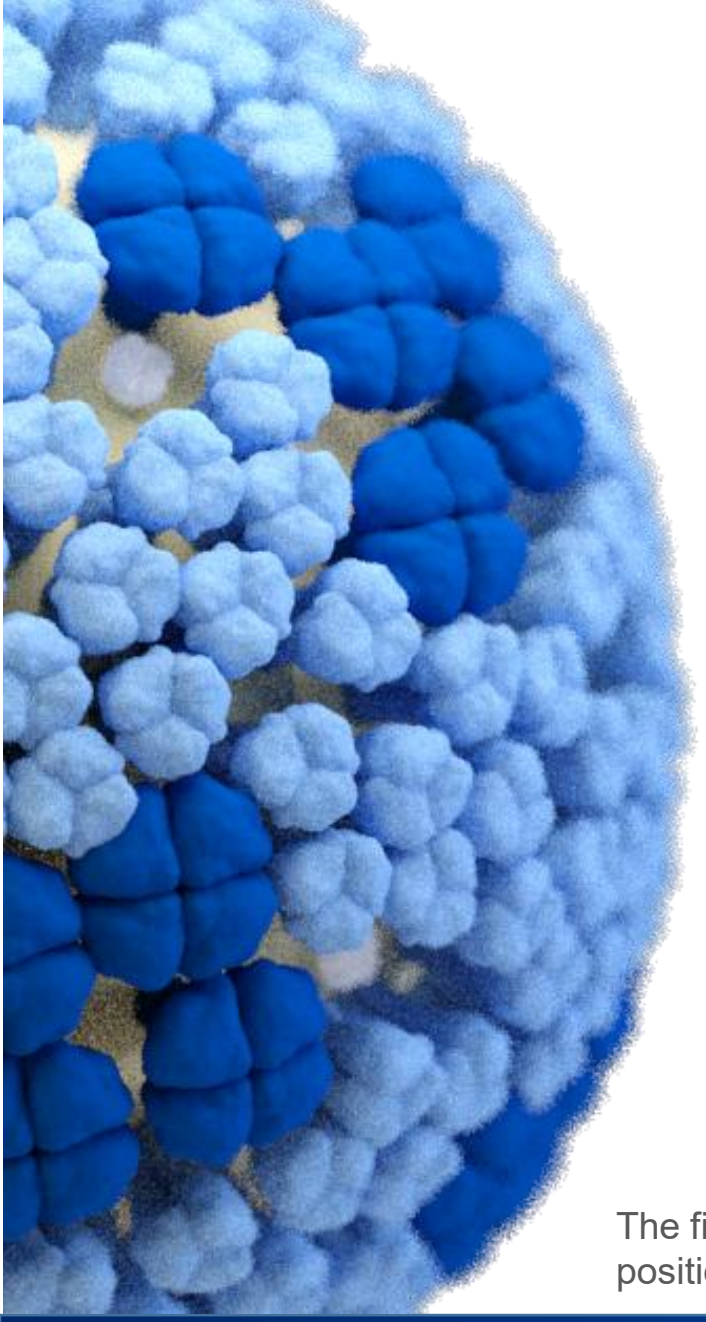


Information For The Vaccine And Related Biological Products Advisory Committee CBER, FDA

Global Influenza Virus Surveillance and Characterization October 1, 2026

Rebecca Kondor, Ph.D.
Influenza Division
National Center for Immunization and Respiratory Diseases
Centers for Disease Control and Prevention
Atlanta, GA 30333

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Global Influenza Vaccine Composition Recommendations for the 2027 Southern Hemisphere

It is recommended that vaccines for use in the 2027 southern hemisphere influenza season contain the following:

Trivalent: Egg-based Vaccines
- **an A/Missouri/11/2025 (H1N1)pdm09-like virus HA subclade D.3.1;**
- **an A/Darwin/1454/2025 (H3N2)-like virus* HA subclade K; and**
- **a B/Tokyo/EIS13-175/2025* HA subclade C.3.1 (B/Victoria lineage)-like virus.**

Trivalent: Cell-, recombinant protein- or nucleic acid-based Vaccines
- **an A/Missouri/11/2025 (H1N1)pdm09-like virus HA subclade D.3.1;**
- **an A/Darwin/1415/2025 (H3N2)-like virus* HA subclade K; and**
- **a B/Pennsylvania/14/2025* HA subclade C.3.1 (B/Victoria lineage)-like virus.**

*** Different from what was recommended for the 2026 southern hemisphere season but the same as the 2026-27 northern hemisphere season**

Recommendation and technical reports available at: https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations

Candidate vaccine viruses & publications

- The recommended candidate viruses for vaccine development and production for SH 2027 and FAQ;
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations
- Candidate vaccine viruses and reagents
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses
- Guidance to tropical and subtropical countries: which formulation (northern hemisphere vs. southern hemisphere) and when to start vaccination:
  - https://www.who.int/teams/global-influenza-programme/vaccines/vaccine-in-tropics-and-subtropics
- Zoonotic influenza summary reports and candidate vaccine viruses on H5/H7/H9 and variant influenza vaccine viruses:
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations
  - https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/zoonotic-influenza-viruses-and-candidate-vaccine-viruses

Influenza Vaccine Composition Meeting Decision Process

Goal – To identify influenza antigen(s) that will elicit immunity against diverse/diverging viruses that will likely co-circulate in the future. Ideal antigens confer breadth of immunity to multiple subclades of viruses and reduce risk(s).

Review influenza activity, trends, geography

Epidemiologic and clinical data

Where are recent epidemics occurring

Virus surveillance

Global Influenza Surveillance and Response System (GISRS) labs test 50-150 thousand samples per week year-round: identify influenza positive specimens; type and influenza A subtype

Review laboratory data of recently collected viruses

Genomic Characterization

Genetic subclades that have emerged; geographic spread and proportion; forecasting predominance

Antigenic Characterization

Level of antigenic drift from progenitors and/or vaccine references

Data Sharing and Integration across GISRS

- Genetic and Antigenic data integration
- Phylogenetics
- Phylogeography
- Fitness forecasting
- Antigenic cartography
- Antiviral susceptibility
- Human Serum Panels
- Candidate Vaccine Virus (CVV) Reagent sharing

Human serology data and vaccine effectiveness

Post-vaccination and post-exposure studies

Comparative analysis of co-circulating antigenic variants to identify those that pose the greatest risk of immune escape

Global Influenza Vaccine Effectiveness (GIVE) Collaboration

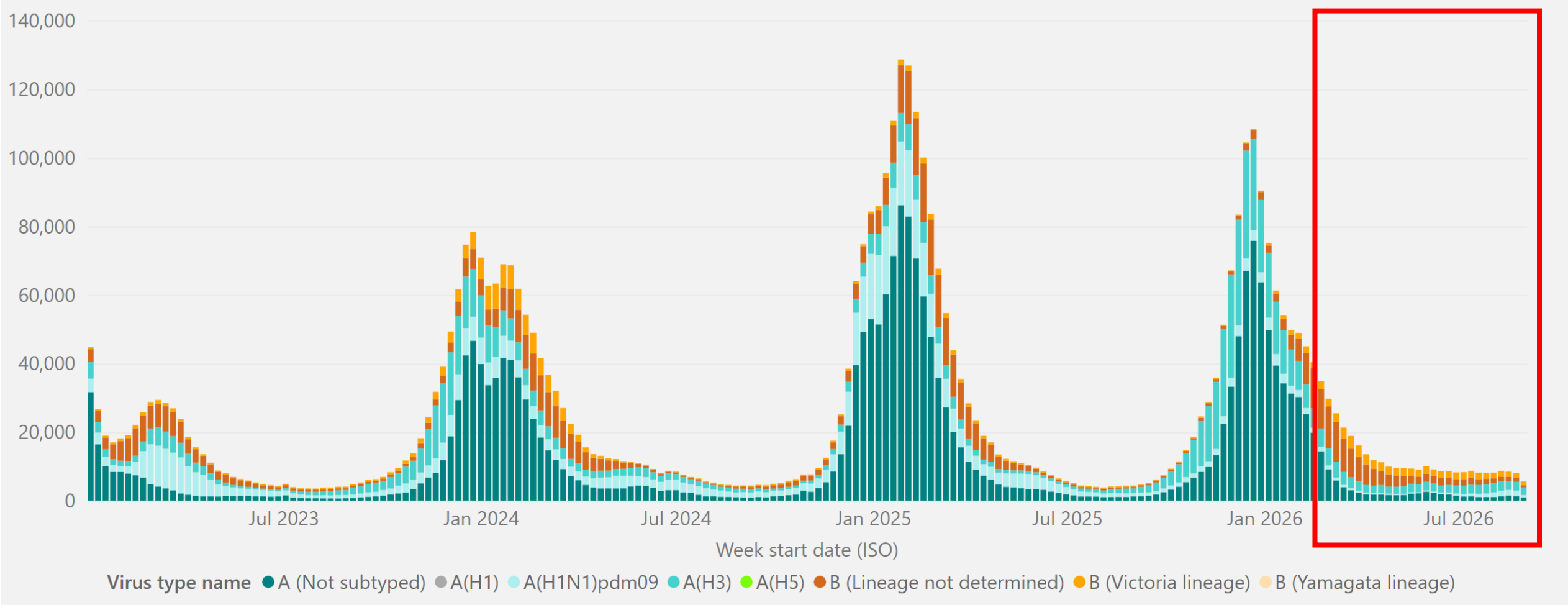
VE studies– previous season and current season interim results

Review Candidate Vaccine Virus availability

New CVVs

- Analysis of the availability and characterization status of candidate vaccine viruses for each platform
- Review of cell or egg-adaptation mutations in CVVs
- Review of high-growth reassortants

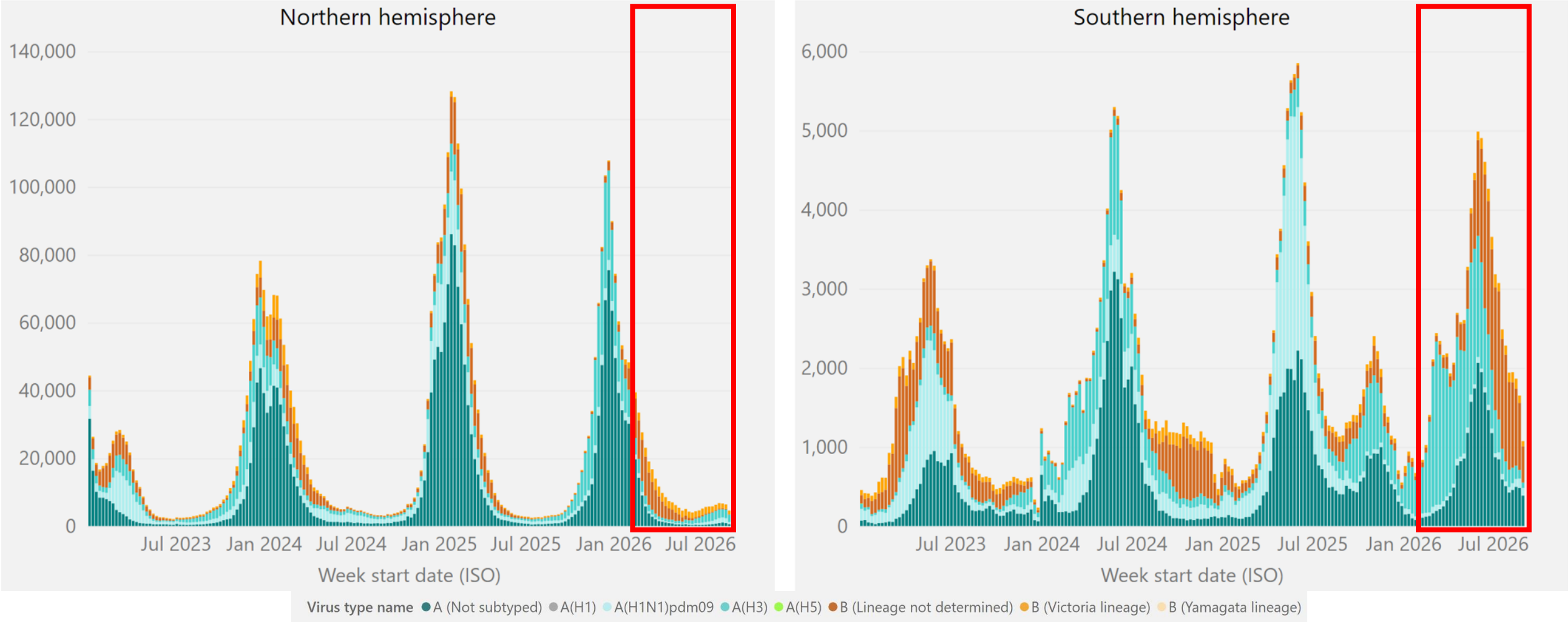
Global Circulation of Seasonal Influenza Viruses Since 2023



Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (13 September 2026)

VCM Information meeting: https://www.youtube.com/@who

Circulation of influenza viruses by hemisphere

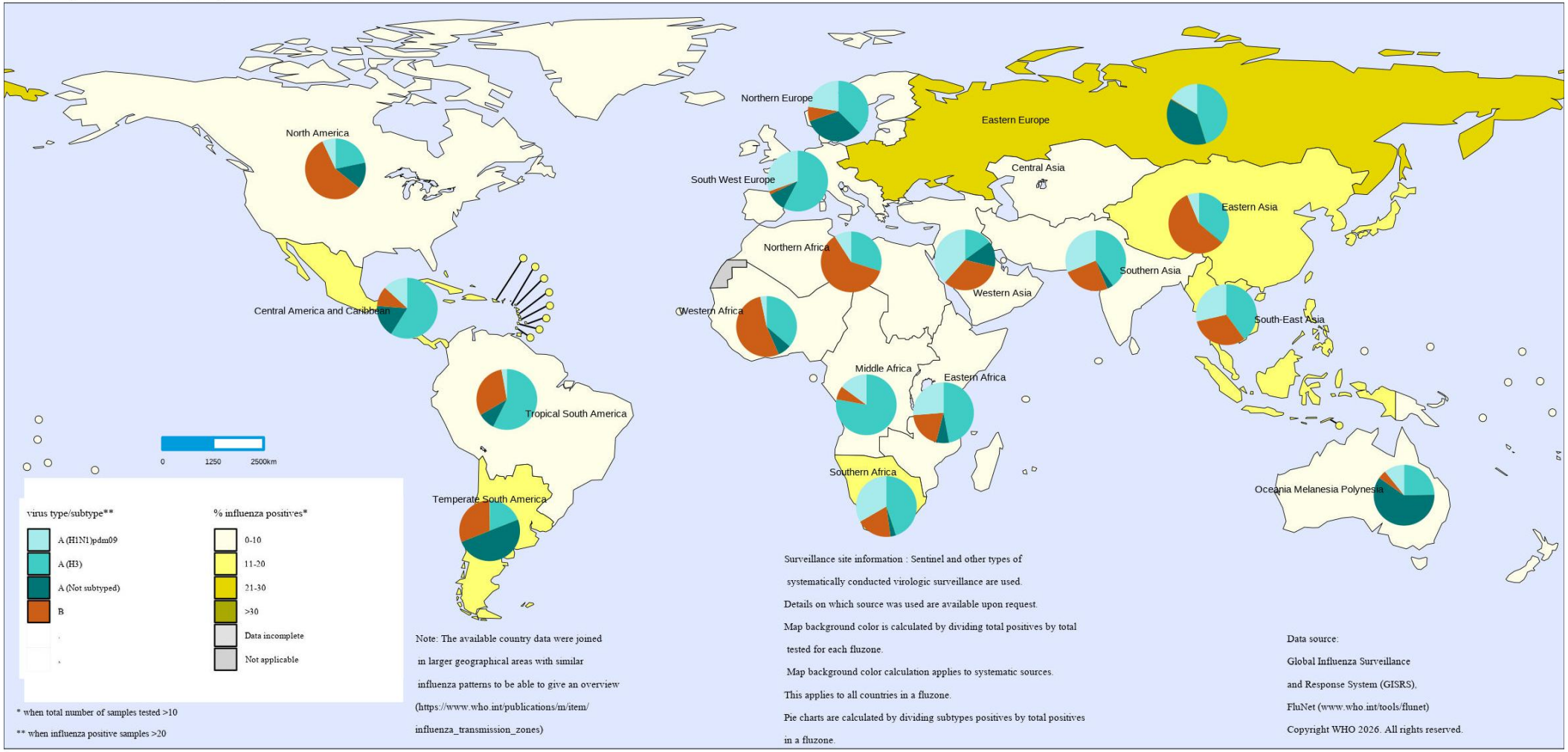


Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (13 September 2026)

VCM Information meeting: https://www.youtube.com/@who

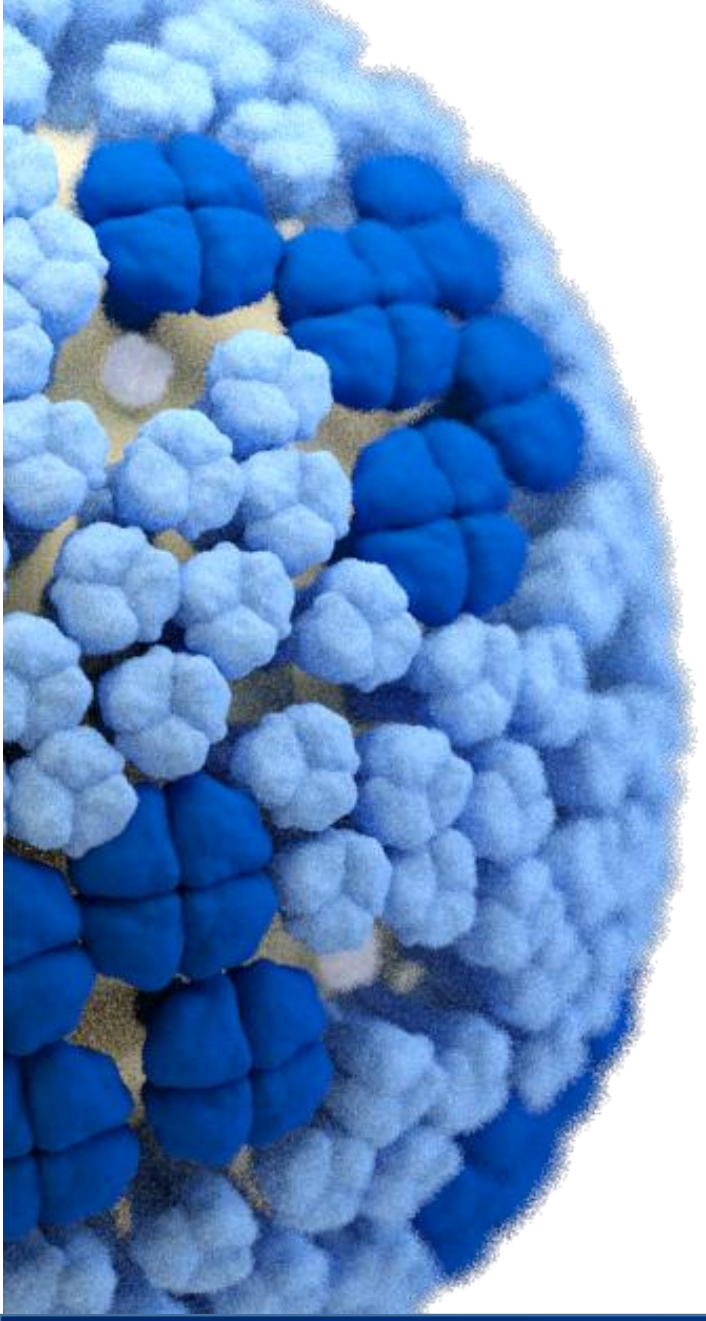
Influenza activity and global distribution of type/subtype
February – September 2026

