Influenza virus characterization

Summary report, Europe, May 2024

Contents

Acknowledgements

This report was prepared by the Worldwide Influenza Centre, Francis Crick Institute (WIC), with contributions from:

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 May 2024.
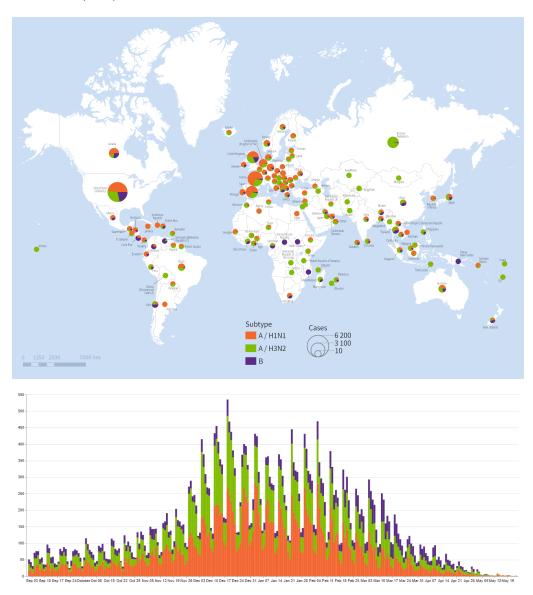
The absence of confirmed detection of naturally occurring B/Yamagata lineage viruses is indicative of very low risk of infection by B/Yamagata lineage viruses. Therefore, it is the opinion of the WHO influenza vaccine composition advisory committee that inclusion of a B/Yamagata lineage antigen in quadrivalent 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.

Influenza by type/subtype

Worldwide
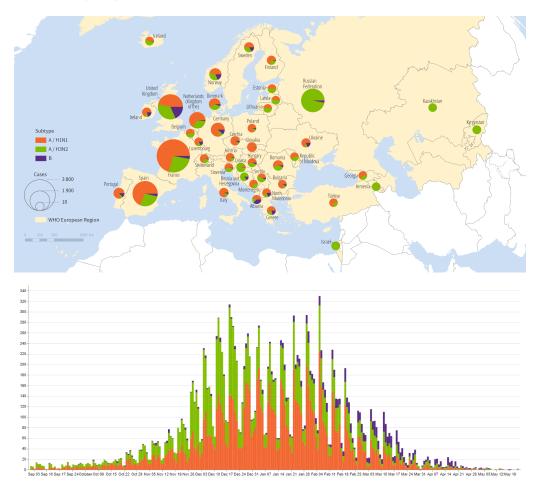
Geographical and time-dependent distribution of influenza viruses with collection dates from 1st September 2023 through to 31st May 2024 as deposited in GISAID (data accessed on 31/05/2024), coloured by Type/subtype. Geographic markers scaled to detection proportions. Full length HA. Map provided by WHO GIS Centre for Health, DNA/DDI. Timeline obtained with Microreact

Globally, influenza detections reached a peak in December 2023, have decreased since the report in January 2024 and continue to be low since the last report in March 2024. The relative proportions of A/H1N1, A/H3N2 and B/Victoria varied by geographic region with predominance of A/H3N2 in Europe and North and Central America and some predominance of A/H1N1 in Asia, Africa and Australia. Some countries showed some predominance of B/Victoria such as Costa Rica, Colombia, Venezuela, Chile, South Africa, Mozambique and Slovenia, as indicated by the different colours in the pie charts by country.

European region

Geographical distribution in the European region of influenza viruses with collection dates from 1st September 2023 through to 31st May 2024 as deposited in GISAID (data accessed on 31/05/2024), coloured by Type/subtype. Geographic markers scaled to detection proportions. Full length HA.Map provided by WHO GIS Centre for Health, DNA/DDI.Timeline obtained with Microreact

In the European region, influenza detections have continued to be low since the last report in March 2024.

The majority of countries which reported detections showed some co-circulation of A/H1N1 and A/H3N2 with predominance of A/H3N2 viruses and sporadic detections of influenza B/Victoria, as indicated by the different colours in the pie charts.

Summary of influenza detections in the WHO European Region, week 35/2023 to 22/2024

Table 1 shows influenza virus detections in the WHO European Region reported to The European Surveillance System (TESSy) database from 1st September 2023 (weeks 35/2023 to 22/2024) compared with the same period in the previous season. For type-percentage calculations, the denominator is total detections; for subtype and lineage, it is the total influenza A subtyped and total influenza B lineage determined, respectively. As not all countries have a true non-sentinel testing denominator, no percentage calculations for total tested are shown (Data taken from Flu News Europe reports and from ERVISS (European Respiratory Virus Surveillance Summary)).
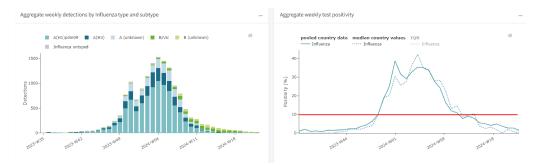
Virus type/subtype/lineage	Cumulative number of detections for weeks 35/2023 to 22/2024				Cumulative number of detections for weeks 35/2022 to 22/2023			
	Sentinel sources	Non-sentinel sources	Totals	%	Sentinel sources	Non-sentinel sources	Totals	%
Influenza A	13293	152339	165632	95	10563	124649	135212	69
A(H1N1)pdm09	8846	24570	33416	73	3131	19816	22947	61
A(H3N2)	2369	9724	12093	27	4310	10427	14737	39
A not subtyped	2078	118045	120123	NA	3122	94406	97528	NA
Influenza B	1416	7913	9329	5	6527	55300	61827	31
Victoria lineage	782	1548	2330	100	1682	3233	4915	100
Yamagata lineage	0	0	0	NA	0	0	0	NA
Lineage not ascribed	634	6365	6999	NA	4845	52067	56912	NA
Total detections	14709	160252	174961	NA	17090	179949	197039	NA
Total tested	96271	1705173	1801444	NA	91929	1814474	1906403	NA

Compared with the same period (weeks 35/2022 to 22/2023), for sentinel surveillance the number of specimens tested is slightly higher, whereas the number of influenza detections has slightly decreased. For non-sentinel surveillance, the number of tested specimens and the number of detections was slightly lower in the current season compare to last season. During the current season, the proportion of influenza A of unknown subtype among sentinel cases has maintained consistently around 15% of the total influenza A detected, compared with 18% in last season; for non-sentinel cases, not-subtyped influenza A detections accounted for 76% of the total influenza A detected in 2023–24, compared with 52% for 2022–23.

