Influenza virus characterization

Summary report, Europe, November 2024

Document number: WHO/EURO:2024-6189-45954-77475

Suggested citation. Influenza virus characterization: summary report, Europe, November 2024. Copenhagen: WHO Regional Office for Europe and Stockholm: European Centre for Disease Prevention and Control; 2024. Licence: CC BY 3.0 IGO.

Cataloguing-in-Publication (CIP) data. CIP data are available at http://apps.who.int/iris.

Sales, rights and licensing. To purchase WHO publications, see http://apps.who.int/bookorders. To submit requests for commercial use and queries on rights and licensing, see http://www.who.int/about/licensing.

Contents

Acknowledgements

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

Prof. Nicola Lewis (Director)
Dr Ruth Harvey (Deputy Director)
Dr Monica Galiano (Head of Molecular Testing and Genomics)
Dr Alex Byrne
Dr Zheng Xiang
Ms Becky Clark
Ms Alice Lilley
Ms Christine Carr
Mr Michael Bennett
Dr Tanya Mikaiel
Ms Abi Lofts
Dr Alize Proust
Ms Chandrika Halai
Dr Karen Cross
Ms Aine Rattigan
Mr Lorin Adams

for the World Health Organization Regional Office for Europe under WHO contract.

Data from The European Surveillance System – TESSy was provided by the respective country and area and accessed through released by ECDC.

We thank all those who have contributed information, clinical specimens and viruses, and associated data to the WHO Global Influenza Surveillance and Response System (GISRS), which provides the basis for our current understanding of recently circulating influenza viruses included in this summary. This report was prepared in part using data reported to the European Surveillance System (TESSy) accessed through the European Respiratory Virus Surveillance Summary (ERVISS). We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from the GISAID EpiFluTM database, which were downloaded for use in the preparation of this report (all submitters of data may be contacted directly via the GISAID website), along with all laboratories who submitted sequences directly to WHO CC London.

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 November 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 1 September 2024 through to 30 November 2024 as deposited in GISAID (data accessed on 02/12/2024), 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 from Respimart.

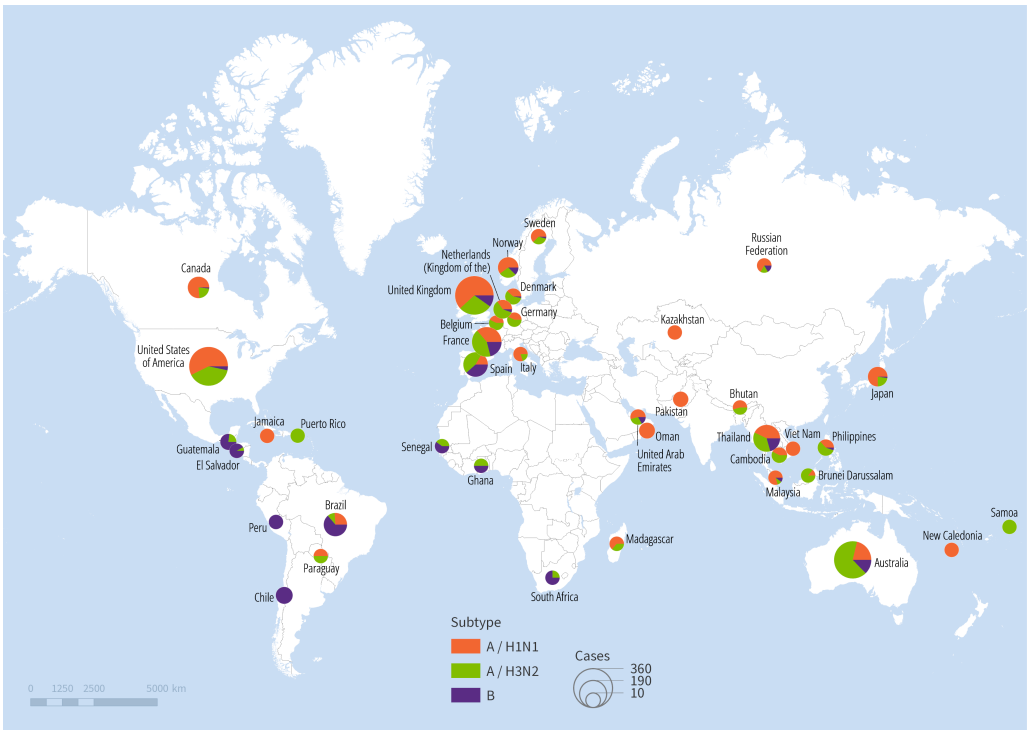


Figure 1: Global distribution of influenza virus subtypes

Globally, influenza detections have slightly increased since the last report in October 2024. The relative proportions of A/H1N1, A/H3N2 and B/Victoria varied by geographic region with with cocirculation of A/H1N1 and A/H3N2 overall and some predominance of B/Victoria. Subtype A/H1N1 predominated in North America, Middle East, United Kingdom, Norway, Sweden, Russian Federation, Japan, Madagascar and Malaysia. Subtype A/H3N2 predominated in some countries in Europe and South East Asia, Australia and Puerto Rico. Some regions and countries showed predominance of B/Victoria such as Central and South America, Senegal and South Africa, as indicated by the different colours in the pie charts by country.

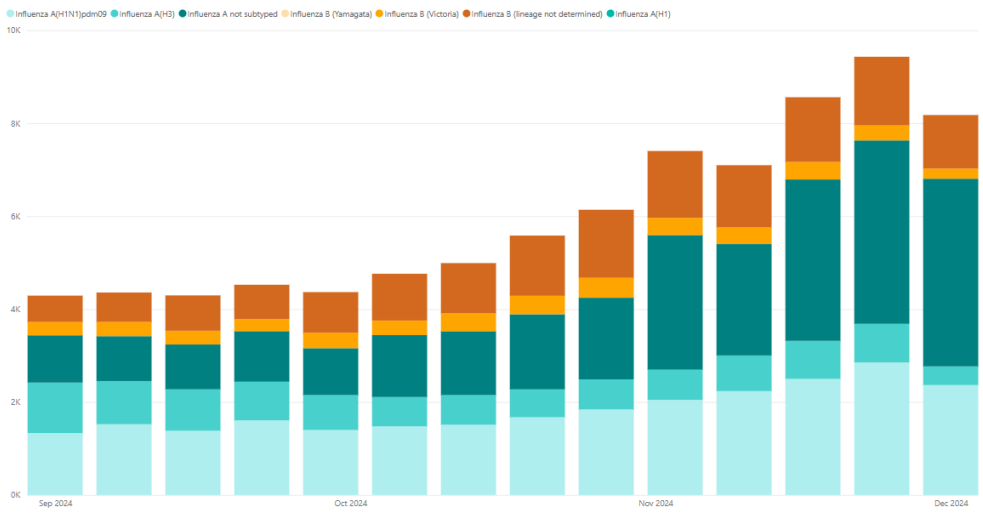


Figure 2: Timeline of circulation of influenza virus subtypes

European region

Geographical distribution in the European region of influenza viruses with collection dates from 1 September 2024 through to 30 November 2024 as deposited in GISAID (data accessed on 02/12/2024), 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 from Respimart.

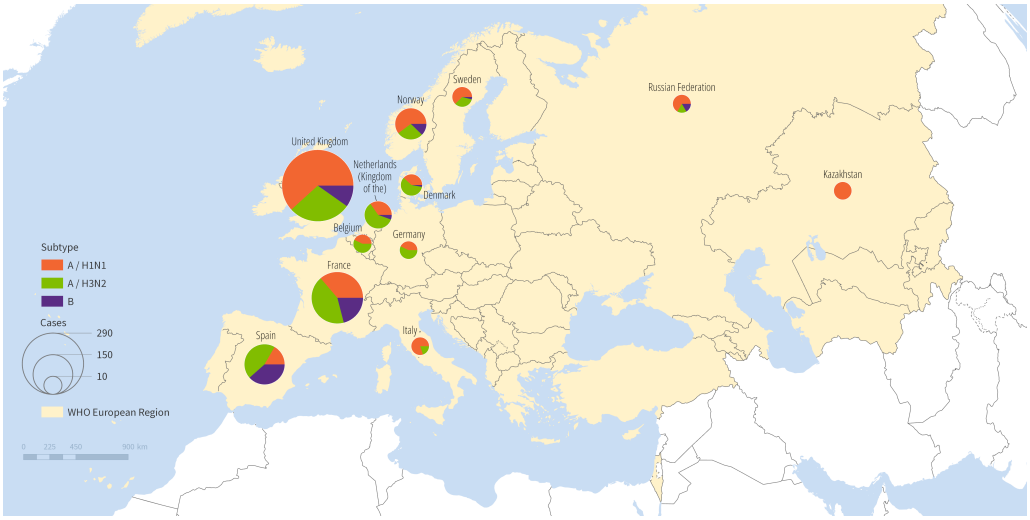


Figure 3: European region - Distribution of influenza virus subtypes

In the European region, influenza detections have increased since the last report in October 2024. The majority of countries which reported detections showed some co-circulation of A/H1N1 and A/H3N2 with predominance of A/H1N1 viruses and sporadic detections of influenza B/Victoria, as indicated by the different colours in the pie charts.

