

May 02, 2022

Letter of Declaration

Dear Sir/Madam who might concern,

We, Green Cross Corporation, the manufacturer of GCFLU Quadrivalent Pre-filled syringe inj. hereby declare that the following strains are recommended composition of influenza virus vaccines for use in the 2022-2023 Northern hemisphere influenza season and are used for the production of GCFLU Quadrivalent PFS inj. 2022-2023:

- H1N1: A/Victoria/2570/2019 IVR-215
- N3N2: A/Darwin/9/2021 SAN-010
- B-Vic: B/Austria/1359417/2021 BVR-26
- B-Yam: B/Phuket/3073/2013

The applied CoPP can be issued on 15th June 2022 from the Ministry of Food and Drug Safety(MFDS) after approval change in Republic of Korea

Attachment

- Recommended composition of influenza virus vaccines for use in the 2022-2023 Northern hemisphere influenza season

Sincerely,



Shin

Yunchul Shin
Head of Regulatory Affairs IV Team
Green Cross Corporation

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Recommended composition of influenza virus vaccines for use in the 2022-2023 northern hemisphere influenza season

February 2022

WHO convenes technical consultations¹ in February and September each year to recommend viruses for inclusion in influenza vaccines² for the northern hemisphere (NH) and southern hemisphere (SH) influenza seasons, respectively. This recommendation relates to the influenza vaccines for use in the NH 2022-2023 influenza season. A recommendation will be made in September 2022 relating to vaccines that will be used for the SH 2023 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 website³.

Seasonal influenza activity

Public health and laboratory responses to the COVID-19 pandemic disrupted the influenza surveillance and/or reporting activities to varying extents in many countries. SARS-CoV-2 mitigation strategies including restrictions on travel, use of respiratory protection, and social-distancing measures in most countries continue to result in decreased influenza transmission. Between September 2021 and January 2022, low numbers of influenza detections were reported and fewer viruses have been available for characterization in comparison to similar time periods prior to the COVID-19 pandemic. Nevertheless, epidemics were reported by a number of countries and regions, with higher detections of influenza activity in the 2021-2022 season than in the 2020-2021 influenza season.

Between September 2021 and January 2022, influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses circulated in low numbers and the relative proportions of the viruses circulating varied among reporting countries. Globally, since September 2021, most influenza virus detections were reported by countries in the temperate zone of the northern hemisphere and countries in the tropics and subtropics. Overall, percent positivity of influenza viruses during this period was less than 3%. In contrast, the average percent positivity during similar reporting periods prior to the COVID-19 pandemic (2017-2020) was 17%.

In the temperate zone of the northern hemisphere, influenza activity was lower than in the corresponding reporting periods before the COVID-19 pandemic. However, compared with the 2020-2021 influenza season, countries reported increases of over 2.5-fold in the number of specimens tested for influenza and over 35-fold in the number of influenza viruses detected. Influenza A was predominant in most countries while influenza B predominated in a few countries in the temperate zone of the northern hemisphere. In north Africa, influenza virus detections were reported by Algeria, Egypt, Morocco and Tunisia with a predominance of A(H3N2). In Asia, both influenza A and B viruses were detected in most reporting countries except in China where influenza B predominated. Of the subtyped influenza A viruses, A(H3N2) predominated. In Afghanistan, Iraq, Islamic Republic of Iran, Kazakhstan, Kyrgyzstan, Lebanon, Mongolia, Syrian Arab Republic and Uzbekistan, only A(H3N2) viruses were reported. Influenza A(H3N2) predominated in most countries in Europe and North America with influenza B viruses also detected. In France, influenza A(H1N1)pdm09 predominated.

