		MDCK1	5a.2a (C.1)	2024-09-26	19440450		Normal inhibition	Normal inhibition	Failed
A/Estonia/177710/2024	cs	2024-01-21	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.8)	2024-09-11	19406644				
A/Estonia/177687/2024	cs	2024-01-21	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.8)	2024-09-11	19406633				
A/Estonia/177675/2024	cs	2024-01-20	H1pdm	2024-08-30		Virus not recovered	cs				no sequence			
A/Estonia/177672/2024	cs	2024-01-17	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.8)	2024-09-11	19406649				
A/Estonia/177612/2024	cs	2024-01-16	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.9)	2024-09-11	19406635				
A/Estonia/177563/2024	cs	2024-01-15	H1pdm	2024-08-30	2024-09-11		cs	5a.2a (C.1)	2024-09-11	19406777		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177563/2024	cs	2024-01-15	H1pdm	2024-08-30	2024-09-11		MDCK1	5a.2a (C.1)	2024-09-26	19440449		Normal inhibition	Normal inhibition	Normal inhibition

(continued)

					Antigenic characterisation			Genetic characterisation				Antiviral susceptibility phenotypic testing		
Virus name	Original passage sent	Collection date	Type/Subtype	Date received	HI table date	HI comments	WIC Passage history	Genetic clade	Submitted to GISAID	EPI Accession	Sequencing comments	Oseltamivir	Zanamivir	Baloxavir marboxil
A/Estonia/177593/2024	cs	2024-01-12	H1pdm	2024-08-30		Failed sequence – not cultured	cs				no sequence			
A/Estonia/177592/2024	cs	2024-01-11	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.9)	2024-09-11	19406776				
A/Estonia/177568/2024	cs	2024-01-11	H1pdm	2024-08-30	2024-09-24		cs	5a.2a (C.1.9)	2024-09-11	19406779		Normal inhibition	Normal inhibition	
A/Estonia/177568/2024	cs	2024-01-11	H1pdm	2024-08-30	2024-09-24		MDCK1	5a.2a (C.1.9)	2024-10-08	19465925		Normal inhibition	Normal inhibition	
A/Estonia/177534/2024	cs	2024-01-10	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.8)	2024-09-11	19406778				
A/Estonia/177408/2024	cs	2024-01-02	H1pdm	2024-08-30		Virus not recovered	cs	5a.2a (C.1.8)	2024-09-11	19406519				
A/Estonia/179133/2024	cs	2024-03-04	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409565				
A/Estonia/179133/2024	cs	2024-03-04	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440409				
A/Estonia/178187/2024	cs	2024-02-13	H3	2024-08-30	2024-09-10		cs				no sequence			
A/Estonia/178187/2024	cs	2024-02-13	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.1)	2024-09-26	19440408				
A/Estonia/178093/2024	cs	2024-02-12	H3	2024-08-30		Virus not recovered	cs				no sequence			
A/Estonia/178200/2024	cs	2024-02-08	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409564		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/178200/2024	cs	2024-02-08	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440411		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177999/2024	cs	2024-02-03	H3	2024-08-30	2024-09-19		cs	2a.3a.1 (J.2)	2024-09-11	19409562		Insufficient Titre	Insufficient Titre	
A/Estonia/177999/2024	cs	2024-02-03	H3	2024-08-30	2024-09-19		SIAT2	2a.3a.1 (J.2)	2024-09-26	19440477		Insufficient Titre	Insufficient Titre	
A/Estonia/178001/2024	cs	2024-01-30	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.1)	2024-09-11	19409563		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/178001/2024	cs	2024-01-30	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.1)	2024-09-26	19440410		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177892/2024	cs	2024-01-26	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409561				
A/Estonia/177892/2024	cs	2024-01-26	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440413				
A/Estonia/177843/2024	cs	2024-01-23	H3	2024-08-30		Virus not recovered	cs	2a.3a.1 (J.2)	2024-09-11	19409560				
A/Estonia/177610/2024	cs	2024-01-15	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409559		Insufficient Titre	Insufficient Titre	
A/Estonia/177610/2024	cs	2024-01-15	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440412		Insufficient Titre	Insufficient Titre	
A/Estonia/177562/2024	cs	2024-01-12	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409557		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177562/2024	cs	2024-01-12	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440415		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177583/2024	cs	2024-01-10	H3	2024-08-30		Virus not recovered	cs				no sequence			
A/Estonia/177566/2024	cs	2024-01-10	H3	2024-08-30	2024-09-10		cs	2a.3a.1 (J.2)	2024-09-11	19409558		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177566/2024	cs	2024-01-10	H3	2024-08-30	2024-09-10		SIAT1	2a.3a.1 (J.2)	2024-09-26	19440414		Normal inhibition	Normal inhibition	Normal inhibition
A/Estonia/177533/2024	cs	2024-01-09	H3	2024-08-30		Virus not recovered	cs	2a.3a.1 (J.2)	2024-09-11	19409556				