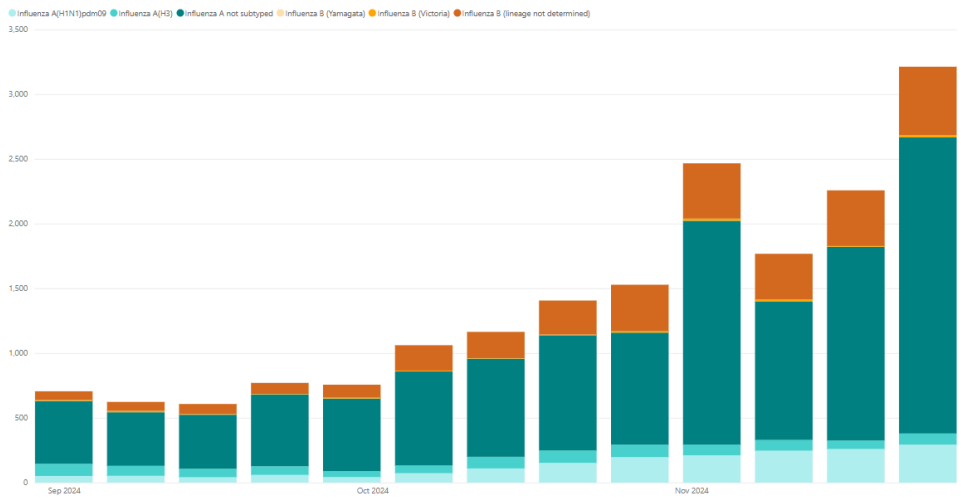


Figure 4: European region - Timeline of circulation of influenza virus subtypes

Summary of influenza detections in the WHO European Region, week 35/2024 to 48/2024

Table 1 shows influenza virus detections in the WHO European Region reported to The European Surveillance System (TESSy) database from 1 September 2024 to 30 November 2024 (weeks 35/2024 to 48/2024) 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)).

Table 1. Sentinel and non-sentinel influenza detections. Comparison of current season 2024-25 with last season 2023-24

	Cumulative number of detections for weeks 35/2024 to 48/2024				Cumulative number of detections for weeks 35/2023 to 48/2023			
Virus type/subtype/lineage	Sentinel sources	Non-sentinel sources	Totals	%	Sentinel sources	Non-sentinel sources	Totals	%
Influenza A	970	18116	19086	83	1144	12248	13392	92
A(H1N1)pdm09	383	1697	2080	66	571	2117	2688	53
A(H3N2)	215	877	1092	34	417	1988	2405	47
A not subtyped	372	15542	15914	NA	156	8143	8299	NA
Influenza B	267	3597	3864	17	80	1054	1134	8
Victoria lineage	45	82	127	100	9	78	87	100
Yamagata lineage	0	0	0	NA	0	0	0	NA
Lineage not ascribed	222	3515	3737	NA	71	976	1047	NA
Total detections	1237	21713	22950	NA	1224	13302	14526	NA
Total tested	43102	730053	773155	NA	46033	610380	656413	NA

Compared with the same period within last season (weeks 35/2023 to 48/2023), the number of specimens tested has slightly decreased while number of influenza detections was similar for sentinel samples. For non-sentinel samples, the number of specimens tested was higher in the current season, as well as the number of influenza detections, accounting for a 60% increase of positive cases from last season.

So far during the current season, the proportion of influenza A of unknown subtype among sentinel cases represents 38% of the total influenza A detected, compared with 14% in last season; for non-sentinel cases, not-subtyped influenza A detections accounted for 86% of the total influenza A detected in 2024–25, compared with 66% for 2023–24.

Relative frequencies of type A vs B influenza viruses continue to show predominance of influenza A with a proportion of 83% compared with 92% in 2023–2024. Currently, in Europe there are variable detections of influenza B (17%), being only a dominant subtype in Spain. Relative frequencies of influenza A subtypes have also shifted, with A/H1N1 viruses increasing from 53% to 66% frequency and a higher proportion of circulating A/H1N1 viruses (66% A/H1N1 vs 34% A/H3N2) compared to last season (53% A/H1N1 vs 47% A/H3N2). A/H1N1 viruses continue to predominate since the last report in October 2024.

Sentinel surveillance system dynamics, week 35/2024 to 48/2024

Figure adapted from ERVISS

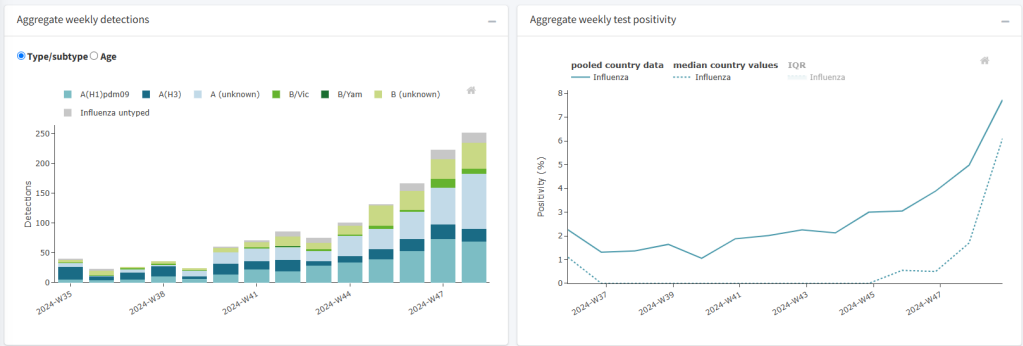


Figure 5: Aggregate sentinel weekly detections

During the period from week 35/2024 to week 48/2024, influenza activity remained at low levels through the reporting period until the last two weeks when it started to approach the epidemic threshold of 10%. Across sentinel surveillance, influenza A/H3N2, A/H1N1 and B/Victoria viruses cocirculated during most of this period with overall predominance of A/H1N1 among subtyped influenza A viruses.

Genetic diversity by Type/Lineage and group

Number of viruses classified by genetic clades (subclades), obtained with full HA sequences as deposited in GISAID and classified using Nextclade. Collection dates 01/09/2024 to 30/11/2024.

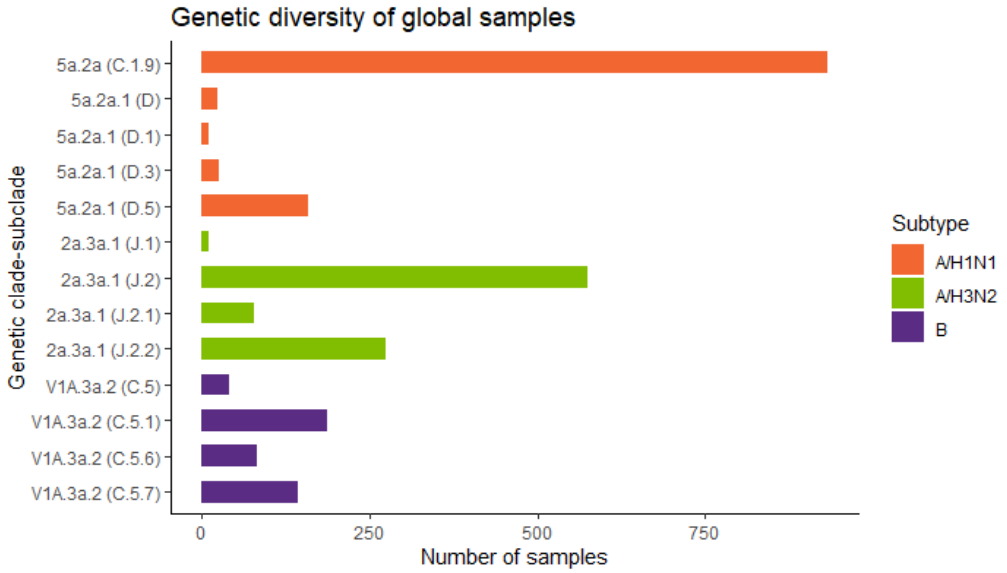


Figure 6: Global proportion of genetic subclades

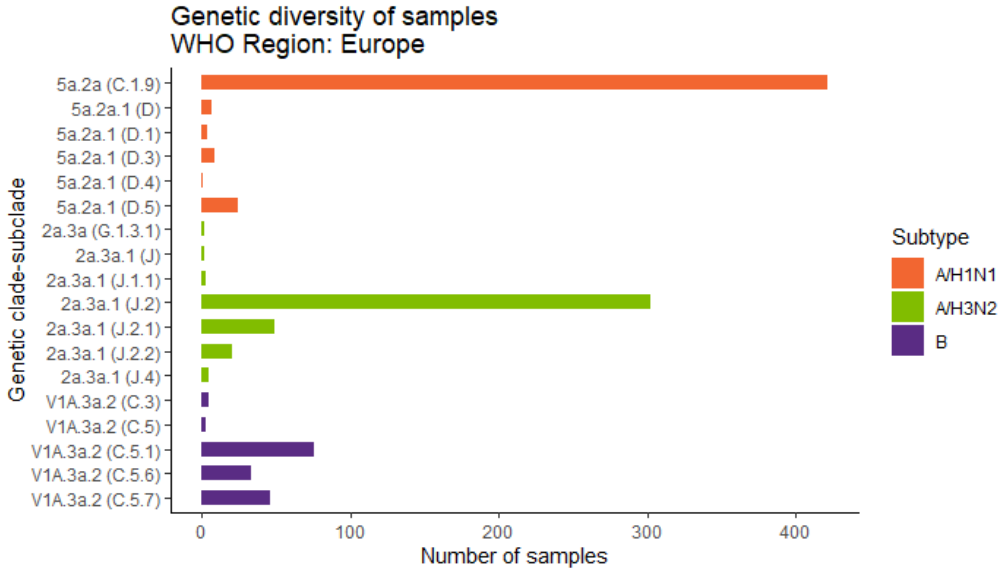


Figure 7: European region - Proportion of genetic subclades

Influenza A/H1N1

Genetic analyses: A/H1N1

6B.1A.**5a.2a** and 6B.1A.**5a.2a.1** clade viruses both continued to circulate with changing relative proportions throughout this period.