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

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>

Influenza activity in tropical and subtropical countries was lower than in the corresponding reporting periods before the COVID-19 pandemic, with co-circulation of influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses. In the tropical countries of Africa, most influenza detections were reported from central, east and west Africa. In east Africa, influenza A(H3N2) predominated in Ethiopia, Kenya and Uganda, while influenza A(H1N1)pdm09 predominated in the United Republic of Tanzania and in Zambia, whereas influenza B predominated in Madagascar and Mozambique. In west Africa, only influenza A viruses were detected, with a predominance of A(H1N1)pdm09 in Ghana, Mali, Mauritania, Niger and Senegal and a predominance of A(H3N2) in Côte d'Ivoire and Togo. In central Africa, Cameroon reported mostly A(H1N1)pdm09, the Democratic Republic of Congo mostly A(H3N2) and South Sudan mostly influenza B. In the tropical countries of Asia, most influenza virus detections were reported from Bangladesh, Bhutan, India, Malaysia, Maldives and Nepal. Influenza B was predominant in India and Nepal and influenza A predominated elsewhere. Of the subtyped influenza A viruses, A(H3N2) was predominant in most reporting countries except in Bangladesh where A(H1N1)pdm09 predominated. In the tropical countries of the Caribbean and Central America, Mexico accounted for most of the detections reported, with A(H3N2) predominating. Dominican Republic, Guatemala, Haiti, Honduras and Nicaragua reported influenza A and B viruses in differing proportions, and of the influenza A viruses that were subtyped, A(H3N2) predominated.

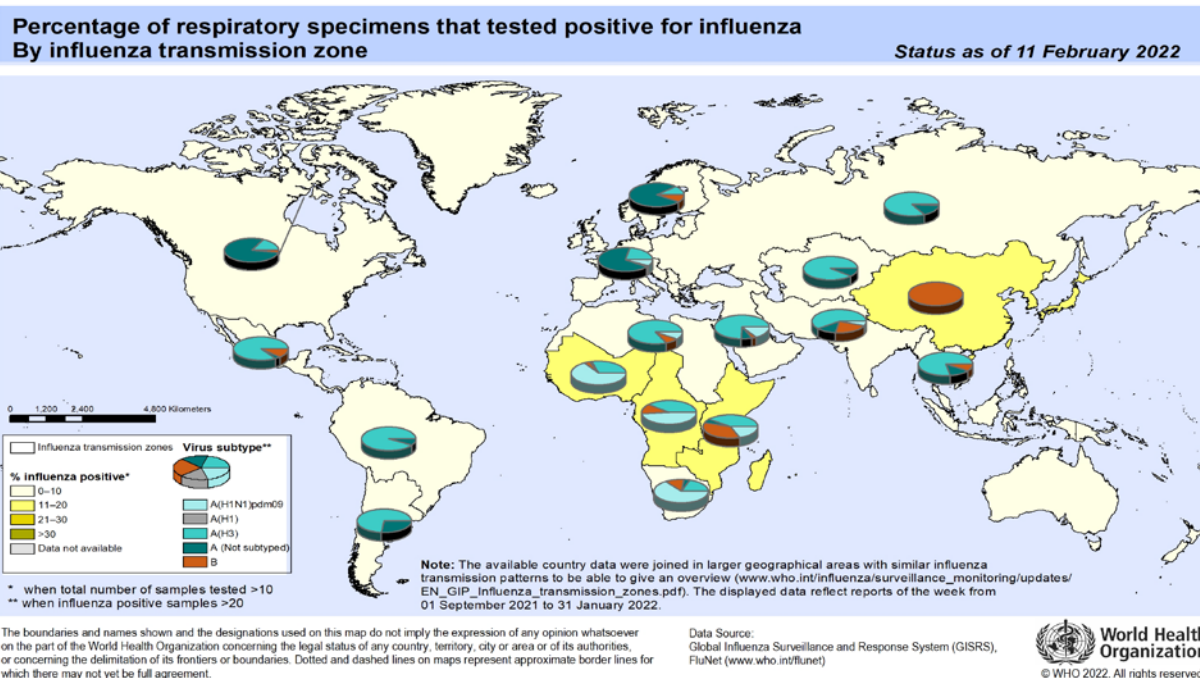
In the temperate zone of the southern hemisphere, overall influenza activity was lower than in the corresponding inter-seasonal reporting periods before the COVID-19 pandemic, though increased detections were reported at the end of 2021 and early 2022 from Brazil, Chile, Paraguay and Uruguay with mainly A(H3N2) viruses detected. Influenza activity was detected outside the timing of the usual season from South Africa where influenza A(H1N1)pdm09 predominated but influenza A(H3N2) and B viruses were also detected. In Oceania, few influenza A and B virus detections were reported, though French Polynesia reported increased influenza A(H3N2) activity.

