Recommended composition of influenza virus vaccines for use in the 2023-2024 northern hemisphere influenza season

February 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 NH 2023-2024 influenza season. A recommendation will be made in September 2023 relating to vaccines that will be used for the SH 2024 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].

Seasonal influenza activity, September 2022 – January 2023

From September 2022 through January 2023, influenza activity was reported in all regions, with many regions having seen activity return to levels typical of pre-COVID-19 pandemic years. During this period, influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses circulated, although the proportions of viruses circulating varied between reporting countries. In most countries, influenza A virus detections outnumbered those of influenza B.

In the temperate zone of the northern hemisphere, influenza activity started increasing in October and reached its highest levels in December. Between January and mid-February 2023, influenza activity decreased in most countries. Overall, influenza A(H3N2) viruses have dominated.

Countries in North America reported a predominance of A(H3N2), with lower levels of A(H1N1)pdm09 and very few influenza B viruses detected.

Countries in northern Europe reported circulation of influenza A(H1N1)pdm09 and A(H3N2) viruses, whereas in countries in south-eastern Europe, A(H3N2) represented the majority of detections. A predominance of A(H1N1)pdm09 viruses was reported from countries in eastern Europe, particularly the Russian Federation.

In northern Africa, A(H3N2) viruses predominated from September through November, while A(H1N1)pdm09 viruses represented the majority of detections in December and January 2023. In recent weeks, however, northern African countries and all regions in Europe have reported an increasing proportion of specimens testing positive for influenza B viruses.

Countries in western Asia had circulation of A(H3N2), A(H1N1)pdm09 and B viruses, while central Asian countries had a predominance of A(H1N1)pdm09 or B viruses. In East Asia (China) influenza activity resulted from the circulation of A(H3N2) viruses through the end of December. An increase in influenza activity since February 2023 in China has been due to the cocirculation of A(H1N1)pdm09 and A(H3N2) viruses.

Tropical and subtropical areas

In countries of Central America and the Caribbean, influenza A(H3N2) predominated. In tropical South America, influenza activity was dominated by influenza A(H3N2), and since January 2023, increasing proportions of influenza A(H1N1)pdm09 and B viruses have been detected.

In Southern and South-East Asia, influenza activity resulted from cocirculation of influenza types or

[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

subtypes in a number of countries. Both A(H1N1)pdm09 and A(H3N2) viruses circulated in India and Nepal, while Pakistan reported codominance of influenza B and A(H1N1)pdm09 viruses. The Islamic Republic of Iran had circulation of A(H3N2), A(H1N1)pdm09 and B viruses. Cambodia, the Lao People's Democratic Republic and Viet Nam experienced cocirculation of A(H3N2) and B viruses. The majority of influenza B virus detections in South-East Asia was reported by Malaysia.

In the tropical and subtropical countries of Africa, influenza activity mostly remained at low levels during this reporting period but persisted in several countries through early January 2023. A(H1N1)pdm09 viruses predominated in eastern Africa (particularly in Ethiopia, Kenya, Madagascar and Mozambique), while A(H3N2) or B viruses represented the majority of influenza detections in western Africa (influenza B viruses in Ghana and Senegal, and A(H3N2) viruses in Togo).