February 01 2026 and September 13 2026



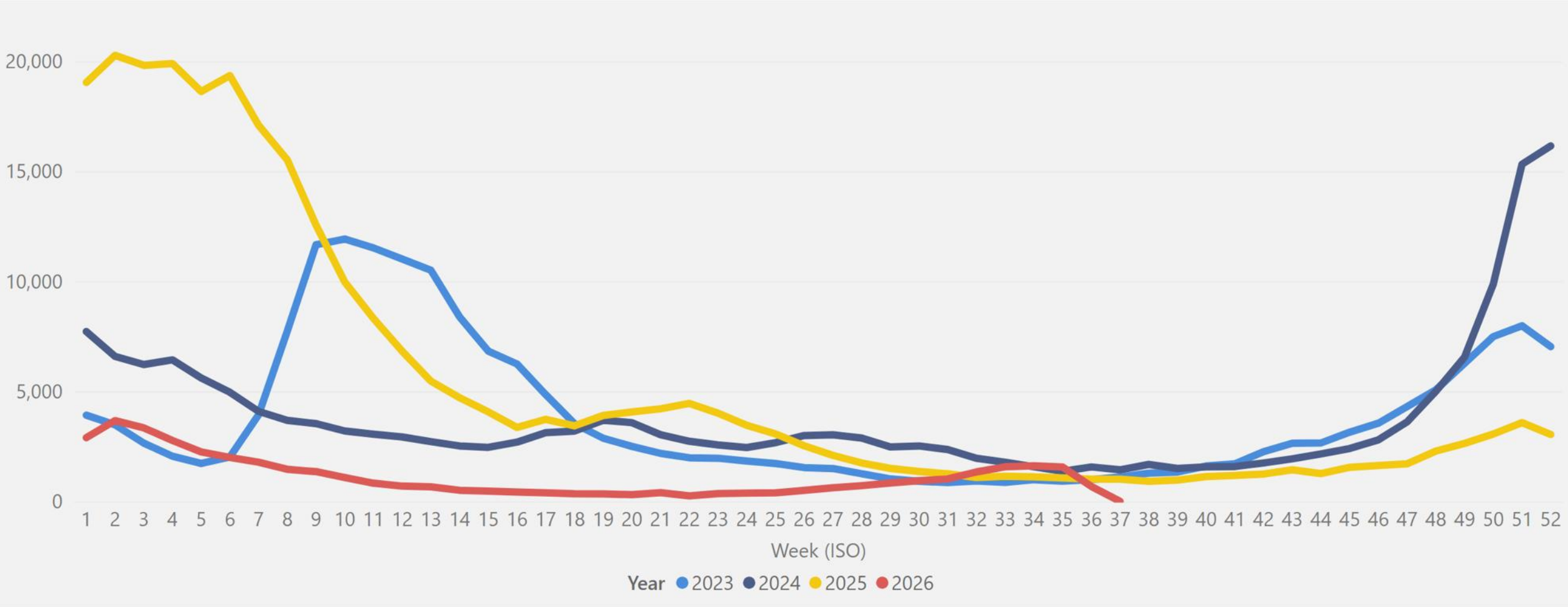
The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area of of its authorities, of concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

VCM Information meeting: https://www.youtube.com/@who



A(H1N1)pdm09 Viruses

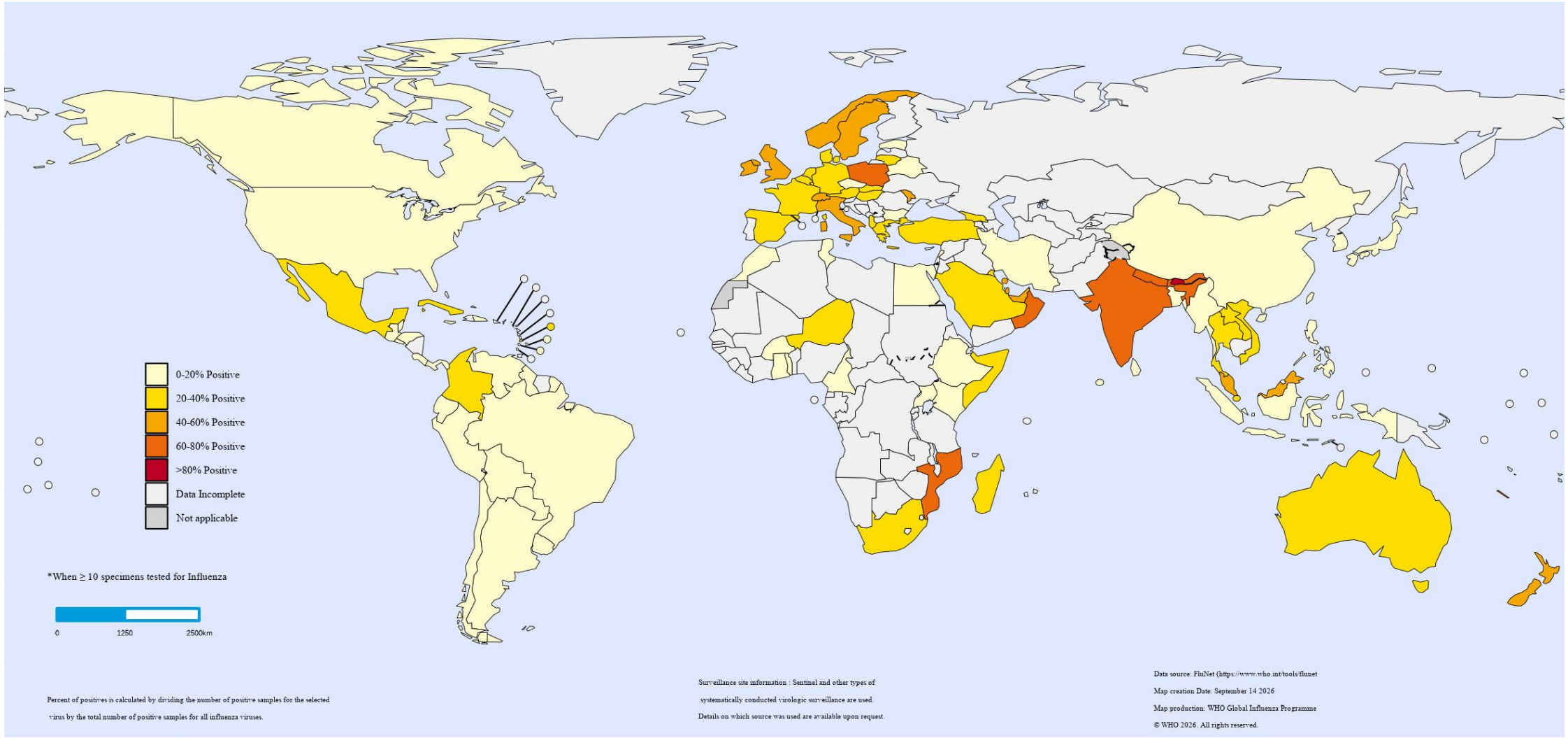
Number of A(H1N1)pdm09 viruses detected by GISRS



GISRS GLOBAL INFLUENZA SURVEILLANCE & RESPONSE SYSTEM

VCM Information meeting: https://www.youtube.com/@who

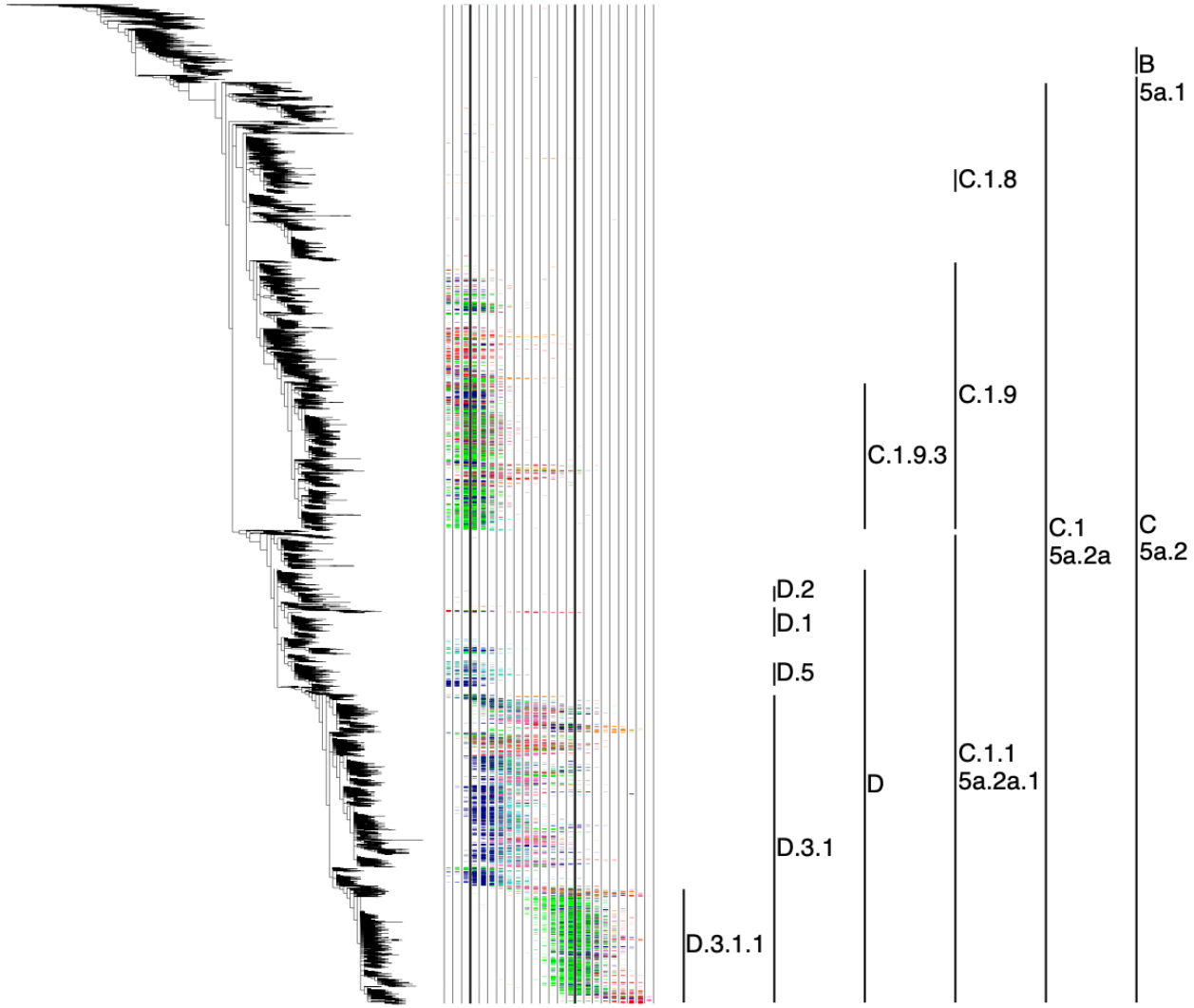
Influenza A(H1N1)pdm09 activity

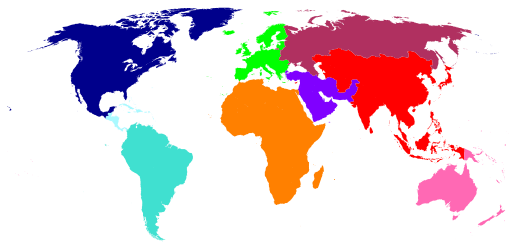


Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (13 September 2026)

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 HA phylogeography





North America
South America
Europe
Africa
Middle East
Russia
E SE Asia
Oceania

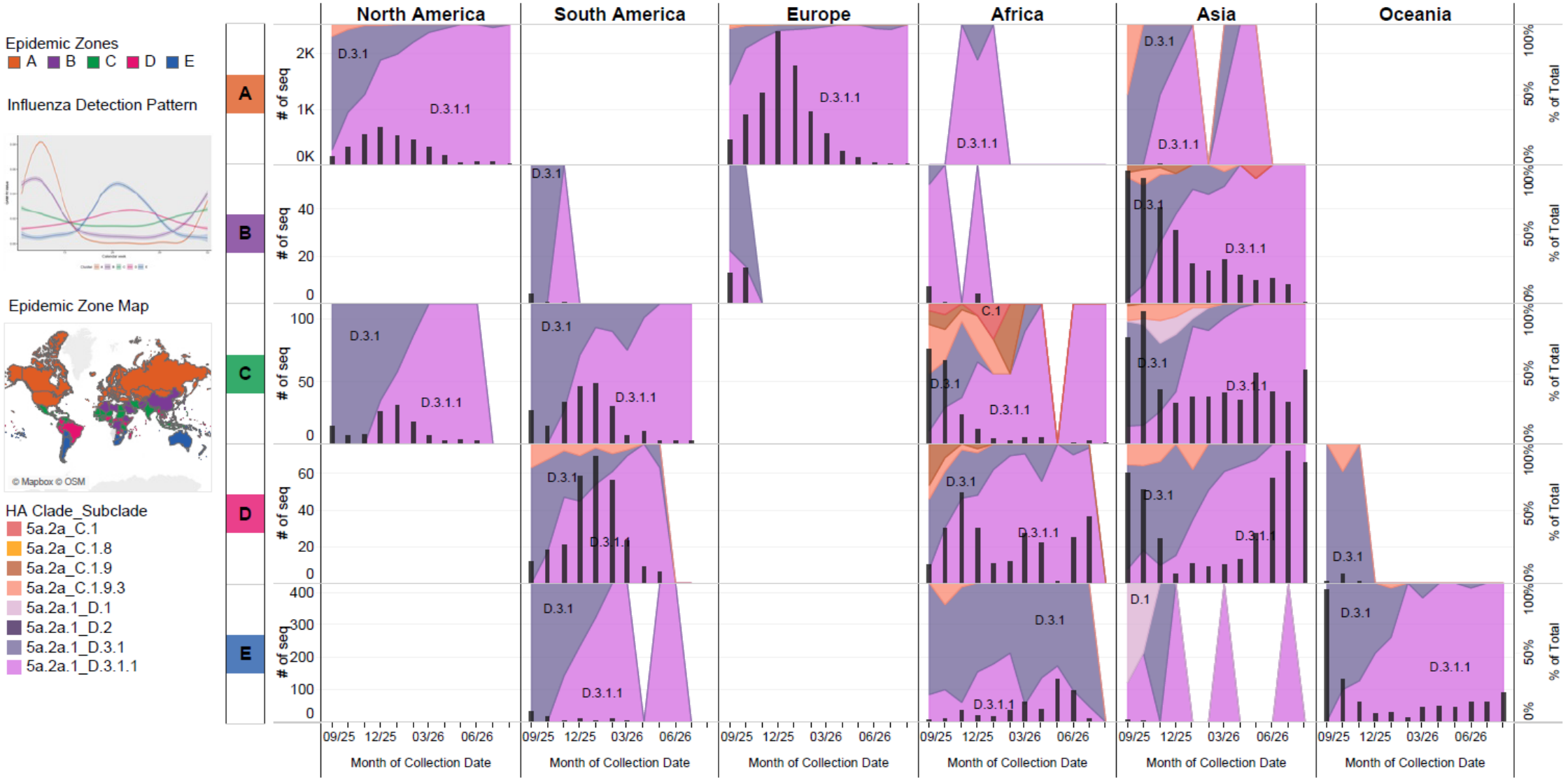
Figure Source: University of Cambridge

Data Source: GISAID

HA and NA clade/subclades: https://clades.nextstrain.org/

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 Extended Diversity Plot



Data Source: GISAID

HA and NA clade/subclades:
https://clades.nextstrain.org/

Antigenic analysis of A(H1N1)pdm09 viruses in HI assays

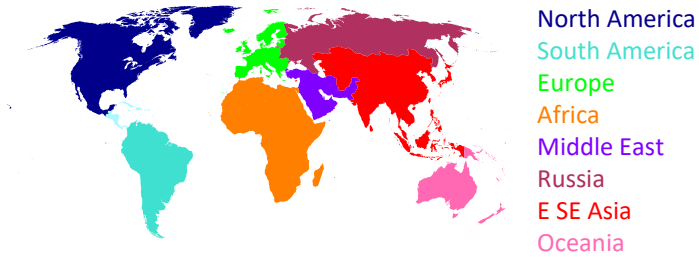
Antisera to southern hemisphere 2026 & northern hemisphere 2026-27 vaccine virus antigens

WHO CC	A/Missouri/11/2025-like Cell 5a.2a.1 (D.3.1)	Low (≥ 8 fold)	WHO CC	A/Missouri/11/2025-like Egg 5a.2a.1 (D.3.1)	Low (≥ 8 fold)
CDC	272 (100%)	0 (0%)	CDC	272 (100%)	0 (0%)
CNIC	36 (97%)	1 (3%)	CNIC	35 (95%)	2 (5%)
FCI	121 (92%)	10 (8%)	FCI	131 (100%)	0 (0%)
NIID	57 (98%)	1 (2%)	NIID	53 (91%)	5 (9%)
VIDRL	337 (94%)	21 (6%)	VIDRL	346 (97%)	12 (3%)
TOTAL	823 (96%)	33 (4%)	TOTAL	837 (98%)	19 (2%)

“Low” reactor represented titers ≥ 8-fold lower than vaccine strain homologous titer by HI

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 HA phylogeography



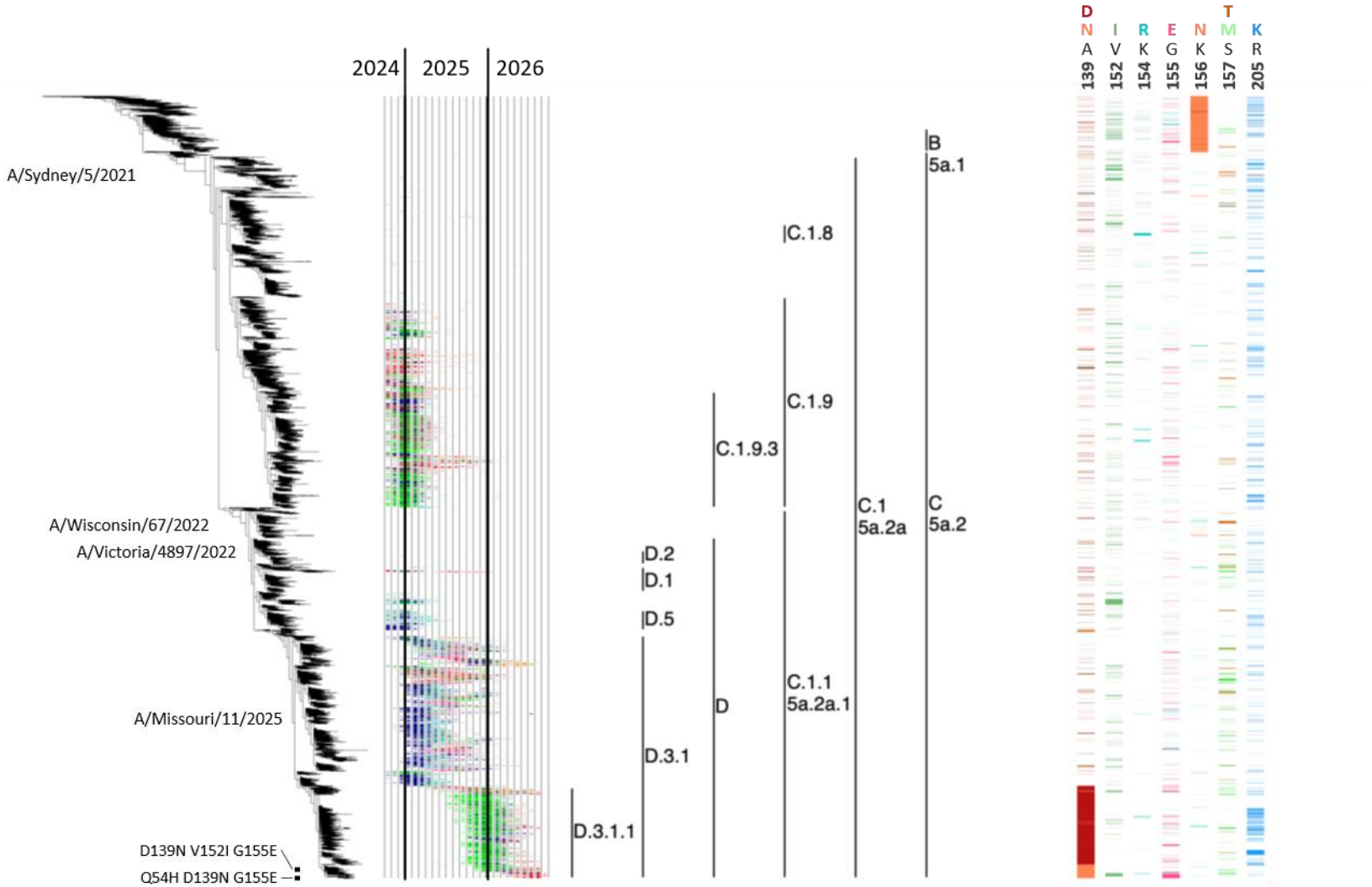


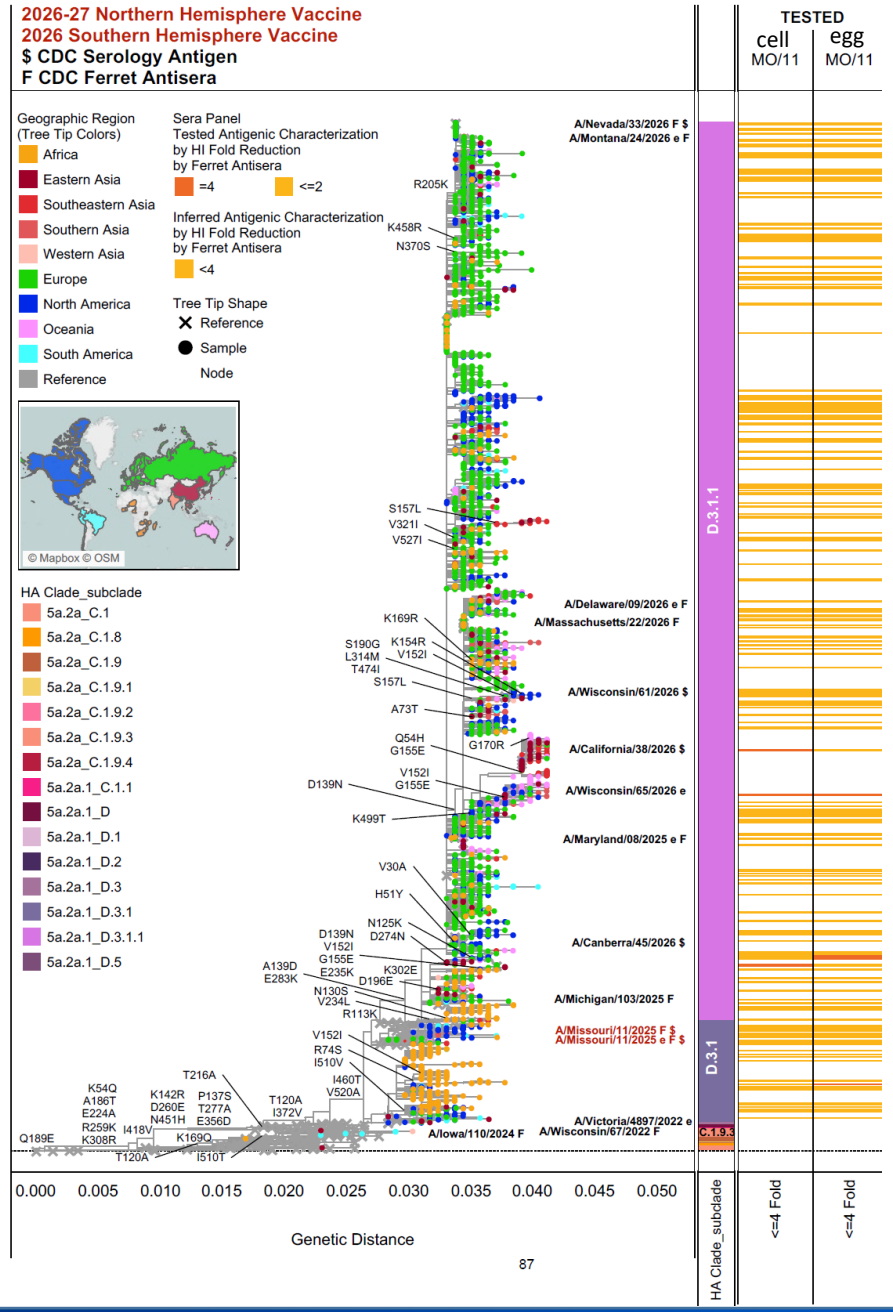
Figure Source: University of Cambridge

Data Source: GISAID

HA and NA clade/subclades: https://clades.nextstrain.org/

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 Integrated Genotype and Phenotype Analysis