Influenza A

Globally, influenza A viruses predominated in most reporting countries during this period. Influenza A detections were reported mainly from countries in the northern hemisphere, from late November 2021 to mid-January 2022. In most reporting countries, areas and territories, both A(H1N1)pdm09 and A(H3N2) subtypes were detected. Influenza A(H1N1)pdm09 was predominant in Bangladesh, France, South Africa and in some tropical countries. Elsewhere, influenza A(H3N2) was predominant.

Influenza B

Globally, influenza B viruses were reported by most countries at a lower frequency than influenza A viruses except in China, Dominican Republic, Haiti, India, Madagascar, Mozambique, Nepal and South Sudan. Of the influenza B viruses where lineage was determined, nearly all belonged to the B/Victoria/2/87 lineage and most were reported from China. Influenza B/Yamagata/16/88 lineage viruses were reported in very low numbers but these have not been confirmed by sequencing or virus isolation.



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/teams/global-influenza-programme/surveillance-and-monitoring/influenza-surveillance-outputs>.

Zoonotic influenza infections

In the period from 24 September 2021 to 23 February 2022, 25 cases of A(H5N6) and 15 cases of A(H9N2) were reported in China and one A(H5N1) case was reported in the United Kingdom of Great Britain and Northern Ireland.

Three cases of A(H1N1)v in the United States of America and one in Denmark were reported in this period. Three cases of A(H1N2)v were reported in Canada (n=1) and the United States of America (n=2). An additional A(H1)v case was reported in the United States of America; the neuraminidase subtype was not determined. One case of A(H3N2)v was reported in the United States of America.

Antigenic and genetic characteristics of recent seasonal influenza viruses, human serology and antiviral susceptibility

Influenza A(H1N1)pdm09 viruses

The few A(H1N1)pdm09 viruses that have circulated since 1 September 2021 had haemagglutinin (HA) genes that belong to phylogenetic clade 6B.1A.5a (**5a**), characterised by HA1 amino acid substitutions N129D, T185I and N260D. Clade 5a has further diverged into two major subclades: **5a.1**, defined by HA amino acid substitutions D187A and Q189E (antigenic site Sb) and **5a.2**, defined by K130N (located in the receptor binding site), N156K (antigenic site Sa), L161I (antigenic site Sa), V250A in HA1 and E179D in HA2 (E506D). Some subclade 5a.1 viruses collected after August 2021 have additional HA1 amino acid substitutions P137S (antigenic site Ca) and G155E (antigenic site Sa). Subclade 5a.2 viruses collected after August 2021 have additional HA1 amino acid substitutions K54Q, A186T (antigenic site Sb), Q189E (antigenic site Sb), E224A (located in the receptor binding site), R259K and K308R. Viruses belonging

to both subclades have circulated during 2021-2022 in different geographic locations. After August 2021, subclade 5a.1 viruses predominated in Europe and Africa while subclade 5a.2 viruses predominated in southern Asia, the Middle East and Australia. In North America, similar numbers of viruses in subclades 5a.1 and 5a.2 were seen.

The antigenic characteristics of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) and virus neutralization (VN) assays with post-infection ferret antisera. Results from viruses with collection dates after August 2021 showed that the majority of 5a.1 viruses were recognized well by antisera raised against the previous vaccine viruses (egg-propagated A/Guangdong-Maonan/SWL1536/2019 and cell culture-propagated A/Hawaii/70/2019). However, 5a.1 viruses with substitutions in the HA1 of P137S and G155E were recognized less well and 5a.2 viruses were recognized poorly by these antisera. Antisera raised against the NH 2021-2022 vaccine viruses (egg-propagated A/Victoria/2570/2019 and cell culture-propagated A/Wisconsin/588/2019) recognized 5a.2 viruses well, but 5a.1 viruses were recognized poorly by these antisera.

