World Health Organization

Recommended composition of influenza virus vaccines for use in the 2024 southern hemisphere influenza season

September 2023

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 2024 influenza season. A recommendation will be made in February 2024 relating to vaccines that will be used for the NH 2024-2025 influenza season. For countries in tropical and subtropical regions, WHO recommendations for influenza vaccine composition (NH or SH) are 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 2023, influenza activity was reported in all zones and the number of detections was comparable to the same reporting period in 2022. However, the predominant virus varied among transmission zones[5] and between countries.

In Africa, influenza A and B viruses co-circulated, with predominance of influenza A and roughly equal circulation of influenza A(H1N1)pdm09 and A(H3N2) across the continent. In Northern Africa, influenza had declined by the start of the current reporting period and remained low, with mainly influenza B detections that peaked in April. In Eastern Africa, influenza A was predominant with both subtypes co-circulating; influenza A activity declined during the reporting period, while the detection of influenza B increased in recent months. In Middle Africa, while overall detections remained low, activity increased during the reporting period; most detections were influenza A with co-circulation of both subtypes. In Southern Africa, influenza activity rose towards the end of April with an A(H3N2) epidemic peak at the end of May and very few detections of influenza B or A(H1N1)pdm09. In Western Africa, there was a peak of A(H1N1)pdm09 activity at the end of February, which had declined by June. This was followed by a gradual resurgence of influenza activity that was initially predominated by A(H1N1)pdm09 viruses with a subsequent increase in A(H3N2) detections towards the end of the reporting period.

In Asia, influenza virus detections peaked in March and declined to low levels by May. Most detections were reported from Eastern Asia, where activity peaked in March with co-circulation of both subtypes and a predominance of A(H1N1)pdm09. In South-East Asia, influenza B activity

[1] https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses
[2] Description of the process of influenza vaccine virus selection and development available at: http://www.who.int/gb/pip/pdf_files/Fluvaccvirusselection.pdf
[3] Influenza in the tropics and sub-tropics: 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
[5] Information in this report is categorized by influenza transmission zones, which are geographical groups of countries, areas or territories with similar influenza transmission patterns. For more information on influenza transmission zones, see: https://www.who.int/publications/m/item/influenza_transmission_zones

steadily declined during this reporting period. Meanwhile, influenza A activity steadily increased during the reporting period, with co-circulation of both subtypes and a predominance of A(H1N1)pdm09. In Southern Asia, both influenza A subtypes and influenza B viruses co-circulated and no clear peaks were identified. In Central Asia, there was minimal activity reported after February. In Western Asia, influenza activity declined during the reporting period with higher detections of influenza A involving both subtypes. Towards the end of the reporting period, there was an increase in A(H3N2) activity.

In Europe, influenza B predominated with co-circulation of A(H1N1)pdm09 and some detections of A(H3N2) viruses. In Eastern, Northern and South-West Europe, influenza B activity peaked in February and declined by June. Influenza A activity declined between February and May and remained low throughout the rest of this reporting period.

In the Americas, influenza activity varied by transmission zone. In North America, there was a decline in influenza A activity from February to March and thereafter activity remained at inter-seasonal levels with a predominance of A(H1N1)pdm09 viruses. Influenza B activity increased during the reporting period, peaked in April and declined by July. In Central America and the Caribbean, influenza activity peaked in June with a predominance of A(H1N1)pdm09 and co-circulation of influenza B viruses. In Tropical South America, an influenza B epidemic occurred with a peak in March followed by a steady decline to the end of this reporting period. During April and May, there was a rise in influenza A activity with a predominance of A(H1N1)pdm09 and minimal detections of A(H3N2) viruses. In Temperate South America, influenza virus detections peaked in May with predominance of A(H1N1)pdm09 and little influenza B or A(H3N2) activity.

In Oceania, influenza detections peaked in June with influenza A and B viruses co-circulating. A predominance of A(H1N1)pdm09 was observed.