5a.2a.1
(D.3.1, D.3.1.1)

5a.2a
(C.1.9, C.1.9.3)

Data Source: GISAID

HA and NA clade/subclades: https://clades.nextstrain.org/

HI antigenic analysis of A(H1N1)pdm09 viruses (1)

Hemagglutination-inhibition test of influenza A/H1pdm09 viruses-0.5%TRBC

				C.1.1	D	D.3.1			K156N	D.3.1.1	G155E	C.1.9.3	HI test date:2026/9/9	
	Strains	Passage History	Sample date	Wisconsin/ 67/22 Cell No.111	Victoria/ 4897/22 Egg No.121	TOKYO/ EIS10-554/24 Cell No.112	Missouri/11/25 Cell No.131	Missouri/11/25 Egg No.142	TOKYO/ EIS11-980/25 Cell No.111	TOKYO/ EIS13-602/25 Cell No.112	TOKYO/ EIS15-043/26 Cell NIID-2026-121	TOKYO/ EIS10-381/24 Cell No.112	Subclade	Amino acid substitution in HA
	REF. Ag.													
	A/Wisconsin/67/2022	S 2 +hCK2		2560	2560	2560	5120	2560	320	2560	2560	2560	C.1.1	—
	A/Victoria/4897/2022	E 3 +1		2560	2560	2560	2560	2560	320	1280	1280	2560	D	D187D/E*, Q223R
	A/TOKYO/EIS10-554/2024	hCK 3	2024/08/10	5120	5120	5120	5120	2560	320	2560	2560	2560	D.3.1	—
	A/Missouri/11/2025	S 2 +hCK1		5120	2560	5120	5120	2560	320	5120	2560	2560	D.3.1	—
	A/Missouri/11/2025	Spf3E1/SpE1		5120	2560	2560	5120	2560	320	2560	2560	2560	D.3.1	Q223R
	A/TOKYO/EIS11-980/2025	hCK 2	2025/03/15	320	80	320	320	160	2560	320	320	160	D.3.1	R113K, K156N*, Q193K*
	A/TOKYO/EIS13-602/2025	hCK 3	2025/08/31	5120	2560	5120	5120	5120	320	2560	5120	5120	D.3.1.1	—
	A/TOKYO/EIS15-043/2026	hCK 2	2026/05/05	640	160	2560	1280	320	160	1280	5120	640	D.3.1.1	D139N*, Q54H, G155E*
	A/TOKYO/EIS10-381/2024	hCK 2	2024/07/15	2560	2560	2560	5120	2560	320	2560	1280	5120	C.1.9.3	I510T, S83P
	TEST Ag.													
1	A/SAITAMA-C/19/2026	MDCK 2 +hCK1	2026/07/02	5120	5120	5120	5120	5120	320	5120	2560	5120	D.3.1.1	D139N*, I96F, V132I, D168D/N(28%)*
2	A/TOCHIGI/496/2026	hCK 2	2026/08/07	5120	5120	5120	5120	5120	320	2560	2560	5120	D.3.1.1	D139N*, I96F, V132I
3	A/Taiwan/C23020/2026	MDCK 2 +hCK2	2026/06/14	5120	2560	5120	5120	2560	320	5120	2560	5120	D.3.1.1	D139N*
4	A/Taiwan/S28759/2026	MDCK 2 +hCK2	2026/06/12	5120	2560	5120	5120	2560	320	5120	2560	5120	D.3.1.1	D139N*
5	A/Seoul/1016/2026	MDCK 2 +hCK1	2026/04/06	5120	2560	5120	5120	2560	320	2560	2560	5120	D.3.1.1	—
6	A/OKINAWA/531/2026	MDCK 1 +hCK1	2026/07/06	5120	2560	2560	5120	2560	320	2560	2560	2560	D.3.1.1	D139N*
7	A/Taiwan/C23031/2026	MDCK 2 +hCK2	2026/06/22	5120	2560	2560	5120	2560	320	2560	1280	2560	D.3.1.1	D139N*, V152I
8	A/YOKOHAMA/17/2026	hCK 1 +1	2026/07/28	1280	320	2560	1280	640	320	1280	5120	1280	D.3.1.1	D139N*, G155E*, Q54H
9	A/Taiwan/S28766/2026	MDCK 2 +hCK2	2026/06/21	1280	320	2560	1280	640	160	1280	5120	1280	D.3.1.1	D139N*, Q54H, G155E*
10	A/NIIGATA/1052/2026	CaCo-2 2 +hCK1	2026/08/03	1280	320	1280	1280	640	320	1280	5120	1280	D.3.1.1	D139N*, G155E*
11	A/SENDAI/7/2026	AX-4 1 +hCK1	2026/08/10	1280	320	1280	1280	640	320	1280	5120	1280	D.3.1.1	D139N*, G155E*, Q54H
12	A/KANAGAWA/IC2541/2026	hCK 1	2026/08/27	1280	320	1280	1280	640	320	1280	5120	640	D.3.1.1	D139N*, G155E*
13	A/KANAGAWA/ZC2519/2026	hCK 1	2026/08/28	1280	320	1280	1280	320	320	640	2560	640	D.3.1.1	D139N*, G155E*, V152I, N287S
14	A/KANAGAWA/ZC2518/2026	hCK 1	2026/08/17	1280	160	1280	1280	640	320	1280	5120	640	D.3.1.1	D139N*, G155E*
15	A/YOKOHAMA/18/2026	hCK 1 +1	2026/08/08	1280	160	1280	1280	640	160	1280	5120	1280	D.3.1.1	D139N*, G155E*, Q54H, G170E*
16	A/KANAGAWA/IC2540/2026	hCK 1	2026/08/27	640	320	1280	1280	640	320	1280	5120	1280	D.3.1.1	D139N/D(37%)*, G155E*
17	A/KANAGAWA/AC2574/2026	hCK 1	2026/08/21	640	320	1280	1280	640	160	1280	5120	640	D.3.1.1	D139N*, G155E*, V152I, N287S
18	A/KANAGAWA/AC2575/2026	hCK 1	2026/08/24	640	320	1280	1280	320	160	1280	5120	640	D.3.1.1	D139N*, G155E*, V152I, N287S

*Antigenic sites

Isolates in phylogenetic tree

Fold reduction

< 4-fold

4-fold

8-fold

8-fold <

ß

C.1.9	T120A, K169Q*
C.1.9.3	S83P, I510T
D.3.1	I460T, V520A
D.3.1.1	R113K, A139D*, E283K, K302E

Source: WHO CC Tokyo

VCM Information meeting: https://www.youtube.com/@who

HI antigenic analysis of A(H1N1)pdm09 viruses (2)

Table H1-11. Antigenic analyses of influenza A(H1N1)pdm09 viruses (Turkey RBC)

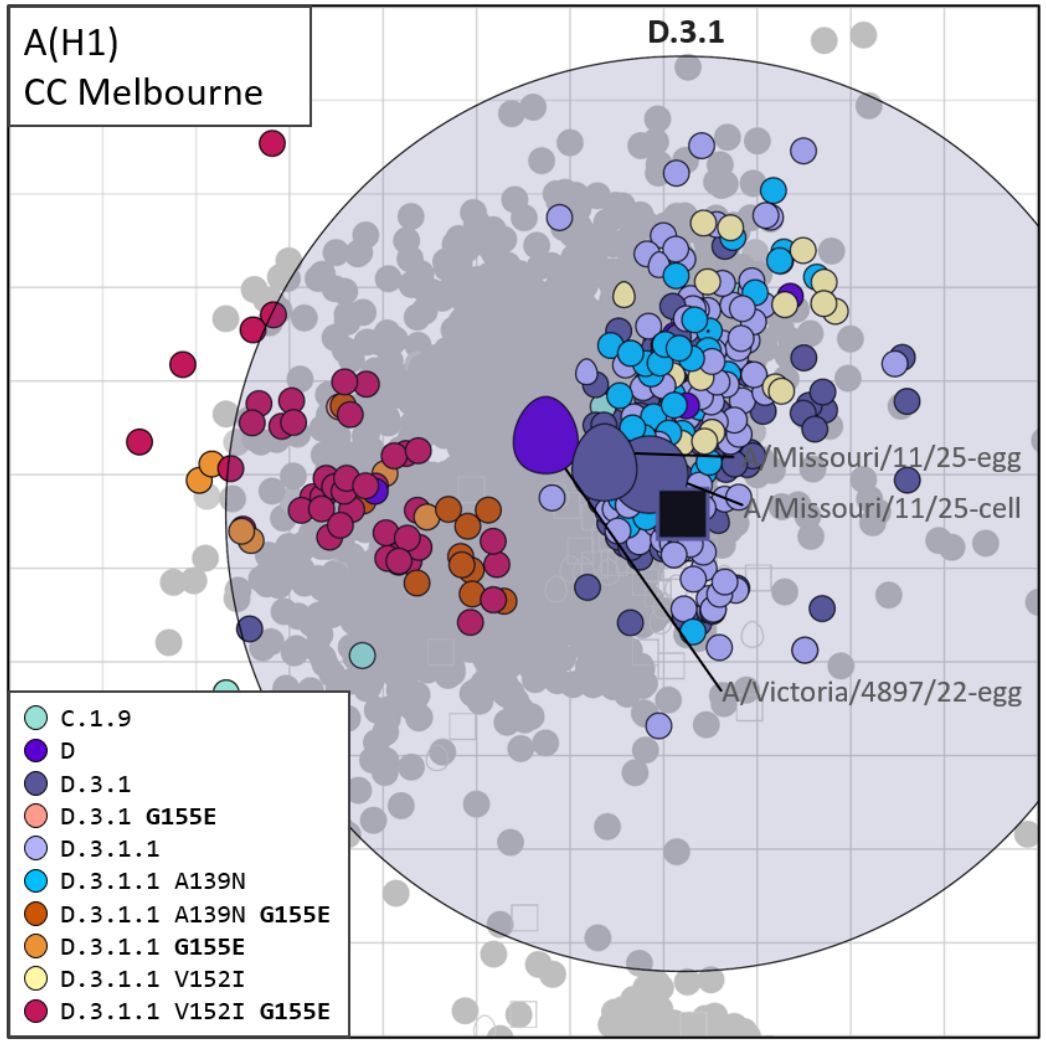
	Viruses	Other information	Genetic group	Collection Date	Passage / Genetic group	Haemagglutination inhibition titre: Post-infection ferret antiserum						
						A/Wisconsin/67/2022	A/Norway/07606/2024	A/Missouri/11/2025	A/Missouri/11/2025	A/Iceland/25-39095/2025	itzerland/UN-IUG-002/2025	A/Iceland/25-36510/2025
					Passage	MDCK	MDCK	MDCK	Egg	MDCK	Egg	Egg
					Ferret number	F04/24	F02/25	F42/25	F02/26	F03/26	F05/26	F15/26
			Genetic group	Collection Date	Genetic group	5a.2a.1 (C.1.1)	5a.2a (C.1.9.3)	5a.2a.1 (D.3.1)	5a.2a.1 (D.3.1)	5a.2a.1 (D.3.1.1)	5a.2a.1 (D.3.1.1)	5a.2a.1 (D.3.1.1)
	REFERENCE VIRUSES											
	A/Wisconsin/67/2022		5a.2a.1 (C.1.1)	2022-10-25	MDCK2	2560	1280	2560	1280	1280	2560	1280
	A/Norway/07606/2024	I166V	5a.2a (C.1.9.3)	2024-10-12	MDCK3	1280	2560	2560	1280	1280	2560	1280
	A/Missouri/11/2025		5a.2a.1 (D.3.1)	2025-01-30	SIAT2/MDCK2	2560	2560	5120	2560	2560	2560	2560
	A/Missouri/11/2025		5a.2a.1 (D.3.1)	2025-01-30	E1/E3	1280	1280	1280	640	1280	1280	1280
	A/Iceland/25-39095/2025		5a.2a.1 (D.3.1.1)	2025-11-19	MDCK2	2560	2560	2560	2560	2560	2560	2560
	A/Switzerland/UN-SNRCI-HUG-002/2025		5a.2a.1 (D.3.1.1)	2025-10-17	E2 (Am1AI1)	2560	1280	2560	1280	1280	2560	2560
	A/Iceland/25-36510/2025		5a.2a.1 (D.3.1.1)	2025-11-02	E2 (Am1AI1)	1280	1280	2560	1280	1280	1280	1280
	TEST VIRUSES											
262531	A/Iceland/10309/2026	Q54H, D139N (egg adap. Q223R)	5a.2a.1 (D.3.1.1)		E2(Am1AI1)	1280	640	1280	640	1280	1280	1280
262513	A/Iceland/26153/2026	D139N (egg adap. Q223R)	5a.2a.1 (D.3.1.1)		E3(Am1AI2)	1280	640	1280	640	640	1280	640
262652	A/Mauritius/4286/2026	G155E (egg adap. D187V)	5a.2a.1 (D.3.1.1)		E3(Am1AI2)	640	320	640	640	320	640	640
262772	A/Hong Kong/444/2026	Q54H, D139N, G155E (egg adap. Q223R)	5a.2a.1 (D.3.1.1)		E3(Am1AI2)	320	320	640	320	160	320	320
262772	A/Hong Kong/444/2026	Q54H, D139N, G155E	5a.2a.1 (D.3.1.1)		MDCK2/MDCK2	640	320	1280	640	640	640	320
263095	A/Hong Kong/525/2026	Q54H,D139N,G155E (+P322L)	5a.2a.1 (D.3.1.1)		MDCK2/MDCK1	320	80	320	160	160	320	160
263097	A/Hong Kong/520/2026	Q54H,D139N,G155E (+V173I)	5a.2a.1 (D.3.1.1)		MDCK2/MDCK1	320	160	640	320	320	320	320
263099	A/Hong Kong/524/2026	D139N,V152I,G155E,E235K	5a.2a.1 (D.3.1.1)		MDCK2/MDCK1	640	320	640	320	320	640	320
263105	A/Hong Kong/430/2026	Q54H,D139N,G155E	5a.2a.1 (D.3.1.1)		MDCK1/MDCK1	640	320	1280	640	320	640	640
	< relates to the lowest dilution of antiserum used					Vaccine SH 2025 NH 2025-26		Vaccine SH 2026 NH 2026-27				

< 4-fold 4-fold 8-fold > 8-fold < not recognised by the antiserum

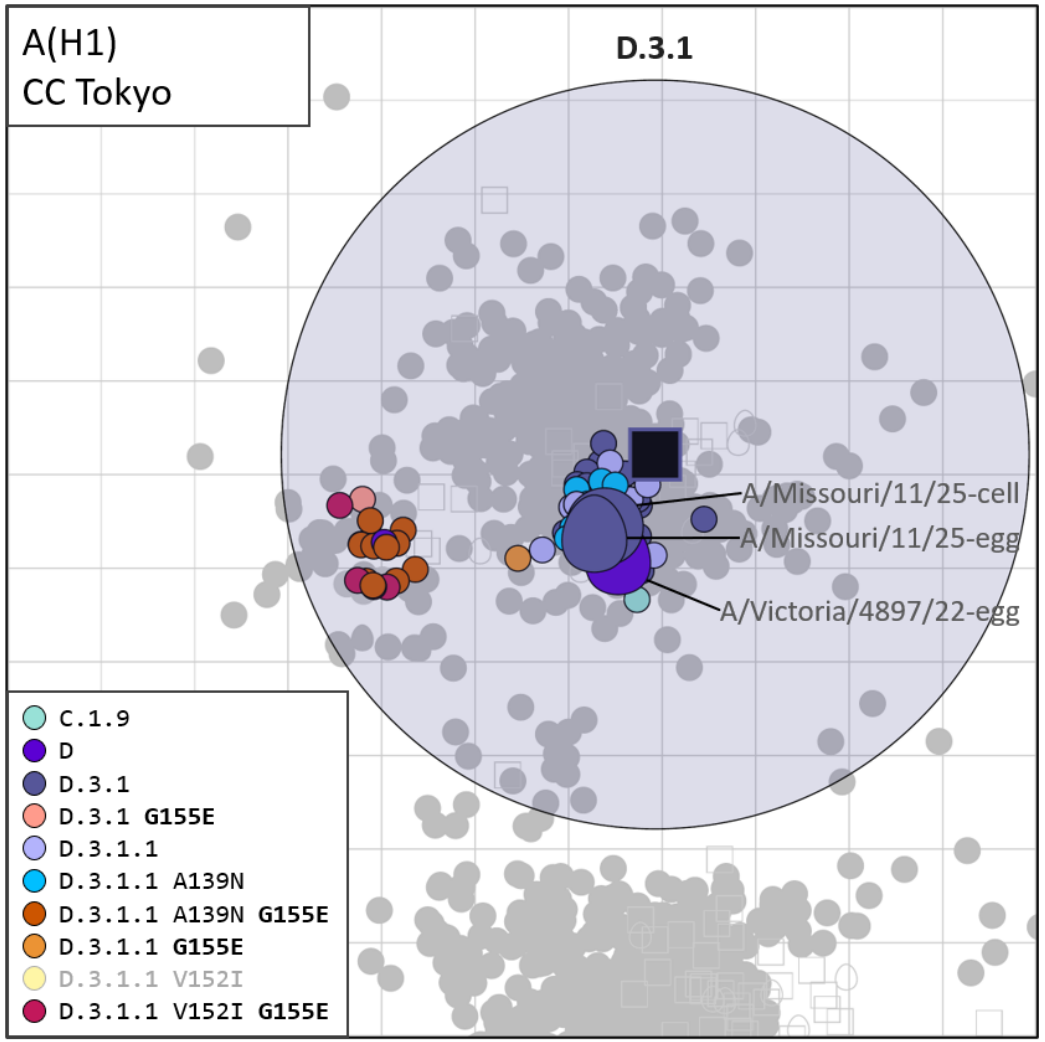
Source: WHO CC London

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 antigenic cartography (1)



A/Missouri/11/25-cell serum circle
(within 8-fold of homologous titer)