The SH 2024 winter season was characterised by predominance of clade 5a.2a subclades C.1.9 and C.1.8 with minor circulation of clade 5a.2a.1 subclade D. Since September 2024, subclades C.1.9 continues to predominate, with minor cocirculation of a recently emerged subclade 5a.2a.1 (D.5) and other 5a.2a.1 subclades, whereas subclade C.1.8 has not been detected so far.

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, K308R and I418V, the majority (>80%) of H1pdm viruses sequenced globally belong to subclade C.1.9, characterised by substitution K169Q. Other 5a.2a subclades such as C.1.8 and C.1.7 were not detected so far into the NH winter season.

Within the 5a.2a.1 viruses, characterised by substitutions P137S, K142R, D260E, T277A, E356D and N451H, major subclade D (former C.1.1.1) with T216A represented by A/Victoria/4897/2022 has split into 5 subclades, of which the most recently emerged subclade D.5 characterised by R45K is the most frequently detected. Subclade D.5 and other 5a.2a.1 subclades have only been detected in significant proportions in the Americas and Madagascar.

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

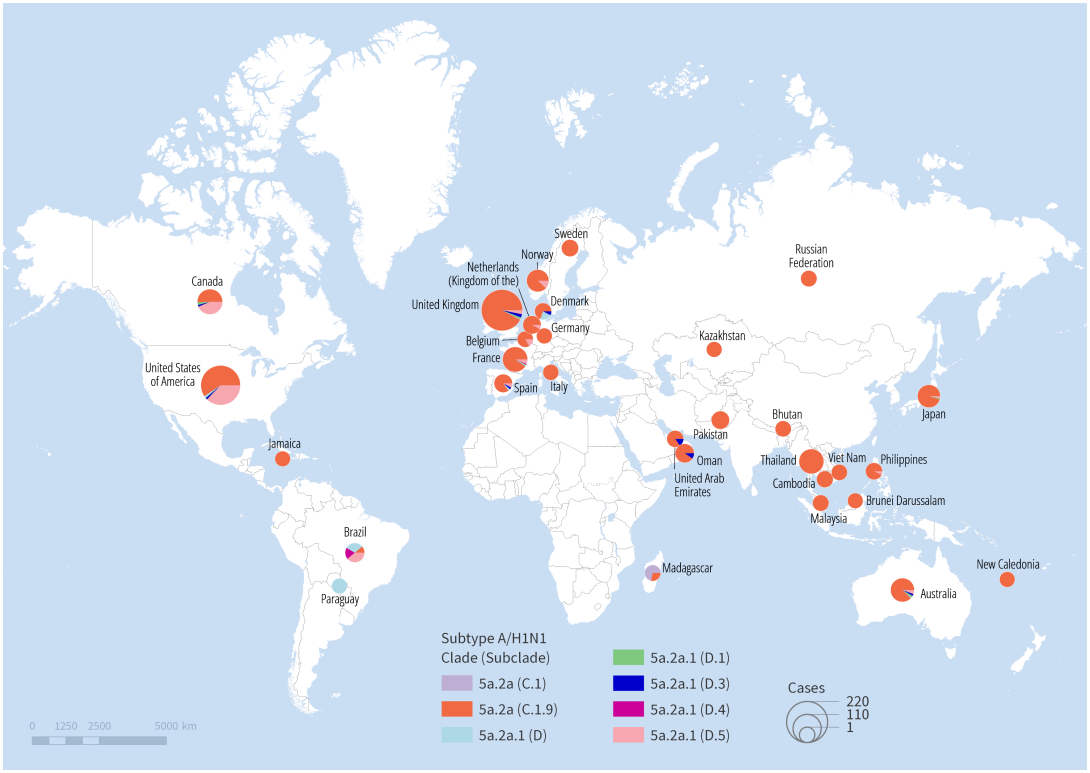


Figure 8: Global geographical distribution of influenza A/H1N1 genetic clades (subclades)

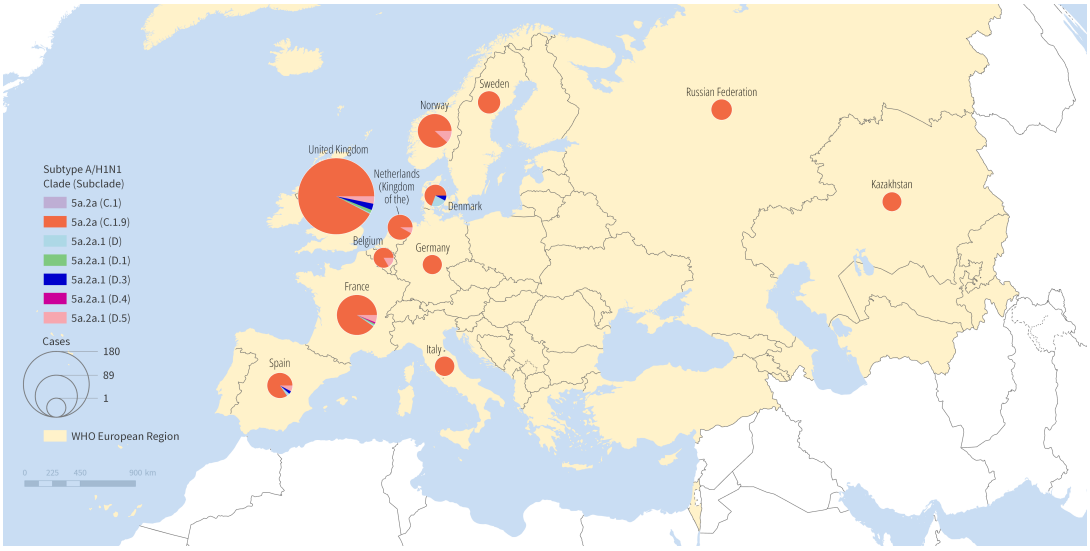


Figure 9: European region - Geographical distribution of influenza A/H1N1 genetic clades (subclades)

Global time-dependent variation in frequencies of genetic clades (subclades) of A/H1N1 viruses, collection dates 01/09/2024 to 30/11/2024.

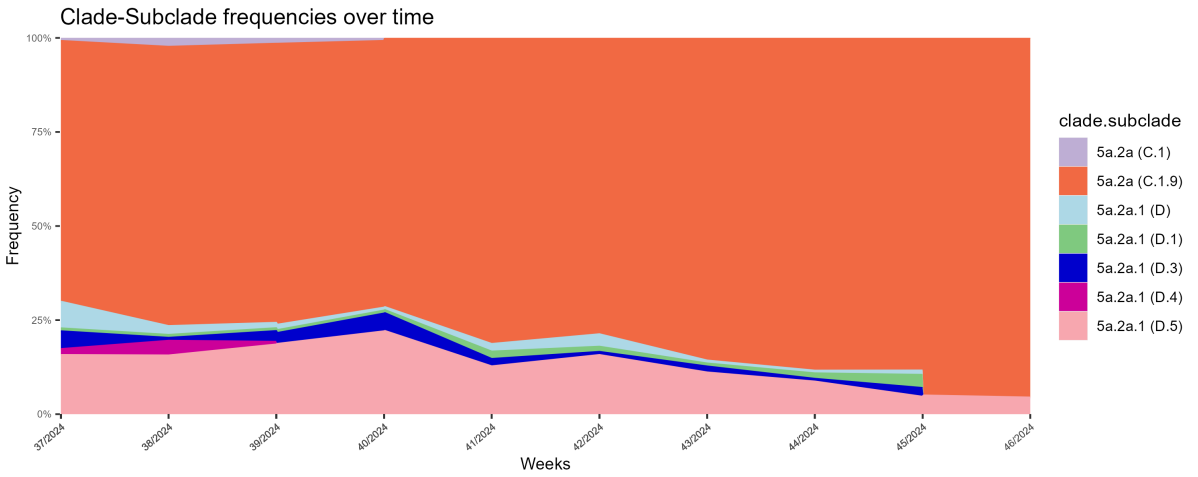


Figure 10: Global time-dependent variation in frequencies of A/H1N1 genetic clades (subclades)

Maximum likelihood Phylogenetic trees: A/H1N1

Maximum likelihood (ML) phylogenetic trees inferred using Iqtree2 from HA sequence data obtained from GISAID. 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.

Phylogenetic tree in Figure 11 was initially built with all European GISRS A/H1N1 sequences uploaded to GISAID with collection dates from 01/09/2024 to 30/11/2024, downsampled using Treemer to retain a representative tree topology of 200 sequences.