Relative frequencies of type A vs B influenza viruses continue to show predominance of influenza A with a proportion of 95% compared with 69% in 2022–2023. Currently, in Europe there are sporadic detections of influenza B (5%), and predominance was circumscribed to a few countries. Relative frequencies of influenza A subtypes have also shifted, with A/H1N1 viruses increasing from 61% to 73% frequency, and a higher proportion of circulating A/H1N1 viruses (73% A/H1N1 vs 27% A/H3N2) compared to last season (61% A/H1N1 vs 39% A/H3N2).

Sentinel surveillance system dynamics, week 35/2023 to 22/2024
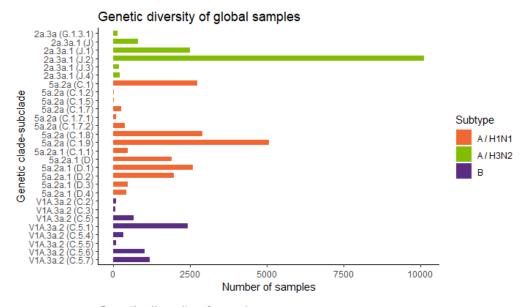
Figure adapted from ERVISS
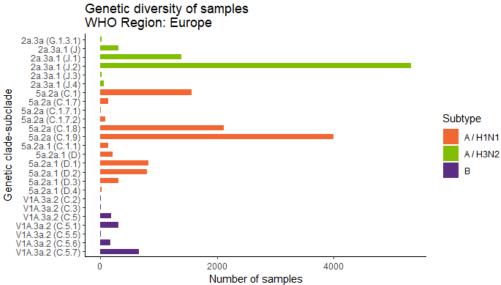
During the period from week 35/2023 to week 22/2024, influenza activity remained at low levels through the reporting period until week 46 when it started to increase, crossing the epidemic threshold of 10% in week 50. This marks a late start of the influenza season when compared with the previous season where the epidemic threshold of 10% had been crossed by week 45.Influenza activity peaked briefly in week 1 and then again in week 5, then started to decrease until it fell below the 10% threshold in week 11. Since the last report in week 13, influenza activity remained low in the European region.

Across sentinel surveillance, influenza A/H3N2 and A/H1N1 viruses cocirculated with predominance of A/H1N1 during most of this period, with overall frequencies of 79% for A/H1N1 and 21% for A/H3N2. From week 8 onwards the proportion of influenza B increased slightly, to become predominant in week 13, although overall influenza detections are low.

Genetic diversity by Type/Lineage and group

Genetic diversity of global samples

Genetic diversity of samples
WHO Region: Europe

Influenza A/H1N1

Genetic analyses: A/H1N1
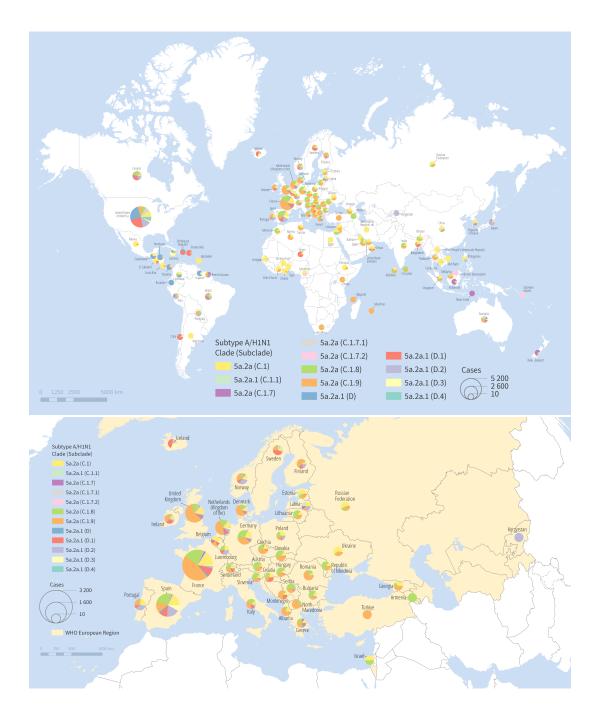
6B.1A.**5a.2a** and 6B.1A.**5a.2a.1** clade viruses both continued to circulate with differing relative proportions depending on region, with an overall predominance of 5a.2a viruses.

In Europe, both 5a.2a and 5a.2a.1 viruses were detected, with 5a.2a increasing in frequency over time until predominating in 70% of A/H1N1 sequenced viruses by week 07/2024, then decreasing to 60% by week 16/2024.
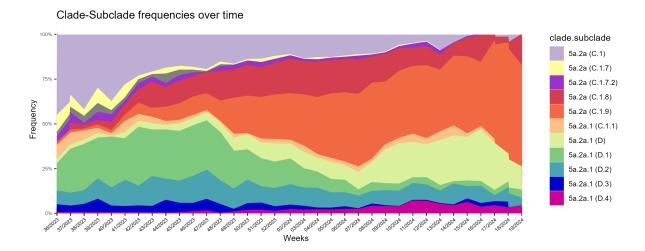
Within the 5a.2a viruses, characterised by substitutions K54Q, A186T, E224A, R259K and K308R, several subclades were observed: subclade C.1 defined by substitution I418V (reference A/Sydney/5/2021) which split into two further subclades: C.1.8, characterised by V47I with I96T in most sequences, and C.1.9, with substitution K169Q (no references assigned yet); the majority of H1pdm viruses sequenced in Europe, Africa and Asia belong to these three subclades. 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. This subclade has been further split into subclades C.1.7.1, circulating mostly in Australia, and C.1.7.2 with T120A and K142R circulating in low frequencies in several countries.

