Recommended composition of influenza virus vaccines for use in the 2025-2026 northern hemisphere influenza season

February 2025

WHO convenes technical consultations[1] in February and September each year to recommend viruses for inclusion in influenza vaccines[2] for the northern hemisphere (NH) and southern hemisphere (SH) influenza seasons, respectively. This recommendation relates to the influenza vaccines for use in the NH 2025-2026 influenza season. A recommendation will be made in September 2025 relating to vaccines that will be used for the SH 2026 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 website[3].

National or regional authorities approve the composition and formulation of 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 influenza[4].

Seasonal influenza activity

From September 2024 through January 2025, influenza activity was reported in all *transmission zones*. Overall activity was lower compared to the same reporting period in 2023-2024. The predominant viruses varied among transmission zones and between countries.

In Africa, influenza activity varied by transmission zone, and the frequency of reported detections was generally low in all regions. In *Northern Africa*, influenza activity peaked in December, with a predominance of A(H3N2) detections. In *Western Africa*, influenza A(H3N2) detections were predominant during September, followed by an increase in influenza B detections during October, with decreased detections and co-circulation of influenza A and B viruses late in the reporting period. In *Middle Africa*, influenza activity peaked in October with more detections of A(H3N2) until November followed by higher detections of A(H1N1)pdm09 in December and January. In *Eastern Africa*, detections of influenza A were predominant during September, while influenza B predominated from November onwards, although there was co-circulation of A(H1N1)pdm09 and A(H3N2) viruses and influenza B throughout the reporting period. In *Southern Africa* influenza activity remained low following a decrease in influenza detections of predominantly B/Victoria lineage viruses early in the reporting period.

In Asia, influenza virus detections increased during the reporting period. Influenza A viruses were predominant in all transmission zones, although there was a relatively higher proportion of influenza B

[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

detections in *Western Asia* and to a lesser extent *South East Asia* compared to other transmission zones. Most influenza detections were reported from *Eastern Asia*, with increased activity and predominant detections of A(H1N1)pdm09 viruses from November onwards. In *South East Asia* there was sustained influenza A activity with a predominance of A(H1N1)pdm09 detections across the reporting period, with a slight peak in activity in January. Influenza A(H1N1)pdm09 detections predominated in *Southern Asia*, with an increase in activity during November and December, along with much lower co-circulation of A(H3N2) and influenza B viruses. In *Central Asia*, influenza detections were low with an increase of A(H1N1)pdm09 detections from November onwards and a small increase in influenza B detections in January. There was sustained influenza activity in *Western Asia*, with a predominance of influenza A(H1N1)pdm09 detections, although A(H3N2) and influenza B viruses co-circulated in lower proportions throughout the reporting period.

In Europe, influenza activity was substantially greater in December and January compared to earlier in the reporting period, with a predominance of influenza A, although co-circulation of influenza B was detected in *Eastern Europe* and *South West Europe*. Influenza A(H1N1)pdm09 predominated among detections in *Northern Europe*, while there was roughly equal co-circulation of A(H1N1)pdm09 and A(H3N2) viruses in *Eastern Europe*. In *South West Europe*, there was co-circulation of both subtypes but with a lower proportion of A(H3N2) detections. Activity in *Eastern* and *South West Europe* remained elevated in January while activity peaked in December in *Northern Europe*.

In the Americas, influenza activity varied by transmission zone. Activity in *North America* increased from November onwards, with most activity identified as influenza A and roughly equal proportions of A(H1N1)pdm09 and A(H3N2) viruses among subtyped viruses. In *Central America and the Caribbean*, influenza activity increased from November onwards with influenza A predominating; most detections were A(H3N2) viruses, though A(H1N1)pdm09 viruses were detected in increasing proportions near the end of the reporting period and influenza B viruses were detected at low levels throughout the reporting period. Influenza activity occurred across the reporting period in *Tropical South America*, with a sustained higher proportion of influenza B and decreasing influenza A detections until December; there was a greater proportion of A(H1N1)pdm09 among influenza A subtyped viruses, although A(H3N2) co-circulated. Influenza B detections were also predominant in *Temperate South America*, with decreasing activity in December and January; there was low but sustained influenza A activity throughout the reporting period.