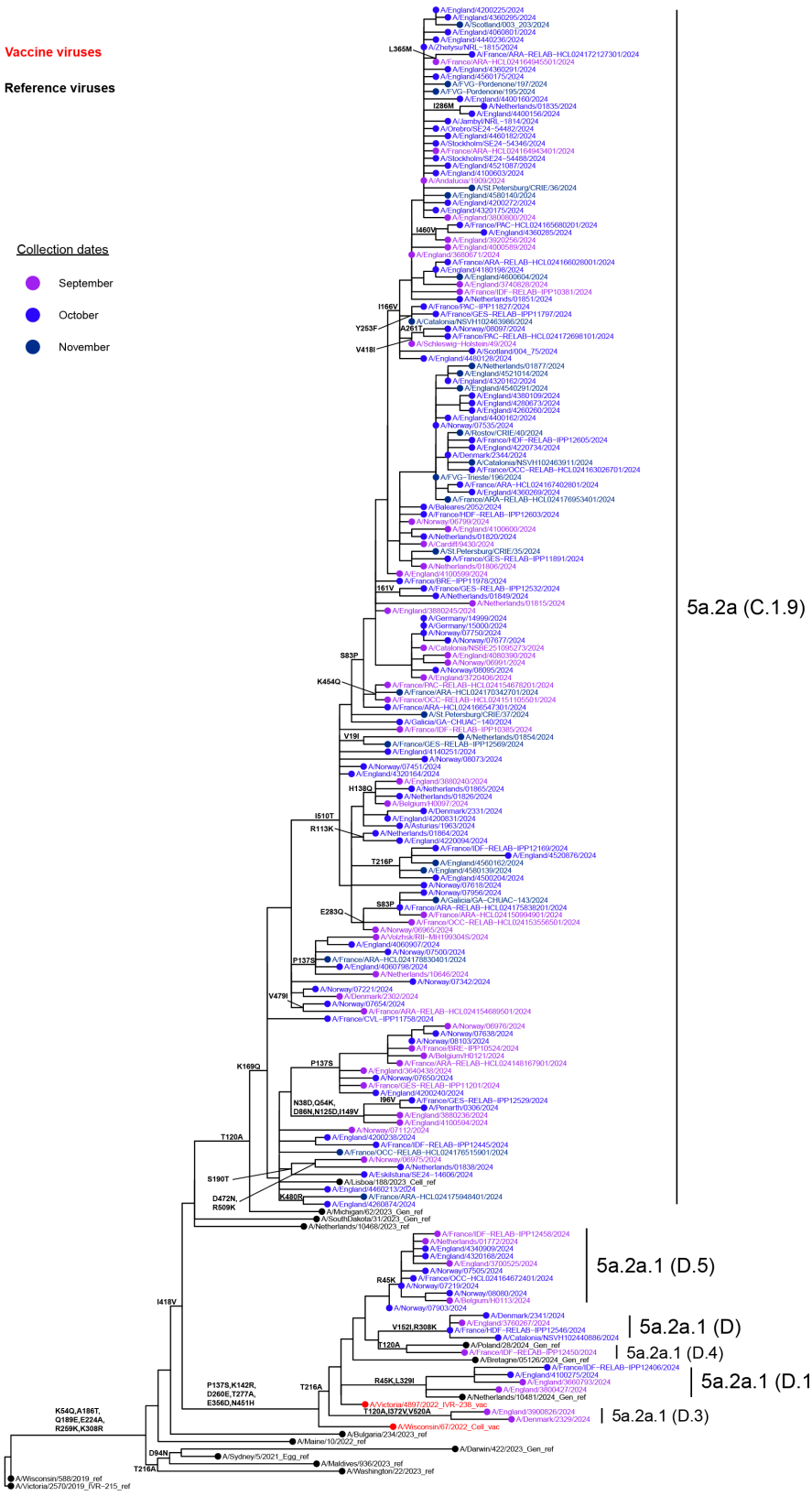


Figure 11: ML phylogenetic tree, 200 representative European GISRS A/H1N1 sequences from 1 September 2024 to 30 November 2024

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

NH 2023-24, 2024-25 and SH 2024 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 reduced recognition was observed with the cell- based A/Wisconsin/67/2022 strain that was not seen with the egg-based A/Victoria/4897/2022.

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

Table 2. A/H1N1 HI reagents and references

Virus	Genetic group	Virus passage	Ferret ID
A/Sydney/5/2021	5a.2a (C.1)	MDCK3/MDCK4	F46/22
A/Victoria/4897/2022	5a.2a.1 (D)	SIAT2/MDCK3	F05/23
IVR-238 (A/Victoria/4897/2022)	5a.2a.1 (D)	E3/D6/E1	F07/23
A/Wisconsin/67/2022	5a.2a.1 (C.1.1)	MDCK2	F17/23
A/Lisboa/188/2023	5a.2a.1 (C.1)	SIAT1/MDCK2	F09/24

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.

The SH 2024 winter season was characterised by predominance of subclade 2a.3a.1 (J.2). Since September 2024, subclade J.2 continues to predominate globally.

During this reporting period, the great majority of H3 viruses detected belong to clade 2a.3a.1 subclade J, vaccine reference A/Thailand/8/2022 (substitutions E50K, I140K and I223V). Subclade J split into 4 further subclades: of these, subclade J.2 (reference A/Croatia/10136RV/2023) characterised by N122D (-CHO) and K276E became the dominant subclade, predominating in the majority of continents with >90% frequency. Two subclades were recently designated within J.2: J.2.1 with substitution P239S (reference A/West Virginia/51/2024) detected in minor proportions in Europe, Thailand, United Arab Emirates, Japan and US, and J.2.2 with substitution S124N (reference A/Lisboa/216/2023) which predominated in South East Asia, Australia and Senegal, and circulated in minor proportions in Europe, Japan and US. Subclade J.1 was also split into a further subclade J.1.1 with substitution S145N (reference A/Canberra/331/2023) which was detected with low frequency in Bhutan, Australia, UK and US.

Other subclades such as J.4 and G.1.3.1 were detected very sporadically during this period.
Convergent evolution was observed with several sequences in separate clades characterised by substitutions such as S124N, S145N and fewer viruses with substitutions N158K and K189R.

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

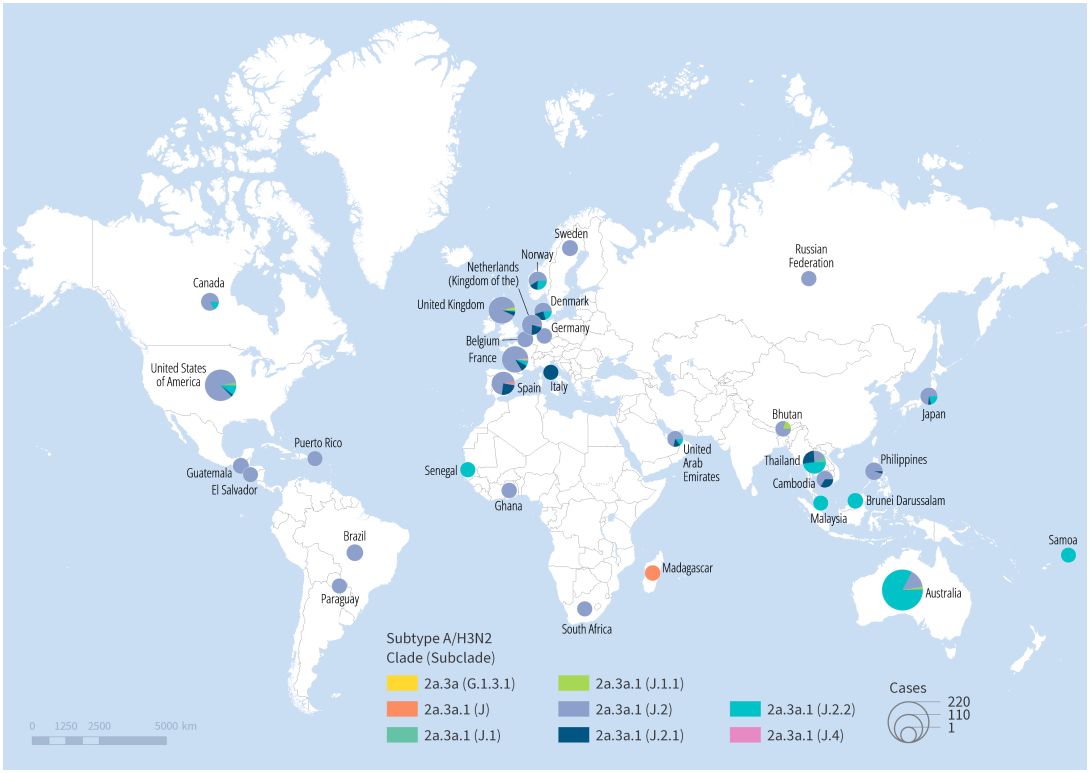


Figure 12: Global geographical distribution of influenza A/H3N2 genetic clades (subclades)

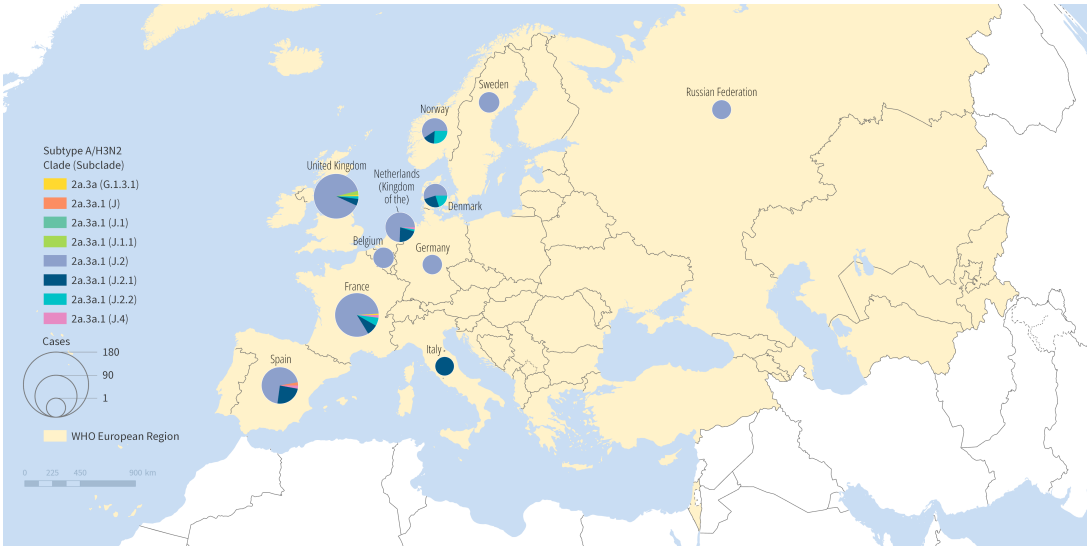


Figure 13: European region - Geographical distribution of influenza A/H3N2 genetic clades (subclades)

Global time-dependent variation in frequencies of genetic clades-subclades of A/H3N2 viruses, collection dates 01/09/2024 to 30/11/2024.