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, detected in the Americas, which has split into four subclades: D.1 with R45K, which predominates in Sweden, Iceland, Niger, Chile, Dominican Republic and Puerto Rico; D.2 with R113K and V427I, which predominates in Japan, Kyrgyzstan and Peru; D.3 with T120A and I372V circulating in several countries and D.4 with T120A detected in US and Brazil. 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 circulating with decreasing frequencies in Brazil, US, Eastern Europe and South East Asia.

Global and European geographical distribution of influenza A/H1N1 genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade.Geographic markers scaled to detection proportions. Map provided by WHO GIS Centre for Health, DNA/DDI
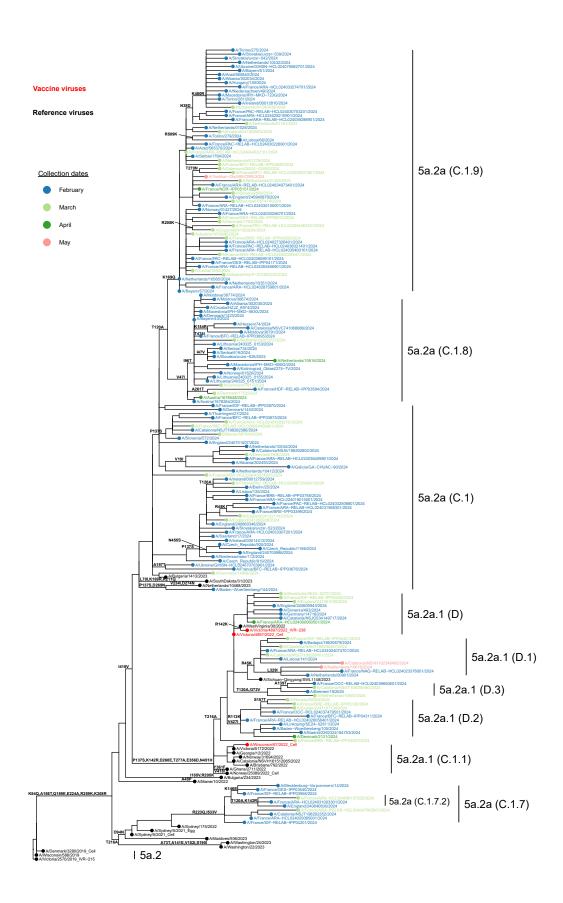
Global time-dependent variation in frequencies of genetic clades-subclades of A/H1N1 viruses collected since 1st September 2023.

Clade-Subclade frequencies over time

Maximum likelihood Phylogenetic tree: A/H1N1

Maximum likelihood phylogenetic tree inferred using Iqtree2 from HA sequence data obtained from GISAID from 1st September onwards. Trees were manually curated and, if sequence numbers were > 200, downsampled using Treemer to retain a representative tree topology of 200 sequences with emphasis on viruses from the European region. Annotation of amino acids substitutions was performed with Treetime ancestral reconstruction; all reference viruses and tree nodes with more than one sequence were annotated. References and CVVs are marked as Cell or Egg.

Summary of the antigenic properties of A/H1N1 viruses circulating in the reporting period

Both cell- and egg-based NH 2023–24 strain (A/Victoria/4897/2022) recognises both 5a.2a and 5a.2a.1 well.

For an overall picture of the genetic and antigenic relationships across viruses collected during the past season, see the Annex.

A/H1N1: References

Virus	Genetic group	Virus passage	Ferret ID
IVR-215 (A/Victoria/2570/2019)	5a.2	E4/D7/E3	F37/21
A/Sydney/5/2021	5a.2a	MDCK3/MDCK3	F46/22
A/Sydney/5/2021	5a.2a	E3/E3	F04/22
A/Victoria/4897/2022	5a.2a.1	SIAT2/MDCK2	F05/23
IVR-238 (A/Victoria/4897/2022)	5a.2a.1	E3/D6/E1	F07/23
A/Wisconsin/67/2022	5a.2a.1	MDCK2	F17/23

Influenza A/H3N2

Genetic analyses: A/H3N2
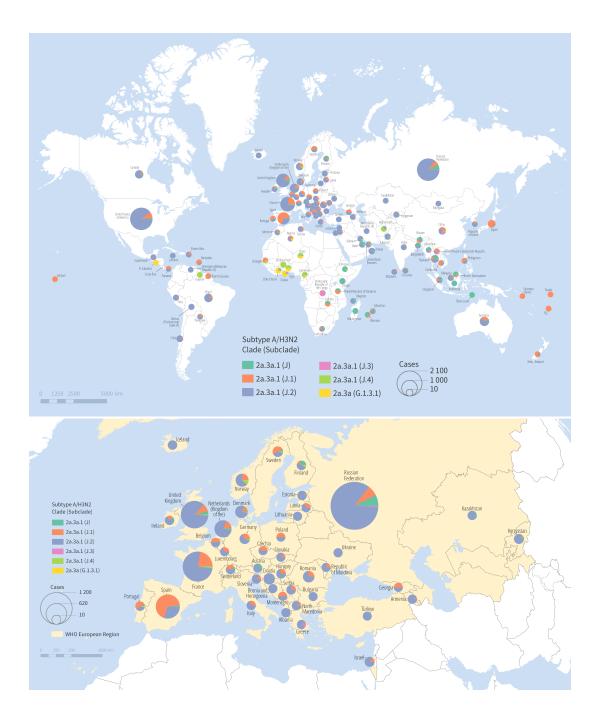
Please note that within clade 2a.3a.1, former subclade H and derivatives (H.1 to H.4) have been renamed as J (J.1 to J.4).