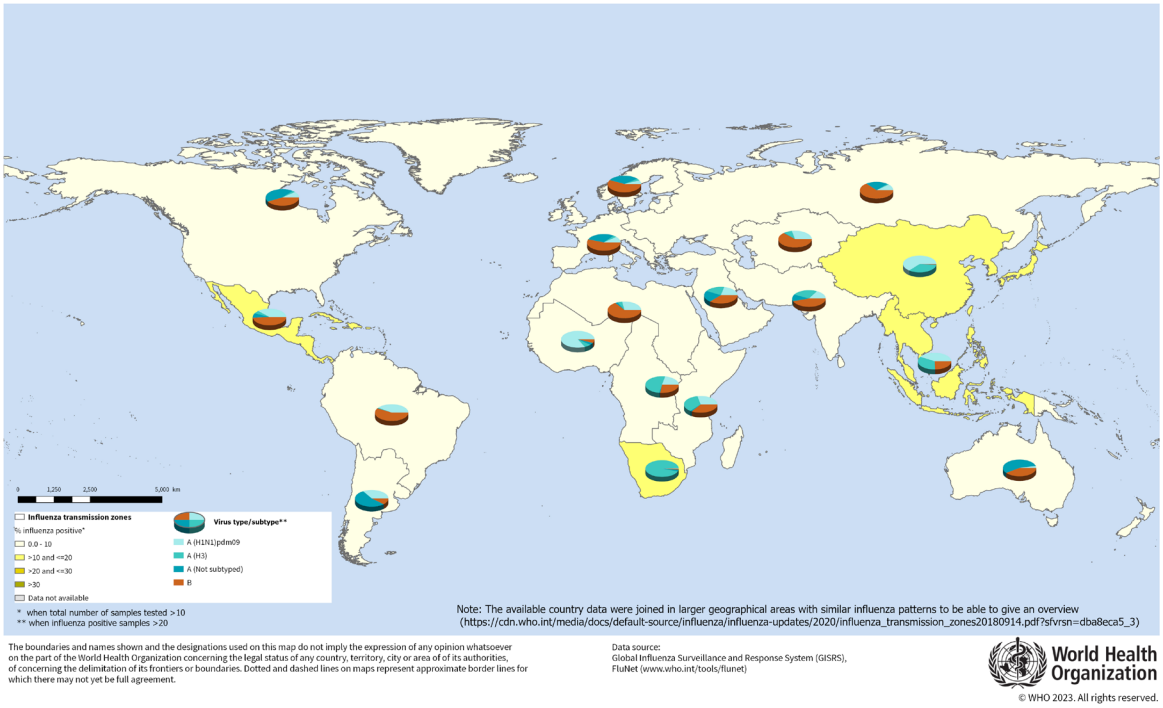
Influenza A

Globally, influenza A virus detections outnumbered influenza B virus detections. Influenza A(H1N1)pdm09 and A(H3N2) viruses were reported in most transmission zones and A(H1N1)pdm09 was more frequently detected in all continents. However, in Eastern, Middle and Southern Africa, and Southern and Western Asia more A(H3N2) viruses were detected.

Influenza B

Globally, influenza B virus detections were lower than those for influenza A. However, in some regions, influenza B predominated, including Europe, Northern Africa and Tropical South America. All circulating influenza B viruses, where lineage was confirmed by GISRS laboratories, belonged to the B/Victoria/2/87 lineage.

Distribution of influenza virus type/subtype by influenza transmission zone, between February 2023 and August 2023



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

During the period from 21 February to 22 September 2023, sporadic cases were reported following exposure to infected birds and swine in most cases. Four cases of A(H5N6), one case of A(H3N8) and five cases of A(H9N2) were reported in China, two cases of A(H5N1) were reported in Cambodia, one case of A(H5N1) was reported in Chile and four A(H5N1) detections were reported in the United Kingdom of Great Britain and Northern Ireland.
Single cases of A(H1N1)v were reported in Brazil and the Kingdom of the Netherlands in this period. Three cases of A(H1N2)v were reported in Taiwan, China (n=1) and the United States of America (n=2). One case of A(H3)v was reported in the United States of America.

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

Influenza A(H1N1)pdm09 viruses

Since 1 February 2023, A(H1N1)pdm09 viruses circulated globally and predominated in most geographic regions. The vast majority of haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 6B.1A.5a.2 clade, with only 1% of HA genes characterized belonging to the 6B.1A.5a.1 clade.