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 from 1 February 2024 until 31 August 2024 informed the WHO influenza vaccine composition meeting (VCM) in September 2024 when recommendations were made for the Southern hemisphere (SH) 2025 influenza season. At the September 2024 VCM it was recommended to change the A(H3N2) vaccine components for the 2025 SH season. Previously, at the February 2024 VCM, which focused on data from viruses collected from 1 September 2023 until 31 January 2024, it was also recommended to change the A(H3N2) vaccine components for the 2024–2025 NH season

It is recommended that vaccines for use in the 2025 SH influenza season contain the following:

Trivalent: Egg-based Vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Croatia/10136RV/2023 (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/District of Columbia/27/2023 (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 reported as confirmed detection or sequences released in GISAID as of 30 September 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.

Seasonal 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, 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, see Annex) 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.1.2)**
            - signature amino acid substitutions Clade 5a.2a (C.1) + A48P
            - Reference virus: A/Maine/10/2022
        - **Clade 5a.2a (C.1.3)**
            - signature amino acid substitutions Clade 5a.2a (C.1) + A73T, A141E, V152I, S190I, T216A
            - Reference virus: A/Washington/22/2023
        - **Clade 5a.2a (C.1.4)**
            - signature amino acid substitutions Clade 5a.2a (C.1) + S85P, H273Q, V321I
            - Reference virus: A/Maldives/936/2023
        - **Clade 5a.2a (C.1.5)**
            - signature amino acid substitutions Clade 5a.2a (C.1) + I185V
            - Reference virus: A/Bulgaria/234/2023
        - **Clade 5a.2a (C.1.6)**
            - signature amino acid substitutions Clade 5a.2a (C.1) 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 (C.1) + I533V
            - Reference virus: A/Darwin/422/2023

- **Clade 5a.2a (C.1) + I418V**
    - Reference virus: A/Netherlands/10468/2023
    - **Clade 5a.2a (C.1.8)**
        - signature amino acid substitutions Clade 5a.2a (C.1) + I418V + V47I
        - Reference virus: A/Michigan/62/2023
    - **Clade 5a.2a (C.1.9)**
        - signature amino acid substitutions Clade 5a.2a (C.1) + I418V + K169Q
        - Reference virus: A/Lisboa/188/2023
- **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 (D, former 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.1 (D.1)**
        - signature amino acid substitutions Clade 5a.2a.1 (D) + R45K
        - Reference virus: A/Netherlands/10481/2024
    - **Clade 5a.2a.1 (D.2)**
        - signature amino acid substitutions Clade 5a.2a.1 (D) + R113K, V427I
        - Reference virus: A/Bretagne/05126/2024
    - **Clade 5a.2a.1 (D.3)**
        - signature amino acid substitutions Clade 5a.2a.1 (D) + T120A, I372V
        - Reference virus: not assigned yet
    - **Clade 5a.2a.1 (D.4)**
        - signature amino acid substitutions Clade 5a.2a.1 (D) + T120A
        - Reference virus: A/Poland/28/2024