Human serology studies used 17 serum panels from children (6 months to 17 years), adults (18-64 years) and older adults (≥ 65 years) who had received egg-based quadrivalent inactivated vaccines (standard or high dose), cell culture-based quadrivalent inactivated vaccines or recombinant-based quadrivalent vaccines formulated for NH 2021-2022. Egg-based vaccines contained antigens from A/Victoria/2570/2019 (H1N1)pdm09-like, A/Cambodia/e0826360/2020 (H3N2)-like, B/Washington/02/2019-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) viruses. Cell culture-based and recombinant vaccines contained A/Wisconsin/588/2019 (H1N1)pdm09-like, A/Cambodia/e0826360/2020 (H3N2)-like, B/Washington/02/2019-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens.

Human serology studies were conducted with these serum panels using HI assays for A(H1N1)pdm09 viruses. Antibodies induced by A/Wisconsin/588/2019 (H1N1)pdm09-like vaccine viruses reacted well with subclade 5a.2 viruses. Post-vaccination HI geometric mean titres (GMTs) against some cell culture-propagated subclade 5a.1 viruses were reduced in some serum panels.

Of 190 A(H1N1)pdm09 viruses collected after August 2021 and examined by genetic and/or phenotypic analysis, none showed evidence of reduced inhibition by neuraminidase inhibitors. Of 158 A(H1N1)pdm09 viruses examined by genetic and/or phenotypic analysis, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir.

Influenza A(H3N2) viruses

Phylogenetic analysis of the HA gene of A(H3N2) viruses collected since 1 September 2021 showed the vast majority fell into genetic clade 3C.2a1b.2a.2 (**2a.2**) with the HA1 substitutions Y159N, T160I (resulting in the loss of a glycosylation site), L164Q, G186D, D190N, F193S and Y195F. The 2a.2 HA further diversified into genetic groups containing H156Q, H156S and D53G, or H156S and D53N. Viruses from three other HA clades were also detected: 3C.2a1b.1a (**1a**) with HA1 substitutions T135K (resulting in the loss of a glycosylation site), A138S, G186D, D190N, F193S and S198P; 3C.2a1b.1b (**1b**) with HA1 substitutions T135K (resulting in the loss of a glycosylation site), S137F, A138S and F193S; and 3C.2a1b.2a.1 (**2a.1**) with HA1 substitutions G186S, F193S, Y195F and S198P. Viruses with 1b HA were predominant in African countries (Côte d'Ivoire, Madagascar, Niger and South Africa) and sporadically identified in very small numbers in Armenia, Australia and the UK. HA clade 1a viruses were detected in Ethiopia, Italy, Sweden and Togo. Viruses with 2a.2 HA have become predominant globally and were detected in all regions.

Antigenic characterization of A(H3N2) viruses was performed by HI and VN assays. Ferret antisera raised against cell culture- and egg -propagated A/Cambodia/e0826360/2020-like viruses (2a.1), representing the vaccine viruses for the NH 2021-2022 influenza season, recognized viruses in clade 2a.2 poorly. The small number of viruses with HA genes belonging to 3C.2a1b subclades 1a and 1b were recognized well by ferret antisera raised against cell culture-propagated A/Cambodia/e0826360/2020-like viruses but not those against egg-propagated A/Cambodia/e0826360/2020-like viruses. Ferret antisera raised against cell culture-propagated A/Darwin/6/2021-like and egg-propagated A/Darwin/9/2021-like viruses (2a.2), representing the vaccine viruses for the SH 2022 influenza season, generally recognized 2a.2 viruses well but reacted poorly with 2a.1, 1a and 1b viruses.

Human serology studies were conducted with serum panels as described above using HI and VN assays. When compared to titres against cell culture-propagated A/Cambodia/e0826360/2020-like 2a.1 vaccine viruses, post-vaccination GMTs against many cell culture-propagated 2a.2 viruses were significantly reduced in most serum panels. GMTs against the 2a.1 viruses tested were not reduced.

Of 1023 influenza A(H3N2) viruses examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analysis, one showed evidence of reduced inhibition by zanamivir and had an A246V substitution in the neuraminidase. Of 962 A(H3N2) tested for the endonuclease inhibitor baloxavir susceptibility by genetic and/or phenotypic analysis, none showed evidence of reduced susceptibility to baloxavir.

Influenza B viruses

Globally, influenza B viruses represented 26% of the viruses detected since 1 September 2021 and, of those tested, all belonged to the B/Victoria/2/87 lineage. There have been no confirmed B/Yamagata/16/88 lineage virus detections after March 2020.