Clade 3C.2a1b.2a.2 (renamed as **2**) predominated since February 2023 in all geographic regions where A/H3N2 circulated.
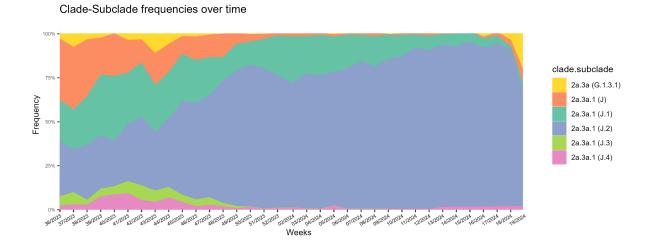
During this reporting period, the great majority of H3 viruses detected belong to clade 2a.3a.1, which share substitution E50K with clade 2a.3a and present additional substitutions I140K and I223V (subclade J, reference A/Thailand/8/2022). Some viruses from subclade J clustered in a separate branch with 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 and El Salvador.

Global and European geographical distribution of influenza A/H3N2 genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade.Geographic markers scaled to detection proportions. Map provided by WHO GIS Centre for Health, DNA/DDI

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

Clade-Subclade frequencies over time

Maximum likelihood phylogenetic tree: A/H3N2

Maximum likelihood phylogenetic tree inferred using Iqtree2 from HA sequence data obtained from GISAID from 1st September onwards. Trees were manually curated and, if sequence numbers were > 200, downsampled using Treemer to retain a representative tree topology of 200 sequences with emphasis on viruses from the European region. Annotation of amino acids substitutions was performed with Treetime ancestral reconstruction; all reference viruses and tree nodes with more than one sequence were annotated. References and CVVs are marked as Cell or Egg.

Vaccine viruses

Reference viruses

Collection dates
- February
- March
- April
- May

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

2a.3a.1 (J)

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

2a.3a.1 (J)

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

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

2a.3a

Summary of the antigenic properties of A/H3N2 viruses circulating in the reporting period

We note 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.

For an overall picture of the genetic and antigenic relationships across viruses collected during the past season, see the Annex.

A/H3N2: HI reagents and references

Virus	Genetic group	Virus passage	Ferret ID
A/Thuringen/10/2022	2b	P1/SIAT2	F36/22
A/Stockholm/5/2021	2a	SIAT0/SIAT3	F35/21
A/Darwin/9/2021	2a	E3/E4	F39/21
A/Catalonia/NSVH161512067/2022	2a.1b	SIAT1/SIAT3	F41/22
A/Albania/289813/2022	2a.3a.1	MDCK1	F21/23
A/Brandenburg/15/2022	2a.3a.1	E5(Am1AI2)	F18/23
A/Switzerland/28719/2022	2b	SIAT1	F29/23
A/Massachusetts/18/2022	2a.3a.1	SIAT3/SIAT1	F36/23
A/California/122/2022	2a.3a.1	E1/E1	F33/23
A/Thailand/08/2022	2a.3a.1	E3/E1	F34/23
IVR-237(A/Thailand/08/2022)	2a.3a.1	E3/D7/E1	F35/23

Influenza B

Genetic analyses: B/Victoria

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.
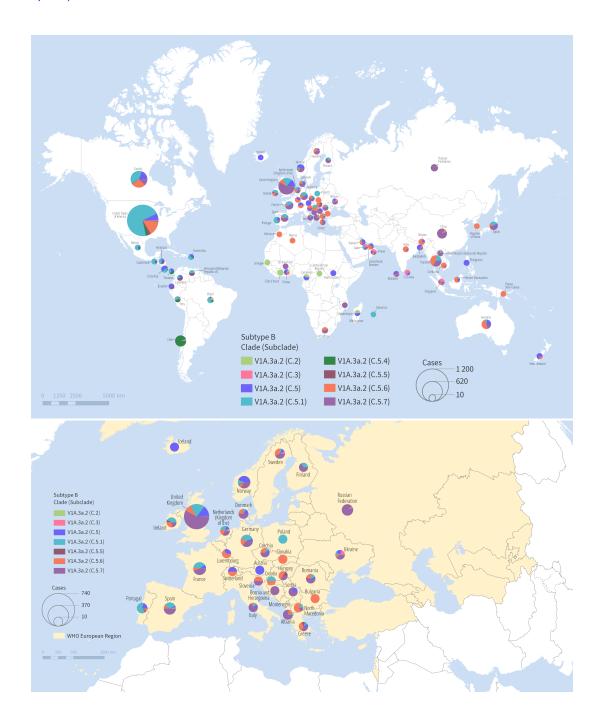
During this reporting period, only a minority of B/Victoria viruses were detected and characterised in Europe. Within V1A.3a.2, subclade C.5 characterised by D197E represents the majority of influenza B viruses characterised during the current influenza season. The most frequent subclades observed within C.5 are: C.5.1 with E183K represented by B/Catalonia/2279261NS/2023, as the dominant subclade predominating in North America and some countries in Central America, Brazil and Portugal and detected in several other countries in minor proportions; C.5.6 (B/Norway/08717/2023) with D129N predominating in Australia, South East Asia, Middle East and some European countries; C.5.7 (no reference assigned yet) with E183K and E128G predominating in China, Japan, Russian Federation, South Africa and some countries in Europe. Other subclades such as C.5.4 (B/Slovenia/924/2023) with V117I, E128K, A154T and K326R were detected in Chile and Peru, and C.5.5 (B/Paraguay/2102/2023) with R80G, E184K were detected in Colombia, Venezuela and the US.