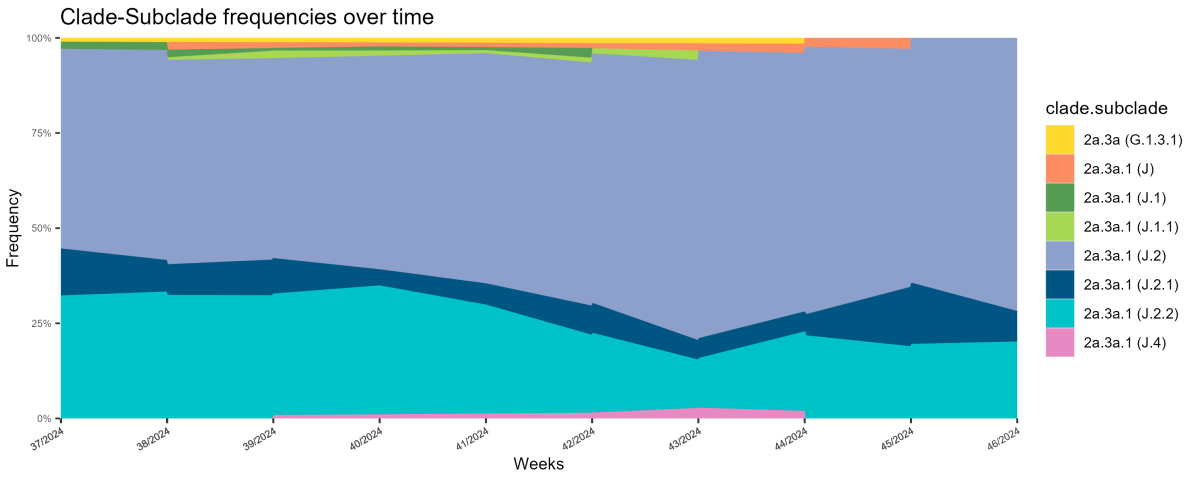


Figure 14: Global time-dependent variation in frequencies of A/H3N2 genetic clades (subclades)

Maximum likelihood phylogenetic tree: A/H3N2

Maximum likelihood phylogenetic trees inferred using Iqtree2 from HA sequence data obtained from GISAID. 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.

Phylogenetic tree in Figure 15 was initially built with all European GISRS A/H3N2 sequences uploaded to GISAID with collection dates from 1 September 2024 to 30 November 2024, downsampled using Treemer to retain a representative tree topology of 200 sequences.

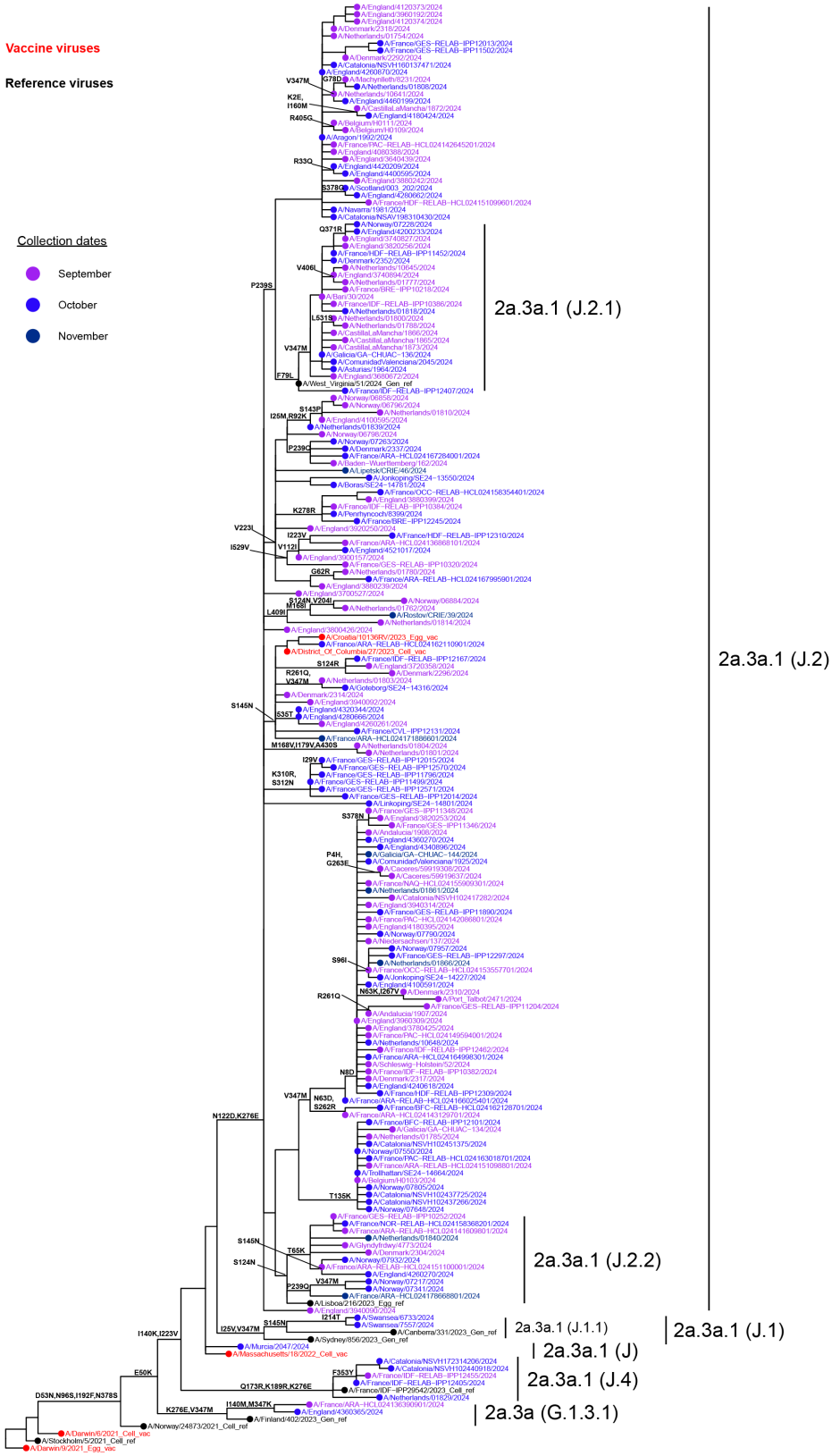


Figure 15: ML phylogenetic tree, 200 representative European GISRS A/H3N2 sequences from 1 September 2024 to 30 November 2024

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

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.

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

Table 3. A/H3N2: HI/MN reagents and references

Virus	Genetic group	Virus passage	Ferret ID
A/Albania/289813/2022	2a.3a.1 (J)	MDCK1	F21/23
A/Massachusetts/18/2022	2a.3a.1 (J)	SIAT3/SIAT1	F36/23
A/Thailand/08/2022	2a.3a.1 (J)	E3/E1	F34/23
A/Sydney/856/2023	2a.3a.1 (J.1)	SIAT1/SIAT2	F01/24
A/Croatia/10136/RV/2023	2a.3a.1 (J.2)	SIAT3	F06/24
A/Croatia/10136/RV/2023	2a.3a.1 (J.2)	E3 (Am1Al2)	F16/24
A/Netherlands/10563/2023	2a.3a.1 (J.2)	MDCK-MIX2/SIAT2	F08/24
A/Slovenia/49/2024	2a.3a.1 (J.2)	MDCKx/SIAT2	F11/24
A/Lisboa/216/2023	2a.3a.1 (J.2)	E3 (Am1Al2)	F15/24
A/Norway/12374/2023	2a.3a.1 (J.4)	SIAT4	F21/24
A/France/IDF-IPP29542/2023	2a.3a.1 (J.4)[K189R]	MDCK1/SIAT2	F22/24
A/BurkinaFaso/3131/2023	2a.3a.1 (J.4)[K189R]	SIAT3	F32/24

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.

The SH 2024 winter season was characterised by cocirculation of subclades V1A.3a.2 C.5.1, C.5.4, C.5.6, C.5.7 and basal C.5, with predominance of C.5.7 and C.5.1 towards the end of the season. During this reporting period, only a minority of B/Victoria viruses were detected and characterised in Europe. Since September 2024, the majority of B/Victoria viruses detected belong to subclades C.5.7 and C.5.1.

Within V1A.3a.2 subclade C.5 (characterised by D197E) the most frequent subclades observed are C.5.1 with E183K represented by B/Catalonia/2279261NS/2023 as the dominant subclade predominating in Central and South America, Portugal, France, Denmark and Canada, and C.5.7 with E183K and E128G represented by B/Guangxi-Beiliu/2298/2023 predominating in South East Asia, UK and Sweden, with both subclades being detected in minor proportions in several countries worldwide. Subclade C.5.6 (reference B/Switzerland/329/2024) with D129N predominated in South Africa and United Arab Emirates and was detected in minor proportions in some countries in South East Asia and Europe.

Outside of C.5 viruses, subclade C.3 (E128K, A154E, S208P, B/Moldova/2030521/2023) was detected with low frequency in Norway.

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

No B/Yamagata lineage viruses have been detected since March 2020, except for a reported detection in the Netherlands which has been unable to be confirmed by lineage-specific RT-PCR or sequencing.