HA gene sequences of characterized B/Victoria lineage viruses belonged to clade 1A, nearly all belonging to subclade 1A.3 which has a triple amino acid deletion in HA1 (positions 162-164) and the substitution K136E. Viruses with HA genes encoding further substitutions of N150K, G184E, N197D (resulting in the loss of a glycosylation site) and R279K in HA1 have predominated (group 1A.3a). Within this group there are two main subgroups, one with additional HA1 substitutions V220M and P241Q (**3a.1**) and the other with HA1 substitutions A127T, P144L and K203R (**3a.2**). Subgroup 3a.1 viruses were only detected in China. 3a.2 viruses have predominated in Asia (including China), Africa, Europe and Oceania, while in North America, viruses in 1A.3 and 3a.2 have been detected in similar proportions, and in Kenya and Madagascar 1A.3 viruses have dominated. 3a.2 viruses have shown further genetic divergence, with additional HA1 amino acid substitutions encoded in viruses from different geographic locations.

Antigenic analysis showed that the few viruses in subclade 1A.3 were recognized well by ferret antisera raised against B/Washington/02/2019-like viruses, while the much greater numbers of viruses from subgroups 3a.1 and 3a.2 were recognized poorly. Post-infection ferret antisera raised against B/Sichuan-Jingyang/12048/2019-like viruses (3a.1) recognized viruses in subgroup 3a.1 well but recognized subgroup 3a.2 viruses less well. Post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2) recognized viruses from subgroup 3a.2 well but recognized other viruses less well.

Human serology studies were conducted with serum panels as described above. When compared to titres against cell culture-propagated B/Washington/02/2019-like vaccine virus, post-vaccination HI GMTs against some cell culture-propagated 3a.1 viruses were reduced and, for most serum panels, the reductions

were more pronounced for 3a.2 viruses. When compared to titres against the egg-propagated B/Washington/02/2019 vaccine virus, HI GMTs against the majority of 3a.1 and 3a.2 viruses were significantly reduced. Serology studies were not performed for the B/Yamagata lineage.

Of 455 influenza B/Victoria lineage viruses collected since 1 September 2021 and examined by genetic and/or phenotypic analysis, one had a NA amino acid substitution (D197N) associated with reduced susceptibility to neuraminidase inhibitors. Of 457 B/Victoria lineage viruses collected in this period, none showed evidence of reduced susceptibility to baloxavir from sequencing of the PA gene.

Recommended composition of influenza virus vaccines for use in the 2022-2023 northern hemisphere influenza season

Influenza A(H1N1)pdm09 viruses collected since 1 September 2021 had HA genes that belonged to two subclades, 5a.1 and 5a.2. Viruses belonging to both subclades have circulated in different geographic locations during 2021-2022. Ferret antisera raised against the NH 2021-2022 A(H1N1)pdm09 vaccine components (egg-propagated A/Victoria/2570/2019 and cell culture-propagated A/Wisconsin/588/2019) recognized 5a.1 viruses poorly, but recognized 5a.2 viruses well. Human serology assays showed that antibodies induced by the A/Wisconsin/588/2019 (H1N1)pdm09-like vaccine component reacted well with subclade 5a.2 viruses but GMTs were reduced against some subclade 5a.1 viruses.

The vast majority of A(H3N2) viruses collected since 1 September 2021 had HA genes that belonged to genetic group 3C.2a1b.2a2. The majority of recently circulating viruses were recognized poorly by ferret antisera raised against cell- and egg- propagated reference viruses representing the A(H3N2) vaccine components of the NH 2021-2022 influenza season (A/Cambodia/e0826360/2020). However, ferret antisera raised against 3C.2a1b.2a.2 viruses, such as cell culture-propagated A/Darwin/6/2021 or egg-propagated A/Darwin/9/2021, inhibited 3C.2a1b.2a.2 test viruses well. Human serology assays showed that, when compared to titres against cell culture-propagated A/Cambodia/e0826360/2020-like 2a.1 vaccine viruses, post-vaccination GMTs against many cell culture-propagated 2a.2 viruses were significantly reduced in most serum panels.