Outside of C.5 viruses, other subclades such as C.2 (T182A, D197E, B/Netherlands/10335/2023) were detected in Africa and Brazil, and C.3 (E128K, A154E, S208P, B/Norway/5216/2023) was detected in very low proportions across the globe.
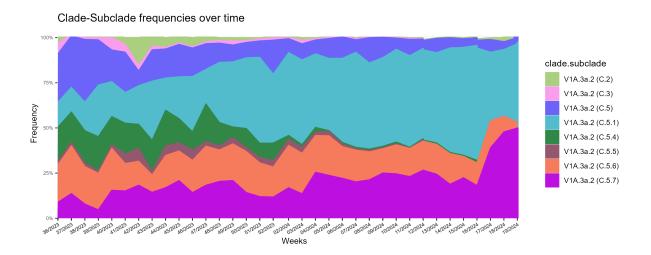
No Clade V1A.3 viruses were detected since 1st February 2023.

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

Global and European geographical distribution and time-dependent frequencies of influenza B/Victoria genetic clades (subclades) viruses, obtained with full HA sequences as deposited in GISAID and classified using Nextclade.Geographic markers scaled to detection proportions. Map provided by WHO GIS Centre for Health, DNA/DDI
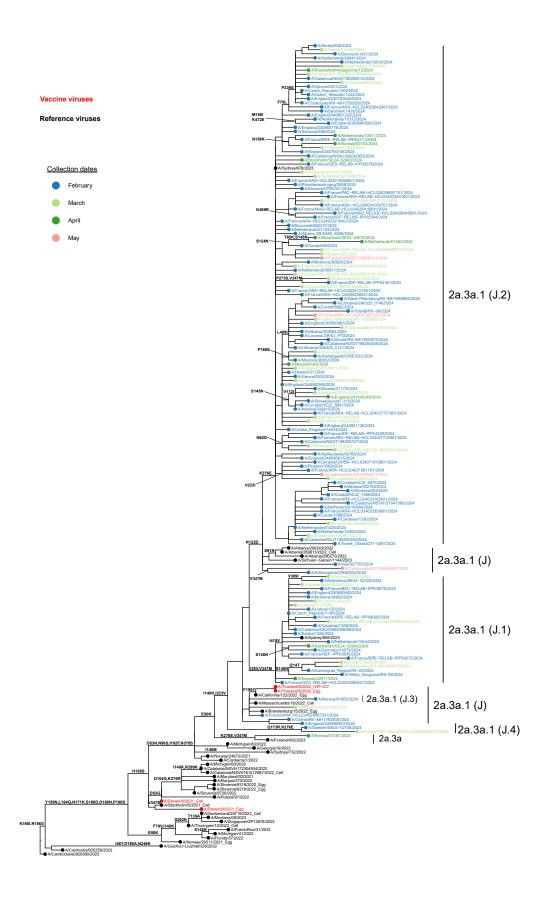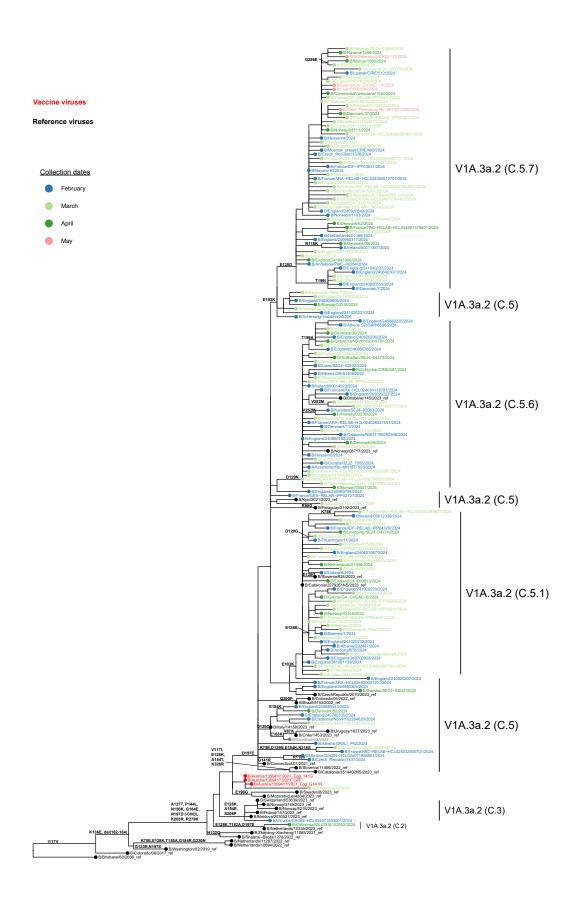
Global time-dependent variation in frequencies of genetic clades-subclades of B/Victoria viruses collected since 1st September 2023.

Clade-Subclade frequencies over time

Maximum likelihood phylogenetic tree: B/Victoria

Maximum likelihood phylogenetic tree inferred using Iqtree2 from HA sequence data obtained from GISAID from 1st September onwards. Trees were manually curated and, if sequence numbers were > 200, downsampled using Treemer to retain a representative tree topology of 200 sequences with emphasis on viruses from the European region. Annotation of amino acids substitutions was performed with Treetime ancestral reconstruction; all reference viruses and tree nodes with more than one sequence were annotated. References and CVVs are marked as Cell or Egg.

Summary of the antigenic properties of B/Victoria lineage viruses circulating in the reporting period

Very few B/Victoria viruses collected since 1st September have been phenotypically characterized by haemagglutination inhibition (HI). All V1A.3a.2 viruses tested were well-recognised by antisera raised against B/Austria/1359417/2021 and -like viruses.

For an overall picture of the genetic and antigenic relationships across viruses collected during the past season, see the Annex.

B/Victoria: Reagents and references

Virus	Genetic group	Virus passage	Ferret ID
B/Brisbane/60/2008	V1A	E4/E4	sheep pool
B/Stockholm/3/2022	V1A.3a.2	SIAT1/MDCK3	F28/22
B/Austria/1359417/2021	V1A.3a.2	SIAT1/MDCK4	NIB F01/21
B/Austria/1359417/2021 G141	V1A.3a.2	E3/E5	F15/21
B/Austria/1359417/2021 G141R	V1A.3a.2	E3/E5	F44/21

Antiviral susceptibility testing

At the WIC, influenza viruses detected within the WHO European Region since 1st September 2023 (weeks 35/2023 to 22/2024) were assessed for phenotypic and/or genotypic susceptibility to antivirals. Of these, 208 A/H1N1, 232 A/H3N2 and 54 B/Victoria viruses were phenotypically assessed against oseltamivir and zanamivir. All viruses showed Normal Inhibition (NI) by both NAIs.