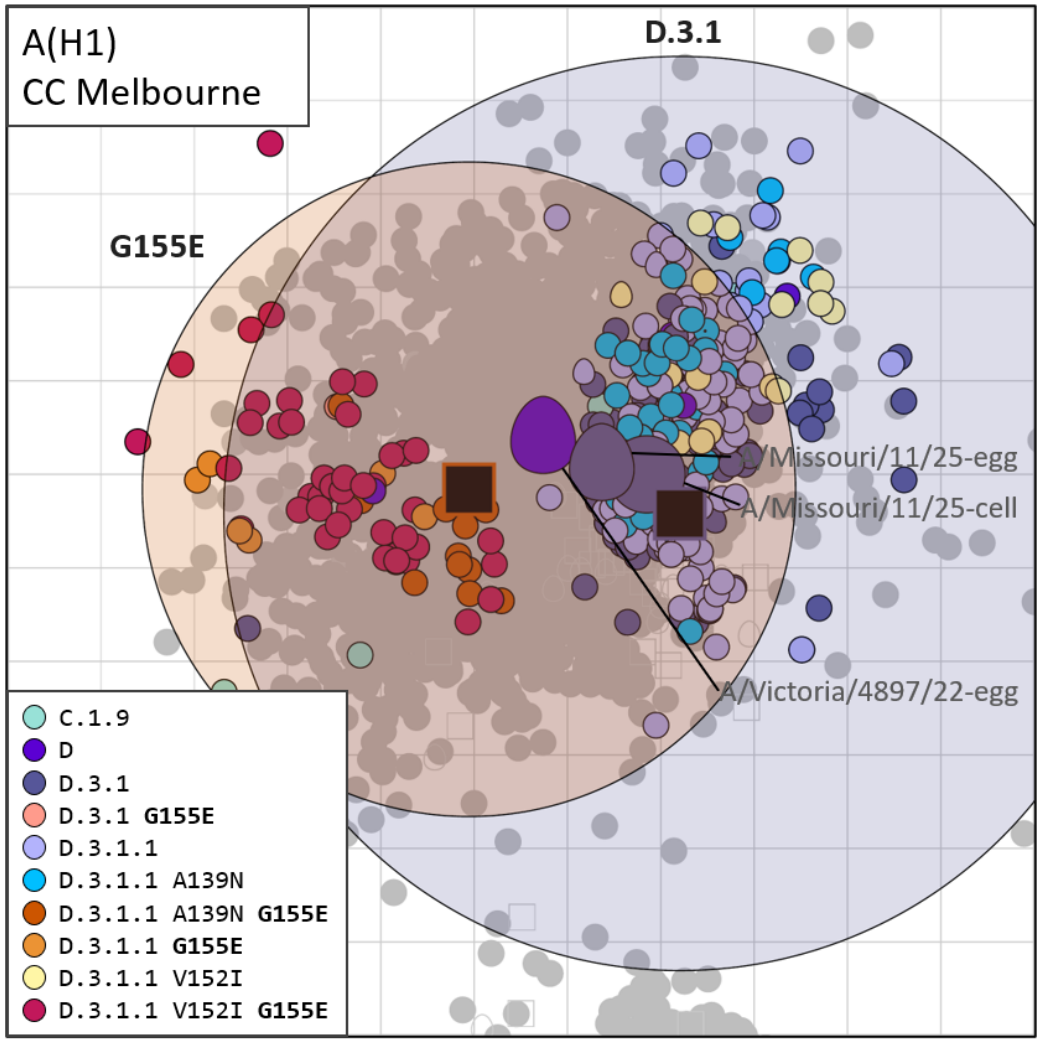


A/Missouri/11/25-egg serum circle
(within 8-fold of homologous titer)

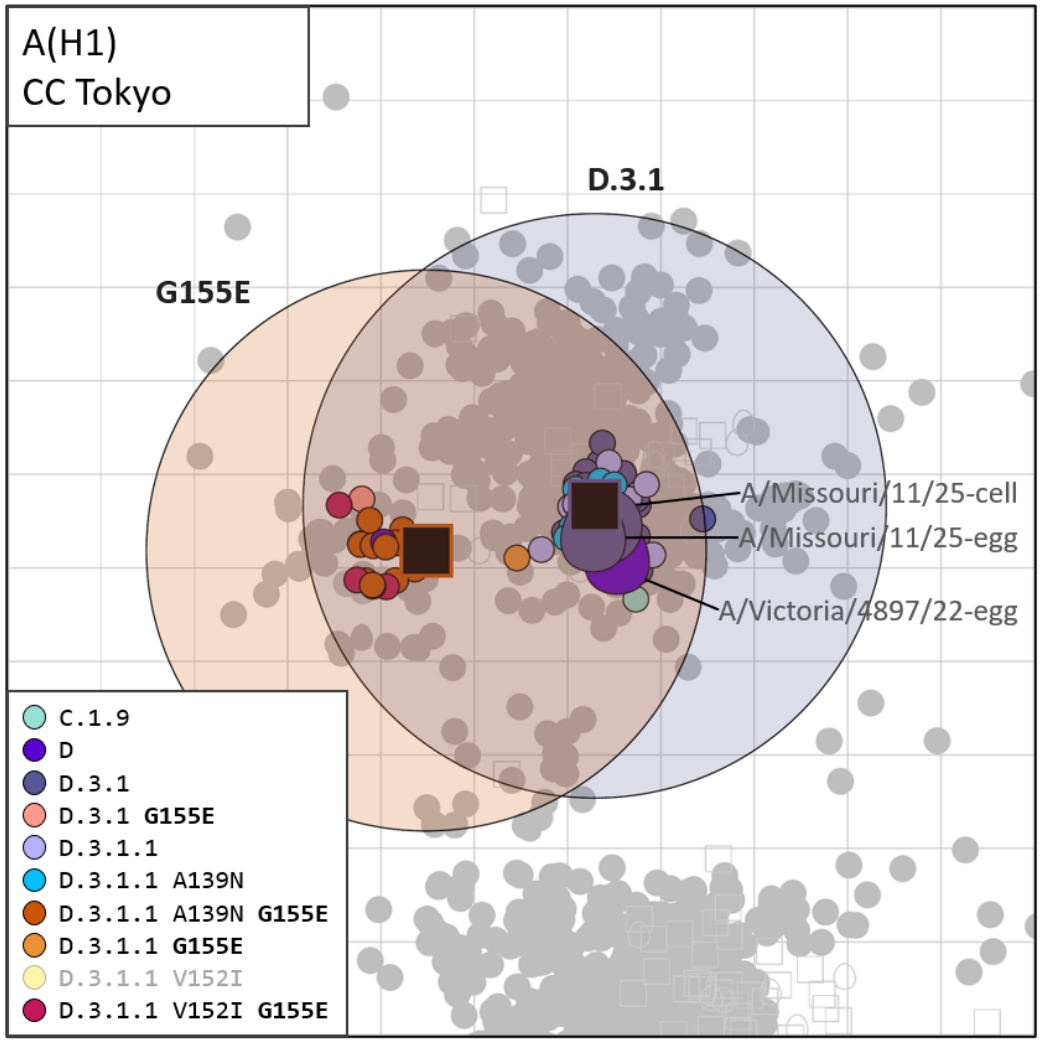
Source: University of Cambridge

VCM Information meeting: https://www.youtube.com/@who

A(H1N1)pdm09 antigenic cartography (2)



A/Missouri/11/25-cell and A/Sydney/81/26 (155E)-cell serum circles
(within 8-fold of homologous titer)



A/Missouri/11/25-cell and A/Tokyo/EIS15-043/26 (155E)-cell serum circles
(within 8-fold of homologous titer)

Source: University of Cambridge

VCM Information meeting: https://www.youtube.com/@who

Human post-vaccination serum analysis of A(H1N1)pdm09 viruses

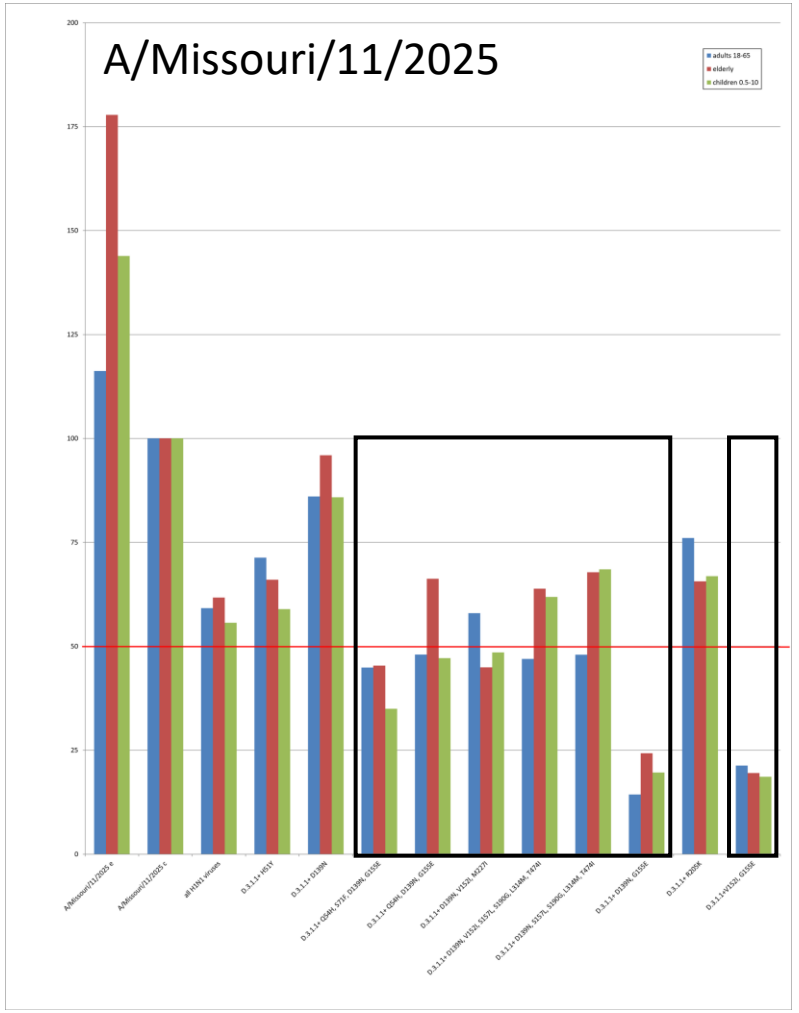
Human serology studies used seven serum panels from children (<10 years), adults (18 to 64 years) and older adults (≥65 years) who had received egg-propagated inactivated (standard or adjuvanted) or cell culture-propagated inactivated vaccines with SH 2026 influenza vaccine formulations.

Recent A(H1N1)pdm09 viruses with HA genes from subclade D.3.1.1 were analyzed in HI assays using these human serum panels. When compared to the post-vaccination geometric mean titers (GMTs) to cell culture-propagated A/Missouri/11/2025 (H1N1)pdm09-like vaccine reference viruses, with amino acid substitutions e.g.:

Q54H, D139N, G155E,

or D139N, V152I, G155E,

or D139N, V152I, S157L, S190G.



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Influenza A(H1N1)pdm09: antiviral susceptibility

Neuraminidase inhibitors

- Of 1,029 A(H1N1)pdm09 virus clinical samples and isolates examined by genetic and/or phenotypic analyses, 15 viruses showed evidence of reduced susceptibility to neuraminidase inhibitors (NAIs):
  - 7 had an H275Y neuraminidase (NA) substitution alone or in combination with S247N substitution
  - 8 had S247N combined with I223V, I223T or Q136K substitutions

Endonuclease inhibitors

- Of 1,331 A(H1N1)pdm09 viruses examined by genetic and/or phenotypic analyses, no viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil

Influenza A(H1N1)pdm09 summary (1)

Phylogenetics of A(H1N1)pdm09 HA genes

- During this reporting period, the majority of A(H1N1)pdm09 viruses sequenced globally belonged to subclade D.3.1.1, characterized by R113K, A139D, E283K and K302E.
- Genetic diversity of the HA in subclade D.3.1.1 viruses increased during this reporting period.
- Emerging viruses within subclade D.3.1.1 with an additional substitution of G155E increased in recent weeks and belonged to several genetic groups characterized by different combinations of additional amino acid substitutions.
- Viruses from subclade D.3.1 with substitutions T120A, I372V, I460T and V520A still predominated in South Africa and circulated in minor proportions in some countries in Central America, Africa, Asia and Oceania.

Influenza A(H1N1)pdm09 summary (2)

Antigenic characteristics of A(H1N1)pdm09 viruses

- Post-infection ferret antisera raised against viruses from subclade D.3.1 (e.g., A/Missouri/11/2025) recognized most recently circulating viruses from D.3.1 and D.3.1.1 well.
- However, post-infection ferret antisera raised against viruses from C.1.9.3, D.3.1 and D.3.1.1 subclades showed reduction in recognition of viruses from the D.3.1.1. clade with additional substitutions including at position G155E.

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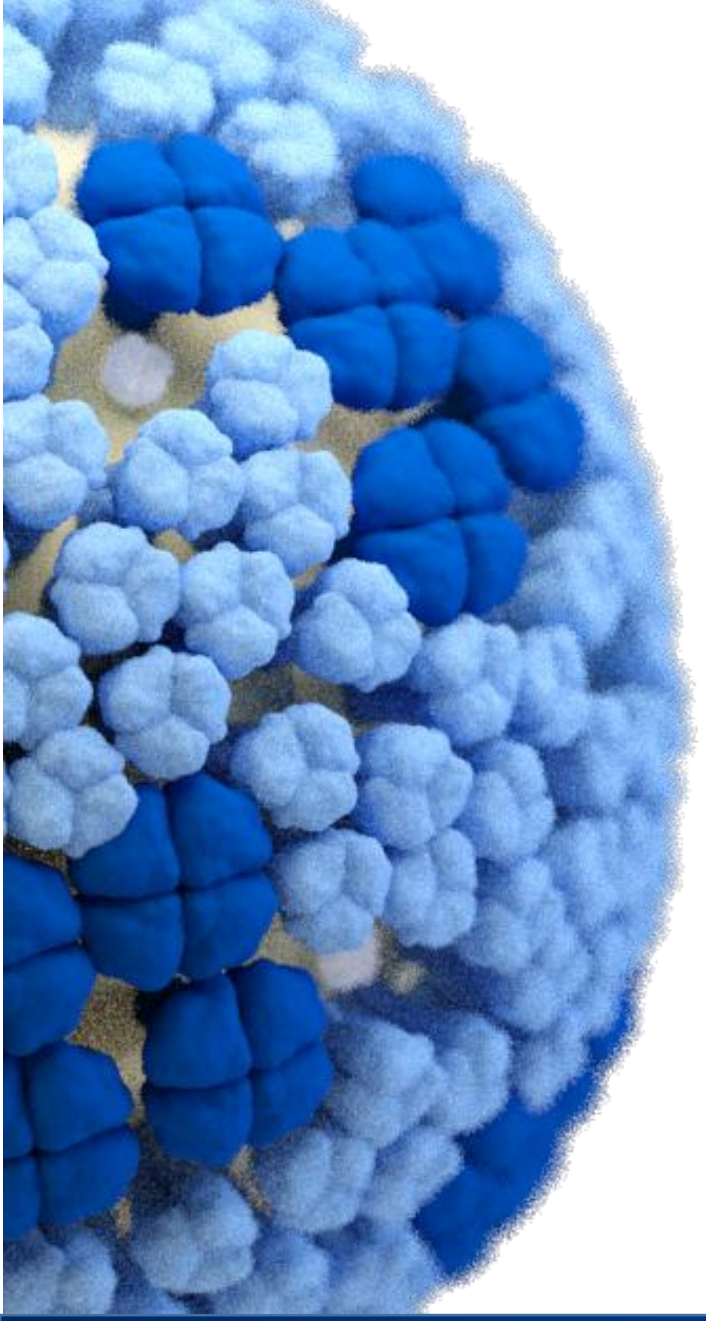
Influenza A(H1N1)pdm09 summary (3)

Human serology studies

- Recent A(H1N1)pdm09 viruses with HA genes from 5a.2a.1 subclade D.3.1.1 were analyzed in HI assays using human serum panels.
- When compared to the post-vaccination geometric mean titers (GMTs) to egg- or cell culture-propagated A/Missouri/11/2025 (H1N1)pdm09-like vaccine reference viruses, postvaccination GMTs were significantly reduced for some recently circulating viruses from subclade D.3.1.1 with amino acid substitutions Q54H, D139N, G155E, or D139N, V152I, G155E, or D139N, V152I, S157L, S190G in several serum panels.

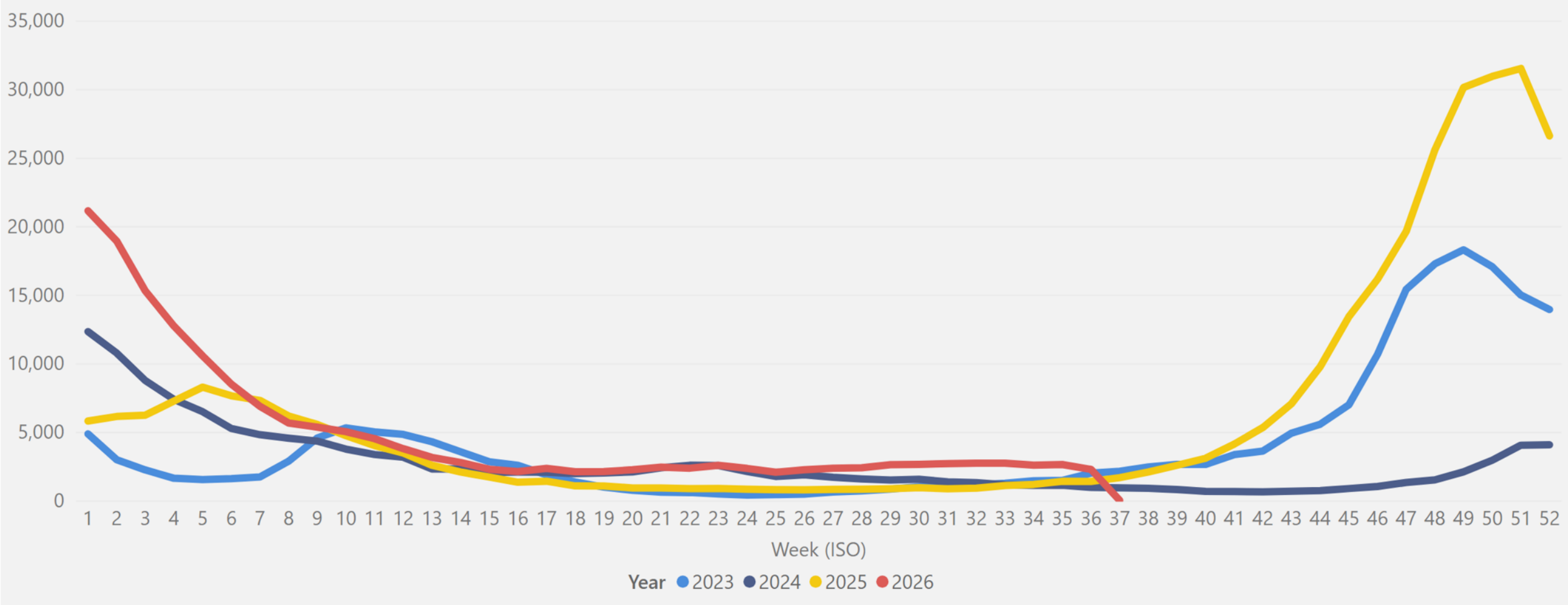
The data supported maintaining A/Missouri/11/2025 (H1N1)pdm09-like (D.3.1) viruses as the A(H1N1)pdm09 vaccine antigens for the 2027 southern hemisphere.