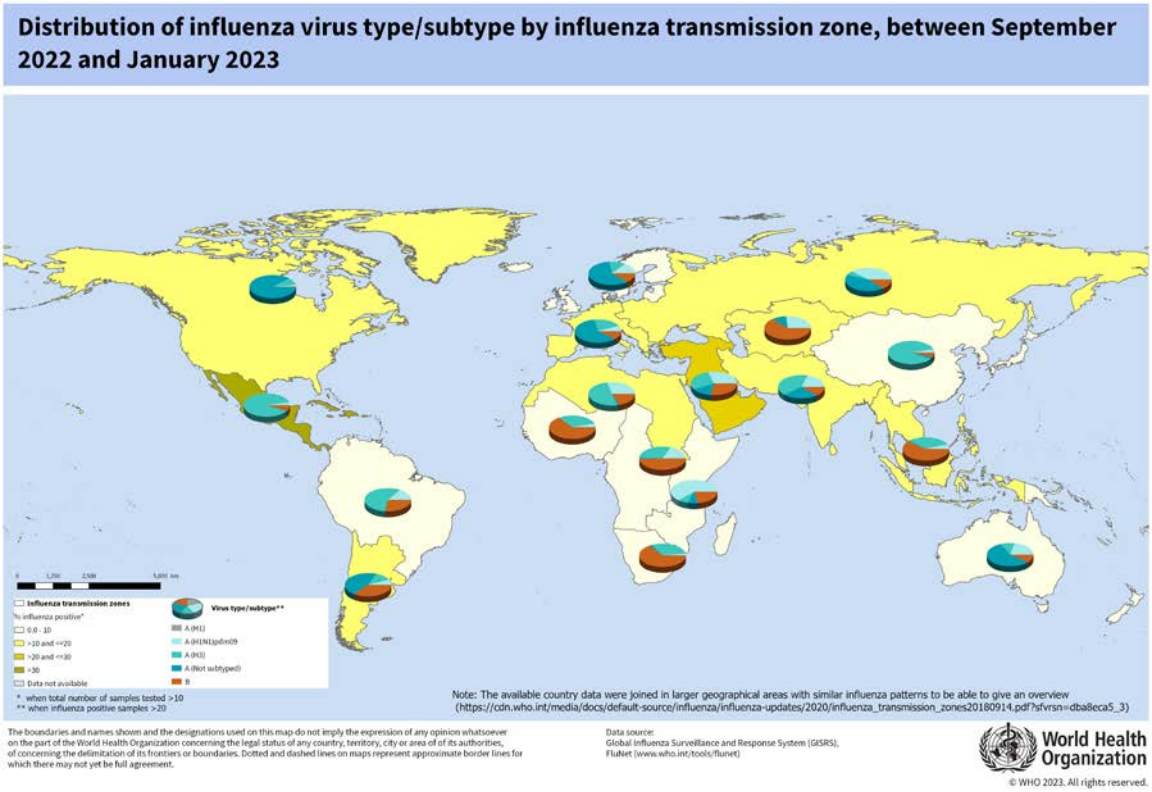
In the temperate zone of the southern hemisphere, the timing of influenza activity and proportions of viruses detected varied between reporting countries. A few countries detected high numbers of influenza viruses during this time period while influenza activity in other countries remained at inter-seasonal levels.

Influenza A virus detections predominated from September to November in South America. However, influenza B virus detections increased after November, to become the majority of viruses reported in some countries such as Argentina and Paraguay. Chile reported high influenza activity with the majority of detections being A(H3N2) viruses.

A few countries in South America (Argentina and Chile) experienced a peak of influenza virus detections during their summer months. South Africa also experienced a wave of influenza activity from September through mid-November with influenza B and A(H3N2) viruses detected.

In Oceania, influenza activity since September has been low and continued to remain at inter-seasonal levels except in Fiji. Influenza detections in Fiji were A(H1N1)pdm09 viruses.

Globally, all circulating influenza B viruses, where lineage was confirmed, belonged to the B/Victoria/2/87 lineage.



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

In the period from 20 September 2022 to 20 February 2023, three human cases of A(H5N6), two cases of A(H5N1) and eight cases of A(H9N2) infection in China were reported. Additional A(H5N1) detections in humans were reported in Ecuador (1), Spain (2) and Viet Nam (1).

Three cases of A(H1N1)v virus infection were reported, one in Brazil and two in China. Two cases of A(H1N2)v virus infection were reported, one each in the Netherlands and Taiwan, China. Two cases of A(H3N2)v virus infection were reported in the United States of America (USA).

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

Influenza A(H1N1)pdm09 viruses

Since 1 September 2022 A(H1N1)pdm09 viruses have circulated and were characterized from all geographic regions. Genetically characterized viruses had haemagglutinin (HA) genes that belong to two major phylogenetic clades: 5a.1 and 5a.2, with 5a.2 viruses representing the vast majority.

All viruses expressing clade 5a.2 HA genes collected since January 2022 have further diversified belonging to a newly designated subclade, 5a.2a, with additional HA1 amino acid substitutions K54Q, A186T, Q189E, E224A, R259K and K308R, some of which are located in antigenic site Sb. For viruses expressing 5a.2a HA genes, many have additional HA1 substitutions of P137S, K142R, D260E and T277A, and are designated as subclade 5a.2a.1 (e.g., A/Wisconsin/67/2022). Many of these viruses also have HA1 substitution T216A. Viruses within subclades 5a.2a and 5a.2a.1 cocirculated with regional differences in proportionality; subclade 5a.2a.1 viruses predominated in North America and many countries in South America and Europe.