Phenotypic testing for susceptibility to baloxavir marboxil was performed for 168 A/H1N1, 169 A/H3N2 viruses and 32 B/Victoria viruses, with all of them showing Normal Inhibition.

Genotypic assessment of 762 A/H1N1, 410 A/H3N2 and 86 B/Victoria neuraminidase (NA) gene sequences from influenza viruses detected within the WHO European Region since 1st September 2023 and received at the WIC did not find any marker associated with reduced susceptibility to NAI, except for one A/H1N1 with substitution H275Y (phenotypic test pending), 25 A/H1N1 viruses with a S247N substitution (phenotypic test showing NI)and 3 A/H1N1 viruses with a double substitution S247N + I223V; these double mutant viruses showed slightly reduced inhibition which was just under the 10-fold reduction threshold, still classified as NI.

For 690 A/H1N1, 404 A/H3N2 and 87 B/Victoria viruses where PA gene sequencing was successful, no markers associated with reduced inhibition by baloxavir marboxil were identified, except for one A/H1N1 virus with substitution E23K (slightly reduced inhibition, under RI threshold) and an A/H3N2 virus with I38V (phenotypic test pending).

Summaries of data submitted to TESSy

Genetic characterization

(According to the guidance produced for TESSy reporting at the beginning of the 2023–2024 influenza season)

Overall, 5910 viruses detected from week 35/2023 to 22/2024 were genetically characterized:

• Of 3868 A/H1N1 viruses, all belonged to clade 6B.1A.5a.2 (clade **5a.2**) with 2662 (69%) represented by A/Sydney/5/2021 (5a.2a), 1155 (30%) by A/Victoria/4897/2022 (5a.2a.1) and 44 (1%) by A/Wisconsin/67/2022 (5a.2a.1), while two (<1%) viruses were unclassified and five (<1%) were allocated to the 'Subgroup Not Listed' category.

• Of 1538 A/H3N2 viruses, all belonged to clade (3C.2a1b.2a.2, renamed as **2**) with 1493 (97%) represented by A/Thailand/8/2022 (clade 2a.3a.1), 30 (2%) represented by A/Darwin/9/2021 (clade 2a), 11 (0.7%) represented by A/Finland/402/2023 (clade 2a.3a) and one virus (<1%) represented by A/Sydney/732/2022 (clade 2a.3b). One (<1%) H3 virus was unclassified and two (<1%) were allocated to the 'Subgroup Not Listed' category.

• Of 504 B/Victoria-lineage viruses,all belonged to clade V1A.3a.2, with 368 (73%) represented by B/Catalonia/2279261NS/2023 (subclade C.5.1), 95 (19%) represented by B/Connecticut/01/2021 (subclade C.5), 38 (7.5%) represented by B/Austria/1359417/2021 (subclade C) and three viruses (<1%) represented by B/Moldova/2030521/2023 (subclade C.3). No viruses were allocated to the 'Subgroup Not Listed' category.

Susceptibility to antivirals

Between weeks 35 and 39/2023, 8 viruses were assessed for susceptibility to neuraminidase inhibitors and 7 were assessed for susceptibility to baloxavir marboxil. Phenotypically and/or genotypically, no markers associated with reduced susceptibility were identified.
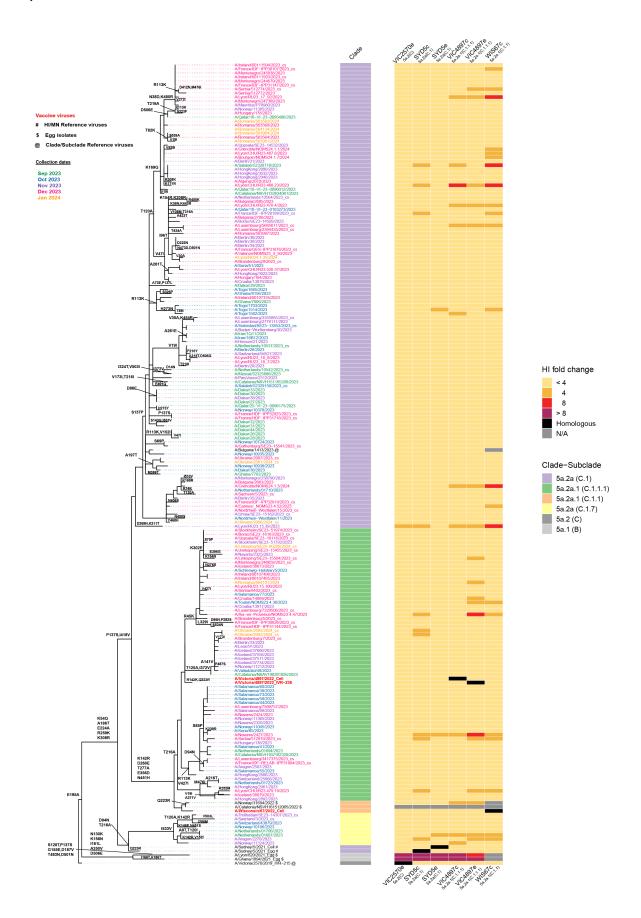
No antiviral susceptibility data was available so far for weeks 40/2023 to 22/2024 of season 2023–2024.

Annex

Heatmapped phylogenetic trees represent the combined genetic and antigenic analyses where the correlation between genetic groups, signature amino acids and their antigenic profile (including microneutralisation for A/H3N2) can be observed.

