

## Recommended composition of influenza virus vaccines for use in the 2023 southern hemisphere influenza season

September 2022

WHO convenes technical consultations<sup>1</sup> in February and September each year to recommend viruses for inclusion in influenza vaccines<sup>2</sup> for the northern hemisphere (NH) and southern hemisphere (SH) influenza seasons, respectively. This recommendation relates to the influenza vaccines for use in the SH 2023 influenza season. A recommendation will be made in February 2023 relating to vaccines that will be used for the NH 2023-2024 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<sup>3</sup>.

### Seasonal influenza activity

**From February through August 2022**, influenza activity was reported in all regions and overall remained lower than in pre-COVID-19 pandemic years, but was at the highest level compared to similar periods since the start of the COVID-19 pandemic. During this period, influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses circulated, although the proportions of the viruses circulating varied among reporting countries.

**In the temperate zone of the northern hemisphere**, increased influenza activity was reported in March and April, declined in May and returned to inter-seasonal levels from June through August. This peak in activity occurred later than usual and followed an earlier peak in late December 2021 and early January 2022.

***In Africa***, influenza B viruses predominated in Egypt, while A(H3N2) viruses predominated in Algeria, Morocco and Tunisia. ***In Asia***, two peaks of influenza detections were noted, in March and in July, with low activity in May. The majority of influenza detections were reported by China, with predominance of influenza B viruses from February through April and A(H3N2) from May to August. In other countries, the timing of peak activity varied. Influenza A(H3N2) viruses predominated in most reporting countries, while A(H1N1)pdm09 predominated in Pakistan and influenza B in Kazakhstan and Oman. ***In Europe***, influenza activity peaked in April and the majority of influenza detections were reported by countries in northern and southwestern Europe: influenza A viruses predominated, with sporadic detections of influenza B. Of the influenza A viruses detected, where subtyping was performed, A(H3N2) was predominant. ***In North America***, influenza activity increased from March through May in the United States of America (USA) and in May in Canada. Influenza A(H3N2) viruses predominated with small proportions of influenza A(H1N1)pdm09 and B. Of the influenza B viruses where lineage was confirmed, all belonged to the B/Victoria/2/87 lineage.

**Influenza activity in tropical and subtropical countries** was slightly lower than in seasons prior to the COVID-19 pandemic. Countries reported influenza A and B detections in varying proportions, with an overall predominance of influenza A viruses.

***In tropical and subtropical countries of Africa***, influenza A(H3N2) viruses were predominant. In Kenya, A(H1N1)pdm09 viruses predominated. While both influenza type A and B viruses co-circulated in the United Republic of Tanzania, and Zambia, the A(H1N1)pdm09 subtype predominated. Influenza B viruses predominated in Côte d'Ivoire and Zimbabwe. Elsewhere, A(H3N2) detections predominated, with the majority of detections reported by Ghana during an epidemic which peaked at the end of May. Uganda reported predominance of influenza A(H3N2) until May followed by A(H1N1)pdm09 and B

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

<sup>2</sup> Description of the process of influenza vaccine virus selection and development available at: [http://www.who.int/gb/pip/pdf\\_files/Fluvaccirusselection.pdf](http://www.who.int/gb/pip/pdf_files/Fluvaccirusselection.pdf)

<sup>3</sup> Influenza in the tropics and sub-tropics: <https://www.who.int/teams/global-influenza-programme/vaccines/vaccine-in-tropics-and-subtropics>

viruses.

***In the tropical countries of south and south-east Asia***, the timing of influenza activity and proportions of detected viruses varied among reporting countries. Influenza A(H1N1)pdm09 predominated in India and Pakistan, A(H3N2) in Bangladesh, Bhutan, Cambodia, Malaysia, the Maldives, the Philippines, Singapore, Sri Lanka, Thailand and Timor-Leste; influenza B in Lao People's Democratic Republic but with a recent upsurge in A(H3N2) activity. In Nepal, A(H1N1)pdm09 and A(H3N2) viruses circulated in similar proportions.

***In the tropical countries of Central America, the Caribbean and South America***, the peak of influenza activity varied among reporting countries. Brazil, Mexico, Nicaragua, Panama and Peru reported the majority of influenza detections in this region. Influenza A(H3N2) predominated in most reporting countries, with few detections of A(H1N1)pdm09 and influenza B viruses.

**In the temperate zones of the southern hemisphere**, influenza activity remained low until March when regional to widespread activity was reported by a number of countries, with a majority of influenza A(H3N2) viruses and, to a lesser extent, A(H1N1)pdm09 and B viruses. In temperate South America, influenza activity peaked in March in Argentina and in May to June in Chile, Paraguay and Uruguay, with the majority of detections being influenza A(H3N2) in these countries. In South Africa, the season began in May and peaked in June, with the majority of detections reported as influenza A(H1N1)pdm09. As influenza activity declined, greater proportions of A(H3N2) and B viruses were detected. In Oceania, high levels of influenza A(H3N2) activity, with few detections of A(H1N1)pdm09 and influenza B viruses, were reported in June and July. In Australia, influenza activity increased in May, and peaked in mid-June which was earlier than in typical seasons. Of the influenza B viruses where lineage was determined, only B/Victoria/2/87-like viruses were reported.