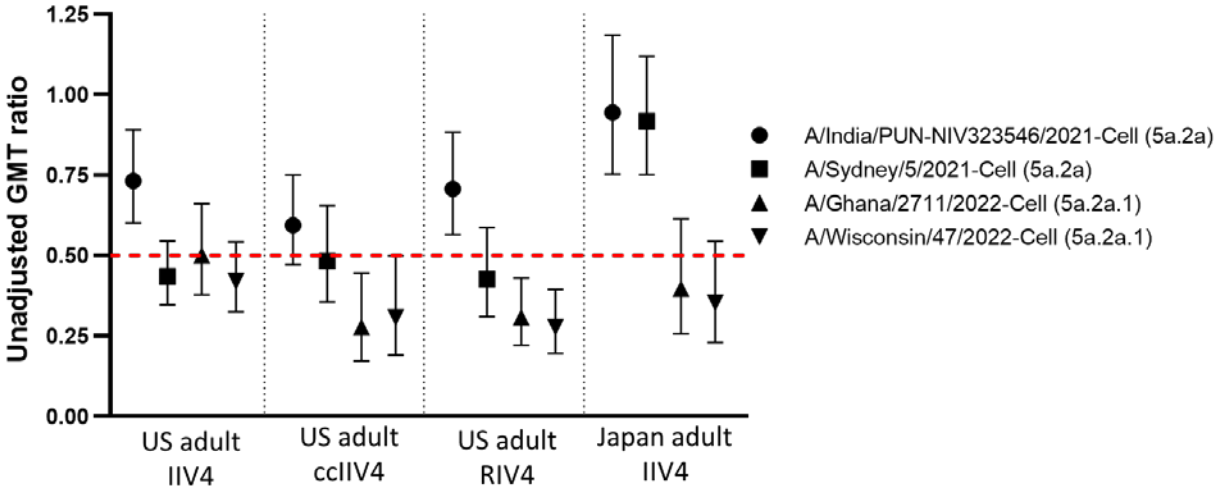
The antigenic characteristics of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) assays with post-infection ferret antisera. HI results for viruses with collection dates since 1 September 2022 showed that ferret antisera raised against the previous vaccine viruses (cell culture-propagated A/Wisconsin/588/2019-like and egg-propagated A/Victoria/2570/2019-like 5a.2 viruses) recognized the small number of 5a.1 test viruses poorly, however viruses in subclades 5a.2a and 5a.2a.1 were recognized well 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 17 serum panels from children (6 months to 17 years), adults (18-64 years) and elderly adults (≥65 years) who had received egg-based quadrivalent inactivated vaccines (standard or adjuvanted), cell culture-based quadrivalent inactivated vaccines or recombinant quadrivalent vaccines formulated for the NH 2022-2023 season. NH 2022-2023 egg-based vaccines contained antigens from A/Victoria/2570/2019 (H1N1)pdm09-like, A/Darwin/09/2021 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) viruses; cell culture- and recombinant-based vaccines contained A/Wisconsin/588/2019 (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) vaccine antigens.

Using these serum panels, reactivities of antibodies induced by 5a.2 A/Victoria/2570/2019 or A/Wisconsin/588/2019 (H1N1)pdm09-like vaccine antigens against recent A(H1N1)pdm09 viruses were determined using HI assays. Compared to the responses to the egg- and cell culture-propagated

A(H1N1)pdm09 vaccine viruses, post-vaccination geometric mean titres (GMTs) were reduced significantly in most serum panels against most recent A(H1N1)pdm09 viruses of subclades 5a.2a and 5a.2a.1 as well as some viruses of clade 5a.1.

Fig. 1. A(H1N1)pdm09 post-vaccination human serology analysis.



Geometric mean titre (GMT) ratios comparing post-vaccination antibody responses of test viruses relative to the response to cell culture-propagated A/Wisconsin/588/2019 vaccine reference virus in human serology studies using HI assay. Serum panels from adult volunteers from the USA received NH 2022-2023 standard dose egg-based inactivated quadrivalent vaccine (US IIV4), NH 2022-2023 cell culture-based inactivated quadrivalent vaccine (US ccIIV4), NH 2022-2023 recombinant influenza quadrivalent vaccine (US RIV4) and for the Japan panel adults received NH 2022-2023 standard dose egg-based inactivated quadrivalent vaccine (Japan IIV4). Serum panels were tested against the **5a.2a** and **5a.2a.1** viruses indicated. GMT ratios and 90% confidence intervals are shown. Dashed line indicates 50% GMT ratio threshold.