These outputs were generated by the London WHO Collaborating Centre at the WIC for the NH 2024–2025 February VCM with influenza viruses with collection dates between 1st September 2023 and 31st February 2024.
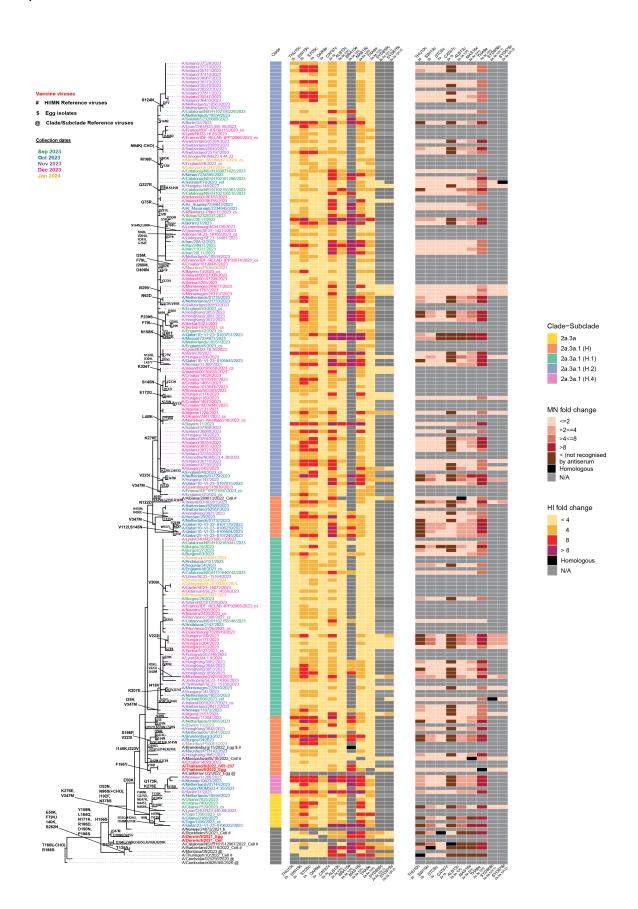
A/H1N1

HI titres show that the SH2023 vaccine strain (A/Sydney/5/21 cell 5a.2), the cell- and egg-based NH 2023–24 strain (A/Victoria/4897/2022) recognises both 5a.2a and 5a.2a.1 well.

Reference Virus	clade	<4-fold difference		4-fold difference		>4-fold difference		
		number	percentage	number	percentage	number	percentage	total
IVR-215 (A/Victoria/2570/2019) Egg	5a.2	278	99.6	1	0.4	0	0.0	279
A/Sydney/5/2021 Cell	5a.2a	265	95.0	14	5.0	0	0.0	279
A/Sydney/5/2021 Egg	5a.2a	276	98.9	3	1.1	0	0.0	279
A/Victoria/4897/2022 Cell	5a.2a.1	268	96.1	10	3.6	1	0.4	279
IVR-238 (A/Victoria/4897/2022) Egg	5a.2a.1	261	93.5	16	5.7	2	0.7	279
A/Wisconsin/67/2022 Cell	5a.2a.1	253	90.7	21	7.5	5	1.8	279
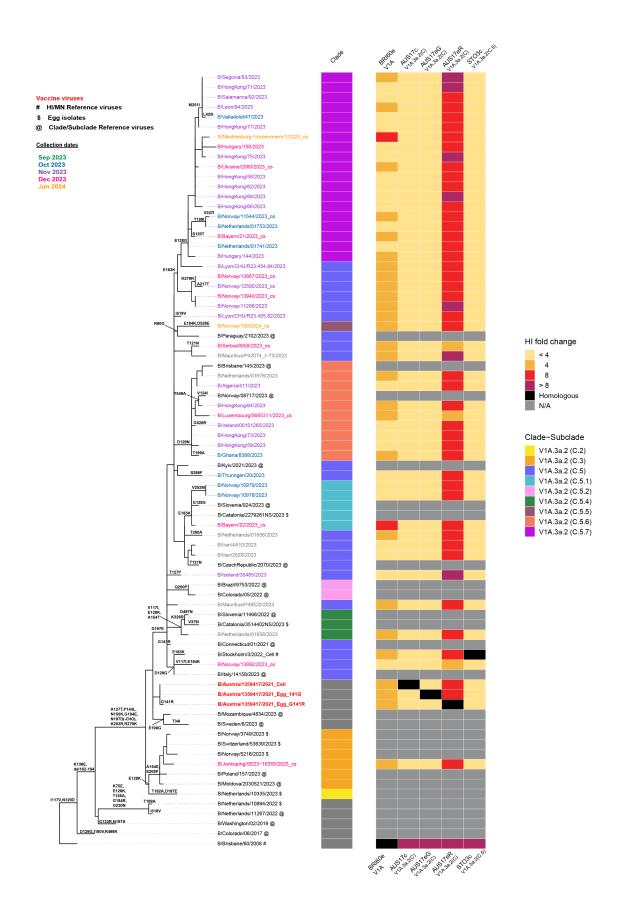
A/H3N2

We note 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.

Reference Virus	clade	<4-fold difference		4-fold difference		>4-fold difference		total
		number	percentage	number	percentage	number	percentage	
A/Thuringen/10/2022 Cell	2b	146	61.6	80	33.8	11	4.6	237
A/Switzerland/28719/2022 Cell	2b	55	23.2	121	51.1	61	25.7	237
A/Stockholm/5/2021 Cell	2a	96	40.5	103	43.5	38	16.0	237
A/Darwin/9/2021 Egg	2a	206	86.9	30	12.7	1	0.4	237
A/Catalonia/NSVH161512067/2022 Cell	2a.1b	57	24.1	129	54.4	51	21.5	237
A/Albania/289813/2022 Cell	2a.3a.1	194	81.9	31	13.1	12	5.1	237
A/Brandenburg/15/2022 Egg	2a.3a.1	2	3.3	13	21.7	45	75.0	60
A/Massachusetts/18/2022 Cell	2a.3a.1	96	40.5	99	41.8	42	17.7	237
A/Thailand/08/2022 Egg	2a.3a.1	174	73.4	59	24.9	4	1.7	237