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

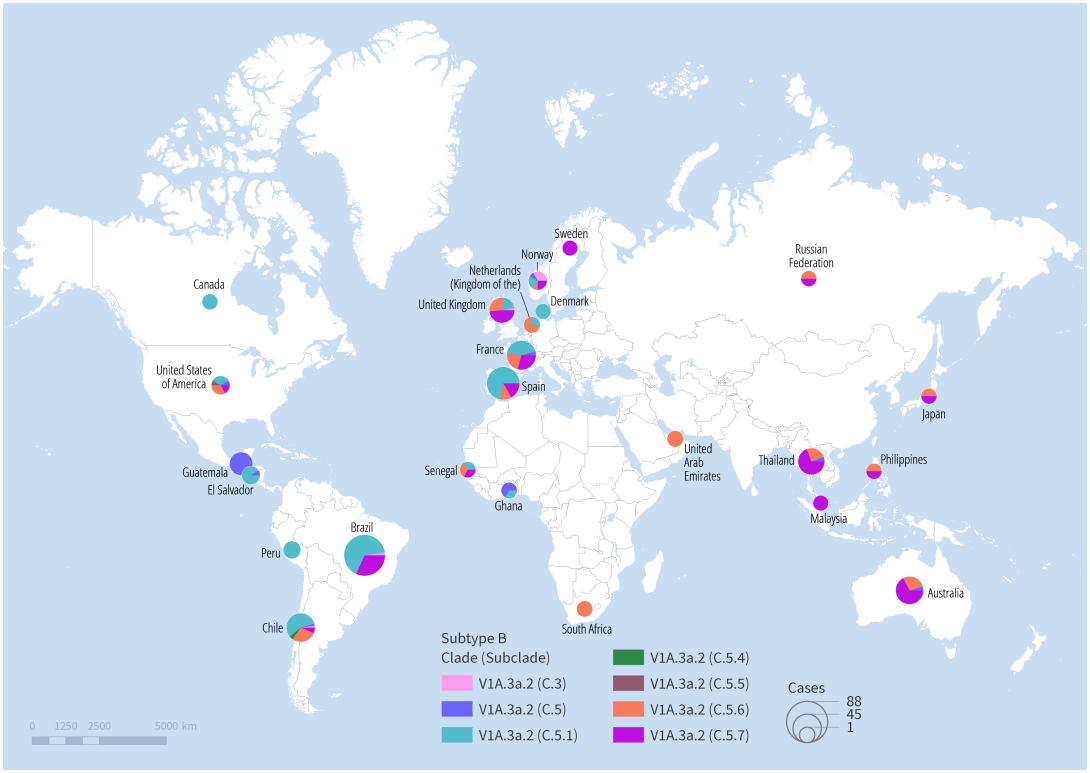


Figure 16: Global geographical distribution of influenza B/Victoria genetic clades (subclades)

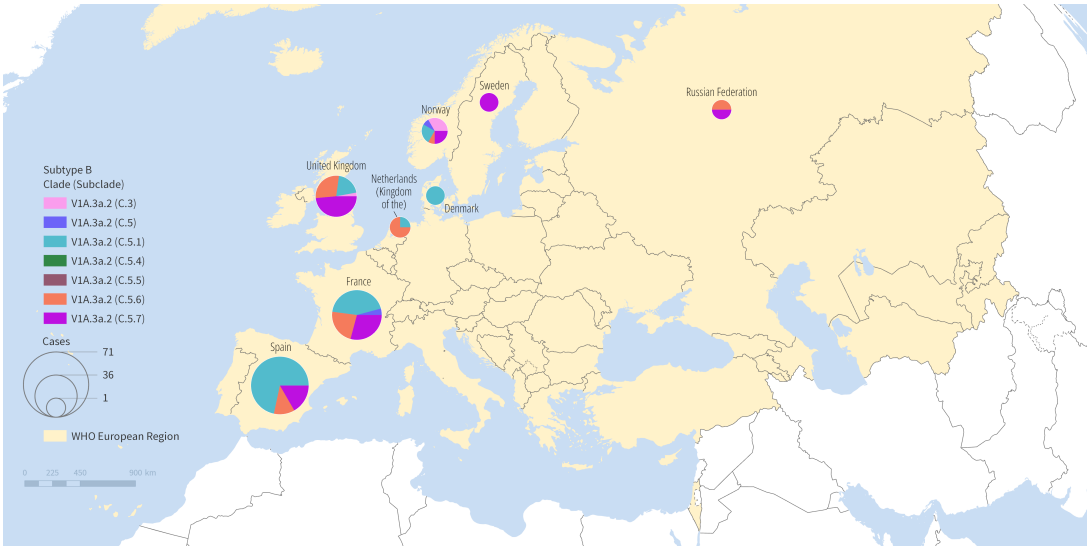


Figure 17: European region - Geographical distribution of influenza B/Victoria genetic clades (subclades)

Global time-dependent variation in frequencies of genetic clades-subclades of B/Victoria viruses, collection dates 01/09/2024 to 30/11/2024.

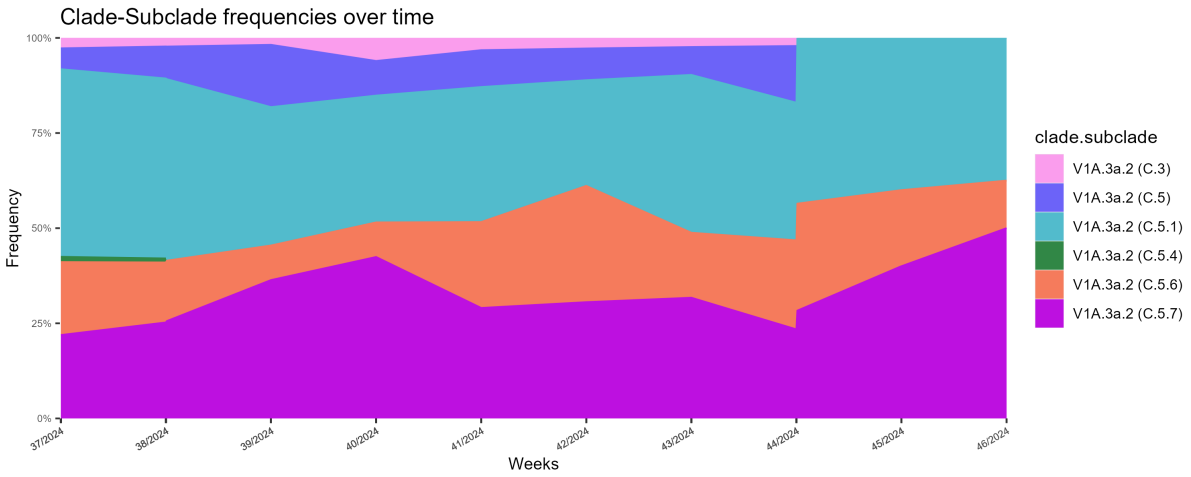


Figure 18: Global time-dependent variation in frequencies of B/Victoria genetic clades (subclades)

Maximum likelihood phylogenetic tree: B/Victoria

Maximum likelihood phylogenetic trees inferred using Iqtree2 from HA sequence data obtained from GISAID. 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.

Phylogenetic tree in Figure 19 was initially built with all European GISRS B/Victoria sequences uploaded to GISAID with collection dates from 1 September 2024 to 30 November 2024, downsampled using Treemer to retain a representative tree topology of 200 sequences.

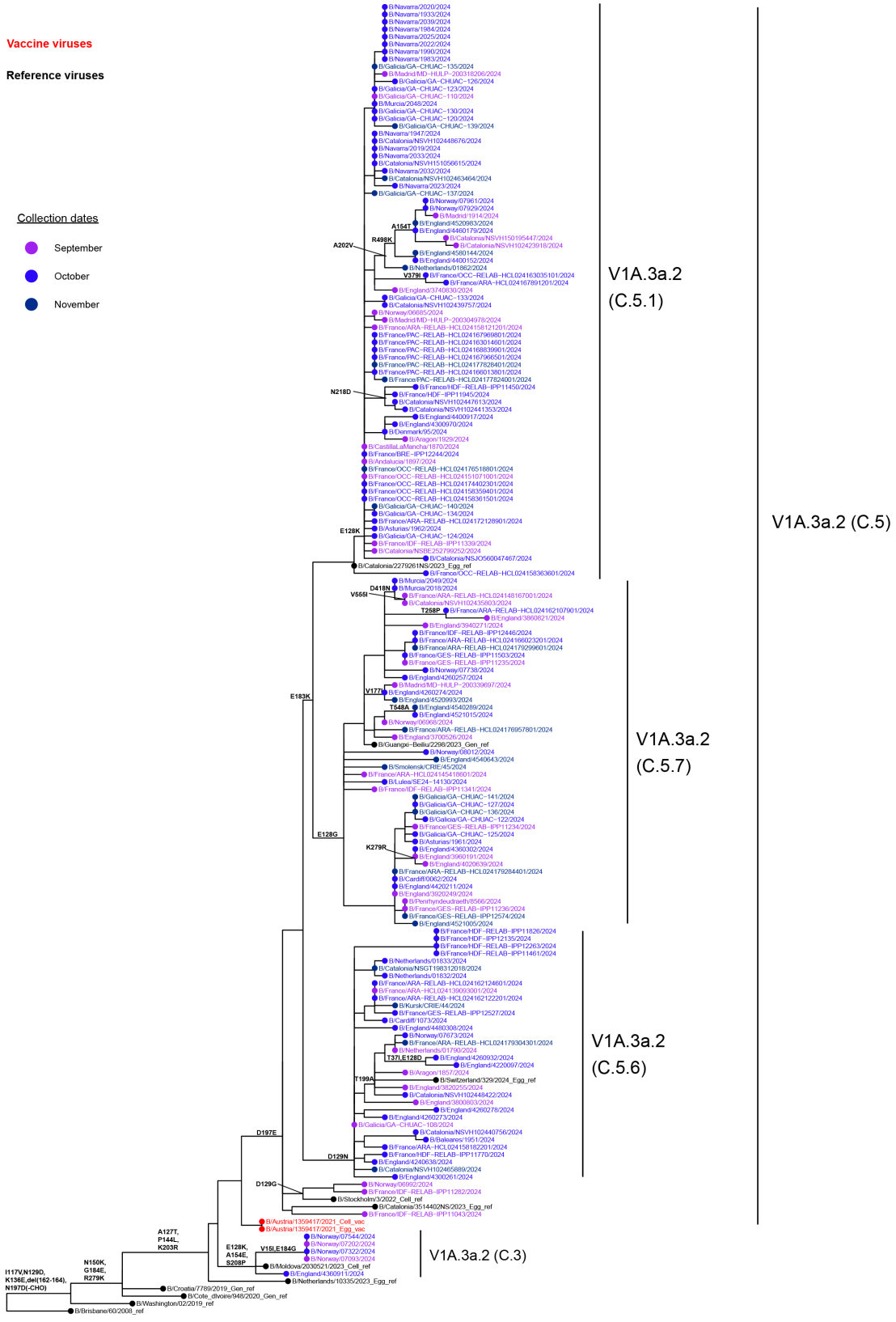


Figure 19: ML phylogenetic tree, 200 representative European GISRS B/Victoria sequences from from 1 September 2024 to 30 November 2024

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

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 previous season, see the Annex.