VCM Information meeting: https://www.youtube.com/@who



A(H3N2) Viruses

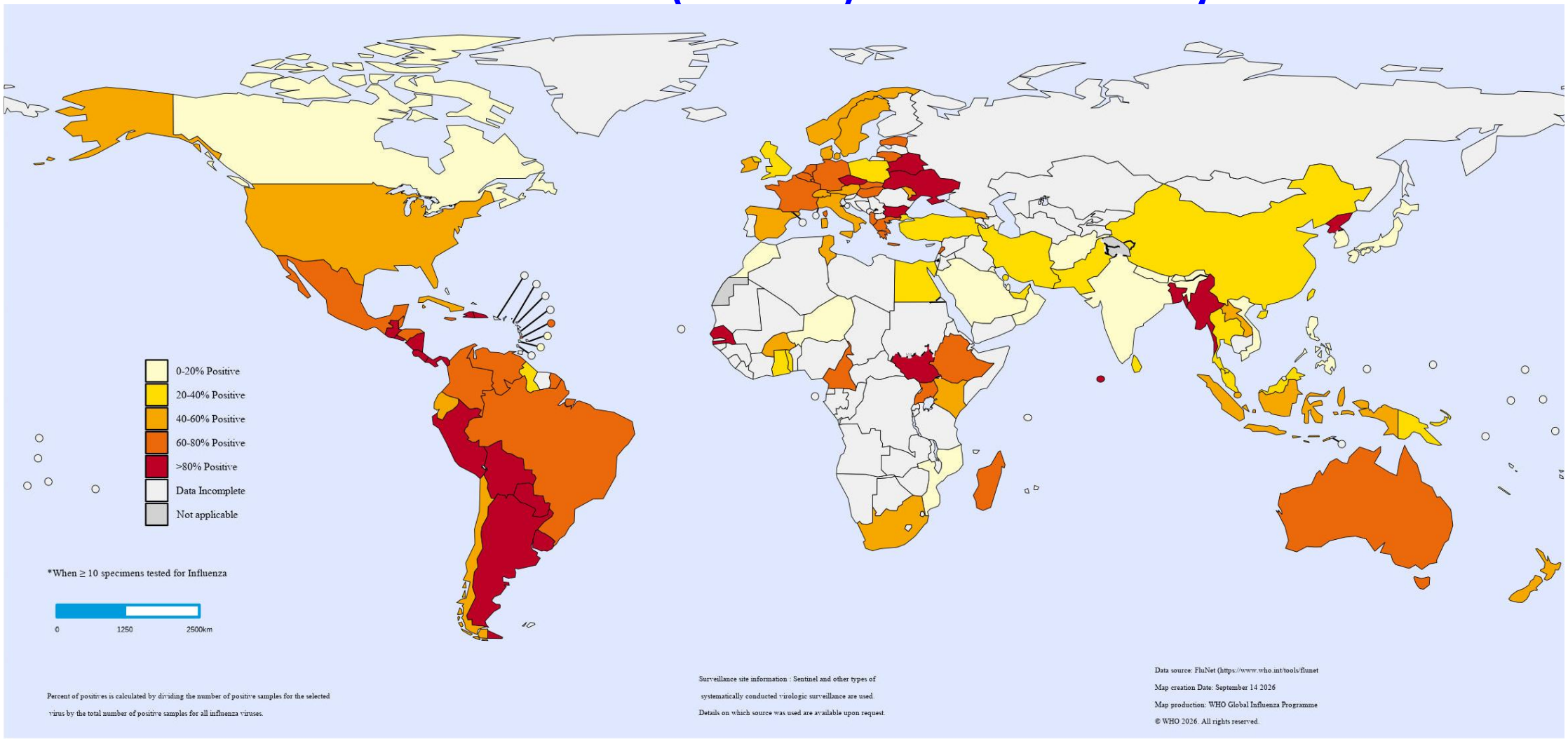
Number of A(H3N2) viruses detected by GISRS



Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (13 September 2026)

VCM Information meeting: https://www.youtube.com/@who

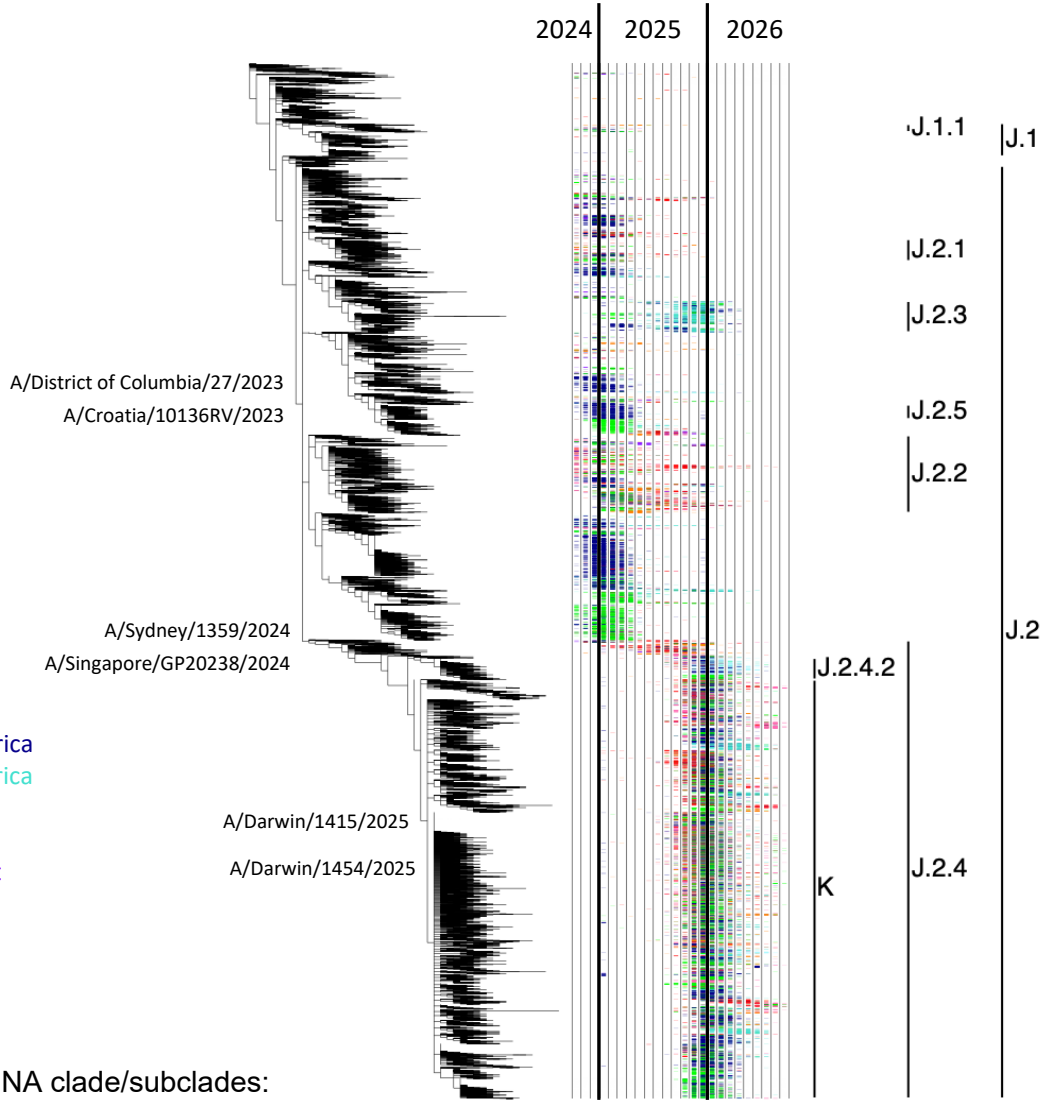
Influenza A(H3N2) virus activity



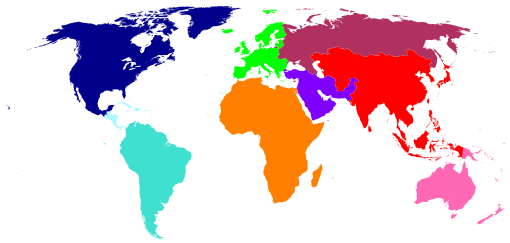
Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (13 September 2026)

VCM Information meeting: https://www.youtube.com/@who

A(H3N2) HA phylogeography







North America
South America
Europe
Africa
Middle East
Russia
E SE Asia
Oceania

J.2.3: N158K, K189R S378N

J.2.2: S124N

J.2.4: T135K, K189R
J.2.4.2 : F79V, T135K, S144N, N158D, I160K, T328A

K: K2N, T135K, S144N, N158D, I160K, Q173R, T328A, and S378N

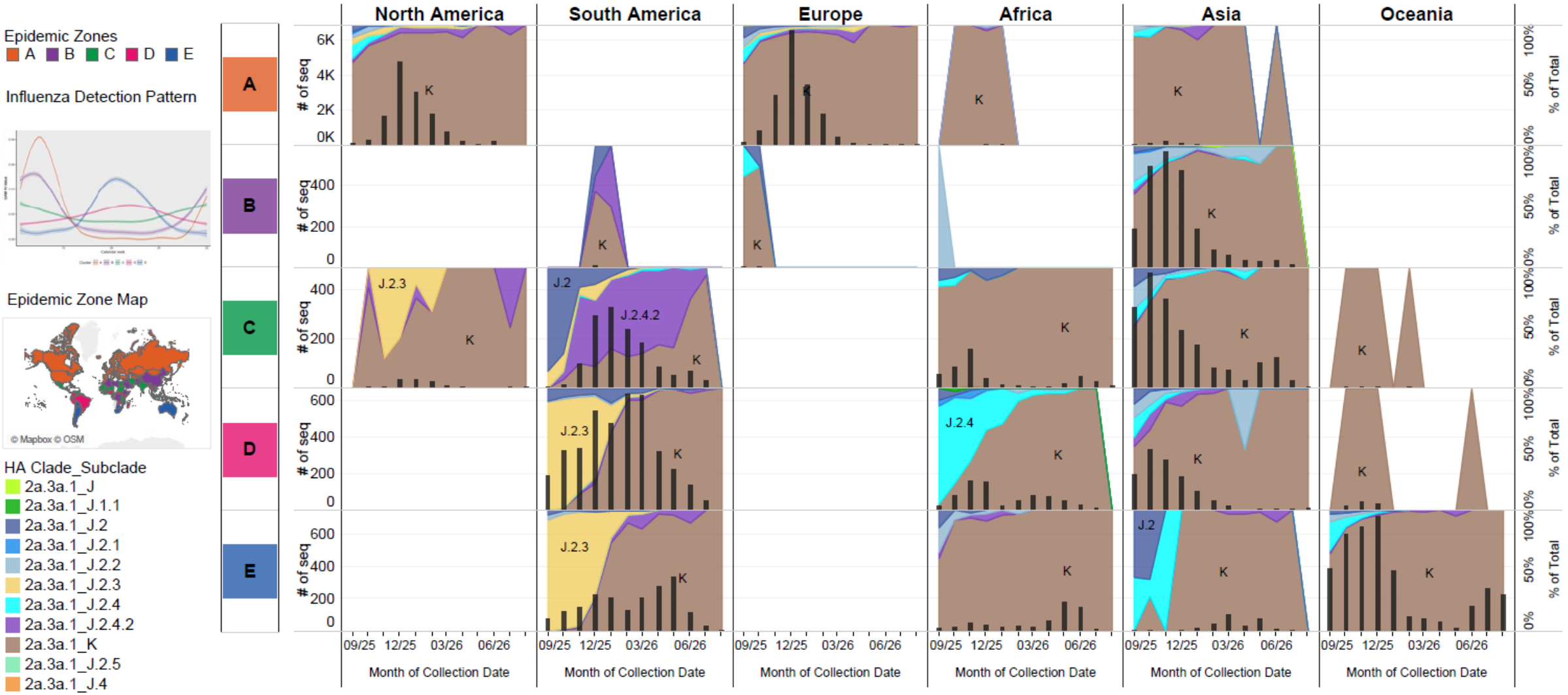
Figure Source: University of Cambridge

Data Source: GISAID

HA and NA clade/subclades: https://clades.nextstrain.org/

VCM Information meeting: https://www.youtube.com/@who

A(H3N2) Extended Diversity Plot



Data Source: GISAID

HA and NA clade/subclades:
https://clades.nextstrain.org/

Antigenic analysis of A(H3N2) viruses in HI assays (1)

Antisera to southern hemisphere 2026 vaccine virus antigens

WHO CC	A/Sydney/1359/2024-like Cell 2a.3a.1 (J.2.4)	Low (≥ 8 fold)	WHO CC	A/Singapore/GP20238/2024-Like Egg 2a.3a.1 (J.2.4)	Low (≥ 8 fold)
CDC	317 (92%)	26 (8%)	CDC	323 (94%)	20 (6%)
CNIC	308 (77%)	94 (23%)	CNIC	116 (29%)	286 (71%)
FCI	134 (72%)	52 (28%)	FCI	87 (47%)	99 (53%)
NIID	48 (94%)	3 (6%)	NIID	46 (90%)	5 (10%)
VIDRL	540 (77%)	162 (23%)	VIDRL	530 (75%)	172 (25%)
Total	1347 (80%)	337 (20%)	Total	1102 (65%)	582 (35%)

"Low" reactor represented titers ≥ 8-fold lower than vaccine strain homologous titer by HI

VCM Information meeting: https://www.youtube.com/@who

Antigenic analysis of A(H3N2) viruses in HI assays (2)

Antisera to northern hemisphere 2026-27 vaccine virus antigens

WHO CC	A/Darwin/1415/2025-like Cell 2a.3a.1 (K)	Low (≥ 8 fold)	WHO CC	A/Darwin/1454/2025-Like Egg 2a.3a.1 (K)	Low (≥ 8 fold)
CDC	318 (93%)	25 (7%)	CDC	325 (95%)	18 (5%)
CNIC	329 (90%)	38 (10%)	CNIC	303 (83%)	64 (17%)
FCI	175 (94%)	11 (6%)	FCI	156 (84%)	30 (16%)
NIID	39 (98%)	1 (3%)	NIID	49 (96%)	2 (4%)
VIDRL	697 (99%)	5 (1%)	VIDRL	694 (99%)	8 (1%)
Total	1558 (95%)	80 (5%)	Total	1527 (93%)	122 (7%)

“Low” reactor represented titers ≥ 8-fold lower than vaccine strain homologous titer by HI

VCM Information meeting: https://www.youtube.com/@who

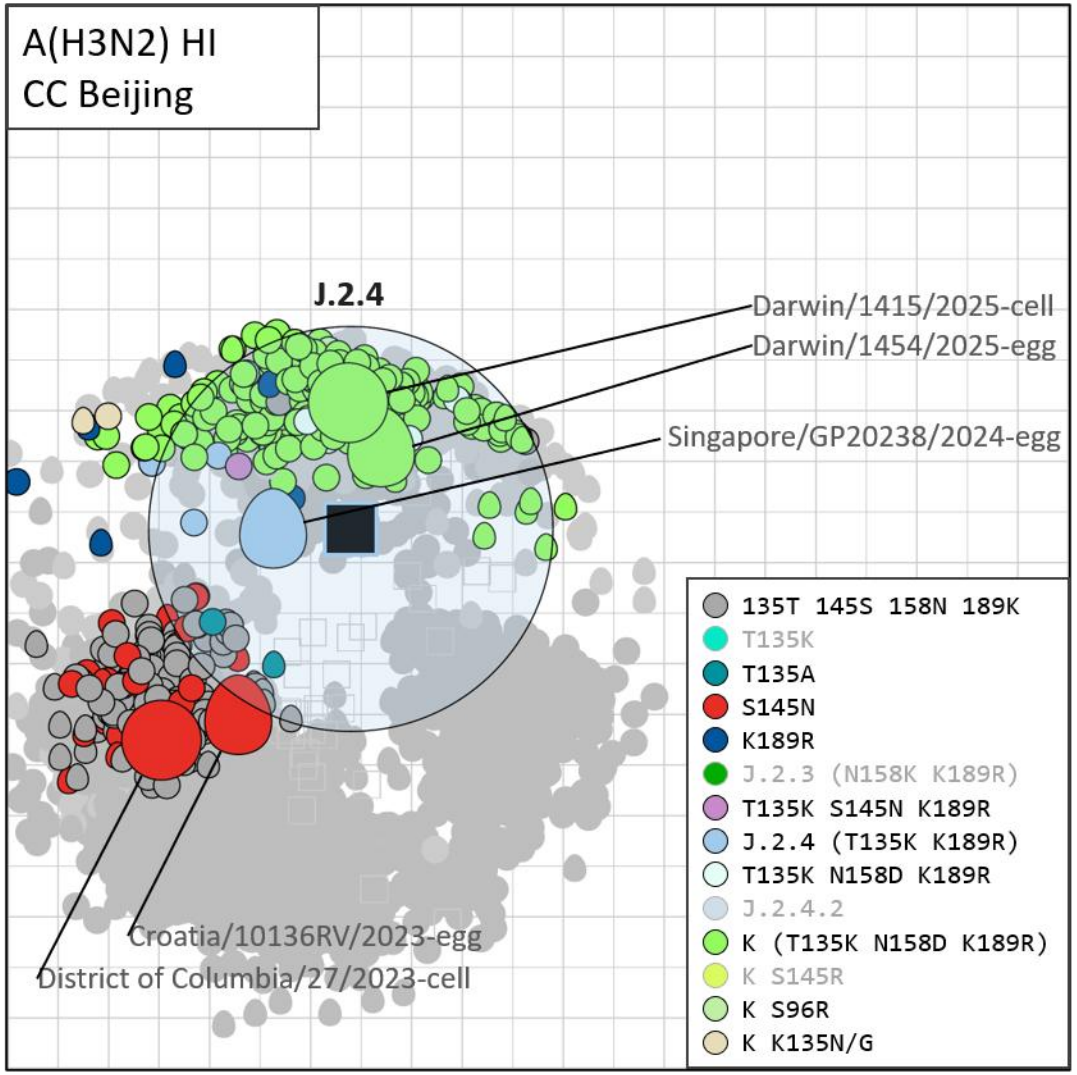
HI antigenic analysis of A(H3N2) viruses

				Reference antisera								
				SIAT1	MDCK1	E2	SIAT2	SIAT2	SH 2026	SH 2026	Passage	Sample
				Syd/1359	Dar/1415	Dar/1454	Perth/19	Syd/99	CELL	EGG	Details	Date
				2a.3a.1	2a.3a.1	2a.3a.1	2a.3a.1	2a.3a.1	sera pool	sera pool		
		Clade>		J.2.4	K	K	K + 135N	K+6D+95G+145N				
1	A/Sydney/1359/2024	2a.3a.1	J.2.4	**640**	320	640	<40	320	320	640	SIAT2	
2	A/Darwin/1415/2025	2a.3a.1	K	320	**1280**	640	160	1280	320	640	SIAT4	
3	A/Darwin/1454/2025	2a.3a.1	K	320	1280	**1280**	160	1280	320	640	E2	
4	A/Perth/19/2026	2a.3a.1	K+135N	<40	160	40	**320**	40	160	160	SIAT2	
5	A/Sydney/99/2026	2a.3a.1	K+6D+95G+145N	80	320	320	80	**640**	160	160	SIAT2	
5	A/Sydney/270/2026	2a.3a.1	K	160	640	320	80	320	160	320	SIAT2	31/07/2026
6	A/Victoria/324/2026	2a.3a.1	K	160	640	640	80	640	160	320	SIAT1	09/07/2026
7	A/Palmerston North/4/2026	2a.3a.1	K	160	640	640	160	640	320	320	SIAT1, SIAT1	17/07/2026
8	A/Victoria/342/2026	2a.3a.1	K+6D+95G+145N	80	320	320	80	640	160	160	SIAT1	08/08/2026
9	A/Sydney/309/2026	2a.3a.1	K+6D+95G+145N	160	640	640	160	1280	160	320	SIAT1	10/08/2026
10	A/Sydney/314/2026	2a.3a.1	K+6D+95G+145N	160	640	640	80	1280	160	320	SIAT1	13/08/2026
11	A/Sydney/293/2026	2a.3a.1	K+6D+95G+145N+149G	320	640	640	160	1280	320	320	SIAT1	12/08/2026
12	A/Victoria/345/2026	2a.3a.1	K+6D+95G+145N+223I	80	320	320	80	640	160	160	SIAT1	27/07/2026
13	A/Maldives/2709/2026	2a.3a.1	K+96R	160	640	640	80	320	160	160	SIAT1	19/06/2026
14	A/Darwin/176/2026	2a.3a.1	K+96R	160	640	640	160	640	320	320	SIAT1	17/08/2026
15	A/Tasmania/115/2026	2a.3a.1	K+223I	160	640	640	160	640	160	320	SIAT1	09/08/2026
16	A/Victoria/341/2026	2a.3a.1	K+223I	80	320	320	40	320	160	160	SIAT1	10/08/2026
17	A/Sri Lanka/38/2026	2a.3a.1	K+328T	160	640	640	80	640	320	320	SIAT2	13/08/2026
18	A/Queensland/107/2026	2a.3a.1	K+328T	160	640	640	80	640	320	320	SIAT1	13/08/2026

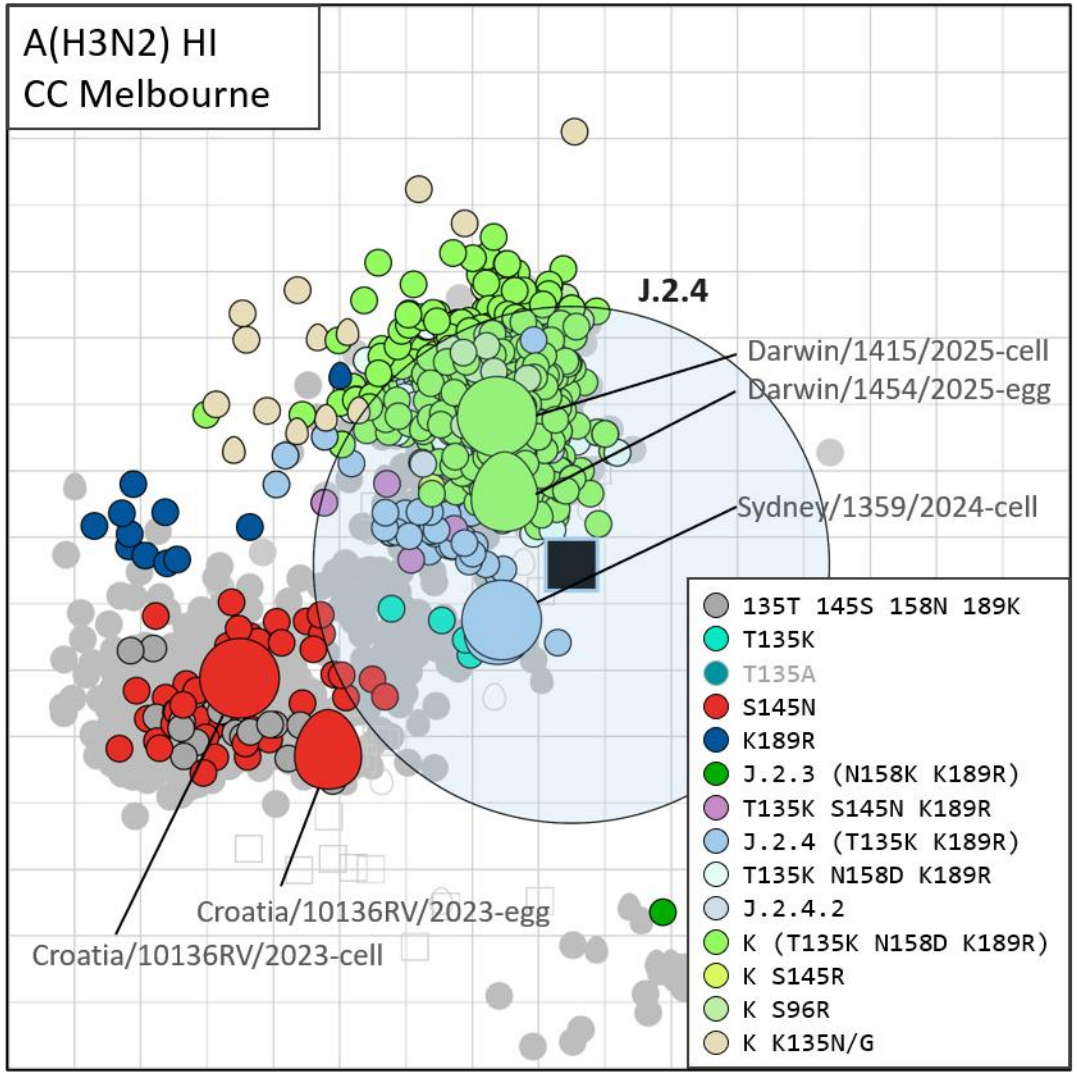
Source: WHO CC Melbourne

VCM Information meeting: https://www.youtube.com/@who

A(H3N2) antigenic cartography (1)



Singapore/GP20238/2024-cell serum circle
(within 8-fold of homologous titer)

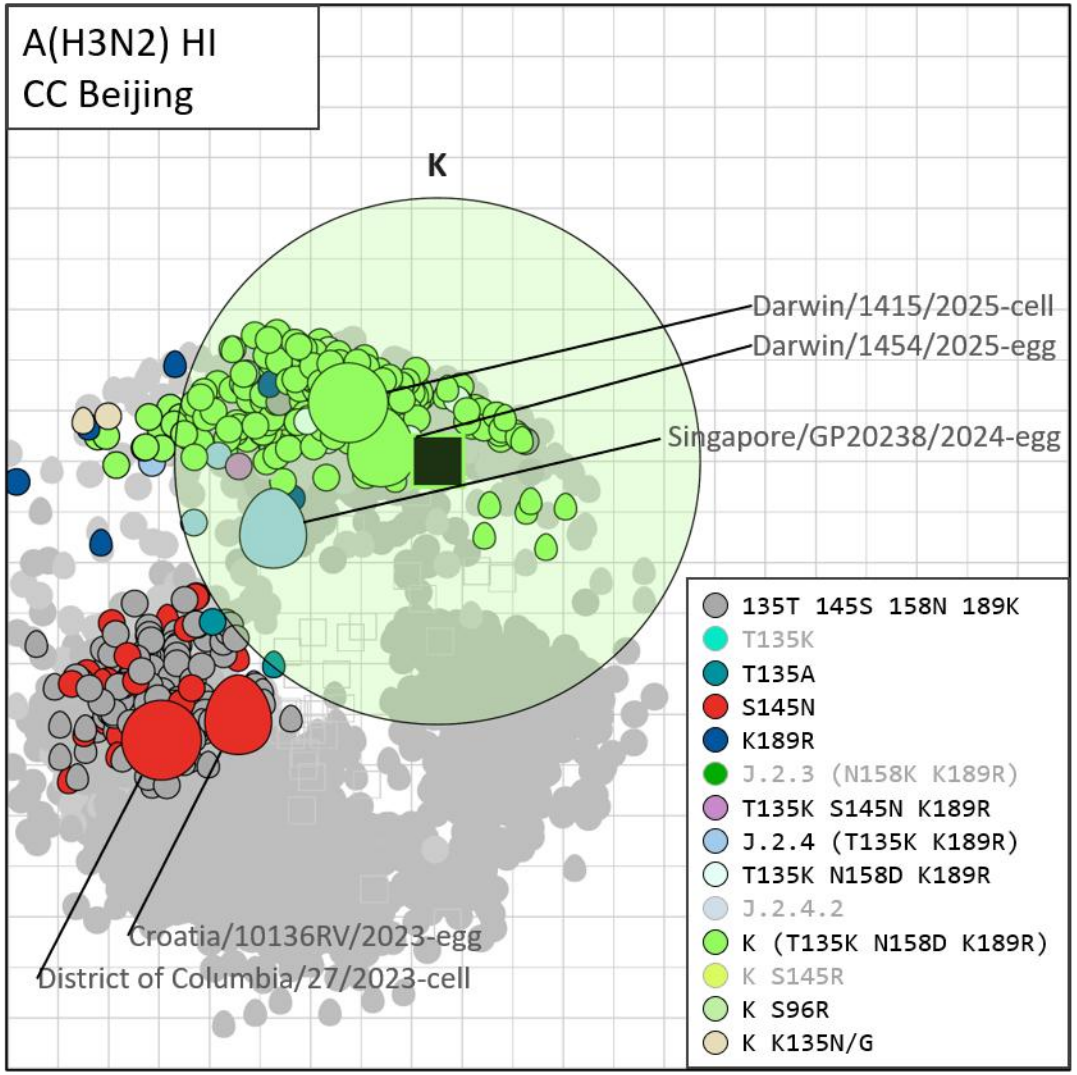


Singapore/GP20238/2024-egg serum circle
(within 8-fold of homologous titer)

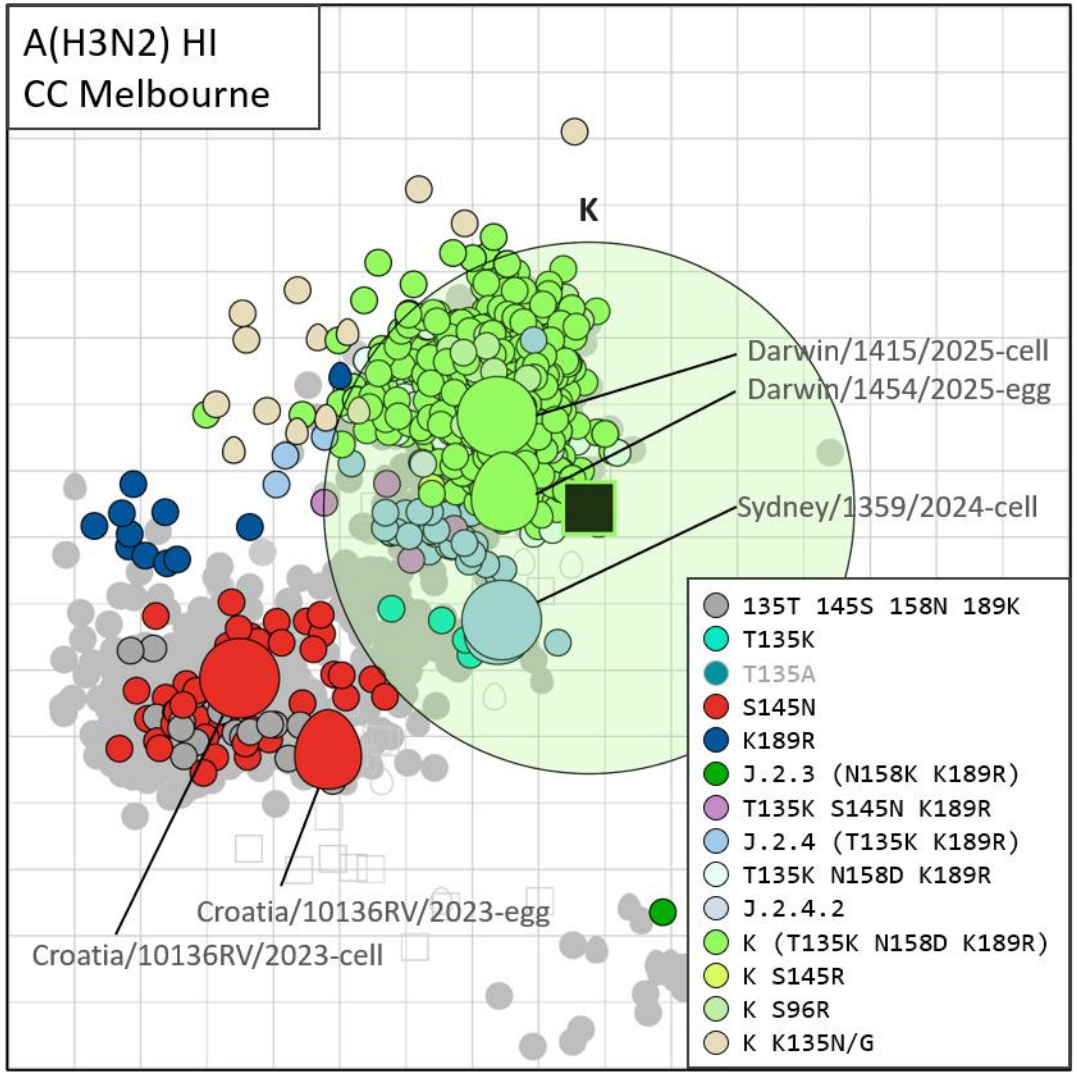
Source: University of Cambridge

VCM Information meeting: https://www.youtube.com/@who

A(H3N2) antigenic cartography (2)



Darwin/1415/2025-cell serum circle
(within 8-fold of homologous titer)



Darwin/1454/2025-egg serum circle
(within 8-fold of homologous titer)

Source: University of Cambridge

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Human post-vaccination serum analysis of A(H3N2) viruses

WHO Collaborating Center (CC): Human Serological Panels
A(H3N2) -- HI & MN Protocol [CELL]

				J.2.4 - SYD/1359-LIKE						J.2.4.2 - NM/01	WI/114-LIKE				+S96R (CHO-) MO/149	+D60E +S96R (CHO-) DAR/142		+S96R (CHO-) +S265N LBN/ILI-26	+R33Q +S124N DE/31	+F79I +K207Q GA/38-LIKE		+F79I +K207Q +D348X +L532V TOKYO/EIS15-097		+S91N +K135N (CHO+) PERTH/19						+K135G +A272T +D408N VIC/192	+N6D +S95G +S145N SYD/99		+N6D +S95G +S145N +S149G SYD/174	+G62E +S145R +D493E VT/22	+H56L +T155A +A328T VIC/268		+T128I (CHO-) +P277X +I230V TOKYO/EIS91-014		J.2.3 +K264T AK/08	+S54N +G78S +S145N +N216H KY/24
				SYD/1359				MS/37		-	WI/114		DAR/1415		-	-		-	-	GA/38	UKR/4736	-		-					-	-	-	-	-	-		-		-	
				CELL				CELL		CELL	CELL		CELL		CELL	CELL		CELL	CELL	CELL	CELL	CELL		CELL					CELL	CELL	CELL	CELL	CELL	CELL		CELL		CELL	
				MHRA HI	NIID HI	VIDRL HI	VIDRL MN	CDC MN	CBER MN	CDC MN	CDC MN	CBER MN	NIID HI	VIDRL HI	CDC MN	VIDRL HI	VIDRL MN	MHRA HI	CDC MN	CDC MN	MHRA HI	CBER MN	NIID HI	CDC MN	CBER MN	MHRA HI	NIID HI	VIDRL HI	VIDRL MN	MHRA HI	VIDRL HI	VIDRL MN	CDC MN	CBER HI	VIDRL HI	MN	MHRA HI	NIID HI	CBER MN	CDC MN
A/SYDNEY/1359/2024-LIKE CELL	Pediatric (2-9Y)	IIV3 (Fluzone)	Australia	40	160	230	275	301	32	138	151	X	88	118	134	90	108	28	170	130	X	X	85	90	X	23	66	85	61	X	71	126	75		73	75	X	80	X	115
	Adult (18-59Y)	IIV3	Peru					420		195	244				138				177	186														152						122
	Adult (18-64Y)	ccIIV3 (Flucelvax)	Australia	61	223	229	205	513	34	200	√	X	√	√	320	128	89	36	303	256	√	X	√	109	X	26	115	103	54	√	94	√	121		103	85	√	√	X	217
		IIV3 (Fluzone)	Australia	56	264	348	303	821	22	434	√	X	√	√	√	164	132	√	459	485	√	X	√	125	X	26	125	112	74	√	112	√	128		139	112	√	143	X	279
		IIV3	South Africa					394		√	√				130				197	226														260						166
	Elderly (≥60Y)	IIV3	Peru					187		√	√				100				√	80														97						73
	Elderly (≥65Y)	aIIV3 (Fluad)	Australia	49	194	294	329	676	23	329	311	X	√	169	329	112	115	26	378	249	26	X	√	125	X	15	89	89	64	26	70	160	82		85	94	√	97	X	286
										5 (71.4)	3 (42.9)	0 (0.0)	1 (25.0)	2 (50.0)	6 (85.7)	4 (100.0)	4 (100.0)	3 (75.0)	6 (85.7)	7 (100.0)	1 (25.0)	0 (0.0)	1 (25.0)	4 (100.0)	0 (0.0)	4 (100.0)	4 (100.0)	4 (100.0)	4 (100.0)	1 (25.0)	4 (100.0)	2 (50.0)	4 (100.0)	3 (100.0)	4 (100.0)	4 (100.0)	0 (0.0)	3 (75.0)	0 (0.0)	7 (100.0)

Geometric Mean Titer (GMT) ratios between reference and test antigens are calculated with 90% confidence intervals (CI) for each cohort and panel location. Unadjusted model results are shown. If the CI lower bound is greater than 50%, it is statistically non-inferior (95% confidence level); otherwise, it is *possibly* inferior. Heat map cells are colored using the GMT ratio lower bound. Blue indicates statistical non-inferiority and orange denotes *possible* inferiority. Numbers shown are post-vaccination GMTs for the unadjusted model. They are shown for *reference antigens* and possibly inferior test antigens. Marks, √ or X, denote statistically significant non-inferiority when the reference virus GMT is ≥ 40 or < 40, respectively. **Number** and **percent** (in parentheses) of *possibly* inferior responses are summarized below the heat map.

Microneutralization (MN) protocol results reported by CBER, CDC, and VIDRL are indicated in addition to all hemagglutination inhibition (HI) assay trends.

CDC and CBER applied the alternative J.2.4 A/MISSISSIPPI/37/2025 reference virus as the cell-based panel reference.

Included Strains: A/ALASKA/08/2025 (AK/08); A/DARWIN/1415/2025 (DAR/1415); A/DARWIN/142/2026 (DAR/142); A/DELAWARE/31/2026 (DE/31); A/GEORGIA/38/2026 (GA/38); A/KENTUCKY/24/2026 (KY/24); A/LEBANON/ILI-26/2026 (LBN/ILI-26); A/MISSISSIPPI/37/2025 (MS/37); A/MISSOURI/149/2026 (MO/149); A/NEW MEXICO/01/2026 (NM/01); A/PERTH/19/2026 (PERTH/19); A/SYDNEY/1359/2024 (SYD/1359); A/SYDNEY/174/2026 (SYD/174); A/SYDNEY/99/2026 (SYD/99); A/TOKYO/EIS15-097/2026 (TOKYO/EIS15-097); A/TOKYO/EIS91-014/2026 (TOKYO/EIS91-014); A/UKRAINE/4736/2025 (UKR/4736); A/VERMONT/22/2026 (VT/22); A/VICTORIA/192/2026 (VIC/192); A/VICTORIA/268/2026 (VIC/268); A/WISCONSIN/114/2025 (WI/114)

Statistically non-inferior = √
Statistically non-inferior but reference virus GMT < 40 = X

GMT Ratio Lower-Bound (90% CI)
0.0 ≥ 1.0

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Influenza A(H3N2): antiviral susceptibility

Neuraminidase inhibitors

- Of 2,350 influenza A(H3N2) viruses examined by genetic and/or phenotypic analyses, one virus showed evidence of reduced susceptibility to NAIs with an NA S331R substitution.

Endonuclease inhibitors

- Of 2,462 A(H3N2) viruses examined by genetic and/or phenotypic analyses, one virus showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil, with a PA K34R substitution.

Influenza A(H3N2) summary (1)

Phylogenetics of A(H3N2) HA genes

- Phylogenetic analysis of the HA gene sequences of A(H3N2) viruses collected since February 2026 showed that the majority of circulating viruses globally belonged to subclade K (characterized by K2N, T135K, S144N [a potential addition of an N-glycosylation site], N158D, I160K, Q173R, T328A and S378N).
- There was still low proportions of viruses circulating from J.2 subclades, notably J.2.2 (characterized by S124N) in Asia, J.2.3 (characterized by N158K, K189R and S378N) in the Americas, J.2.4 (characterized by T135K [a potential loss of an N-glycosylation site] and K189R) in Asia and J.2.4.2 (characterized by F79V, T135K, S144N [a potential addition of an N-glycosylation site], N158D, I160K and T328A) in most regions.

Influenza A(H3N2) summary (2)

Antigenic characteristics of A(H3N2) viruses

- Post-infection ferret antisera raised against cell culture-propagated A/Sydney/1359/2024-like and egg-propagated A/Singapore/GP20238/2024-like J.2.4 viruses, representing the A(H3N2) component for the SH 2026 influenza vaccines, recognized most J.2.4 viruses and many subclade J.2.4.2 and K viruses well.
- However, J.2.4.2 and K subclade viruses were better recognized by post-infection ferret antisera raised against cell culture-propagated A/Darwin/1415/2025-like and egg-propagated A/Darwin/1454/2025-like (subclade K) viruses.

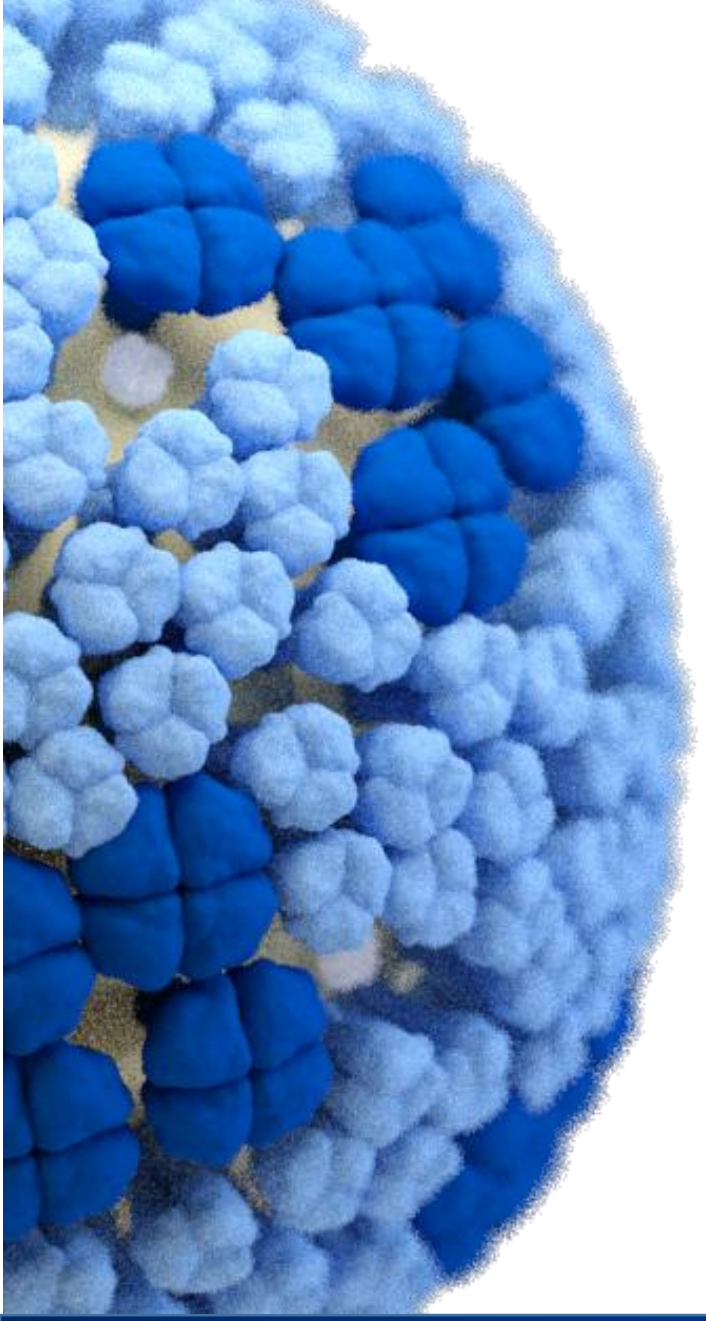
Influenza A(H3N2) summary (3)

Human serology studies

- Human serology studies were conducted using the serum panels as described above by HI and virus neutralization (VN) assays with recently circulating A(H3N2) viruses with HA genes from subclades J.2.3, J.2.4.2 and K.
- When compared to titers against cell-propagated A/Sydney/1359/2024-like and egg-propagated A/Singapore/GP20238/2024-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against many of the recent viruses in J.2.3, J.2.4.2 and K subclades tested were significantly reduced in many serum panels.

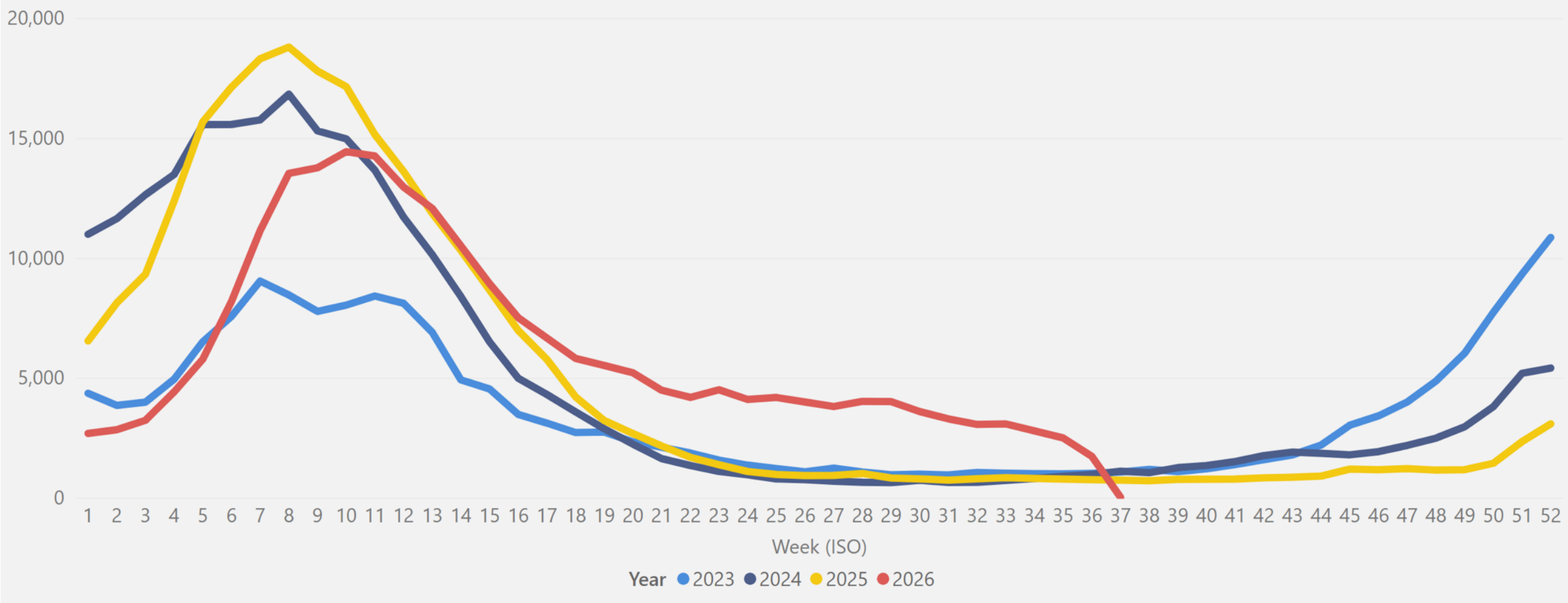
The data supported recommending an update to the cell-propagated A/Darwin/1415/2025 (H3N2)-like (K) virus and an egg-propagated A/Darwin/1454/2025 (H3N2)-like (K) virus as the A(H3N2) vaccine antigens for the 2027 southern hemisphere.

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Influenza B Viruses

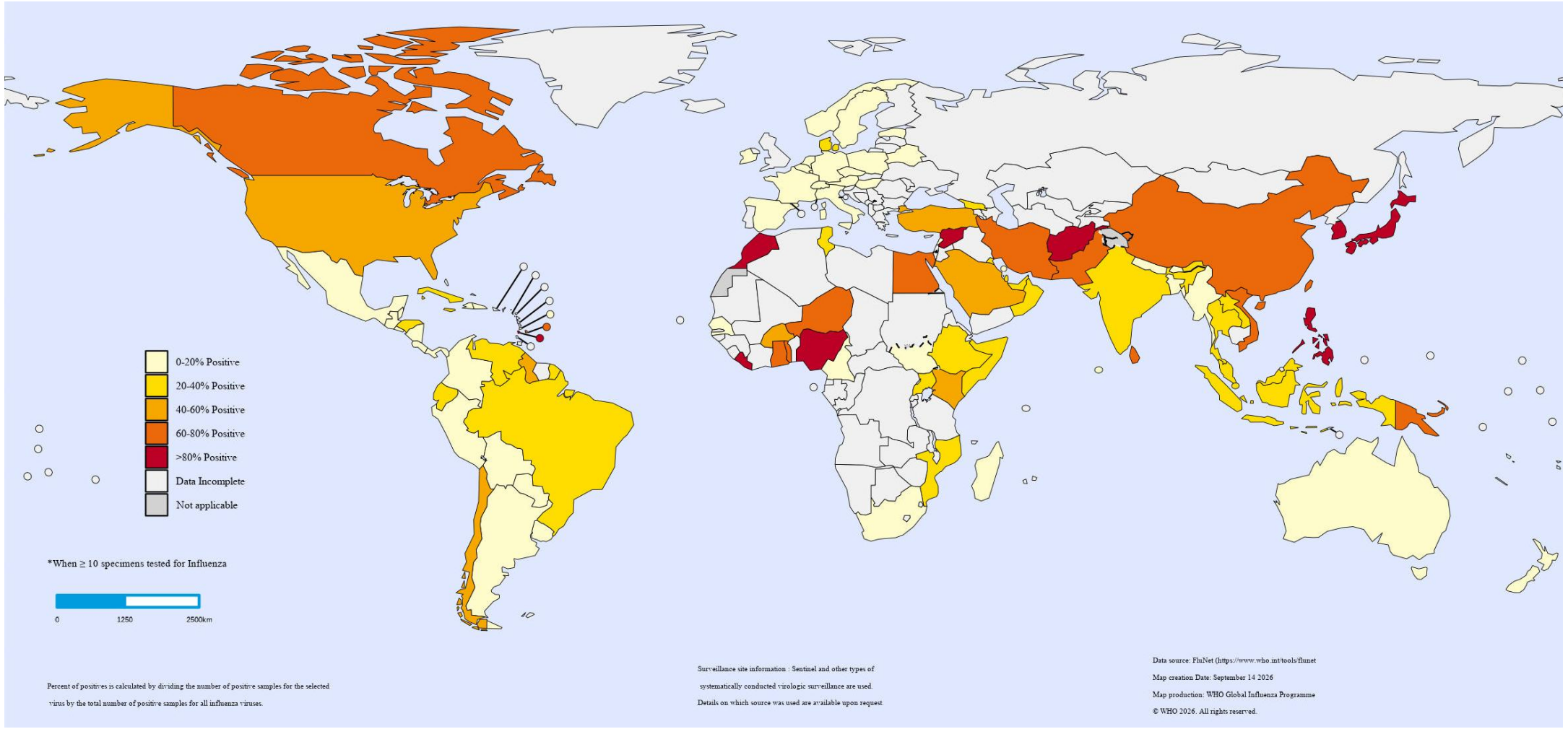
Number and Percentage of B viruses detected by GISRS



GISRS GLOBAL INFLUENZA SURVEILLANCE & RESPONSE SYSTEM

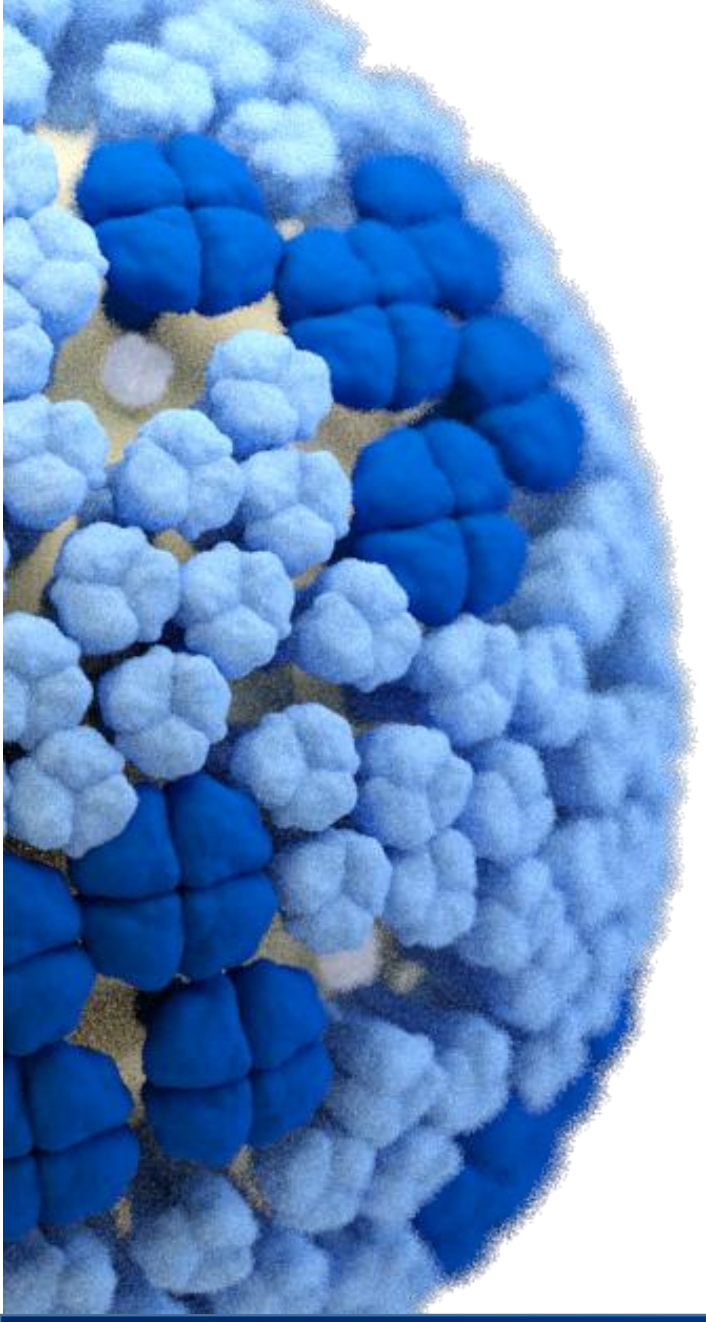
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Influenza B virus activity



Data source: FluNet, (https://www.who.int/tools/flunet),
Global Influenza Surveillance and Response System (September 13, 2026)

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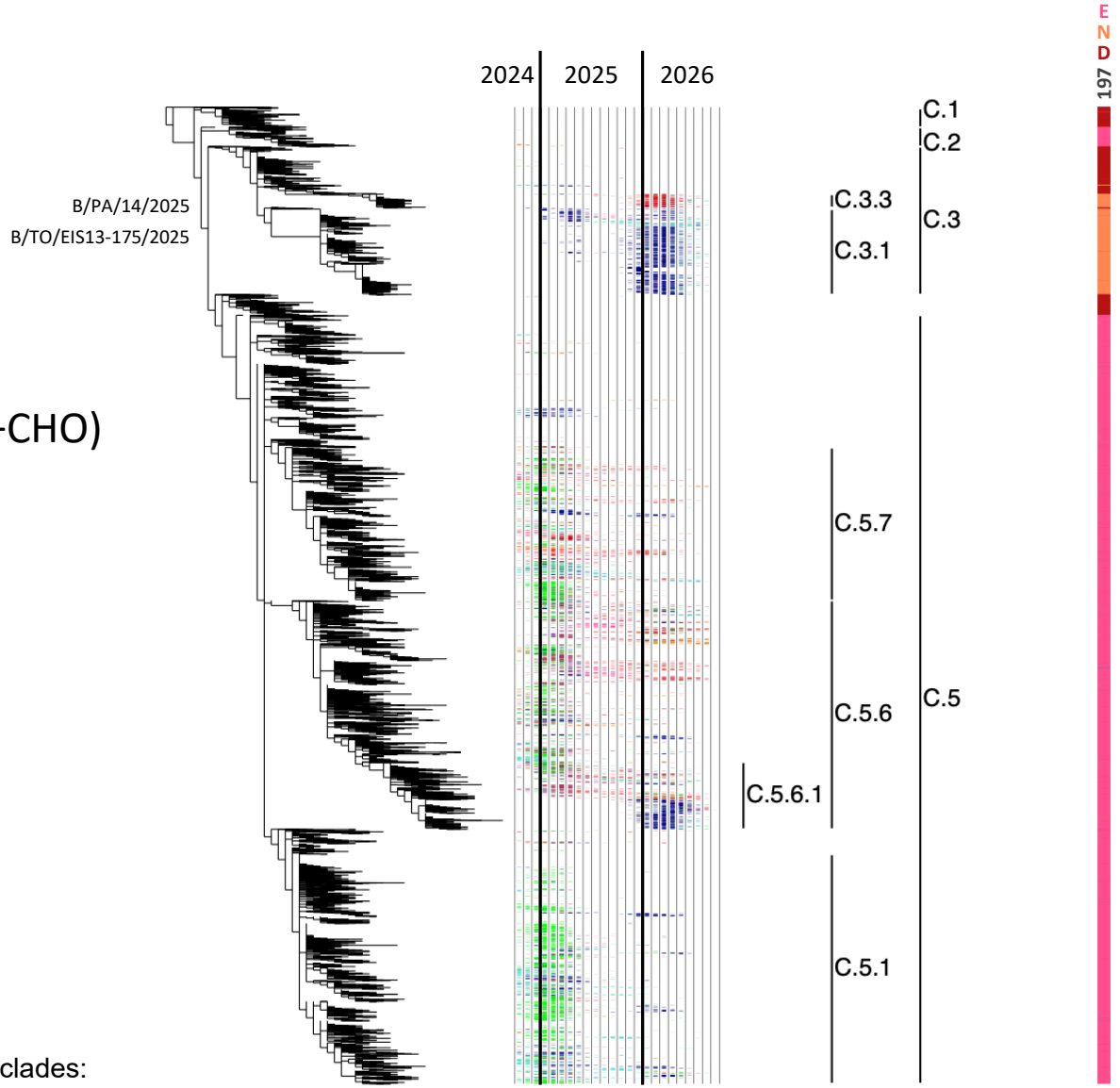
Influenza B/Victoria Viruses

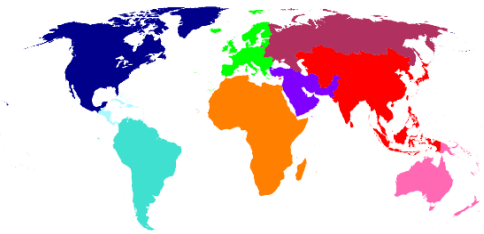
B/Victoria HA phylogeography

C3:
-E128K, A154E, S208P

C.3.1: -P208S & D197N (+CHO)
C.3.3:-S208P, S255P, I267V & D197N(+CHO)

C.5, C.5.1, C.5.6, C.5 and **C.5.7**
-various substitutions, all have D197E





North America
South America
Europe
Africa
Middle East
Russia
E SE Asia
Oceania

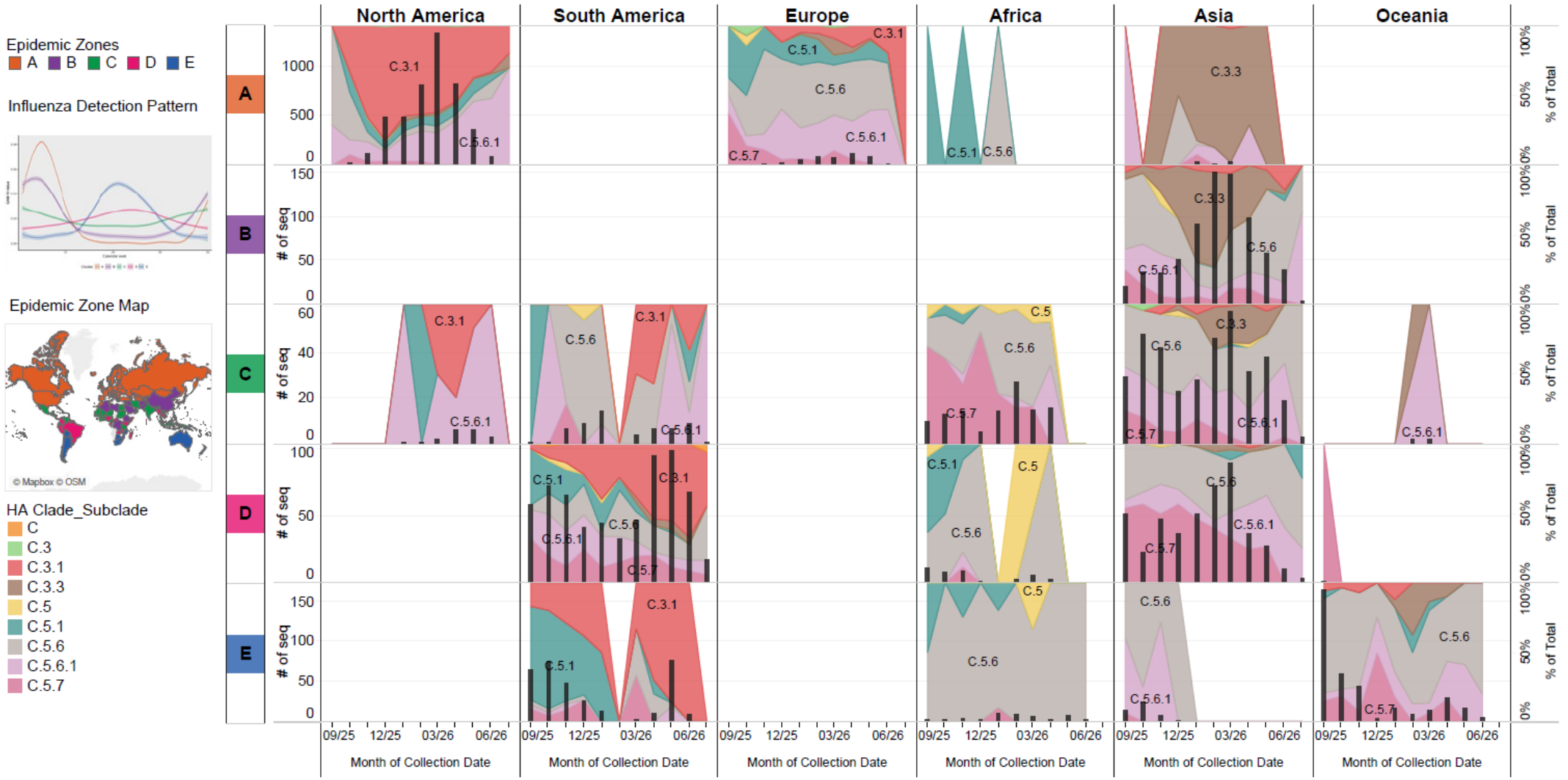
Figure Source: *University of Cambridge*

Data Source: GISAID

HA and NA clade/subclades:
https://clades.nextstrain.org/

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B/Victoria Extended Diversity Plot



Data Source: GISAID

HA and NA clade/subclades:
https://clades.nextstrain.org/

Antigenic analysis of B/Victoria viruses in HI assays (1)

Antisera to southern hemisphere 2026 vaccine virus antigens

WHO CC	B/Austria/1359417/2021-like Cell Clade V1A.3a.2 (C)	Low (≥ 8 fold)	WHO CC	B/Austria/1359417/2021-like Egg Clade V1A.3a.2 (C)	Low (≥ 8 fold)
CDC	113 (44%)	143 (56%)	CDC	111 (43%)	145 (57%)
CNIC	769 (99%)	10 (1%)	CNIC	761 (98%)	18 (2%)
FCI	48 (72%)	19 (28%)	FCI	1 (1%)	70 (99%)
NIID	9 (6%)	146 (94%)	NIID	14 (9%)	141 (91%)
VIDRL	170 (89%)	22 (11%)	VIDRL	170 (89%)	22 (11%)
TOTAL	1109 (77%)	340 (23%)	TOTAL	1057 (73%)	396 (27%)

“Low” represented titers ≥ 8-fold lower than vaccine strain homologous titer

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Antigenic analysis of B/Victoria viruses in HI assays (2)

Antisera to northern hemisphere 2026-27 vaccine virus antigens

WHO CC	B/Pennsylvania/14/2025-like Cell Clade V1A.3a.2	Low (≥ 8 fold)	WHO CC	B/Tokyo/EIS13-175/2025-like Egg V1A.3a.2 (C.3.1)	Low (≥ 8 fold)
CDC	256 (100%)	0 (0%)	CDC	100 (45%)	120 (55%)
CNIC	342 (98%)	7 (2%)	CNIC	551 (94%)	35 (6%)
FCI	71 (100%)	0 (0%)	FCI	50 (70%)	21 (30%)
NIID	137 (99%)	1 (1%)	NIID	10 (6%)	145 (94%)
VIDRL	191 (99%)	1 (1%)	VIDRL	152 (89%)	18 (11%)
TOTAL	997 (99%)	9 (1%)	TOTAL	863 (72%)	339 (28%)

"Low" represented titers ≥ 8-fold lower than vaccine strain homologous titer

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HI antigenic analysis of B/Victoria lineage viruses