Of 1 361 A(H1N1)pdm09 viruses collected since 1 September 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analyses, four viruses had a H275Y and one virus had a S247G substitution in the neuraminidase. Of the four viruses with a H275Y substitution, three were available for phenotypic analysis and showed highly reduced inhibition by oseltamivir and peramivir, and normal inhibition by zanamivir and laninamivir. The virus with a S247G substitution in the neuraminidase showed reduced inhibition by oseltamivir and normal inhibition by zanamivir, peramivir and laninamivir. Of 1 107 A(H1N1)pdm09 viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil.

Influenza A(H3N2) viruses

Phylogenetic analysis of the HA gene of A(H3N2) viruses collected since 1 September 2022 showed that two major clades circulated in this period: clade 1, complete classification 3C.2a1b.2a.**1** and clade 2, complete classification 3C.2a1b.2a.**2**. Clade 1 HA genes have evolved into subclade 1a.1 (typically encoding I48T and K171N substitutions) and were detected primarily in viruses circulating in China. The clade 2 HA genes (typically encoding Y159N, T160I, L164Q, G186D and D190N substitutions) predominated in all geographic regions and have evolved into multiple subclades. Owing to substantial evolution and cocirculation of multiple clade 2 HA subclades, new designations were developed to better define and track the HA evolution (Table 1); a labelled phylogeny can be visualized at nextstrain/flu/seasonal/h3n2/ha/2y. Four subclades (i.e., 2a-2d) have evolved and are undergoing diversifying and parallel evolution.

Table 1: 2023 H3 3C.2a1b.2a subclade designations

Subclade	Defining amino acid substitutions
2a	Clade 2 + H156S
2a.1	Subclade 2a + D53G, D104G, K276R
2a.1a	Subclade 2a.1 + L157I, K220R
2a.1b	Subclade 2a.1 + I140K, R299K
2a.2	Subclade 2a + D53G, R201L, S219Y
2a.3	Subclade 2a + D53N, N96S, I192F
2a.3a	Subclade 2a.3 + E50K
2a.3a.1	Subclade 2a.3a + I140K
2a.3b	Subclade 2a.3a + I140M
2b	Clade 2 + E50K, F79V, I140K
2c	Clade 2 + S205F, A212T
2d	Clade 2 + G62R, H156Q, S199P

+ indicates the additional amino acid substitutions typically found in each subclade

The various HA subclades were found in different regions globally and viruses with HA genes from multiple subclades cocirculated in several geographic regions in varying proportions. In Europe, the 2b HA predominated, while in Africa 2a.3 HA and its subclades (2a.3a and 2a.3a.1) predominated. The HA genes of viruses circulating in Asia were predominantly 2a.3a.1, 2a.3b or 2b and in Oceania, 2a.1, 2a.3a.1, 2a.1b and 2b HA containing viruses cocirculated at low levels. In North America, primarily 2b, 2a.1b and 2a.1 HA genes were detected. In central and South America, 2b and 2a.3 HA genes were detected. Globally, the HA subclades that predominated over the past 6 months were 2b, 2a.3a.1 and 2a.1b.

Generally, ferret antisera raised against cell culture-propagated A/Darwin/6/2021-like viruses and egg-propagated A/Darwin/9/2021-like viruses, representing the clade 2a vaccine viruses for the NH 2022-2023 and SH 2023 influenza seasons, recognized viruses expressing 2a (including subclades) HA genes well. However, viruses expressing 2b HA genes reacted less well with these antisera. Viruses expressing clade 1a.1 HA genes were recognized well by ferret antisera raised against cell culture-propagated A/Cambodia/e0826360/2020-like viruses (clade 1a) but were generally recognized poorly by ferret antisera raised against clade 2a vaccine viruses.

Human serology studies were conducted with serum panels as described above using HI and virus neutralization (VN) assays. When compared to titres against cell culture-propagated A/Darwin/6/2021-like vaccine reference viruses, post-vaccination VN GMTs against recent A(H3N2) viruses with clade 2a (including 2a.1b, 2a.3a.1), 2b, and 1a.1 HA genes were not significantly reduced in most serum panels. Reductions of GMTs were observed when compared to egg-propagated A/Darwin/9/2021-like reference viruses.