All viruses expressing clade 5a.2 HA genes collected since 1 February 2023 have further diversified into designated subclades: the 5a.2a, with additional HA1 amino acid substitutions K54Q, A186T,

Q189E, E224A, R259K and K308R; and the 5a.2a.1 subclade containing viruses expressing HA genes with additional HA1 substitutions P137S, K142R, D260E and T277A (e.g., A/Wisconsin/67/2022). Many of the 5a.2a.1 viruses also have the HA1 substitution T216A. Viruses within subclades 5a.2a and 5a.2a.1 co-circulated, with regional differences in proportions and continued genetic diversification within both subclades. Subclade 5a.2a viruses predominated in Asia, Africa, Europe and Oceania, while subclade 5a.2a.1 viruses predominated in North America and parts of Central and South 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 1 February 2023 showed that ferret antisera raised against the SH 2023 vaccine viruses (cell culture-propagated A/Sydney/5/2021-like and egg-propagated A/Sydney/5/2021-like 5a.2a viruses) recognized the very small number of 5a.1 test viruses poorly; however, viruses in subclades 5a.2a and 5a.2a.1 were well recognized by these antisera. Ferret antisera raised against cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022 from the 5a.2a.1 subclade recognized viruses in both 5a.2a and 5a.2a.1 subclades well.

Human serology studies used five serum panels from Australian children (1-10 years) and adults (18-64 years) who had received standard egg-based quadrivalent inactivated vaccines, elderly adults (aged 65+ years) who had received adjuvanted egg-based vaccines, and adults (18-64 years) who had received cell culture-based quadrivalent inactivated vaccines. All vaccines were SH 2023 formulations containing antigens from A/Sydney/5/2021 (H1N1)pdm09-like, A/Darwin/6/2021 (H3N2)-like (cell-based) or A/Darwin/9/2021 (H3N2)-like (egg-based), B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) viruses.

Using these serum panels, antibody reactivities induced by the 5a.2a A/Sydney/5/2021 (H1N1)pdm09-like vaccine against recent A(H1N1)pdm09 viruses were determined using HI assays. Compared to the responses of the cell culture-propagated and/or- egg-propagated A(H1N1)pdm09 vaccine viruses, post-vaccination geometric mean titres (GMTs) were not significantly reduced for the majority of 5a.2a viruses. However, post vaccination GMTs were significantly reduced in some serum panels against recent A(H1N1)pdm09 viruses belonging to subclade 5a.2a.1. The reductions were more pronounced when compared to egg-propagated A/Sydney/5/2021 reference virus.

Of 5012 A(H1N1)pdm09 viruses collected since 1 February 2023 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analyses of clinical samples and isolates; 13 had an H275Y substitution, one had a mixture of H275H/Y, one had substitutions H275Y and D199G, one had an E119A substitution, one had a Q136K substitution, and one had an S247G substitution in the NA. Phenotypic analysis of the 13 virus isolates with H275Y showed highly reduced inhibition by oseltamivir and normal inhibition by zanamivir. Additional phenotypic analysis of four showed highly reduced inhibition by peramivir and normal inhibition by laninamivir. The virus isolate with a mixture of H275H/Y showed reduced inhibition by oseltamivir and peramivir and normal inhibition by zanamivir and laninamivir. The virus isolate with E119A in the NA showed reduced inhibition by zanamivir and normal inhibition by oseltamivir. The virus isolate with Q136K in the NA showed highly reduced inhibition by zanamivir and normal inhibition by oseltamivir. The virus isolate with S247G was not available for phenotypic testing. Of 1843 A(H1N1)pdm09 viruses examined by genetic and/or phenotypic analyses, two showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil. One virus isolate had an I38V substitution in the polymerase (PA) and another had PA substitutions K34R and E198K.

Influenza A(H3N2) viruses

While A(H3N2) viruses circulated globally since 1 February 2023, they were the predominant A virus in only a few geographic regions. Phylogenetic analysis of the HA gene of A(H3N2) viruses showed that the vast majority of viruses circulating in this period belonged to clade 2 (complete classification 3C.2a1b.2a.**2**). Owing to substantial evolution and co-circulation of multiple clade 2 HA groups,

subclade designations[6] were developed to better define and track the HA evolution. The various HA subclades were found in different regions globally and viruses with HA genes from multiple subclades co-circulated in several geographic regions in varying proportions.

Among viruses with clade 2 HA genes which co-circulated during this period, three subclades predominated: 2a.1b (typically encoding D53G, D104G, I140K, K276R, R299K), 2a.3a.1 (typically encoding E50K, G53N, N96S (CHO+), I140K, I192F, I223V, N378S), and 2b (typically encoding E50K, F79V, I140K). Of these, subclade 2a.3a.1 (e.g., A/Massachusetts/18/2022) predominated globally. 2a.1b viruses were detected mainly in North America and Europe, 2a.3a.1 viruses were detected mainly in Africa, Asia, North America and Oceania, and 2b viruses circulated globally.

Generally, post-infection ferret antisera raised against the SH 2023 vaccine viruses (cell culture-propagated A/Darwin/6/2021-like viruses and egg-propagated A/Darwin/9/2021-like 2a viruses) recognized viruses expressing 2a (including subclades) HA genes well. However, some viruses expressing 2a.3a.1 or 2b HA genes reacted less well with these antisera. Additionally, ferret antisera raised against recent 2b viruses did not recognize some viruses in 2a subclades well. Ferret antisera raised against 2a.3a.1-like viruses (e.g., cell-propagated A/Massachusetts/18/2022 and egg-propagated A/Thailand/8/2022) recognized most circulating viruses well (Table 1).

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

		Reference Antisera					
		1	2	3	4	5	6
		A9049 E5 Camb/e0826360	A9231 SIAT2 Dar/6	A9358 E4 Dar/9	A9671 SIAT2 Thai/8	F0221 E3/D1 Thai/8	A9674 SIAT1 Sth Aust/389
Reference viruses	Clade	1a	2a	2a	2a.3a.1	2a.3a.1	2b
A/Cambodia/e0826360/2020	1a	**640**	320	160	80	160	80
A/Darwin/6/2021	2a	80	**1280**	80	40	160	160
A/Darwin/9/2021	2a	160	640	**320**	80	320	320
A/Thailand/8/2022	2a.3a.1	80	640	160	**320**	640	80
A/Thailand/8/2022	2a.3a.1	160	1280	320	320	**1280**	640
A/South Australia/389/2022	2b	80	160	80	40	80	**320**
Test viruses							
A/Sydney/510/2023	2a.3a.1	80	640	80	320	1280	80
A/Sydney/513/2023	2a.3a.1	80	320	80	320	1280	80
A/Sydney/555/2023	2a.3a.1	80	320	160	160	640	80
A/Auckland/50/2023	2a.3a.1	40	320	80	160	1280	40
A/Singapore/GP1582/2023	2a.3a.1	80	640	80	160	640	80
A/Singapore/GP7270/2023	2a.3a.1	80	640	80	160	1280	80
A/South Australia/48/2023	2a.3a.1	40	320	80	160	640	40
A/Sydney/639/2023	2a.3a.1	40	320	40	160	1280	40
A/Sydney/710/2023	2a.3a.1	<40	320	40	160	640	40
A/Victoria/2107/2023	2a.3a.1	40	320	40	160	640	40
A/Philippines/52/2023	2a.3b	80	640	80	160	640	40
A/Brisbane/273/2023	2a.1b	40	640	80	<40	80	40

Human serology studies used 10 serum panels from children (6 months to 17 years), adults (18-64 years) and older adults (≥65 years) who had received egg-based trivalent or quadrivalent inactivated vaccines (standard or adjuvanted) or cell culture-based quadrivalent inactivated vaccines. Egg-based vaccines contained A/Sydney/5/2021 (H1N1)pdm09-like (SH 2023 formulation) or A/Victoria/2570/2019 (H1N1)pdm09-like (NH 2023-2024 formulation) plus A/Darwin/9/2021 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and, for quadrivalent vaccine, B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens. Cell culture-based vaccines contained A/Sydney/5/2021 (H1N1)pdm09-like, A/Darwin/6/2021 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens for the SH 2023 formulation.

When compared to titres against cell-propagated A/Darwin/6/2021-like vaccine reference viruses, post-vaccination HI and virus neutralization (VN) GMTs against some recent A(H3N2) viruses from the 2a.1b, 2a.3a.1 and 2b genetic subgroups were significantly reduced in some serum panels. The

[6] A labelled phylogeny can be visualized at https://nextstrain.org/flu/seasonal/h3n2/ha/2y

reductions were more pronounced when compared to egg-propagated A/Darwin/9/2021 reference virus.

Of 2 240 influenza A(H3N2) viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to NAIs. Of 1 092 A(H3N2) viruses examined by genetic and/or phenotypic analyses, 10 showed evidence of reduced susceptibility to endonuclease inhibitor baloxavir marboxil. Three virus isolates had an I38T substitution, one virus isolate had a mixture of I38M/T/I substitutions, one virus isolate had a mixture of I38T/I substitutions, three virus isolates had an E199G substitution, and one virus isolate had an E199K substitution in the PA protein. However, one virus isolate that showed reduced susceptibility to baloxavir marboxil did not have any substitutions in the PA that are known to confer reduced susceptibility.

Influenza B viruses

Globally, influenza B viruses represented approximately one-third of the viruses detected since 1 February 2023, and all of those characterized belonged to the B/Victoria/2/87 lineage. There have been no confirmed detections of circulating B/Yamagata/16/88 lineage viruses after March 2020.

The HA genes of B/Victoria lineage viruses characterized during this period belonged to clade 1A.3 which share the encoded amino acid substitutions G133R and K136E, and a triple amino acid deletion (positions 162-164) in HA1. A small number of viruses expressing 1A.3 HA genes with additional substitutions T73I and N233K (resulting in the loss of a glycosylation site) in HA1 were detected in North and Central America. The vast majority of clade 1A.3 HA genes encode further substitutions N150K, G184E, N197D (resulting in the loss of a glycosylation site) and R279K in HA1 and are designated as 1A.3a. The 1A.3a HA diversified into two main subclades, one with additional HA1 substitutions V220M and P241Q (designated as 3a.1) and the other with HA1 substitutions A127T, P144L and K203R (designated as 3a.2). Viruses with 3a.1 HA genes have continued to decline and very few were detected in this period. The 3a.2 HA genes have predominated globally with most recent circulation in Africa and Oceania. The 3a.2 HA genes have diversified further, with the majority sharing the substitution D197E in HA1.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2) recognized representative viruses from various clusters of 3a.2 HA genes well. The small number of viruses in clade 1A.3 were recognized well by ferret antisera raised against B/Washington/02/2019-like viruses (1A.3) and were poorly recognized by ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2).

In human serology studies using most of the serum panels described above, post-vaccination HI GMTs against recent B/Victoria lineage viruses of clade 3a.2 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021 vaccine viruses. Significant reductions were detected with most serum panels for viruses with HAs of the 1A.3 clade. Due to the lack of recent viruses, serology studies were not performed for the B/Yamagata lineage.
Of 2 334 influenza B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, six showed evidence of highly reduced susceptibility to NAIs. Five of these viruses had a K360E substitution and one virus had an H134Y substitution in the NA gene. Of 1 356 B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil.
GISRS NICs lineage-tested 15 878 influenza B viruses collected between 1 February and 31 August 2023. Fifteen detections which were initially reported as B/Yamagata lineage viruses were further investigated and 13 were confirmed to be B/Victoria lineage viruses or negative for influenza, while two were not available for confirmation and did not yield sequence results or virus isolates. These data indicate that B/Yamagata lineage viruses are no longer circulating in the population and therefore are unlikely to cause future epidemics, although GISRS laboratories will continue to test for B/Yamagata viruses. While influenza vaccines are safe and effective, the manufacture and use of inactivated and live attenuated vaccines containing B/Yamagata lineage viruses pose a theoretical risk of reintroduction

of B/Yamagata lineage virus into the population. This risk can be mitigated by the removal of B/Yamagata lineage viruses from the vaccines. Therefore, it is the opinion of the WHO influenza vaccine composition advisory committee that the inclusion of a B/Yamagata antigen as a component of influenza vaccines is no longer warranted, and every effort should be made to exclude it as soon as possible.

Recommended composition of influenza virus vaccines for use in the 2024 southern hemisphere influenza season

The vast majority of the A(H1N1)pdm09 viruses collected since 1 February had HA genes belonging to clade 5a.2 (i.e., 6B.1A.5a.2). Subclade 5a.2a viruses were mainly detected in Africa, Asia, Europe and Oceania, while subclade 5a.2a.1 viruses were mainly detected in North America, Central America and South America. Post-infection ferret antisera raised against the SH 2023 A(H1N1)pdm09 vaccine components (cell culture- and egg-propagated A/Sydney/5/2021 (5a.2a)) recognized 5a.2a and 5a.2a.1 viruses well, but recognized 5a.1 viruses poorly. However, some human serology panels showed reduced post-vaccination GMTs against a number of recently circulating 5a.2a and 5a.2a.1 viruses when compared to titres against cell culture-propagated or egg-propagated A/Sydney/5/2021 (H1N1)pdm09-like vaccine viruses.

The vast majority of A(H3N2) viruses collected since 1 February 2023 have HA genes derived from clade 2 (i.e., 3C.2a1b.2a.2) and have diversified into several new subclades. Some recently circulating viruses showed reduced recognition by post-infection ferret antisera raised against NH 2022-2023 and SH 2023 vaccine viruses, cell culture-propagated A/Darwin/6/2021 and egg-propagated A/Darwin/9/2021 (2a). Human serology assays showed that post-vaccination GMTs against A(H3N2) viruses with HA genes representing 2a.3a.1, 2a.1b and 2b genetic subgroups were significantly reduced in some serum panels compared to titres against cell-propagated A/Darwin/6/2021-like vaccine reference viruses.

All circulating influenza B viruses characterized since 1 February 2023 were of the B/Victoria/2/87 lineage. Most recent viruses expressed HA genes belonging to subclade 3a.2 (i.e., 1A.3a.2). A few viruses belonging to clade 1A.3 were detected in North and Central America. Nearly all circulating viruses were recognized well by post-infection ferret antisera raised against cell culture- and egg-propagated B/Austria/1359417/2021-like viruses (3a.2). Human serology assays showed that post-vaccination GMTs against representative B/Victoria lineage viruses expressing 3a.2 HA genes were not significantly reduced compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021 vaccine virus.

The WHO convenes technical consultations[7] each year to recommend viruses for inclusion in influenza vaccines[8]. 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.

For trivalent vaccines for use in the 2024 southern hemisphere influenza season, the WHO recommends the following:

Egg-based vaccines

- **an A/Victoria/4897/2022 (H1N1)pdm09-like virus;**
- **an A/Thailand/8/2022 (H3N2)-like virus; and**
- **a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.**

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

Cell culture- or recombinant-based vaccines

- **an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;**
- **an A/Massachusetts/18/2022 (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 absence of confirmed detection of naturally occurring B/Yamagata lineage viruses is indicative of very low risk of infection by B/Yamagata lineage viruses. Therefore, it is the opinion of the WHO influenza vaccine composition advisory committee that inclusion of a B/Yamagata lineage antigen in quadrivalent influenza vaccines is no longer warranted, and every effort should be made to exclude this component as soon as possible.

Lists of prototype viruses for egg-propagated, cell culture-propagated and recombinant-based vaccines together with candidate vaccine viruses (CVVs) suitable for use in human vaccine production are available on the WHO website[9]. A list of reagents for vaccine standardization, including those for this recommendation, can also be found on the WHO website.

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

- Biotherapeutics Section, Laboratories Branch, Medical Devices and Product Quality Division, 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
- fax: +441707641050 (email: enquiries@nibsc.org)
- 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:

- WHO Collaborating Centre for Reference and Research on Influenza, VIDRL, Peter Doherty Institute, 792 Elizabeth Street, Melbourne, Victoria 3000, Australia (fax: +61393429329, 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:

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

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, fax: +86 10 5890 0851, email: whocc-china@cnic.org.cn, website: http://www.chinaivdc.cn/cnic/en).

WHO provides fortnightly updates[10] of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website[11].

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 EpiFluTM 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.

[10] https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-updates
[11] 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 2024 southern 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 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: Bill&Melinda Gates Foundation, IFPMA, Innovative Medicines Initiative and PATH.
WHO CC and ERL NIID Tokyo	Dr Hideki Hasegawa	None
WHO CC London	Dr Nicola Lewis	Following items were declared: • Invited speaker and panel member on event organized by Seqirus. No payment 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 for the period from October 2022-June 2023
WHO CC Koltsovo	Dr Vasily Marchenko	None
WHO CC Melbourne	Dr Kanta Subbarao	All items declared and listed below belong to Dr Subbarao's Research Unit: • Received significant financial support for research activities CRADA from Seqirus for development of cell-based manufacturing technologies. Ceased 2019. • Received significant financial support for research activities from IFPMA for isolation of influenza viruses in hens' eggs as potential vaccine strains for development as influenza vaccine strains. Ceased 2019. • Received non-monetary support from Roche, GSK, Biocrvst and Romark 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	Following items were declared: • Participated in a Sanofi next generation influenza vaccine advisory panel, November 2022. No renumeration received. • Participated in a Seqirus-sponsored session at Options XI for the Control of Influenza meeting in Belfast, September 2022. No renumeration for participation or travel received. • Participated in Seqirus' National Influenza Educational Webinar on Tuesday 22 March 2022 as a virtual speaker. Topic was on impact of COVID-19 on influenza activity. No renumeration received. • Participated in a virtual ROCHE advisory board meeting on insights into antiviral use in future influenza pandemics on 25 October 2021. No renumeration received.
WHO CC Atlanta	Dr David Wentworth	Below item declared and listed below belong to Dr Wentworth'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. Being co-inventor with others and employers: • Intellectual Property in a patent on influenza reassortment and another on modified bat influenza viruses and their uses. Both are USA patents and are not licensed.
WHO ERL CBER Silver Spring	Dr Zhiping Ye	None

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