In Oceania, influenza detections were highest early in the reporting period, with decreasing activity until November, and a small increase during December and January; most detections were influenza A, with A(H3N2) initially predominant among subtyped viruses, and a higher proportion of A(H1N1)pdm09 viruses during December and January.

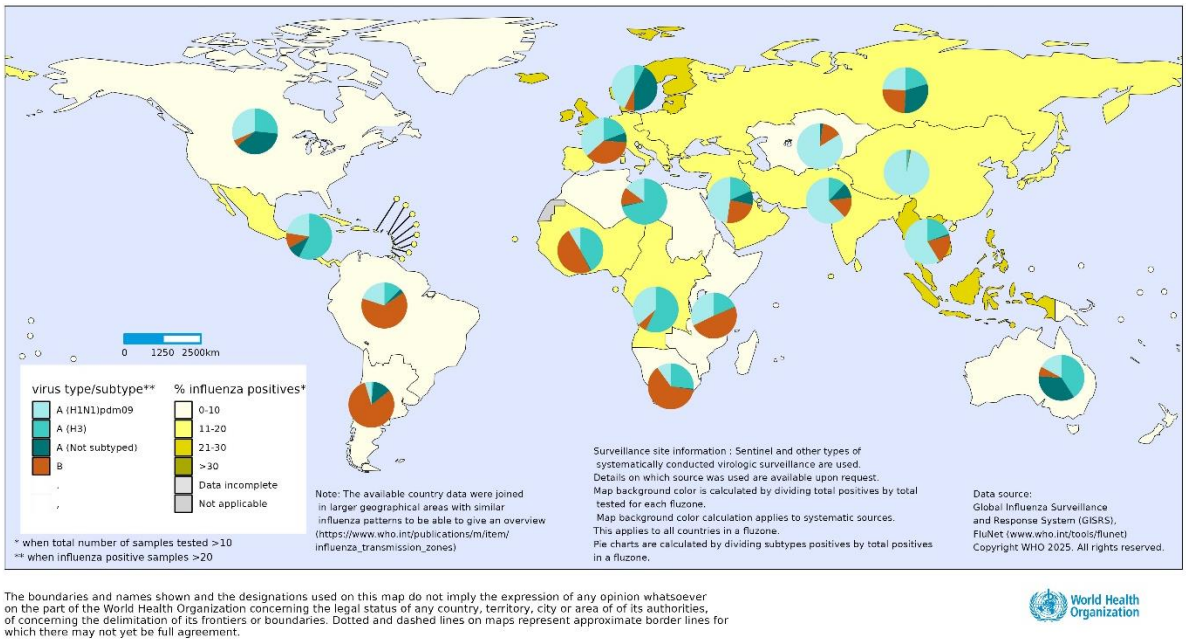
Influenza A

Globally, influenza A virus detections greatly outnumbered those of influenza B, although the predominating subtype varied across transmission zones. Among the subtyped A virus detections, A(H1N1)pdm09 viruses were detected more frequently throughout the reporting period in all transmission zones in Asia; in *Tropical* and *Temperate South America*; and in *Northern* and *South West Europe*. Influenza A(H3N2) viruses predominated in *Central America and the Caribbean; Oceania Melanesia and Polynesia*; and *Northern and Western Africa*. *Eastern Europe* and *North America* reported similar proportions of influenza A(H1N1)pdm09 and A(H3N2) viruses. Detections in *Eastern, Middle* and *Southern Africa* and *Central Asia* were low, with fluctuations in the predominant subtype.

Influenza B

Globally, influenza B virus detections were lower than those of influenza A, with predominance only in *Tropical* and *Temperate South America*, and *Eastern* and *Southern Africa*. Influenza B viruses were detected at roughly comparable levels to influenza A in *Western Africa*. All influenza B viruses where lineage was confirmed belonged to the B/Victoria lineage. There was one reported detection of a B/Yamagata virus in *South West Europe*, but this detection was not confirmed.

Distribution of Influenza virus type/subtype by influenza transmission zone, between 01 September 2024 and 31 January 2025



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 24 September 2024, sporadic zoonotic influenza infections were reported, in most cases, following exposure to infected birds, dairy cattle or swine. Single cases of A(H5N1) were reported from Canada, Cambodia, and the United Kingdom of Great Britain and Northern Ireland, and 49 cases were reported from the United States of America (USA). Seven cases of A(H5) were reported from the USA and one from Viet Nam. Sixteen cases of A(H9N2) and one case of A(H10N3) were reported from China. One A(H1N1)v case was reported from China and one A(H1N2)v case was reported from the USA.

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

Influenza A(H1N1)pdm09 viruses

Since September 2024, A(H1N1)pdm09 viruses circulated globally and predominated in Brazil, East Asia, Europe, India, Madagascar, Middle East, and South Africa. The haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades. Viruses from both clades continued to co-circulate in varying proportions across regions: 5a.2a viruses were predominant in Africa, Asia, the Caribbean, Europe, and Oceania, while 5a.2a.1 viruses were predominant in South America. In North America, both clades co-circulated. Clade 5a.2a HA genes have further diversified into designated subclades C.1, C.1.8, C.1.9, C.1.9.1, C.1.9.2, C.1.9.3, C.1.9.4, while clade 5a.2a.1 HA genes diversified into D, D.1, D.2, D.3, D.4, D.5[5]. Viruses from subclade C.1.9 and C.1.9.3 were predominant in many countries whereas viruses from subclades D and D.5 were predominant in South America. In North America, C.1.9.3, D.3 and D.5 viruses co-circulated with the proportion of D.3 viruses increasing. 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 2024 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.

Human serology studies used sixteen serum panels from children (6 months to 18 years), adults (18 to 64 years) and older adults (≥65 years) who had received egg-propagated inactivated (standard dose or high dose), cell culture-propagated inactivated or recombinant haemagglutinin (HA) trivalent or quadrivalent vaccines with NH 2024-2025 influenza vaccine formulations or egg-propagated or cell culture-propagated quadrivalent inactivated vaccines with SH 2024 influenza vaccine formulations. Egg-based vaccines contained A/Victoria/4897/2022 (H1N1)pdm09-like, A/Thailand/8/2022 (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 HA vaccines contained A/Wisconsin/67/2022 (H1N1)pdm09-like, A/Massachusetts/18/2022 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and, in quadrivalent vaccines, B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens.

Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a (subclades C.1, C.1.8, C.1.9, C.1.9.1, C.1.9.2, C.1.9.3, C.1.9.4) and 5a.2a.1 (subclades D and D.5) 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 not significantly reduced for most recently circulating viruses.

Of 2 492 A(H1N1)pdm09 virus clinical samples and isolates examined by genetic and/or phenotypic analyses, 61 viruses showed evidence of reduced susceptibility to neuraminidase inhibitors (NAIs): 56 had an H275Y NA substitution (42 of which were detected in China), two had a mixture of H275Y/H, two had an I223K, and one had I223V and S247N. Of 1 754 A(H1N1)pdm09 viruses examined by genetic and/or

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

phenotypic analyses, four viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil: one virus had an E23G PA substitution, one had a mixture of E23K/E, one had an E199G, and one had a mixture of E199K/E.

Influenza A(H3N2) viruses

Phylogenetic analysis of the HA gene sequences of A(H3N2) viruses collected since September 2024 showed that the vast majority of viruses belonged to clade 2a.3a.1, with only small numbers of 2a.3a viruses detected in Africa, Europe and North America. Further diversification within clade 2a.3a.1 HA genes into subclades (J.1-J.4)[6] has occurred with viruses expressing HA N122D and K276E substitutions (J.2) predominating globally. Viruses with I25V and V347M HA substitutions (J.1) co-circulated at very low levels globally. Viruses expressing 2a.3a.1 (J.4) were detected at low levels in Africa and viruses expressing 2a.3a.1 (J.3) were detected at very low levels in Asia. While the majority of viruses collected since September belong to subclade J.2, viruses with HA substitution P239S (J.2.1) circulated at low levels globally, while viruses with HA substitution S124N (J.2.2) predominated in Oceania and circulated globally at low levels. Further diversity in the HA of J.2 viruses was observed globally in separate emerging clades characterized by substitutions such as S145N, T135K (with potential loss of N-glycosylation), N158K, K189R or V223I.

Post-infection ferret antisera raised against cell culture-propagated A/Massachusetts/18/2022-like viruses and egg-propagated A/Thailand/8/2022-like viruses (clade 2a.3a.1), representing the vaccine viruses for the NH 2024-2025 influenza seasons, showed reduced reactivity against many recent viruses, with greater reductions observed for viruses with either N158K or K189R HA substitutions or both. Ferret antisera raised against J.2 subclade viruses with the S145N substitutions (e.g., cell-propagated A/District of Columbia/27/2023 and egg-propagated A/Croatia/10136RV/2023 reference viruses) representing the vaccine viruses for the SH 2025 influenza season recognized the majority of circulating viruses well.

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 2a.3a.1 subclades J.1.1, J.2, J.2.1, J.2.2 and J.4. When compared to titres against cell-propagated A/Massachusetts/18/2022-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against the majority of the recent viruses were significantly reduced.

Of 1 844 influenza A(H3N2) viruses examined by genetic and/or phenotypic analyses, no virus showed evidence of reduced susceptibility to NAIs. Of 1 846 A(H3N2) viruses examined by genetic and/or phenotypic analyses, three viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil. Of these, each had an I38T, I38T/I, I38T/M/I substitution respectively.

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

Influenza B viruses

Since September 2024, 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 period belonged to clade 3a.2 with HA substitutions A127T, P144L and K203R. Viruses with clade 3a.2 HA genes have diversified further, with the vast majority sharing the substitution D197E, along with further amino acid substitutions, forming several subclades, the most predominant being designated as C.5.1, C.5.6 and C.5.7[7]. Other subclades were detected at low frequencies.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2), representing the vaccine viruses for the NH 2024-2025 and SH 2025 influenza seasons, recognized the vast majority of viruses including those with additional HA substitutions within the C.5.1, C.5.6 and C.5.7 subclades well.

In human serology studies using the serum panels described above, post-vaccination HI GMTs against recent B/Victoria lineage viruses across the genetic diversity of clade 3a.2 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses. Serology studies were not performed for B/Yamagata lineage viruses, except for a USA population immunity study performed by CDC which showed good levels of seropositivity against B/Phuket/3073/2013, which is the vaccine virus in current quadrivalent vaccines.

Of 671 influenza B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced or highly reduced susceptibility to NAIs. Of 673 B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil.

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

Recommended composition of influenza virus vaccines for use in the 2025-2026 northern hemisphere influenza season

Since September 2024, A(H1N1)pdm09 viruses circulated globally and predominated in many regions. The HA genes of viruses that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades and have further diversified. Post-infection ferret antisera raised against the SH 2024, the NH 2024-2025 and the SH 2025 A(H1N1)pdm09 vaccine viruses (cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022) from the 5a.2a.1 clade recognized 5a.2a and 5a.2a.1 viruses well. In human serology studies, post-vaccination GMTs were not significantly reduced for recently circulating A(H1N1)pdm09 viruses when compared to the responses to cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like vaccine reference viruses.

Since September 2024, A(H3N2) viruses circulated globally and predominated in several regions. The majority of A(H3N2) viruses collected had HA genes derived from 2a.3a.1 subclade J.2 and have continued to diversify. Post-infection ferret antisera raised against recent J.2 viruses (including those with HA S145N substitution represented by A/District of Columbia/27/2023 and A/Croatia/10136RV/2023) showed improved recognition of recently circulating viruses compared to NH 2024-25 A(H3N2) vaccine viruses (cell culture-propagated A/Massachusetts/18/2022 and egg-propagated A/Thailand/8/2022). Human serology assays showed that post-vaccination GMTs against A(H3N2) viruses with HA genes representing J.2 subclades were significantly reduced in most serum panels compared to titres against cell culture-propagated A/Massachusetts/18/2022-like vaccine reference viruses.

Since September 2024, influenza B viruses circulated at lower levels than influenza A viruses globally, predominating in only a few regions. All circulating influenza B viruses characterized were from the B/Victoria lineage. All recent viruses expressed HA genes belonging to clade 3a.2. Circulating viruses were recognized well by post-infection ferret antisera raised against SH 2024, NH 2024-2025 and SH 2025 B/Victoria lineage vaccine viruses (cell culture- and egg-propagated B/Austria/1359417/2021). Human serology assays showed that post-vaccination GMTs against nearly all representative B/Victoria lineage viruses expressing 3a.2 HA genes were not significantly reduced compared to titres against cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses.

WHO convenes technical consultations[8] each year to recommend viruses for inclusion in influenza vaccines[9]. National or regional authorities are responsible for approving the composition and formulation of vaccines used in each country and should consider the use and relative benefit(s) of trivalent or quadrivalent influenza vaccines.

[8] https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses
[9] Description of the process of influenza vaccine virus selection and development available at: http://www.who.int/gb/pip/pdf_files/Fluvaccvirusselection.pdf

For trivalent vaccines for use in the 2025-2026 northern hemisphere influenza season, the WHO recommends the following:

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.**

Cell culture-, recombinant protein- or nucleic acid-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.**

The recommendation for the B/Yamagata lineage component of quadrivalent influenza vaccines remains unchanged from previous recommendations:

- **a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.**

The continued absence of confirmed detection of naturally occurring B/Yamagata lineage viruses after March 2020 is indicative of a very low risk of infection by B/Yamagata lineage viruses. Consistent with previous recommendations, it remains 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.

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 website[10]. 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, 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, USA (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:

[10] https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses

• 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, 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: influenzavirussurveillance@cdc.gov, website: http://www.cdc.gov/flu/).
• WHO Collaborating Centre for Reference and Research on Influenza, The Francis Crick Institute, 1 Midland Road, London NW1 1AT, 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 updates[11] of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website[12].

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 WOAH/FAO Network of Expertise on Animal Influenza (OFFLU), who contributed information, clinical specimens, viruses and associated data; WHO Collaborating Centres of GISRS, the U.S. Centers for Disease Control and Prevention, and the U.S. Food and Drug Administration/Center for Biologics Evaluation and Research 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.

[11] Current respiratory virus update: https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-updates
[12] 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 2025-2026 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
TGA, Canberra	Dr Pearl Bamford	None
MHRA, London	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: IFPMA, Innovative Medicines Initiative and PATH.
NIID, Tokyo	Dr Hideki Hasegawa	None
CDC, Atlanta	Dr Rebecca Kondor	The item declared and listed below belongs to Dr Kondor's Research Unit: • Received significant financial support for research activities CRADA from Seqirus for development of cell-based manufacturing technologies for influenza vaccines.
The Francis Crick Institute, London	Dr Nicola Lewis	Following items were declared: • Invited speaker and panel member on event organized by Seqirus. No renumeration received. The items declared and listed below belong to Dr Lewis's Research Unit: • 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.
VECTOR, Novosibirsk	Dr Vasily Marchenko	None

VIDRL, Melbourne	Dr Patrick Reading	The items declared and listed below belong to Dr Reading's Research Unit: • 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.
IVDC, Beijing	Dr Dayan Wang	None
St. Jude Children's Research Hospital, Memphis	Dr Richard Webby	Following items were declared: • Invited speaker and participant at events organized by Seqirus, Sanofi and Roche. No renumeration received.
CBER, Silver Spring	Dr Zhiping Ye	None

Based on the WHO assessment, the interests declared by Drs Engelhardt, Kondor, Lewis, Reading and Webby 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, Reading and Webby should continue to serve as Advisers.