B/Victoria

Vaccine viruses
\#   HI/MN Reference viruses
$ Egg isolates
@   Clade/Subclade Reference viruses

Collection dates
Sep 2023
Oct 2023
Nov 2023
Dec 2023
Jan 2024

Clade

BRI60e V1A
AUS17c V1A.3a.2(C)
AUS17eG V1A.3a.2(C)
AUS17eR V1A.3a.2(C)
STO3c V1A.3a.2(C.5)

B/Segovia/93/2023
B/HongKong/71/2023
B/Salamanca/92/2023
B/Leon/94/2023
M251I
L425I
B/Valladolid/47/2023
B/HongKong/77/2023
B/Mecklenburg–Vorpommern/1/2024_cs
B/Hungary/150/2023
B/HongKong/75/2023
B/Ukraine/2060/2023_cs
B/HongKong/58/2023
B/HongKong/62/2023
B/HongKong/68/2023
B/HongKong/66/2023
V247I
T199I   B/Norway/11544/2023_cs
B/Netherlands/01753/2023
S120T   B/Bayern/21/2023_cs
E128G   B/Netherlands/01741/2023
B/Hungary/144/2023
E183K   B/Lyon/CHU/R23.454.84/2023
K279R   B/Norway/13867/2023_cs
A217T   B/Norway/12590/2023_cs
B/Norway/13940/2023_cs
B/Norway/11286/2023
I519V   B/Lyon/CHU/R23.455.82/2023
R80G   E184K,D526E   B/Norway/100/2024_cs
B/Paraguay/2102/2023 @
T121N   B/Serbia/8059/2023_cs
B/Mauritius/P42074_I–73/2023
B/Brisbane/145/2023 @
B/Netherlands/01676/2023
B/Algeria/411/2023
T548A   V124I   B/Norway/08717/2023 @
B/HongKong/64/2023
G528R   B/Luxembourg/5685311/2023_cs
B/Ireland/00101265/2023
D129N   B/HongKong/73/2023
B/HongKong/59/2023
T199A   B/Ghana/8388/2023
B/Kyiv/2021/2023 @
S286F   B/Thuringen/20/2023
V252M   B/Norway/10979/2023
B/Norway/10978/2023
E128G   B/Slovenia/924/2023 @
E183K   B/Catalonia/2279261NS/2023 $
T260A   B/Bayern/22/2023_cs
B/Netherlands/01656/2023
B/Iran/4A10/2023
B/Iran/28Z8/2023
T121N   B/CzechRepublic/2070/2023 @
T127P   B/Iceland/35485/2023
Q200P   B/Brazil/9753/2022 @
B/Colorado/05/2022 @
V117I,   B/Mauritius/P49520/2023
E128K,   D497N   B/Slovenia/11466/2022 @
A154T   K326R   V379I   B/Catalonia/3514402NS/2023 $
D197E   B/Netherlands/01658/2023
G141R   B/Connecticut/01/2021 @
E183K   B/Stockholm/3/2022_Cell #
V117I,E184K   B/Norway/13892/2023_cs
D129G   B/Italy/14158/2023 @
B/Austria/1359417/2021_Cell
B/Austria/1359417/2021_Egg_141G
G141R   B/Austria/1359417/2021_Egg_G141R
B/Mozambique/4834/2023 @
T34I   B/Sweden/8/2023 @
A127T,P144L,   E198G
N150K,G184E,
N197D(–CHO),
K203R,R279K
B/Norway/3749/2023 $
B/Switzerland/53639/2023 $
B/Norway/5216/2023 $
A154E   B/Jonkoping/SE23–16355/2023_cs
S208P
K136E,   E128K   B/Poland/157/2023 @
del162-164   B/Moldova/2030521/2023 @
K75E,   T182A,D197E   B/Netherlands/10335/2023 $
E128K,   B/Netherlands/10894/2022 $
T155A,   T199A   B/Netherlands/11267/2022 @
G184R,   I318V
G230N
I117V,N129D   B/Washington/02/2019 @
G133R,N197S   B/Colorado/06/2017 @
D129G,I180V,R498K   B/Brisbane/60/2008 #

HI fold change
< 4
4
8
> 8
Homologous
N/A

Clade−Subclade
V1A.3a.2 (C.2)
V1A.3a.2 (C.3)
V1A.3a.2 (C.5)
V1A.3a.2 (C.5.1)
V1A.3a.2 (C.5.2)
V1A.3a.2 (C.5.4)
V1A.3a.2 (C.5.5)
V1A.3a.2 (C.5.6)
V1A.3a.2 (C.5.7)

BRI60e V1A
AUS17c V1A.3a.2(C)
AUS17eG V1A.3a.2(C)
AUS17eR V1A.3a.2(C)
STO3c V1A.3a.2(C.5)

Very few B/Victoria viruses collected since 1st September have been phenotypically characterized by haemagglutination inhibition (HI). All V1A.3a.2 viruses tested were well-recognised by antisera raised against B/Austria/1359417/2021 and -like viruses.

Reference Virus	clade	<4-fold difference		4-fold difference		>4-fold difference		total
		number	percentage	number	percentage	number	percentage	
B/Brisbane/60/2008 Egg	V1A	24	40.7	32	54.2	3	5.1	59
B/Austria/1359417/2021 Cell	V1A.3a.2	59	100	0	0	0	0	59
B/Austria/1359417/2021 Egg G141	V1A.3a.2	59	100	0	0	0	0	59
B/Austria/1359417/2021 Egg G141R	V1A.3a.2	0	0	4	6.8	55	93.2	59
B/Stockholm/3/2022 Cell	V1A.3a.2	59	100	0	0	0	0	59

WHO Collaborating Centre reports

A full description of results generated by the London WHO Collaborating Centre at the WIC and used at the February 2024 WHO VCM, and previous ones, can be found at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports