

Recommended composition of influenza virus vaccines for use in the 2026 – 2027 northern hemisphere influenza season

February 2026

WHO convenes technical consultations¹ in February and September each year to recommend viruses for inclusion in influenza vaccines² for the northern hemisphere (NH) and southern hemisphere (SH) influenza seasons, respectively. This recommendation relates to the influenza vaccines for use in the NH 2026–2027 influenza season. A recommendation will be made in September 2026 relating to vaccines that will be used for the SH 2027 influenza season. WHO guidance for choosing between the NH and SH formulations for countries in tropical and subtropical regions is available on the WHO Global Influenza Programme website³.

National or regional authorities approve the composition and formulation of influenza vaccines used in each country. National public health authorities are responsible for making recommendations regarding the use of the vaccine. WHO has published recommendations on the prevention of influenza⁴.

Seasonal influenza activity

From September 2025 through January 2026, influenza activity was reported in all *transmission zones*. Overall influenza virus detections were higher compared to the same reporting period in 2024–2025 but peaked in December 2025 for this recent period compared to February 2025 for the previous period. During this reporting period, influenza A viruses predominated, although the proportion of virus detections varied among transmission zones.

In Africa, influenza activity increased during the start of the reporting period, with a predominance of influenza A viruses in all transmission zones. In *Eastern, Northern, and Western Africa*, among subtyped influenza A viruses, A(H1N1)pdm09 viruses accounted for the majority of detections early in the reporting period while A(H3N2) viruses predominated later in the reporting period. Influenza detections peaked in November in *Western Africa* and December in *Eastern and Northern Africa*. In *Middle Africa*, influenza detections remained low throughout the reporting period with a slight predominance of A(H1N1)pdm09 viruses early in the reporting period. In *Southern Africa*, influenza detections remained low throughout the reporting period, with a predominance of influenza A viruses. In *Northern and Middle Africa*, there was low and sustained influenza B activity throughout the reporting period.

¹ Recommendations for influenza vaccine composition: <https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations>

² Description of the process of influenza vaccine virus selection and development: http://www.who.int/gb/pip/pdf_files/Fluvaccvirusselection.pdf

³ Vaccines in tropics and subtropics: <https://www.who.int/teams/global-influenza-programme/vaccines/vaccine-in-tropics-and-subtropics>

⁴ Vaccines against influenza WHO position paper – May 2022. Wkly Epidemiol Rec 2022; 97 (19): 185 - 208. Available at: <https://iris.who.int/handle/10665/354264>

In Asia, influenza activity increased during the start of the reporting period in *South East* and *Western Asia*, from October in *Central and Eastern Asia*, and from November in *Southern Asia*, with a predominance of influenza A viruses in all transmission zones. Most influenza detections were reported from *Eastern Asia*, where activity peaked in early December. In *Southern Asia*, influenza activity also peaked in December; in *Central Asia* influenza activity peaked in November, and in *Western and South East Asia*, influenza activity peaked in October. Among subtyped influenza A viruses, A(H3N2) viruses accounted for the majority of detections in all transmission zones; detections of A(H1N1)pdm09 and influenza B viruses remained low in most transmission zones throughout the reporting period, except in *Eastern Asia* where there was a substantial rise in influenza B viruses in recent weeks.

In Europe, influenza activity increased from mid-September in *Northern Europe*, from October in *South West Europe* and from mid-November in *Eastern Europe*, with a predominance of influenza A viruses in all transmission zones. Influenza detections peaked in December in *Northern and South West Europe* but remained elevated through January. Influenza detections continued to increase through January in *Eastern Europe*. Among subtyped influenza A viruses, A(H3N2) viruses predominated. In *South West Europe*, detections of A(H1N1)pdm09 viruses slightly increased in mid-November. In *Eastern and Northern Europe*, detections of A(H1N1)pdm09 and influenza B viruses remained low throughout the reporting period.

In the Americas, influenza activity increased from the start of the reporting period in *Temperate and Tropical South America* and from November in *North America* and *Central America Caribbean*. Influenza A viruses accounted for most detections, and influenza B virus detections remained low throughout the reporting period in all transmission zones, except in *North America* where there was a substantial rise in influenza B viruses in recent weeks. In *North America*, activity peaked in late December. Among subtyped influenza A viruses, there was a predominance of A(H3N2) viruses. In *Central America Caribbean*, influenza activity remained elevated through mid-January with A(H3N2) virus detections predominant from December. In *Tropical South America*, influenza activity peaked in early November and slowly declined until the end of the reporting period. Among subtyped influenza A viruses, A(H3N2) predominated through November then co-circulated at similar proportions to A(H1N1)pdm09 until the end of the reporting period. In *Temperate South America*, influenza activity peaked in mid-November and among subtyped influenza A viruses, A(H3N2) viruses predominated throughout the reporting period.

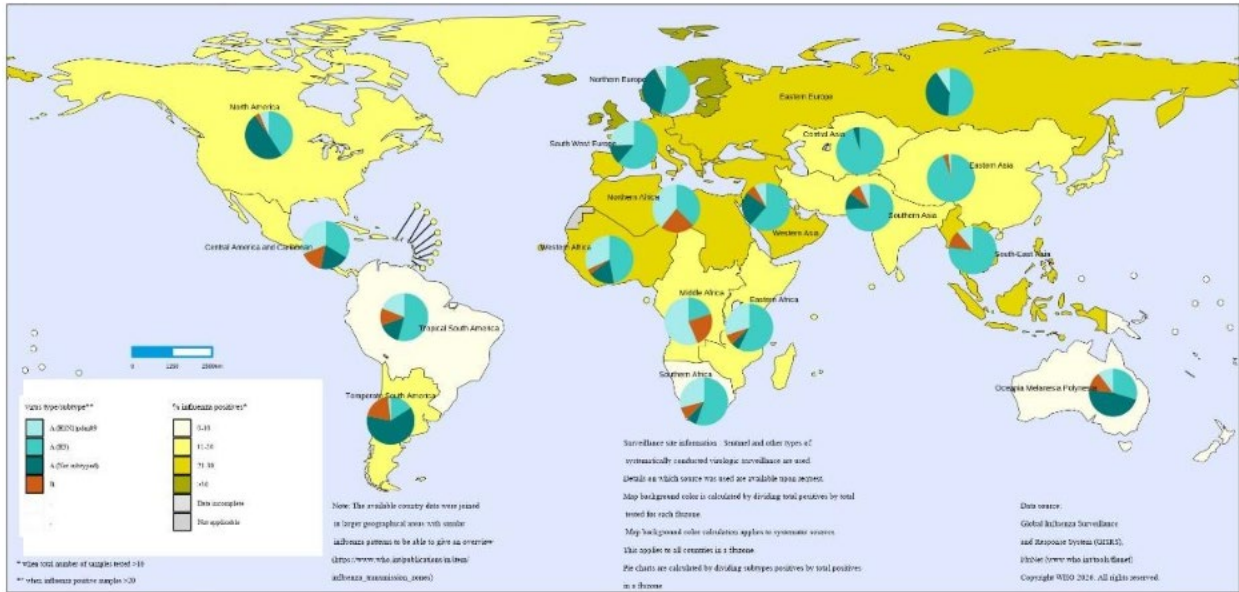
In Oceania, influenza activity decreased until mid-October, increased in December and decreased since mid-December. A(H1N1)pdm09 and B viruses were detected at similar levels until mid-September and A(H3N2) virus detections predominated since then.

Influenza A

Globally, influenza A virus detections greatly outnumbered those of influenza B. Among subtyped influenza A viruses, A(H3N2) viruses predominated throughout the reporting period in most transmission zones. In *Eastern, Northern, Western Africa, Central America Caribbean and Oceania*, influenza A(H1N1)pdm09 virus detections predominated during the first part of the reporting period, and A(H3N2) virus detections predominated in the latter part of the reporting period. Influenza A(H1N1)pdm09 virus detections increased slightly towards the latter part of the reporting period in *Eastern and South West Europe, Central America Caribbean and Tropical South America*. The overall number of influenza detections was low in *Middle and Southern Africa*.

Influenza B

Globally, influenza B virus detections remained low throughout the reporting period. Increases in influenza B virus detections in January were reported in *North America* and *Eastern Asia*. All influenza B viruses where lineage was confirmed belonged to the B/Victoria lineage.



Distribution of Influenza virus type/subtype by influenza transmission zone, between 01 September 2025 and 08 February 2026.

Detailed information by country of the extent of seasonal influenza activity and type/subtype of viruses worldwide is available on the WHO website: <https://www.who.int/tools/flunet>.

Zoonotic influenza

From 23 September 2025, sporadic zoonotic influenza infections were reported, in most cases, following exposure to infected birds, swine or contaminated environments. Single cases of A(H5N1) from Bangladesh, A(H5N2) from Mexico, and A(H5N5) from the United States of America were reported. Three A(H5N1) cases were reported from Cambodia. Fourteen cases of A(H9N2) and one case of A(H10N3) were reported from China. Single cases of A(H1N1)v and A(H1N2)v were reported from China, a case of A(H1N2)v from the United States of America, and a case of A(H3N2)v from Brazil.

Genetic and antigenic characteristics of recent seasonal influenza viruses, human serology and antiviral susceptibility

Influenza A(H1N1)pdm09 viruses

Since September 2025, A(H1N1)pdm09 viruses circulated globally, but did not predominate in any region. The haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades. Viruses from clade 5a.2a subclades C.1, C.1.9 and C.1.9.3 circulated in low numbers, with the largest proportion of detections in Africa⁵. Since September 2025, clade 5a.2a.1 subclades D.3.1 and D.3.1.1 viruses circulated globally. The D.3.1 subclade with substitutions T120A, I372V, I460T and V520A predominated in Western Pacific, Africa, South East Asia and several countries in the Americas. D.3.1.1 viruses characterized by R113K and more recently acquired substitutions A139D, E283K and K302E predominated in some countries in Europe, the Middle East and North America.

The antigenic properties of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) assays with post-infection ferret antisera. HI results for viruses with collection dates since September 2025 showed that ferret antisera raised against cell culture-propagated A/Wisconsin/67/2022-like and egg-propagated A/Victoria/4897/2022-like viruses from the 5a.2a.1 clade recognized viruses in both 5a.2a and 5a.2a.1 clades well. However, post-infection ferret antisera raised against viruses from clade 5a.2a showed some reduction in recognition of the now predominating D.3.1 and D.3.1.1 subclade viruses. Post-infection ferret antisera raised against viruses from subclade D.3.1 (e.g., A/Missouri/11/2025) recognized recently circulating viruses from both 5a.2a and 5a.2a.1 clades well.

Human serology studies used 15 serum panels from children, adults (18 to 64 years) and older adults (≥ 65 years) who had received egg-propagated inactivated (standard, high dose or adjuvanted), cell culture-propagated inactivated or recombinant trivalent or quadrivalent vaccines with NH 2025-2026 influenza vaccine formulations. NH 2025-2026 egg-based vaccines contained A/Victoria/4897/2022 (H1N1)pdm09-like, A/Croatia/10136RV/2023 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and, in quadrivalent vaccines, B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens. Cell culture-propagated and recombinant vaccines contained A/Wisconsin/67/2022 (H1N1)pdm09-like, A/District of Columbia/27/2023 (H3N2)-like and B/Austria/1359417/2021-like (B/Victoria lineage) virus antigens.

Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a (subclade C.1.9.3) and 5a.2a.1 (subclades D.3.1 and D.3.1.1) were analysed in HI assays using these human serum panels. When compared to the responses to cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like vaccine reference viruses, post-vaccination geometric mean titres (GMTs) were significantly reduced for some recently circulating viruses from D.3.1 and D.3.1.1 subclades.

Of 1 161 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): seven had an H275Y neuraminidase (NA) substitution and eight had I223V and S247N substitutions. 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.

⁵ Real-time tracking of influenza A(H1N1)pdm09 evolution: <https://nextstrain.org/seasonal-flu/h1n1pdm/ha/2y?c=subclade>

Influenza A(H3N2) viruses

Phylogenetic analysis of the HA gene sequences of A(H3N2) viruses collected since September 2025 showed that the vast majority of viruses belonged to one of the J.2 subclades⁶, expressing HA N122D and K276E substitutions. HA genes have diversified with many subclades; J.2.2 (characterized by S124N), J.2.3 (characterized by N158K, K189R and S378N), J.2.4 (characterized by T135K [a potential loss of an N-glycosylation site] and K189R), and K (formerly designated as J.2.4.1; characterized by K2N, S144N [a potential addition of an N-glycosylation site], N158D, I160K, Q173R, T328A and S378N). During this reporting period, subclade K viruses were detected in all regions and predominated in many countries. There was still circulation of other J.2 subclades, notably J.2 or J.2.3 in South America, J.2.2 or J.2.4 in Africa and Asia.

Post-infection ferret antisera raised against cell culture-propagated A/District of Columbia/27/2023-like and egg-propagated A/Croatia/10136RV/2023-like (clade 2a.3a.1, subclade J.2) viruses, representing the A(H3N2) component for the NH 2025-2026 influenza vaccines, showed poor recognition with recently circulating subclade J.2.3 (e.g., A/Netherlands/10685/2024), J.2.4 (e.g., A/Sydney/1359/2024) and K (e.g., A/Darwin/1415/2025) viruses. Ferret antisera raised against reference viruses from J.2.3 subclades showed good recognition of viruses expressing HA from J.2.3, but poor recognition of other subclades.

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 SH 2026 influenza vaccines, recognized most J.2.4 viruses and many subclade K viruses well. However, subclade K viruses and J.2.4 viruses with HA substitutions F79V, S144N (addition of a potential N-glycosylation site), N158D, I160K, T328A 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.

Human serology studies were conducted using the serum panels as described above by HI and virus neutralization (VN) assays with recent circulating A(H3N2) viruses with HA genes from subclades J.2, J.2.2, J.2.3, J.2.4, J.2.5 and K. When compared to titres against cell-propagated A/District of Columbia/27/2023-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against many of the recent viruses in all subclades tested were significantly reduced in many serum panels.

⁶ Real-time tracking of influenza A(H3N2) evolution: <https://nextstrain.org/seasonal-flu/h3n2/ha/2y?c=subclade>

Table 1. HI assay of recently circulating A(H3N2) viruses

Reference viruses	Passage level	Clade/ Subgroup	Reference ferret antisera						Collection dates
			A9936	A10020	A9985	A10145	A10162	A10204	
			SIAT3, SIAT4	M2/SIAT2, SIAT1	SIAT1	E4	MDCK1	E2	
			Cro/ 10136RV	Neth/ 10685	Syd/ 1359	Sing/ GP20238	Dar/ 1415	Dar/ 1454	
			J.2	J.2.3	J.2.4	J.2.4	K	K	
A/Croatia/10136RV/2023	SIAT3, SIAT6	J.2	320	<40	40	40	<40	<40	
A/Netherlands/10685/2024	M2/SIAT 2, SIAT3	J.2.3	80	640	<40	<40	<40	<40	
A/Sydney/1359/2024	SIAT3	J.2.4	160	40	320	2560	640	640	
A/Singapore/GP20238/2024	E6	J.2.4	160	160	640	2560	320	320	
A/Darwin/1415/2025	SIAT3	K	40	40	160	640	640	640	
A/Darwin/1454/2025	E2	K	<40	80	320	1280	1280	640	
Test viruses									
A/Darwin/2100/2025	SIAT1	J.2.2	320	<40	40	40	<40	<40	05/10/2025
A/Singapore/GP14404/2025	M1, SIAT1	J.2.2	320	<40	40	40	<40	<40	30/10/2025
A/Victoria/2797/2025	SIAT1	J.2.4	<40	<40	320	640	640	640	14/11/2025
A/Sri Lanka/69/2025	SIAT2	J.2.4	80	40	320	2560	640	640	21/10/2025
A/Tasmania/1035/2025	SIAT1	K	<40	<40	80	320	320	320	04/12/2025
A/Canberra/980/2025	SIAT1	K	<40	<40	80	640	640	320	23/12/2025
A/Sri Lanka/111/2025	SIAT2	K	40	<40	160	640	1280	1280	30/12/2025
A/Cambodia/IKCM250152/2025	SIAT1	K	<40	<40	160	640	640	320	20/12/2025
A/New Caledonia/195/2025	SIAT2	K	<40	<40	80	640	640	640	11/12/2025
A/Nepal/S3684/2025	SIAT1	K	<40	<40	80	320	640	640	15/12/2025

Of 4 458 influenza A(H3N2) viruses examined by genetic and/or phenotypic analyses, two viruses showed evidence of reduced susceptibility to NAIs; both had an NA E119V substitution. Of 4 828 A(H3N2) viruses examined by genetic and/or phenotypic analyses, nine viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil: three had a PA I38T substitution, three had a PA I38I/T substitution, two had a PA I38I/M substitution and one had a PA E199E/G substitution.

Influenza B viruses

Since September 2025, influenza B viruses were detected in all WHO regions, and all those characterized belonged to the B/Victoria lineage. There have been no confirmed detections of circulating B/Yamagata lineage viruses after March 2020.

All HA genes of B/Victoria lineage viruses characterized during this reporting period belonged to clade 3a.2 with HA substitutions A127T, P144L, and K203R. Viruses with clade 3a.2 HA genes have diversified further, forming several subclades (C.1-C.5)⁷. Viruses designated as C.5, C.5.1, C.5.6, C.5.6.1 and C.5.7, 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. Subclade C.3.1 viruses shared additional mutations D197N (addition of a potential N-glycosylation site) and P208S. Recent C.3 viruses which had additional changes D197N (addition of a potential N-glycosylation site), S255P and I267V and C.3.1 viruses have been detected in increasing proportions in Eastern Asia and North America in recent weeks.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2), representing the vaccine viruses for the SH 2026 and NH 2025-2026 influenza seasons, recognized viruses within the C.5.1, C.5.6, C.5.6.1 and C.5.7 subclades well. C.3 and C.3.1 subclade viruses with the HA substitution D197N were recognized poorly. Post-infection ferret antisera raised against cell culture-propagated viruses from subclade C.3.1 (e.g., B/Pennsylvania/14/2025) recognized recently circulating viruses from C.3, C.3.1 and other 3a.2 subclades well. All available egg isolates for subclade C.3 and C.3.1 viruses acquired substitutions that remove the potential N-glycosylation site at HA 197 to 199. Post-infection ferret antisera raised against egg-propagated viruses from subclade C.3.1 (e.g., B/Tokyo/EIS13-175/2025, B/Tokyo/EIS13-011/2025, B/Perth/115/2025) showed reduced recognition of recently circulating viruses from C.3 and C.3.1 subclades compared to that of the cell equivalent.

⁷ Real-time tracking of influenza B/Victoria lineage evolution: <https://nextstrain.org/seasonal-flu/vic/ha/2y?c=subclade>

Table 2. HI assay of recently circulating B/Victoria Lineage viruses

	HA subclade	REFERENCE ANTISERA			
		MDCK	MDCK	MDCK	MDCK
		B/Austria/ 1359417/2021	B/Missouri/ 03/2024	B/Texas/19/2024	B/Pennsylvania/ 14/2025
		C	C.5.6	C.5.7	C.3.1
REFERENCE VIRUSES					
B/Austria/1359417/2021	C	320	1280	2560	40
B/Missouri/03/2024	C.5.6	320	2560	1280	40
B/Texas/19/2024	C.5.7	320	2560	2560	40
B/Pennsylvania/14/2025	C.3.1	20	80	80	80
TEST VIRUSES					
B/Shandong-Huancui/11058/2025	C.3	20	80	160	160
B/Colorado/65/2025	C.3	40	80	160	160
B/Pennsylvania/01/2026	C.3	40	80	160	160
B/Virginia/20/2025	C.3.1	40	80	320	320
B/Sao Paulo/358687134-IAL/2025	C.3.1	20	80	160	160
B/Hawaii/03/2026	C.3.1	40	80	160	160
B/Michigan/04/2026	C.3.1	40	80	160	160
B/Oklahoma/02/2026	C.3.1	40	80	160	160
B/New Hampshire/27/2025	C.3.1	20	40	80	80
B/Bangladesh/2898/2025	C.5.6	320	2560	5120	80
B/New York/43/2025	C.5.6	320	1280	2560	40
B/Kanagawa/Ac2504/2025	C.5.6	320	2560	2560	80
B/Tokyo/EIS13-776/2025	C.5.6.1	320	2560	2560	80
B/Bangladesh/2857/2025	C.5.6.1	320	2560	2560	80
B/North Dakota/02/2026	C.5.6.1	160	1280	1280	40
B/Vietnam/5315/2025	C.5.7	320	2560	5120	80
B/Cameroon/1888/2025	C.5.7	320	1280	5120	40
B/Missouri/36/2025	C.5.7	160	1280	1280	40

In human serology studies, recently circulating B/Victoria lineage viruses with HA genes from clade 3a.2 subclades C.3, C.3.1, C.5.1, C.5.6, C.5.6.1 and C.5.7 were tested using the serum panels described above. When compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference virus, titres against most viruses with HA genes from C.5.1, C.5.6, C.5.6.1 and C.5.7 subclades were not significantly reduced; however, titres against viruses with HA genes from C.3 and C.3.1 were significantly reduced in most serum panels. Serology studies were not performed for B/Yamagata lineage viruses.

Of 549 influenza B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, two showed evidence of reduced or highly reduced susceptibility to NAIs, both with an NA M464T substitution. Of 760 B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, no viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil.

Recommended composition of influenza virus vaccines for use in the 2026-2027 northern hemisphere influenza season

Since September 2025, A(H1N1)pdm09 viruses circulated globally. The majority of viruses had HA genes belonging to the 5a.2a.1 clade which has further diversified into the D.3.1 and D.3.1.1 subclades. Post-infection ferret antisera raised against the northern hemisphere (NH) 2025-2026 A(H1N1)pdm09 vaccine viruses (cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022) and the southern hemisphere (SH) 2026 A(H1N1)pdm09 vaccine viruses A/Missouri/11/2025 recognized D.3.1 and D.3.1.1 viruses well. In human serology studies, post-vaccination geometric mean titres (GMTs) were significantly reduced for some recently circulating A(H1N1)pdm09 viruses when compared to the responses to cell culture-propagated A/Wisconsin/67/2022 A(H1N1)pdm09-like vaccine reference viruses.

Since September 2025, A(H3N2) viruses circulated and predominated globally. The vast majority of A(H3N2) viruses collected had HA genes from subclades of J.2 and have continued to diversify with subclade K (previously designated as J.2.4.1) viruses predominating in most regions. Post-infection ferret antisera raised against NH 2025-2026 influenza season vaccine viruses (cell culture-propagated A/District of Columbia/27/2023 and egg-propagated A/Croatia/10136RV/2023) recognized some J.2 viruses well but showed poor recognition of viruses from subclades J.2.3, J.2.4 and K. Post-infection ferret antisera raised against subclade K viruses (cell culture-propagated A/Darwin/1415/2025 and egg-propagated A/Darwin/1454/2025) showed improved recognition of K viruses compared to post-infection antisera raised against NH 2025-2026 and SH 2026 A(H3N2) vaccine viruses. When compared to titres against cell culture-propagated A/District of Columbia/27/2023-like vaccine reference viruses, human post-vaccination haemagglutinin inhibition (HI) GMTs or virus neutralisation (VN) GMTs against many of the recent viruses in J.2.3, J.2.4 and K subclades were significantly reduced.

Since September 2025, influenza B virus detections remained low globally, although some countries had increased detections in recent weeks. All circulating influenza B viruses characterized belonged to the B/Victoria lineage, and had HA genes belonging to clade 3a.2 with substitutions A127T, P144L and K203R. Post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2), representing the vaccine viruses for the SH 2026 and NH 2025-2026 influenza seasons, recognized viruses within the C.5.1, C.5.6, C.5.6.1 and C.5.7 subclades well. C.3 and C.3.1 subclade viruses with HA substitution D197N were recognized poorly. Post-infection ferret antisera raised against cell culture-propagated viruses from subclade C.3.1 (e.g., B/Pennsylvania/14/2025) recognized recently circulating viruses from C.3, C.3.1 and other 3a.2 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, leading to post-infection ferret antisera raised against egg-propagated viruses from subclade C.3.1 (e.g., B/Tokyo/EIS13-175/2025) showing reduced recognition of recently circulating viruses from C.3 and C.3.1 subclades compared to that of the cell equivalent. Human serology assays showed that post-vaccination titres against most recent B/Victoria lineage viruses with HA genes from subclades C.5.1, C.5.6, C.5.6.1 and C.5.7 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses. Titres against viruses with HA genes from subclade C.3 and C.3.1 were significantly reduced in most serum panels.

