Recommended composition of influenza virus vaccines for use in the 2025 southern hemisphere influenza season

September 2024

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 SH 2025 influenza season. A recommendation will be made in February 2025 relating to vaccines that will be used for the NH 2025-26 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 February through August 2024, influenza activity was reported in all *transmission zones*. Overall, detections were higher compared to the same reporting period in 2023, largely due to higher detections in the Americas. The predominant viruses varied among zones and between countries.

In Africa, influenza activity varied by transmission zone. In *Northern Africa*, influenza activity decreased and remained low during the current reporting period, with similar proportions of influenza A and B viruses and more A(H3N2) detections among influenza A subtyped virus specimens. In *Eastern Africa*, influenza A(H3N2) viruses were detected throughout the reporting period; however, when influenza detections were highest in June to August, A(H1N1)pdm09 viruses initially predominated, while A(H3N2) and B/Victoria virus detections increased towards the end of the reporting period. In *Middle Africa*, while overall influenza detections remained low, activity increased in May and peaked in July; B/Victoria detections were predominant earlier in the reporting period, followed by a predominance of both A(H1N1)pdm09 and A(H3N2) viruses during the period of increased activity, and then by A(H3N2) viruses at the end of the reporting period. In *Southern Africa*, influenza activity increased and peaked in May with a predominance of influenza A(H1N1)pdm09 detections; B/Victoria lineage viruses were detected throughout the reporting period and predominated in August. In *Western Africa*, influenza activity peaked in July with a predominance of A(H3N2) viruses along with continued detections of B/Victoria lineage viruses 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 virus detections decreased during the reporting period. Though influenza B/Victoria lineage viruses predominated during the first few months, A(H1N1)pdm09 viruses predominated through the remainder of the reporting period. These trends were seen in *Eastern Asia*, which accounted for most of the detections reported in Asia. In *South East Asia*, influenza detections remained relatively low throughout the reporting period with some increased activity in July; influenza A virus detections predominated with roughly equal proportions of A(H1N1)pdm09 and A(H3N2), though influenza B viruses were also detected throughout the reporting period. In *Southern Asia*, activity decreased and continued to remain low; while influenza B virus detections predominated earlier in the reporting period, influenza A viruses predominated since May with A(H1N1)pdm09 viruses accounting for the majority of detections in the later months. In *Central Asia*, detections were low with mostly A(H3N2) viruses, and no influenza virus detections were reported since May. In *Western Asia*, influenza activity decreased early in the reporting period and remained stable from May to August with a predominance of influenza A viruses, though influenza B viruses were detected throughout the reporting period; of the subtyped influenza A virus specimens, A(H3N2) detections were slightly higher early in the reporting period and A(H1N1)pdm09 predominated since mid-March.

In Europe, influenza activity decreased and remained low during the reporting period; influenza A viruses predominated, with co-circulation of A(H1N1)pdm09 and A(H3N2) viruses. In *Northern Europe* and *Eastern Europe*, similar proportions of influenza A(H1N1)pdm09 and A(H3N2) viruses were detected, while in *South West Europe*, influenza A(H1N1)pdm09 viruses predominated. Influenza B viruses were detected at low levels throughout the reporting period in all three transmission zones.

In the Americas, influenza activity varied by transmission zone. In *North America*, activity decreased and remained low during the reporting period with roughly equal detections of influenza A and B viruses; there were similar proportions of A(H1N1)pdm09 and A(H3N2) viruses among subtyped influenza A virus specimens. In *Central America and the Caribbean*, influenza activity was elevated throughout most of the reporting period with an increase in May and June and a decrease in July and August; most detections were A(H3N2) viruses, though A(H1N1)pdm09 and B/Victoria lineage viruses were also detected. In *Tropical South America*, influenza activity increased at the start of the reporting period and peaked in March; influenza A viruses predominated with more A(H3N2) viruses detected, though a steady increase of influenza B detections occurred from late May through August as influenza A detections decreased. In *Temperate South America*, influenza activity peaked in June; influenza A viruses were predominant with more A(H3N2) detections among subtyped virus specimens, though influenza B detections increased at the end of the reporting period.

In Oceania, influenza detections increased in May, peaked in early July, and then decreased. Influenza A viruses were predominant with both A(H3N2) and A(H1N1)pdm09 viruses co-circulating. Low levels of influenza B viruses were detected throughout the reporting period.