All influenza B viruses collected since 1 September 2021 were of the B/Victoria/2/87 lineage. Most recent viruses belonged to genetic subgroups 1A.3a.1 or 1A.3a.2, and the latter predominated, showing a wider geographic spread. The great majority of these viruses were recognized poorly by ferret antisera raised against cell culture- and egg-propagated 1A.3 viruses, such as the NH 2021-2022 vaccine virus B/Washington/02/2019. Post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2) inhibited viruses from this subgroup well. Human serology assays showed post-vaccination HI GMTs were significantly reduced against 1A.3a.1 and 1A.3a.2 viruses. No B/Yamagata lineage viruses were available for characterization.

The WHO recommends that quadrivalent vaccines for use in the 2022-2023 northern hemisphere influenza season contain the following:

Egg-based vaccines

- **an A/Victoria/2570/2019 (H1N1)pdm09-like virus;**
- **an A/Darwin/9/2021 (H3N2)-like virus;**
- **a B/Austria/1359417/2021 (B/Victoria lineage)-like virus; and**
- **a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.**

Cell culture- or recombinant-based vaccines

- **an A/Wisconsin/588/2019 (H1N1)pdm09-like virus;**
- **an A/Darwin/6/2021 (H3N2)-like virus;**
- **a B/Austria/1359417/2021 (B/Victoria lineage)-like virus; and**
- **a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.**

The WHO recommends that trivalent vaccines for use in the 2022-2023 northern hemisphere influenza season contain the following:

Egg-based vaccines

- **an A/Victoria/2570/2019 (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/588/2019 (H1N1)pdm09-like virus;**
- **an A/Darwin/6/2021 (H3N2)-like virus; and**
- **a B/Austria/1359417/2021 (B/Victoria 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 website⁴. 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 influenza⁵.

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>)
- Division of Virology, National Institute for Biological Standards and Control, a centre of the 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, the United States of America (email: cbershippingrequests@fda.hhs.gov)
- Centre for Influenza and Respiratory Virus Research, National Institute of Infectious Diseases, 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011, Japan (email: flu-vaccine@nih.go.jp)

⁴ <https://www.who.int/teams/global-influenza-programme/vaccines/who-recommendations/candidate-vaccine-viruses>

⁵ [https://www.who.int/news-room/fact-sheets/detail/influenza-\(seasonal\)](https://www.who.int/news-room/fact-sheets/detail/influenza-(seasonal))

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 updates⁶ of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website⁷.

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

Annex 1

Declarations of interest

Annex 1 Declarations of interest The WHO recommendation on the composition of influenza vaccines for use in the northern hemisphere 2022-2023 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 Canberra	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: IFPMA, Innovative Medicines Initiative and PATH.
WHO CC Koltsovo	Dr Elena Gavrilova	None
WHO CC and ERL NIID Tokyo	Dr Hideki Hasegawa	None
WHO CC London	Dr John McCauley	Following items were declared: • Served on an organizing committee for an educational flu awareness meeting/symposium/teleconferences organized by Seqirus. No payment received. • Served as an advisor on antiviral drug (Baloxavir) and attended a meeting on new influenza inhibitors organized by Roche as part of an ISIRV Antiviral Group. No payment received. • Serving as an advisor on RNA vaccines to Pfizer. No payment received. • Serving as an advisor on carbohydrate-based diagnostics, including influenza to Icen Diagnostics. No payment received. • Member of the advisory committee for the Global Influenza Hospital Surveillance Network. No payment received. • Participant in the Global Influenza Initiative by Sanofi Pasteur. No payment received.

		The items declared and listed below belong to Dr McCauley'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 July 2010- June 2022 - Daily expenses reimbursed by the European Medicines Agency for participation in the meeting on the outcome of Northern Hemisphere WHO Vaccine Selection Meeting to European Medicines Agency to provide advice for European Regulations for the vaccine.
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, Biocryst 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. Being co-owner with NIH of a patent: Influenza Hemagglutinin and Neuraminidase Variants, USA Patent Number: 7,504,109 B2, 17 March 2009. The patent ceased in 2018. No benefit generated or expected from it.
WHO CC Beijing	Dr Dayan Wang	None
WHO CC Memphis	Dr Richard Webby	None
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, McCauley, Subbarao, 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, McCauley, Subbarao, and Wentworth should continue to serve as Advisers.