A(H3N2)

All A(H3N2) viruses detected since February 2023 belong to **Clade 2** (former 3C.2a1b.2a.**2**). Several clades and subclades emerged, of which clade **2a.3a.1 (J)** predominated, with some detection of clade **2a.3a (G.1.3.1).**

- **Clade 2a (G.1)**
    - Signature amino acid substitutions Clade 2 + H156S
    - Vaccine virus: A/Darwin/9/2021

Signature amino acid substitutions are described against A/Darwin/9/2021 from here onwards

- **Clade 2a.3 (G.1.3)**
    - Signature amino acid substitutions Clade 2a + D53N, N96S (+CHO), I192F
    - Reference virus: A/Norway/24873/2021
    - **Clade 2a.3a (G.1.3.1)**
        - 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 (J) + I25V, V347M
      - Reference virus: A/Sydney/856/2023
    - **Clade 2a.3a.1 (J.1.1)**
      - Signature amino acid substitutions Clade 2a.3a.1 (J.1) + S145N
      - Reference virus: A/Canberra/331/2023
  - **Clade 2a.3a.1 (J.2)**
    - Signature amino acid substitutions Clade 2a.3a.1 (J) + K276E
    - Vaccine virus: A/Croatia/10136RV/2023
    - **Clade 2a.3a.1 (J.2.1)**
      - Signature amino acid substitutions Clade 2a.3a.1 (J.2) + P239S
      - Reference virus: A/West Virginia/51/2024
    - **Clade 2a.3a.1 (J.2.2)**
      - Signature amino acid substitutions Clade 2a.3a.1 (J.2) + S124N
      - Reference virus: A/Lisboa/216/2023
  - **Clade 2a.3a.1 (J.3)**
    - Signature amino acid substitutions Clade 2a.3a.1 (J) + V505I
    - Reference virus: none assigned
  - **Clade 2a.3a.1 (J.4)**
    - Signature amino acid substitutions Clade 2a.3a.1 (J) + Q173R, K276E
    - Reference virus: A/France/IDF-IPP29542/2023

Influenza type B viruses

B/Victoria/2/87 lineage

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

Since February 2023, all B/Victoria viruses detected globally belong to **clade V1A.3a.2.**

- **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 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, K203R
        - Vaccine virus: B/Austria/1359417/2021
      - **Clade V1A.3a.2 (C.2)**
        - Signature amino acid substitutions Clade V1A.3a.2 (C) +T182A, D197E, T221A
        - Reference virus: B/Netherlands/10335/2023
      - **Clade V1A.3a.2 (C.3)**
        - Signature amino acid substitutions Clade V1A.3a.2 (C) +E128K, A154E, S208P
        - Reference virus: B/Moldova/2030521/2023
      - **Clade V1A.3a.2 (C.5)**
        - Signature amino acid substitutions Clade V1A.3a.2 (C) +D197E
        - Reference virus: B/Stockholm/3/2022

- **Clade V1A.3a.2 (C.5.1)**
  - Signature amino acid substitutions Clade V1A.3a.2 (C.5) +E183K
  - Reference virus: B/Catalonia/2279261NS/2023
- **Clade V1A.3a.2 (C.5.4)**
  - Signature amino acid substitutions Clade V1A.3a.2 (C.5) +V117I, E128K, A154T, K326R
  - Reference virus: B/Catalonia/3514402NS/2023
- **Clade V1A.3a.2 (C.5.6)**
  - Signature amino acid substitutions Clade V1A.3a.2 (C.5) +D129N
  - Reference virus: B/Switzerland/329/2024
- **Clade V1A.3a.2 (C.5.7)**
  - Signature amino acid substitutions Clade V1A.3a.2 (C.5) +E128G
  - Reference virus: B/Guangxi-Beiliu/2298/2023