Table 4. B/Victoria: HI reagents and references

Virus	Genetic group	Virus passage	Ferret ID
B/Brisbane/60/2008	V1A	E4/E3	sheep pool
B/Austria/1359417/2021	V1A.3a.2 (C)	SIAT1/MDCK4	NIB F01/21
B/Austria/1359417/2021 G141	V1A.3a.2 (C)	E3/E4	F40/21
B/Austria/1359417/2021 G141R	V1A.3a.2 (C)	E3/E5	F44/21
B/Stockholm/3/2022	V1A.3a.2 (C.5)	SIAT1/MDCK3	F28/22

Antiviral susceptibility testing

At the WIC, influenza viruses are routinely assessed for phenotypic and/or genotypic susceptibility to antivirals. No viruses with collection dates since 1 September 2024 were phenotypically assessed against oseltamivir and zanamivir or against baloxavilr marboxil.

Genotypic assessment of 24 A/H1N1, 10 A/H3N2 and 12 B/Victoria neuraminidase (NA) gene sequences found some viruses with markers associated with reduced susceptibility to NAI: one A/H1N1 virus with substitution H275Y and 2 A/H1N1 viruses with S247N (virus isolation and phenotypic tests in progress).

For 21 A/H1N1, 9 A/H3N2 and 12 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 E23G (virus isolation and phenotypic test in progress).

Annex

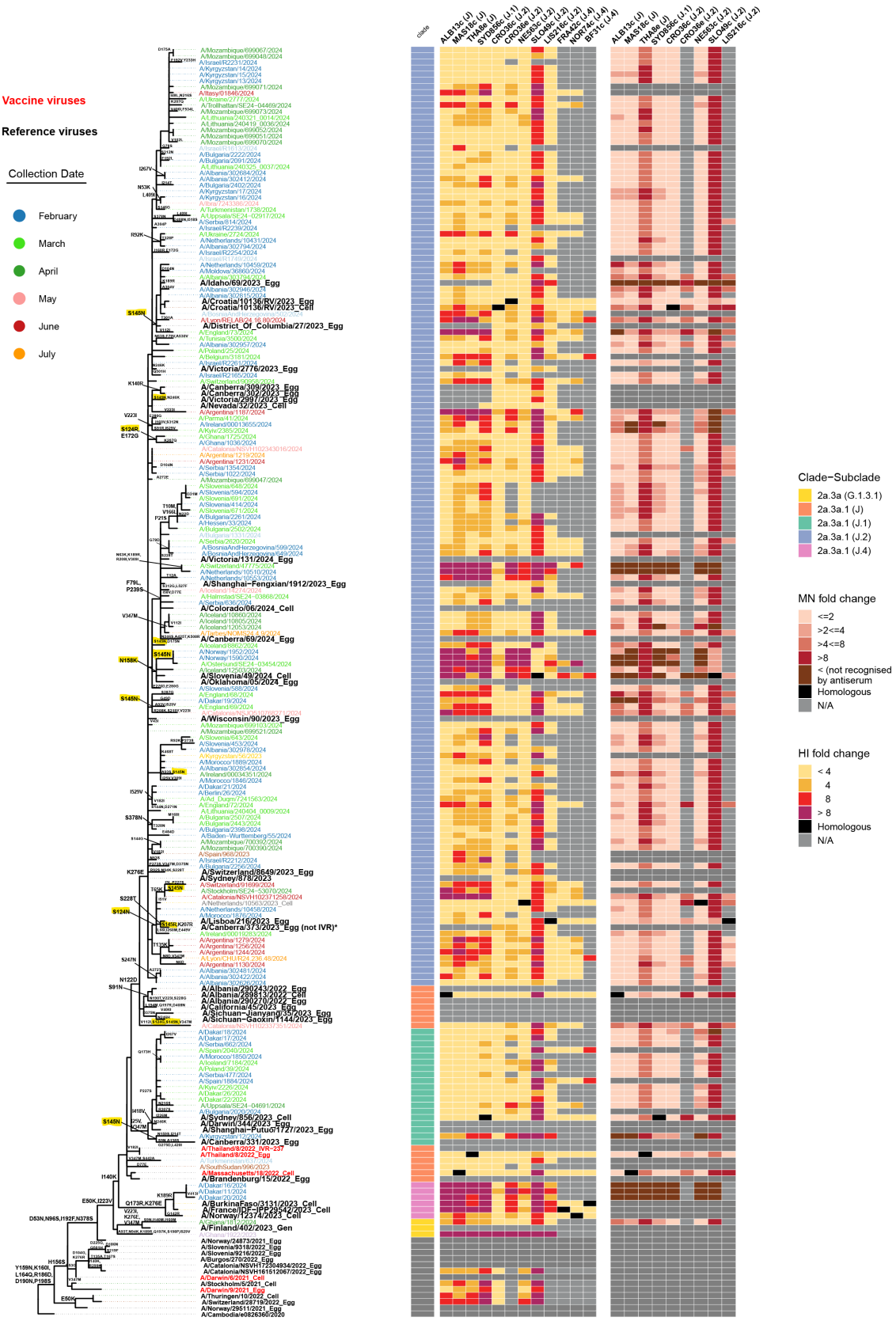
Heatmapped phylogenetic trees represent the combined genetic and antigenic analyses where the correlation between genetic groups, signature amino acids and their antigenic profile (including microneutralisation for A/H3N2) can be observed.

These outputs were generated by the London WHO Collaborating Centre at the WIC for the SH 2025 September VCM with influenza viruses with collection dates between 1 February and 31 August 2024.