For vaccines for use in the 2026-2027 northern hemisphere influenza season, WHO recommends the following:

Egg-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1454/2025 (H3N2)-like virus; and
- a B/Tokyo/EIS13-175/2025 (B/Victoria lineage)-like virus.

Cell culture-, recombinant protein- or nucleic acid-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1415/2025 (H3N2)-like virus; and
- a B/Pennsylvania/14/2025 (B/Victoria lineage)-like virus.

Lists of prototype viruses for egg-, cell culture-, recombinant protein- and nucleic acid-based vaccines together with candidate vaccine viruses (CVVs) suitable for the development and production of human influenza vaccines are available on the WHO website⁸. A list of reagents for vaccine standardization, including those for this recommendation, can also be found on the WHO website.

CVVs and reagents for use in the laboratory standardization of inactivated vaccines may be obtained from:

- Therapeutic Goods Administration, P.O. Box 100, Woden, ACT, 2606, Australia (email: influenza.reagents@health.gov.au; website: <http://www.tga.gov.au>).
- Medicines and Healthcare products Regulatory Agency (MHRA), Blanche Lane, South Mimms, Potters Bar, Hertfordshire, EN6 3QG, the United Kingdom of Great Britain and Northern Ireland (email: enquiries@mhra.gov.uk; website: http://www.nibsc.org/science_and_research/virology/influenza_resource.aspx).
- Division of Biological Standards and Quality Control, Center for Biologics Evaluation and Research, Food and Drug Administration, 10903 New Hampshire Avenue, Silver Spring, Maryland, 20993, the United States of America (email: cbershippingrequests@fda.hhs.gov).
- Research Centre for Influenza and Respiratory Viruses, National Institute of Infectious Diseases, 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japan (email: flu-vaccine@nih.go.jp).

Requests for reference viruses should be addressed to:

- WHO Collaborating Centre for Reference and Research on Influenza, VIDRL, Peter Doherty Institute, 792 Elizabeth Street, Melbourne, Victoria 3000, Australia (email: whoflu@influenzacentre.org; website: <http://www.influenzacentre.org>).
- WHO Collaborating Centre for Reference and Research on Influenza, National Institute of Infectious Diseases, Japan Institute for Health Security 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japan (email: whocc-flu@nih.go.jp).
- Influenza Division, Centers for Disease Control and Prevention, 1600 Clifton Road, Mail Stop H17-5, Atlanta, GA 30329, the United States of America (email: InfluenzaVirusSurvei@cdc.gov; website: <http://www.cdc.gov/flu/>).

⁸ Candidate vaccine viruses: <https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses>

- WHO Collaborating Centre for Reference and Research on Influenza, The Francis Crick Institute, 1 Midland Road, London NW1 1AT, the United Kingdom of Great Britain and Northern Ireland (Tel: +44 203 796 1520 or +44 203 796 2444, email: whocc@crick.ac.uk;
- website: <http://www.crick.ac.uk/research/worldwideinfluenza-centre>).
- WHO Collaborating Centre for Reference and Research on Influenza, National Institute for Viral Disease Control and Prevention, China CDC, 155 Changbai Road, Changping District, 102206, Beijing, China. (tel: +86 10 5890 0851; email: fluchina@ivdc.chinacdc.cn; website: <https://ivdc.chinacdc.cn/cnic/en/>).

WHO provides weekly updates⁹ of global influenza activity. Other information about influenza surveillance, risk assessment, preparedness and response can be found on the WHO Global Influenza Programme website¹⁰.