Of 2 686 influenza A(H3N2) viruses collected since 1 September 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analyses, none showed evidence of reduced inhibition by NAIs. Of 2 429 A(H3N2) viruses examined for endonuclease inhibitor baloxavir marboxil susceptibility by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to endonuclease inhibitor baloxavir marboxil.

Influenza B viruses

Globally, influenza B viruses represented 5.8% of the viruses detected since 1 September 2022, 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 great 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 had previously diversified into two main subclades, one with additional HA1 substitutions V220M and P241Q (designated as **3a.1**; none detected in this time period) and the other with HA1 substitutions A127T, P144L and K203R (designated as **3a.2**). The 3a.2 HA genes have predominated in Africa, Asia (including China), Europe, North America, Oceania, and South America. The 3a.2 HA genes have diversified into numerous clusters, defined by additional HA1 amino acid substitutions, 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 viruses in the 3a.2 subclade 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 the serum panels described above, post-vaccination HI GMTs against recent B/Victoria lineage viruses expressing 3a.2 HA genes were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021 (3a.2) vaccine viruses. Significant reductions were detected with some serum panels for viruses expressing 1A.3 HA genes. Due to the lack of available recent viruses, serology studies were not performed for the B/Yamagata lineage.

Of 472 influenza B/Victoria lineage viruses collected since 1 September 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analyses, none showed evidence of reduced inhibition by NAIs oseltamivir and zanamivir. Of 374 B/Victoria lineage viruses examined by genetic and/or phenotypic analyses, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir marboxil.

Recommended composition of influenza virus vaccines for use in the 2023-2024 northern hemisphere influenza season

The majority of A(H1N1)pdm09 viruses collected since 1 September 2022 had HA genes derived from clade 5a.2 (i.e., 6B.1A.**5a.2**); subclade 5a.2a was mainly detected in countries in Asia and 5a.2a.1 in countries in Europe, South America and North America. Post-infection ferret antisera raised against the NH 2022-2023 and SH 2023 A(H1N1)pdm09 vaccine components (NH: egg-propagated A/Victoria/2570/2019, cell culture-propagated A/Wisconsin/588/2019 (5a.2), and SH: cell culture- and egg-propagated A/Sydney/5/2021 (5a.2a)) recognized 5a.2, 5a.2a, and 5a.2a.1 viruses well, but 5a.1 viruses poorly. However, most serum panels in human serology assays showed markedly 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 A/Wisconsin/588/2019 or egg-propagated A/Victoria/2570/2019 A(H1N1)pdm09-like vaccine viruses.

The vast majority of A(H3N2) viruses collected since 1 September 2022 had HA genes derived from clade 2 (i.e., 3C.2a1b.2a.**2**) and have diversified into several new subclades. However, the majority of recently circulating viruses were recognized well 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 subclades 2a (with its emerging subclades) and 2b were not significantly reduced compared to titres against the cell culture-propagated A/Darwin/6/2021 vaccine virus.

All circulating influenza B viruses characterized since 1 September 2022 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. The great majority of the 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 the cell culture-propagated B/Austria/1359417/2021 vaccine virus.

For trivalent vaccines for use in the 2023-2024 northern hemisphere influenza season, the WHO recommends the following:

Egg-based vaccines

- **an A/Victoria/4897/2022 (H1N1)pdm09-like virus;**
- **an A/Darwin/9/2021 (H3N2)-like virus; and**
- **a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.**

Cell culture- or recombinant-based vaccines

- **an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;**
- **an A/Darwin/6/2021 (H3N2)-like virus; and**
- **a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.**

For quadrivalent egg- or cell culture-based or recombinant vaccines for use in the 2023-2024 northern hemisphere influenza season, the WHO recommends inclusion of the following as the B/Yamagata lineage component:

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

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[4]. A list of reagents for vaccine standardization, including those for this recommendation, can also be found on the WHO website.

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[5].

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)

[4] https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses
[5] Vaccines against influenza WHO position paper - November 2012. Wkly Epidemiol Rec 2012;87(47):461-76. Available at: https://apps.who.int/iris/handle/10665/241994

• 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: 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[6] of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website[7].

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 Global Initiative for Sharing All Influenza Data (GISAID) 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.

[6] https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-updates
[7] 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 2023-2024 Northern Hemisphere Influenza Season was made through a WHO Consultation with relevant WHO Collaborating Centres on Influenza (CCs) and Essential Regulatory Laboratories (ERLs).

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

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

Institution	Representative	Personal interest
WHO ERL 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 Alexander Ryzhikov	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.