Influenza A

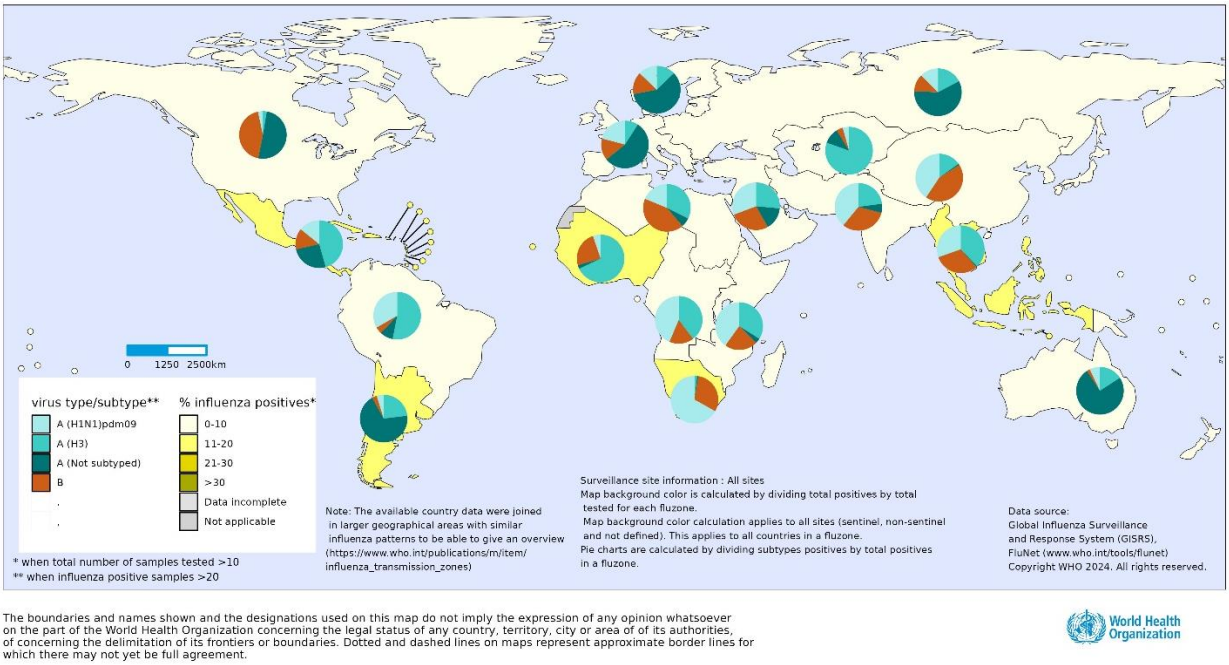
Globally, influenza A virus detections outnumbered those of influenza B. Influenza A(H1N1)pdm09 and A(H3N2) viruses were reported in all transmission zones, although the predominant subtype varied. A(H1N1)pdm09 viruses predominated in *Southern Africa* and *Eastern* and *Southern Asia*. Influenza A(H3N2) viruses predominated in the Americas (apart from *North America*), *Northern* and *Western Africa*, and *Oceania Melanesia and Polynesia*. A(H1N1)pdm09 and A(H3N2) viruses were detected at comparable levels over the reporting period in *Eastern* and *Middle Africa*, *South East* and *Western Asia*,

and *North America*. Europe reported similar proportions of influenza A(H1N1)pdm09 and A(H3N2) viruses with some variation among transmission zones.

Influenza B

Globally, influenza B virus detections were lower than those of influenza A; influenza B viruses did not predominate in the majority of transmission zones throughout the reporting period. However, influenza B viruses co-circulated at similar proportions to influenza A in some transmission zones. All influenza B viruses, where lineage was confirmed, belonged to the B/Victoria lineage. No naturally-occurring B/Yamagata lineage viruses were detected.

Distribution of Influenza virus type/subtype by influenza transmission zone, between 01 February 2024 and 31 August 2024



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.](https://www.who.int/tools/flunet)

Zoonotic influenza

From 20 February 2024, sporadic zoonotic influenza infections were reported, in most cases, following exposure to infected birds, dairy cattle or swine. One imported case of A(H5N1) was reported in Australia; six cases of A(H5N1) were reported in Cambodia; one case of A(H10N3), three cases of A(H5N6), one imported case of A(H5N1) and seven cases of A(H9N2) were reported in China; single cases of A(H9N2) were reported in Ghana and India; nine cases of A(H5N1) and five cases of A(H5) were reported in the United States of America (USA) and single cases of A(H5N1) and A(H9N2) were reported in Viet Nam. A single case of A(H3N2)v was reported in Canada; four cases of A(H3N2)v and four cases of A(H1N2)v were reported in the USA and single cases of A(H1N1)v were reported in the USA and Viet Nam.

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

Influenza A(H1N1)pdm09 viruses

Since February 2024, A(H1N1)pdm09 viruses circulated globally and predominated in Europe, Middle East, South Africa, Brazil, India, and Madagascar. The haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades. Clade 5a.2a HA genes have further diversified into designated subclades C.1, C.1.7, C.1.7.2, C.1.8, C.1.9 and the 5a.2a.1 clade into C.1.1, D, D.1, D.2, D.3, D.4[5]. Viruses from both clades continued to circulate with the C.1.9 subclade predominating in most regions, except in North America and some countries in Central and South America where the D subclades predominated.

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 February 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 five serum panels from adults (18 to 64 years) and older adults (≥65 years) who had received egg-based quadrivalent inactivated (standard or adjuvanted) 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 B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens. Cell culture-propagated vaccines contained A/Wisconsin/67/2022 (H1N1)pdm09-like, A/Massachusetts/18/2022 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens.

Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a and 5a.2a.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 not significantly reduced for most recently circulating viruses.

Of 3 300 A(H1N1)pdm09 virus clinical samples and isolates examined by genetic and/or phenotypic analyses, 63 viruses showed evidence of reduced susceptibility to neuraminidase inhibitors (NAIs). Forty-one had NA substitution H275Y, three had H275Y and S247N, 17 had I223V and S247N, one had S247N, and one had Q136K. Of 2 612 A(H1N1)pdm09 viruses examined by genetic and/or phenotypic analyses, two viruses showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil; one virus had an I38V PA substitution and one had an I38N PA substitution.

[5] Real-time tracking of influenza A/H1N1pdm 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 February 2024 showed that the vast majority of viruses belonged to clade 2a.3a.1, with only small numbers of 2a.3a viruses detected. 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 lower levels in many countries except in a few countries in Asia and Africa where it predominated. Some countries in west Africa also had circulation of viruses in HA subclades 2a.3a (G.1.3.1) and 2a.3a.1 (J.4).

Generally, 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 SH 2024 and NH 2024-25 influenza seasons, recognized many recent clade 2a.3a.1 viruses well, but reduced reactivity was seen for some viruses within the J.2 subclade with either S145N, N158K or K189R HA substitutions or combinations of these substitutions. J.2 viruses with S145N were more frequently detected while those with N158K or K189R were rarely detected. Reduced reactivity was also seen with viruses in the J.4 subclade with K189R substitutions. 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) recognized most circulating viruses well (Table 1).

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

	HA Clade (Subclade)	HA Substitutions	SIAT A/Massachusetts /18/2022 2a.3a.1 (J)	Egg A/Thailand /08/2022 2a.3a.1 (J)	SIAT A/Sydney /856/2023 2a.3a.1 (J.1)	SIAT A/Croatia/ 10136RV/2023 2a.3a.1 (J.2)	Egg A/Croatia/ 10136RV/2023 2a.3a.1 (J.2)	SIAT A/Slovenia /49/2024 2a.3a.1 (J.2)
REFERENCE VIRUSES								
A/Massachusetts/18/2022	2a.3a.1 (J)		**640**	1280	1280	160	320	160
A/Thailand/08/2022	2a.3a.1 (J)		320	**1280**	640	320	640	320
A/Sydney/856/2023	2a.3a.1 (J.1)		320	640	**640**	80	160	80
A/Croatia/10136RV/2023	2a.3a.1 (J.2)	S145N	40	160	160	**160**	160	160
A/Croatia/10136RV/2023	2a.3a.1 (J.2)	S145N	320	640	640	640	**640**	640
A/Slovenia/49/2024	2a.3a.1 (J.2)	N158K	<40	160	<40	80	40	**1280**
TEST VIRUSES								
A/Saudi Arabia/6095/2024	2a.3a (G.1.3.1)		40	80	40	80	80	80
A/Iasi/567841/2024	2a.3a.1 (J.1)		320	640	640	160	320	80
A/Belgium/4741/2024	2a.3a.1 (J.2)		160	320	160	160	160	160
A/Prahova/566118/2024	2a.3a.1 (J.2)		160	320	160	160	160	160
A/Spain/2603/2024	2a.3a.1 (J.2)		160	320	160	160	320	160
A/Cameroon/5947/2024	2a.3a.1 (J.2)		80	160	160	160	160	80
A/Denmark/2186/2024	2a.3a.1 (J.2)		80	160	160	160	160	160
A/Papeete/OMS24.3.54/2024	2a.3a.1 (J.2)		80	160	160	160	160	160
A/Saudi Arabia/12903/2024	2a.3a.1 (J.2)		80	160	160	160	160	160
A/Tarbes/NOMS24.4.9/2024	2a.3a.1 (J.2)		80	160	160	160	160	160
A/Denmark/2208/2024	2a.3a.1 (J.2)	S145N	80	160	160	160	320	160
A/Spain/2562/2024	2a.3a.1 (J.2)	S145N	80	160	160	160	320	160
A/Cameroon/7167/2024	2a.3a.1 (J.2)	S145N	40	80	80	80	160	80
A/Spain/2381/2024	2a.3a.1 (J.2)	S145N	40	80	80	80	160	80
A/Cameroon/6580/2024	2a.3a.1 (J.2)	S145N	<40	40	40	80	80	80
A/Switzerland/47775/2024	2a.3a.1 (J.2)	K189R	<40	40	<40	80	40	<40
A/Switzerland/59652/2024	2a.3a.1 (J.2)	K189R	<40	40	<40	40	80	<40
A/Cameroon/3172/2024	2a.3a.1 (J.4)		80	160	80	80	80	80

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

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, J.1, J.2 and J.4) and 2a.3a (G.1.3.1). When compared to titres against cell-propagated A/Massachusetts/18/2022-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against many recent J.1 and J.2 viruses were significantly reduced in most serum panels.

Of 3 480 influenza A(H3N2) viruses examined by genetic and/or phenotypic analyses, only one virus showed evidence of reduced susceptibility to NAIs and had an amino acid deletion at position 245 in NA. Of 3 269 A(H3N2) viruses examined by genetic and/or phenotypic analyses, 11 showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil. Of these, 10 viruses had an A37I PA substitution and one had an I38T/I PA substitution.

Influenza B viruses

Since February 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].

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 2024 and NH 2024-25 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.

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 the B/Yamagata lineage virus, 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 2 153 influenza B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, six showed evidence of reduced or highly reduced susceptibility to NAIs. Two viruses had NA substitution D197N, two had A245G, one had H273Y and one had I348T. Of 1 685 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/Vic evolution: https://nextstrain.org/seasonal-flu/vic/ha/2y?c=subclade

Recommended composition of influenza virus vaccines for use in the 2025 southern hemisphere influenza season

Since February 2024, A(H1N1)pdm09 viruses circulated globally and predominated in several 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 and NH 2024-25 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. 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.

The majority of A(H3N2) viruses collected since February 2024 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 SH 2024 and 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.1 and 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.

All circulating influenza B viruses characterized since February 2024 were of 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 and NH 2024-25 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 southern 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).

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

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, 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japan (email: whocc-flu@nih.go.jp).
• WHO Collaborating Centre for Surveillance, Epidemiology and Control of Influenza, 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 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 Southern Hemisphere 2025 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 CC Melbourne	Dr Ian Barr	Following items were declared: • Shareholdings (significant) in the company CSL The items declared and listed below belong to Dr Barr's Research Unit: • Received significant financial support for research activities (Collaborative research and development agreement (CRADA)) from Seqirus for development of cell-based manufacturing technologies for influenza vaccines. • 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, GSK and Biocrvst 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 ERL NIBSC 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: 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: • 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: • Invited speaker and panel member to an 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.
WHO CC Koltsovo	Dr Vasily Marchenko	None
WHO CC Beijing	Dr Dayan Wang	None
WHO CC Memphis	Dr Richard Webby	Following items were declared: • Invited speaker and participant at events organized by Seqirus, Sanofi and Roche. No renumeration received.
WHO ERL CBER Silver Spring	Dr Zhiping Ye	None

Based on the WHO assessment of the interest declared by Dr Barr, it was concluded that Dr Barr should continue to serve as an Adviser, considering that the interest was disclosed at the beginning of the consultation, and that, in accordance with the conditions required of all WHO CC Melbourne staff, Dr Barr has agreed to refrain from acquiring additional shares in influenza vaccine manufactures.

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