Acknowledgements

The WHO recommendation on vaccine composition is based on the year-round work of the WHO Global Influenza Surveillance and Response System (GISRS). We thank the National Influenza Centres (NICs) of GISRS, and non-GISRS laboratories including the World Organization for Animal Health (WOAH) and the Food and Agriculture Organization of the United Nations (FAO) Network of Expertise on Animal Influenza (OFFLU), who contributed information, clinical specimens, viruses and associated data; WHO Collaborating Centres of GISRS for their in-depth characterization and comprehensive analysis of viruses; University of Cambridge for performing antigenic cartography and phylogenetic analysis; WHO Essential Regulatory Laboratories of GISRS for their complementary virus analyses and contributions from a regulatory perspective; and laboratories involved in the production of high growth/yield reassortants as candidate vaccine viruses. We also acknowledge the GISAID Global Data Science Initiative for the EpiFlu™ database and other sequence databases which were used to share gene sequences and associated information; modelling groups for virus fitness forecasting; and the Global Influenza Vaccine Effectiveness (GIVE) Collaboration for sharing estimates of influenza vaccine effectiveness on a confidential basis.

⁹ Current respiratory virus update: <https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-updates>

¹⁰ Global Influenza Programme: <https://www.who.int/teams/global-influenza-programme>

Annex 1

Declarations of interest

The WHO recommendation on the composition of influenza vaccines for use in the 2026-2027 Northern Hemisphere Influenza Season was made through a WHO Consultation with relevant WHO Collaborating Centres on Influenza (CCs) and Essential Regulatory Laboratories (ERLs).

In accordance with WHO policy, Directors and experts of the relevant WHO CCs and ERLs, in their capacity as representatives of their respective institutions (“Advisers”), completed the WHO form for Declaration of Interests for WHO experts before being invited to the Consultation. At the start of the Consultation, the interests declared by the Advisers were disclosed to all participants.

The Advisers declared the following personal current or recent (within the past 4 years) financial or other interests relevant to the subject of work:

Institution	Representative	Personal interest
WHO ERL TGA Woden	Dr Pearl Bamford	None
WHO ERL MHRA Potters Bar	Dr Othmar Engelhardt	All items declared and listed below belong to Dr Engelhardt’s Research Unit in the form of contract research and grants from: DIOSynVax, IFPMA, Innovative Medicines Initiative and PATH.
WHO CC and ERL NIID Tokyo	Dr Hideki Hasegawa	None
WHO CC Atlanta	Dr Rebecca Kondor	Below item declared and listed below belong to Dr Kondor’s Research Unit: <ul style="list-style-type: none">• Received significant financial support for research activities CRADA from Seqirus for development of cell-based manufacturing technologies for influenza vaccines.
WHO CC London	Dr Nicola Lewis	Following items were declared: <ul style="list-style-type: none">• Invited speaker and panel member on event organized by Seqirus. No remuneration received. The items declared and listed below belong to Dr Lewis’s Research Unit: <ul style="list-style-type: none">• Received significant financial support for research activities on annual basis from IFPMA for isolation of influenza viruses in hens’ eggs as potential vaccine strains for development as influenza vaccine strains.• Received significant financial support for research activities from FluLab on broadening vaccine responses.
WHO CC Koltsovo	Dr Vasily Marchenko	None
WHO CC Melbourne	Dr Patrick Reading	The items declared and listed below belong to Dr Reading’s Research Unit:

		<ul style="list-style-type: none"> • Received significant financial support for research activities (Collaborative research and development agreement (CRADA)) from Seqirus on isolation of candidate vaccine viruses in cell cultures. • Received significant financial support for research activities through a letter of agreement with IFPMA for isolation of influenza viruses in hens' eggs as potential vaccine strains for development as influenza vaccine strains. • Received non-monetary support from Roche and GSK with supply of antiviral drugs for use in antiviral drug sensitivity testing for surveillance and research purposes. Value not determined. • Received non-monetary support from CSL Limited/Seqirus in the form of Service Agreement for access to animal facilities and provision of some materials. Value not determined.
WHO CC Beijing	Dr Dayan Wang	None
WHO CC Memphis	Dr Richard Webby	None

Based on the WHO assessment, the interests declared by Drs Engelhardt, Kondor, Lewis and Reading were determined not to present a conflict of interest with the objectives of the WHO consultation. Therefore, it was concluded that with disclosure at the beginning of the consultation to all participants, Drs Engelhardt, Kondor, Lewis and Reading should continue to serve as Advisers.