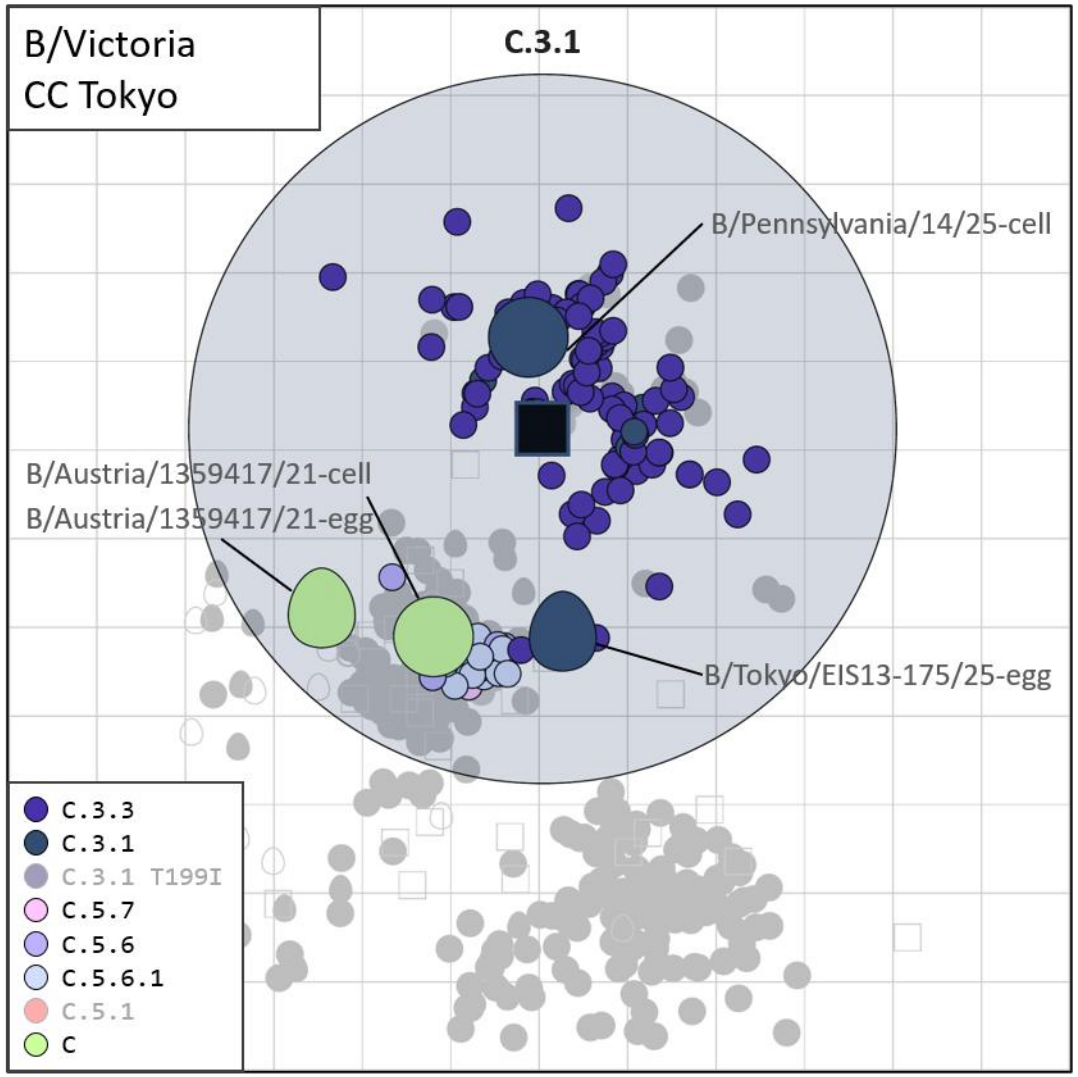
		REFERENCE FERRET ANTISERA							
		C		C.3.1		C.3.3	C.5.6	C.5.6.1	C.5.7
REFERENCE VIRUSES	HA Subclade	CELL AUT/ 1359417	EGG AUT/ 1359417	CELL PA/14	EGG TOK/ EIS13-175	CELL CT/05	CELL MO/03	CELL NM/06	CELL TX/19
B/AUSTRIA/1359417/2021	C	**320**	640	320	320	320	320	640	2560
B/AUSTRIA/1359417/2021	C	320	**640**	320	160	320	160	320	1280
B/PENNSYLVANIA/14/2025	C.3.1	20	40	**320**	20	320	20	40	80
B/TOKYO/EIS13-175/2025	C.3.1	80	160	320	**640**	320	80	320	640
B/CONNECTICUT/05/2026	C.3.3	20	20	320	20	**320**	20	20	40
B/MISSOURI/03/2024	C.5.6	320	640	160	160	320	**320**	640	2560
B/NEW MEXICO/06/2025	C.5.6.1	320	640	160	160	160	320	**640**	1280
B/TEXAS/19/2024	C.5.7	320	640	160	320	320	320	640	**2560**
TEST VIRUSES									
B/NEW HAMPSHIRE/25/2026	C.3	20	20	320	20	320	10	20	40
B/WISCONSIN/10/2026	C.3.1	20	40	640	20	320	20	40	80
B/NEW MEXICO/16/2026	C.3.1	20	40	320	20	320	20	40	80
B/ALASKA/37/2026	C.3.1	20	40	640	20	320	20	40	80
B/DISTRICT OF COLUMBIA/12/2026	C.3.3	20	40	320	20	320	20	40	80
B/VIETNAM/056/2026	C.3.3	20	40	320	20	320	20	40	80
B/VIETNAM/059/2026	C.3.3	20	40	320	20	320	20	40	80
B/WYOMING/01/2026	C.5.1	320	640	320	320	640	320	640	2560
B/NEVADA/03/2026	C.5.1	160	640	160	160	320	160	320	1280
B/HAWAII/31/2026	C.5.1	320	640	320	320	320	320	640	2560
B/GHANA/4455/2026	C.5.6	320	640	320	320	320	320	640	2560
B/PENNSYLVANIA/86/2026	C.5.6	320	640	320	320	320	320	640	2560
B/VIETNAM/038/2026	C.5.6.1	320	640	320	320	320	320	640	2560
B/VIETNAM/100/2026	C.5.6.1	320	640	320	320	320	320	640	2560
B/MINNESOTA/24/2026	C.5.6.1	320	640	320	160	320	320	640	1280
B/PUERTO RICO/11/2026	C.5.6.1	320	640	320	160	320	320	640	2560
B/VIETNAM/094/2026	C.5.7	640	1280	320	640	320	640	1280	2560

≤ 2-fold = 4-fold ≥ 8-fold

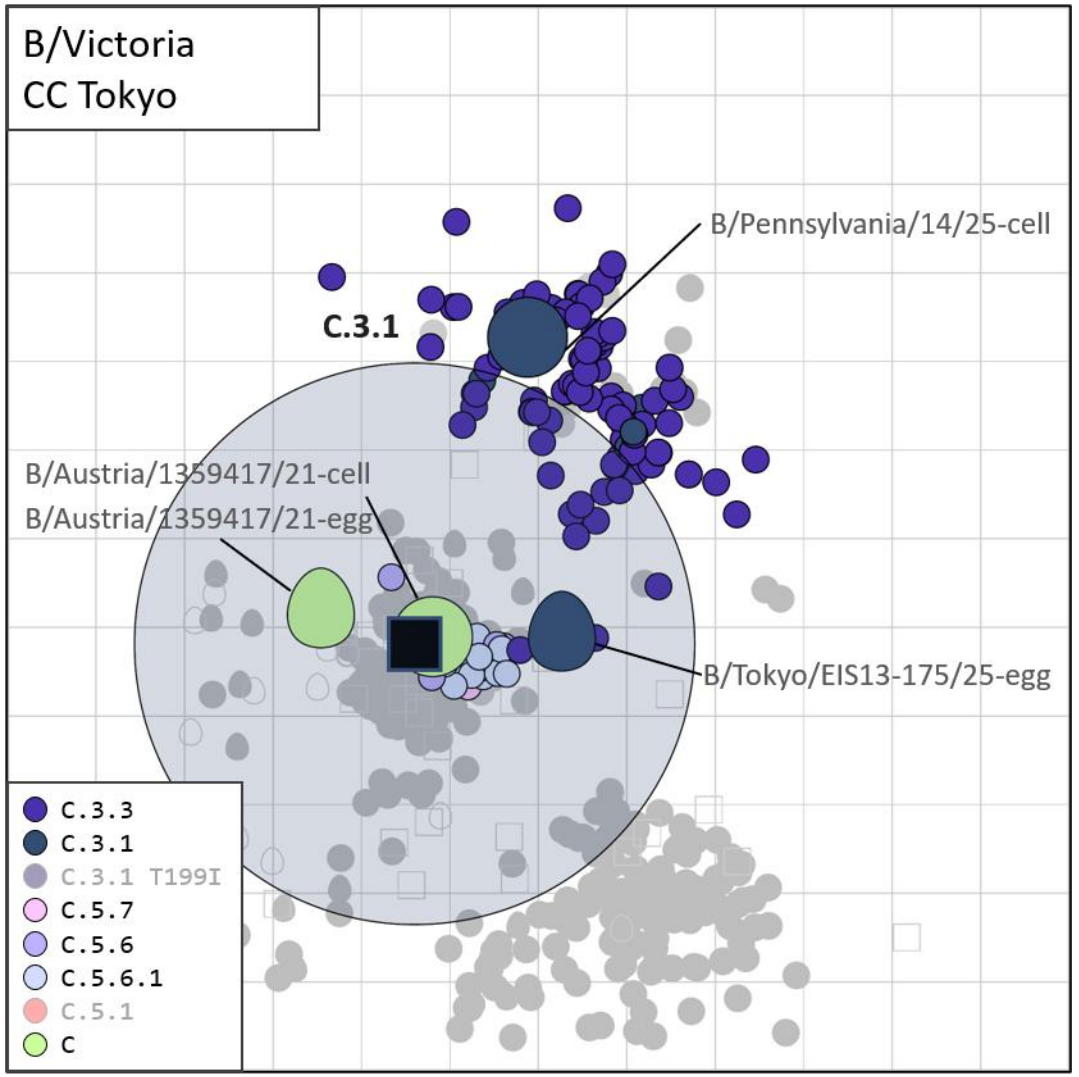
Source: CDC, Atlanta

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B/Victoria antigenic cartography



B/Pennsylvania/14/25-cell serum circle
(within 8-fold of homologous titer)



B/Tokyo/EIS13-175/25-egg serum circle
(within 8-fold of homologous titer)

Source: University of Cambridge

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Human post-vaccination serum analysis of B/Victoria viruses

WHO Collaborating Center (CC): Human Serological Panels
B/Victoria -- HI Protocol [CELL]

				C					C.3.1						C.3.3							C.5.6		C.5.6.1						C.5.7
				-					-					+M156V +T388X +R467X	-			+T199A (CHO-)				+V15X +S277G +V431X		+T199A	+K75E +T221A	-	+P241Q			+R80K +E184K	+N123K +I424V	-
				AUT/1359417					PA/14					TOKYO/ EIS15-095	CT/05-LIKE			VIC/12				YOK/172		MO/03	DAR/93	NM/06	TOKYO/EIS15-052-LIKE			VIC/33	TUR/ P288	GY/1420
				-					-					-	CT/05	WA/2611 016932		-				-		-	-	-	TOKYO/EIS15-052	DAR/81		-	-	-
				CELL					CELL					CELL	CELL	CELL		CELL				CELL		CELL	CELL	CELL	CELL			CELL	CELL	CELL
				CDC	CBER	MHRA	NIID	VIDRL	CDC	CBER	MHRA	NIID	VIDRL	NIID	CBER	VIDRL	CDC	CBER	MHRA	NIID	VIDRL	MHRA	NIID	CDC	VIDRL	CDC	MHRA	NIID	VIDRL	VIDRL	MHRA	MHRA
B/AUSTRIA/1359417/2021 CELL	Pediatric (2-9Y)	IIV3 (Fluzone)	Australia	118	26	130	547	420	9	10	18	155	61	85	14	138	51	X	65	√	180	21	71	√	275	√	51	291	78	√	√	√
	Adult (18-59Y)	IIV3	Peru	86					22								37							√		√						
	Adult (18-64Y)	ccIIV3 (Flucelvax)	Australia	189	42	229	622	329	36	30	35	229	115	174	√	211	94	√	128	√	211	121	143	√	√	√	109	√	160	√	√	√
		IIV3 (Fluzone)	Australia	135	34	179	605	446	32	22	26	256	106	249	23	169	62	X	85	√	179	41	151	√	√	√	92	√	147	√	√	100
		IIV3	South Africa	155					41								77							√		√						
	Elderly (≥60Y)	IIV3	Peru	85					39								√							√		√						
	Elderly (≥65Y)	aIIV3 (Fluad)	Australia	85	26	49	485	189	30	X	22	256	106	211	X	√	47	X	√	√	√	28	169	√	√	√	√	√	103	√	√	√
									7 (100.0)	3 (75.0)	4 (100.0)	4 (100.0)	4 (100.0)	4 (100.0)	2 (50.0)	3 (75.0)	6 (85.7)	0 (0.0)	3 (75.0)	0 (0.0)	3 (75.0)	4 (100.0)	4 (100.0)	0 (0.0)	1 (25.0)	0 (0.0)	3 (75.0)	1 (25.0)	4 (100.0)	0 (0.0)	0 (0.0)	1 (25.0)

Geometric Mean Titer (GMT) ratios between reference and test antigens are calculated with 90% confidence intervals (CI) for each cohort and panel location. Unadjusted model results are shown. If the CI lower bound is greater than 50%, it is statistically non-inferior (95% confidence level); otherwise, it is *possibly* inferior. Heat map cells are colored using the GMT ratio lower bound. Blue indicates statistical non-inferiority and orange denotes *possible* inferiority. Numbers shown are post-vaccination GMTs for the unadjusted model. They are shown for *reference antigens* and possibly inferior test antigens. Marks, √ or X, denote statistically significant non-inferiority when the reference virus GMT is ≥ 40 or < 40, respectively. Number and percent (in parentheses) of *possibly* inferior responses are summarized below the heat map.

Included Strains: B/AUSTRIA/1359417/2021 (AUT/1359417); B/CONNECTICUT/05/2026 (CT/05); B/DARWIN/81/2026 (DAR/81); B/DARWIN/93/2026 (DAR/93); B/GUANGDONG-YUNCHENG/1420/2026 (GY/1420); B/MISSOURI/03/2024 (MO/03); B/NEW MEXICO/06/2025 (NM/06); B/PENNSYLVANIA/14/2025 (PA/14); B/TOKYO/EIS15-052/2026 (TOKYO/EIS15-052); B/TOKYO/EIS15-095/2026 (TOKYO/EIS15-095); B/TURKIYE/P288/2026 (TUR/P288); B/VICTORIA/12/2026 (VIC/12); B/VICTORIA/33/2026 (VIC/33); B/WESTERN AUSTRALIA/2611016932/2026 (WA/2611016932); B/YOKOHAMA/172/2026 (YOK/172)

*In human serology studies using the SH 2026 serum panels, most post-vaccination HI GMTs against recent B/Victoria lineage with HA genes from subclades **C.5.6, C.5.6.1 and C.5.7 were not significantly reduced** when compared to titers against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses.

*Titers against clade **C.3 and subclade C.3.1 were significantly reduced** in most assays.

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B/Victoria lineage antiviral susceptibility

Neuraminidase inhibitors

- Of 2,598 influenza B/Victoria lineage viruses collected since February 1, 2026 were examined by genetic and/or phenotypic analyses, five viruses showed evidence of reduced or highly reduced susceptibility by NAIs

Endonuclease inhibitors

- Of 2,387 B/Victoria lineage viruses examined by genetic and/or phenotypic analyses in this period, no viruses showed evidence of reduced susceptibility to baloxavir marboxil.

Influenza B/Victoria lineage summary (1)

Phylogenetics of B/Victoria lineage HA genes

- Only influenza B/Victoria lineage viruses were available for analysis (no B/Yamagata viruses confirmed after March 2020).
- All viruses characterized belong to subclades C.3 and C.5.
- Viruses designated as C.5, C.5.1, C.5.6, C.5.6.1 and C.5.7,from subclade C.5 all of which had the HA substitution D197E, circulated at varying proportions in different regions.
- Viruses designated as C.3 have HA substitutions E128K, A154E and S208P. Subclades C.3.1 and C.3.3 viruses shared additional mutations D197N (gain of a potential N-glycosylation site.
- Subclade C.3.1 viruses predominated in the Americas, C.3.3 viruses predominated in East Asia, and subclade C.5.6 predominated in Africa, Europe, South East Asia and Oceania.

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Influenza B/Victoria lineage summary (2)

Antigenic characteristics of B/Victoria lineage viruses

- Post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (subclade C), representing the vaccine viruses B component for the SH 2026 influenza vaccines, recognized viruses within the C.5 subclades well. But C.3 and C.3.1 subclade viruses with HA substitution D197N were recognized poorly.
- Post-infection ferret antisera raised against cell culture-propagated B/Pennsylvania/14/2025-like viruses (C.3.1), representing cell-based vaccine viruses for the NH 2026-27 influenza season, recognized recently circulating viruses from C.3 and C.5 subclades well.
- All available egg isolates for subclade C.3 and C.3.1 viruses (e.g., B/Tokyo/EIS13-175/2025) acquired egg-adaptive mutations that remove the potential N-glycosylation site at HA 197 to 199.
- Post-infection ferret antisera raised against egg-propagated B/Tokyo/EIS13-175/2025-like viruses (C.3.1), representing egg-based vaccine viruses for the NH 2026-27 influenza season, recognized most viruses from the C.5 subclades well but showed reduced recognition of C.3 subclades compared to that of the cell equivalent.

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Influenza B/Victoria lineage summary (3)

Human serology studies

- Human serology studies were conducted using SH 2026 influenza vaccine formulation vaccinated serum panels by HI assays with recent B/Victoria viruses with HA genes from subclades C.3, C.3.1, C.5, C.5.6, C.5.6.1 and C.5.7.
- When compared to titers against cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses, titers against many viruses with HA genes from subclades C.5.6 and C.5.6.1 were not significantly reduced in most serum panels except for subclade C.5.6.1 viruses with the amino acid substitution P241Q, which were significantly reduced in some panels.
- In contrast, titers against many viruses with HA genes from subclades C.3.1 and C.3.3 were significantly reduced in most serum panels.

The data supported recommending an update to the cell-propagated B/Pennsylvania/14/2025-like (C.3.1) virus and an egg-propagated B/Tokyo/EIS13-175/2025-like (C.3.1) virus as the B/Victoria vaccine antigens for the 2027 southern hemisphere.

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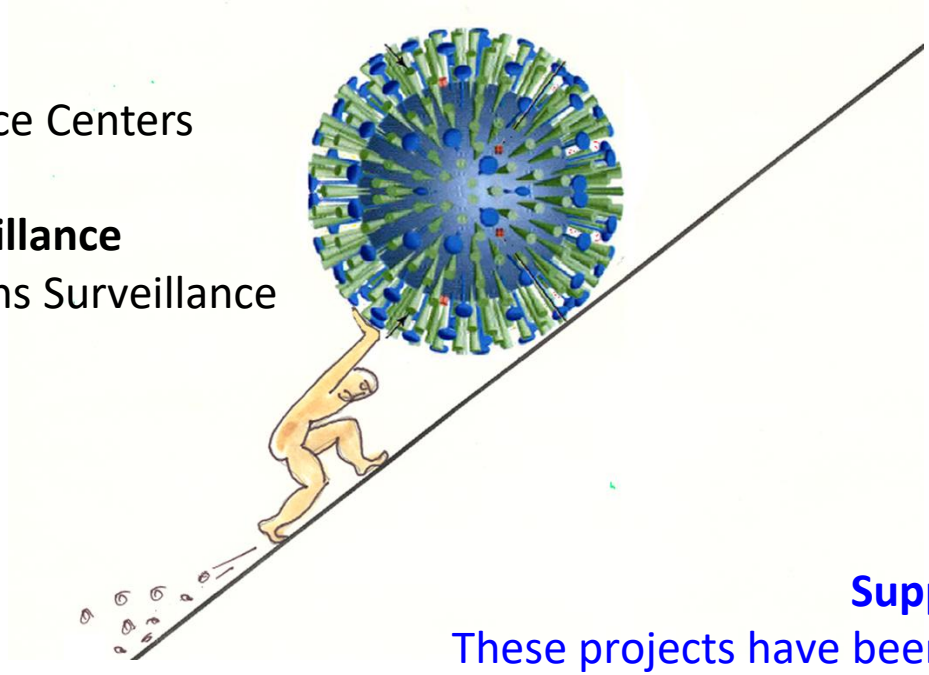
Acknowledgments

CDC Influenza Division and FDA CBER

US Public Health Laboratories
- National Influenza Reference Centers
- APHL

CDC Traveler's Genomic Surveillance

DoD, Global Emerging Infections Surveillance



Global Influenza Surveillance and Response System
- National Influenza Centers
- WHO CCs/ERL
- WHO H5 Ref Labs
- University of Cambridge
- NextStrain
- Previr

Acknowledgements

We gratefully acknowledge all data contributors, i.e., the Authors and their Originating laboratories responsible for obtaining the specimens, and their Submitting laboratories for generating the genetic sequence and metadata and sharing via the GISAID Initiative, on which this research is based.

Support and Disclaimer

These projects have been funded in part with federal funds from US Health and Human Services.

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.