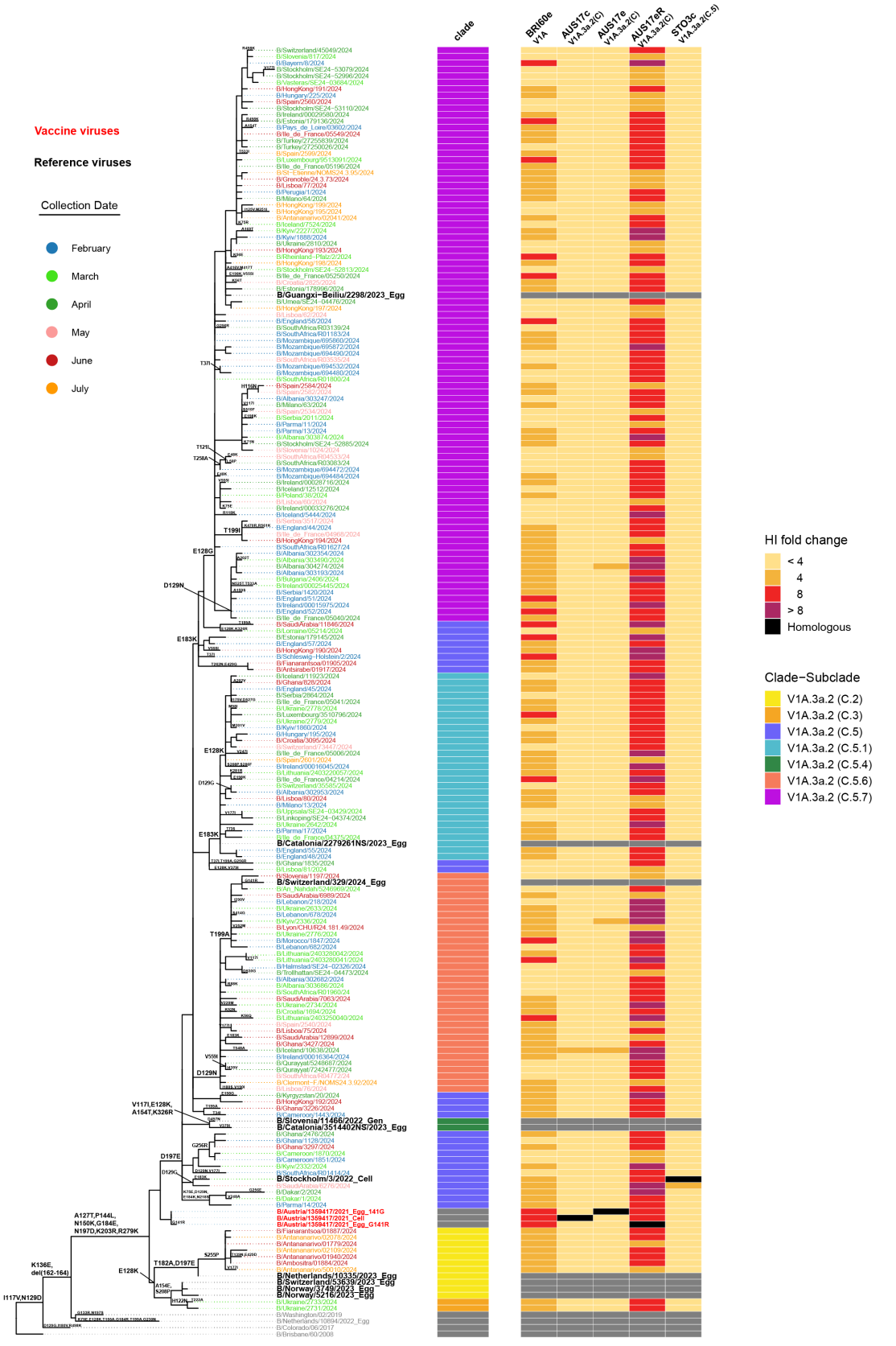
A/H1N1


Vaccine viruses
Reference viruses
Collection Date
February
March
April
May
June
July
clade
VIC2570e
SYD5c (C.1)
SYD5e (C.1)
VIC4897c (D)
VIC4897e (D)
WIS67c (C.1.1)
LIS188c (C.1.9)
HI fold change
< 4
4
8
> 8
N/A
Clade−Subclade
5a.2a (C.1)
5a.2a (C.1.7)
5a.2a (C.1.7.1)
5a.2a (C.1.8)
5a.2a (C.1.9)
5a.2a.1 (C.1.1)
5a.2a.1 (D)
5a.2a.1 (D.1)
5a.2a.1 (D.2)
5a.2a.1 (D.3)
A/Victoria/102/2024_Egg
A/South_Australia/27/2024_Egg
A/Lisboa/188/2023_Cell
A/Victoria/3102/2023_Egg
A/Michigan/62/2023_Egg
A/Canberra/4/2024_Egg
A/Zhejiang−Kecheng/SWL1219/2023_Egg
A/Shanghai−Baoshan/SWL185/2024_Egg
A/Victoria/201/2023_Egg
A/Darwin/7/2023_Egg
A/Victoria/4897/2022_Cell
A/Sichuan−Qingyang/SWL1148/2023_Egg
A/Victoria/3067/2023_Egg
A/Sydney/1/2024_Egg
A/Norway/31694/2022_Egg
A/Catalonia/IBSVH1512065/2022_Egg
A/Wisconsin/67/2022_Cell
A/Norway/25089/2022_Cell
A/Darwin/512/2023_Egg
A/Darwin/422/2023_Egg
A/Sydney/5/2021_Egg
A/Sydney/5/2021_Cell
A/Victoria/705/2023_Egg
A/Sydney/44/2023_Egg
A/Wisconsin/588/2019
A/Victoria/2570/2019_IVR−215
S83P
I510T
T27RN
S83F
P137R
K169Q
N38D
K498R
T120A
A197T
I47V
K154R
I96T
V47TI
D35N
D187V
P137S
I418V
T216A
P137S,K142R,
D260E,T277A,
E356D,N451H
K54Q,A186T,
Q189E,E224A,
R259K,K308R
E195A
I533V
T216A

A/H3N2

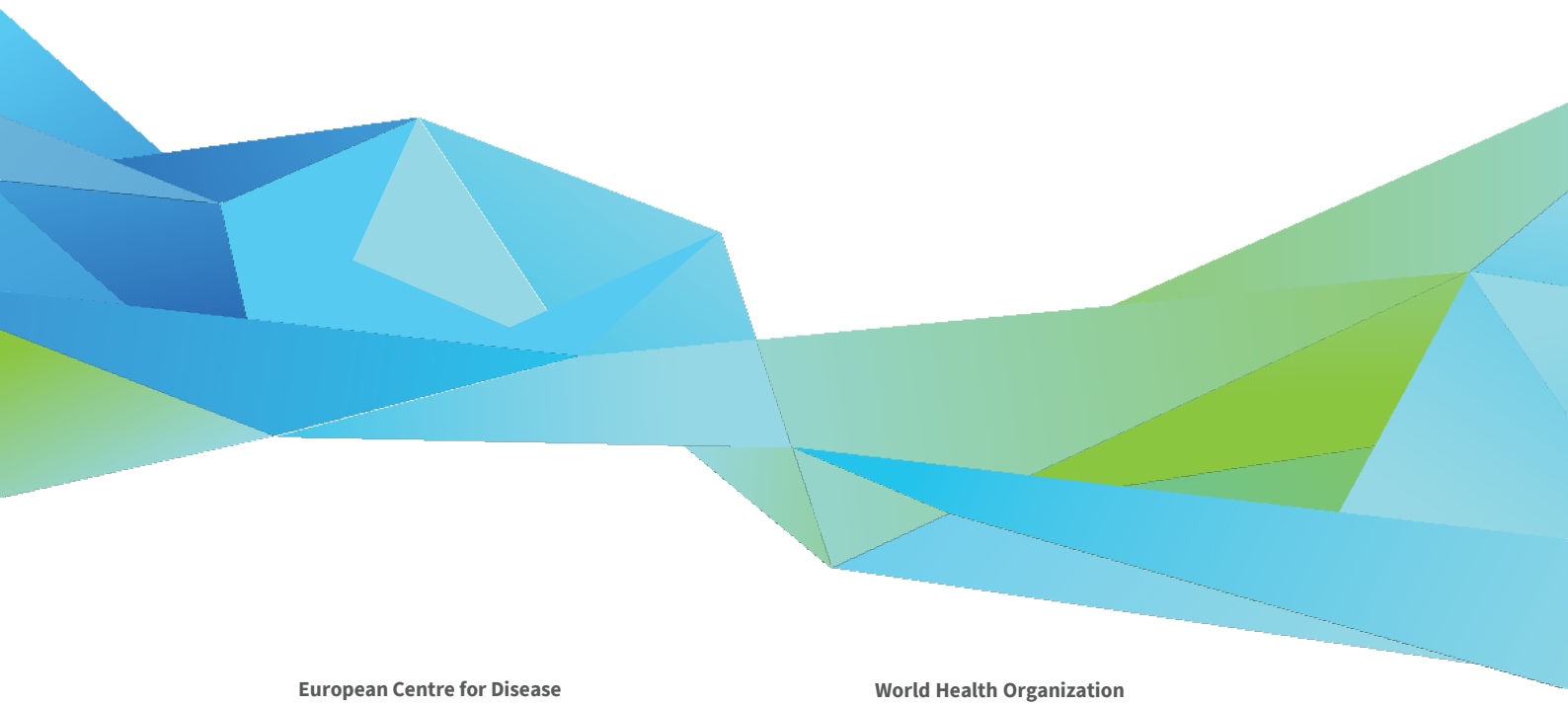

Vaccine viruses
Reference viruses
Collection Date
February
March
April
May
June
July
clade
ALB13c (J)
MAS18c (J)
THA6e (J)
SYD56c (J.1)
CRO36c (J.2)
CRO36e (J.2)
NE56c (J.2)
SLO9c (J.2)
LIS216c (J.2)
FRA84c (J.4)
NOR14c (J.4)
BF31c (J.4)
Clade−Subclade
2a.3a (G.1.3.1)
2a.3a.1 (J)
2a.3a.1 (J.1)
2a.3a.1 (J.2)
2a.3a.1 (J.4)
MN fold change
<=2
>2<=4
>4<=8
>8
< (not recognised by antiserum
Homologous
N/A
HI fold change
< 4
4
8
> 8
Homologous
N/A

B/Victoria


Vaccine viruses
Reference viruses
Collection Date
February
March
April
May
June
July
clade
BR/60e V1A
AUS17c V1A.3a.2(C)
AUS17e V1A.3a.2(C)
AUS17eR V1A.3a.2(C)
STO3c V1A.3a.2(C-5)
HI fold change
< 4
4
8
> 8
Homologous
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.5.4)
V1A.3a.2 (C.5.6)
V1A.3a.2 (C.5.7)
B/Guangxi-Beiliu/2298/2023_Egg
B/Catalonia/2279261NS/2023_Egg
B/Switzerland/329/2024_Egg
B/Slovenia/11466/2022_Gen
B/Catalonia/3514402NS/2023_Egg
B/Stockholm/3/2022_Cell
B/Austria/1359417/2021_Egg_141G
B/Austria/1359417/2021_Cell
B/Austria/1359417/2021_Egg_G141R
B/Netherlands/10335/2023_Egg
B/Switzerland/53639/2023_Egg
B/Norway/3749/2023_Egg
B/Norway/5216/2023_Egg
K136E, del(162-164)
I117V,N129D
A127T,P144L, N150K,G184E, N197D,K203R,R279K
E128K
T182A,D197E
D129N
V117I,E128K, A164T,K326R
D197E
D129G
E183K
T199I
E128G
T121I
T250A
T3R
D129N
E183K
E128K
D129G
T199A
V558I
D129N
G256R
D197E
D129G
S255P
A154E,
I122R,
I117V,N129D

WHO Collaborating Centre reports

A full description of results generated by the London WHO Collaborating Centre at the WIC and used at the September 2025 WHO VCM, and previous ones, can be found at https://www.crick.ac.uk/partnerships/worldwide-influenza-centre/annual-and-interim-reports



European Centre for Disease Prevention and Control (ECDC)

Gustav den III:s Boulevard 40, SE-169 73, Solna, Sweden

Tel. +46 858 60 10 00
Fax +46 858 60 10 01
www.ecdc.europa.eu

Contact us
publications@ecdc.europa.eu

Follow us on Twitter
@ECDC_EU

Like our Facebook page
www.facebook.com/ECDC.EU

World Health Organization Regional Office for Europe

UN City, Marmorvej 51, DK-2100 Copenhagen Ø, Denmark

Tel. +45 45 33 70 00
Fax +45 45 33 70 01
www.who.int/europe

Contact us
eurocontact@who.int

Follow us on Twitter
@WHO_EUROPE

Like our Facebook page
www.facebook.com/WHOEurope

WHO/EURO:2024-6189-45954-77475