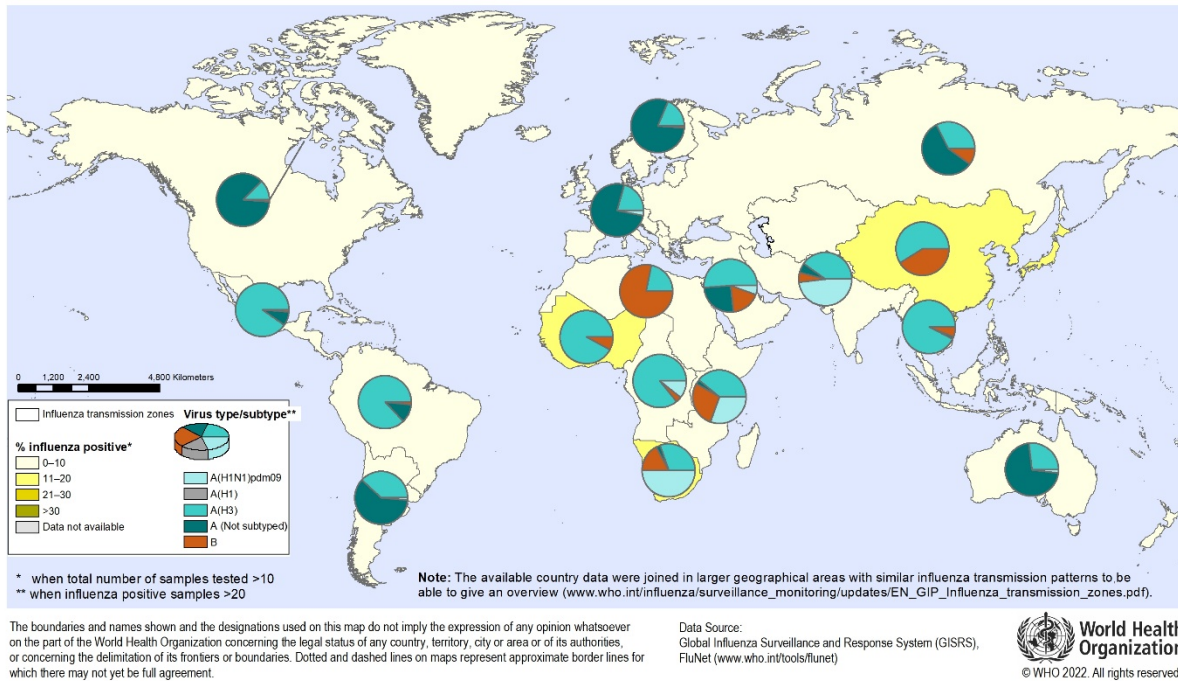
## **Influenza A**

Globally, influenza A virus detections outnumbered those of influenza B during this period. Influenza A(H1N1)pdm09 and A(H3N2) viruses were reported in most regions. In Africa, proportions of influenza A(H1N1)pdm09 and A(H3N2) varied among reporting countries. Influenza A(H1N1)pdm09 viruses were predominant in Kenya, South Africa, United Republic of Tanzania, and Zambia, while elsewhere influenza A(H3N2) dominated. In Asia, A(H3N2) viruses were predominant in all reporting countries except in India and Pakistan where A(H1N1)pdm09 predominated. In Europe, the Americas, and Oceania, both A(H1N1)pdm09 and A(H3N2) viruses co-circulated, with a predominance of A(H3N2).

## **Influenza B**

Globally, influenza B virus detections were much lower than those for influenza A during this period. Influenza B viruses predominated in some countries in Africa (Cote d'Ivoire, Egypt and Zimbabwe) and in Asia (Lao People's Democratic Republic and Oman). All circulating influenza B viruses, where lineage was confirmed, belonged to the B/Victoria/2/87 lineage.

## Distribution of influenza virus type/subtype by influenza transmission zone, between February and August 2022



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 24 February 2022 to 19 September 2022, seven human cases of A(H5N6) virus infection in China and one detection of an A(H5N1) virus in the United States of America were reported. Three cases of A(H9N2) infection were reported in China (2) and Cambodia (1). Two cases of A(H3N8) and one case of A(H10N3) virus infection were reported in China.

Two cases of A(H1N1)v virus infection were reported, one each in China and in Germany, and five cases of A(H1N2)v virus infection were reported in the United States of America. Three cases of A(H3N2)v virus infection were reported in the United States of America.

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

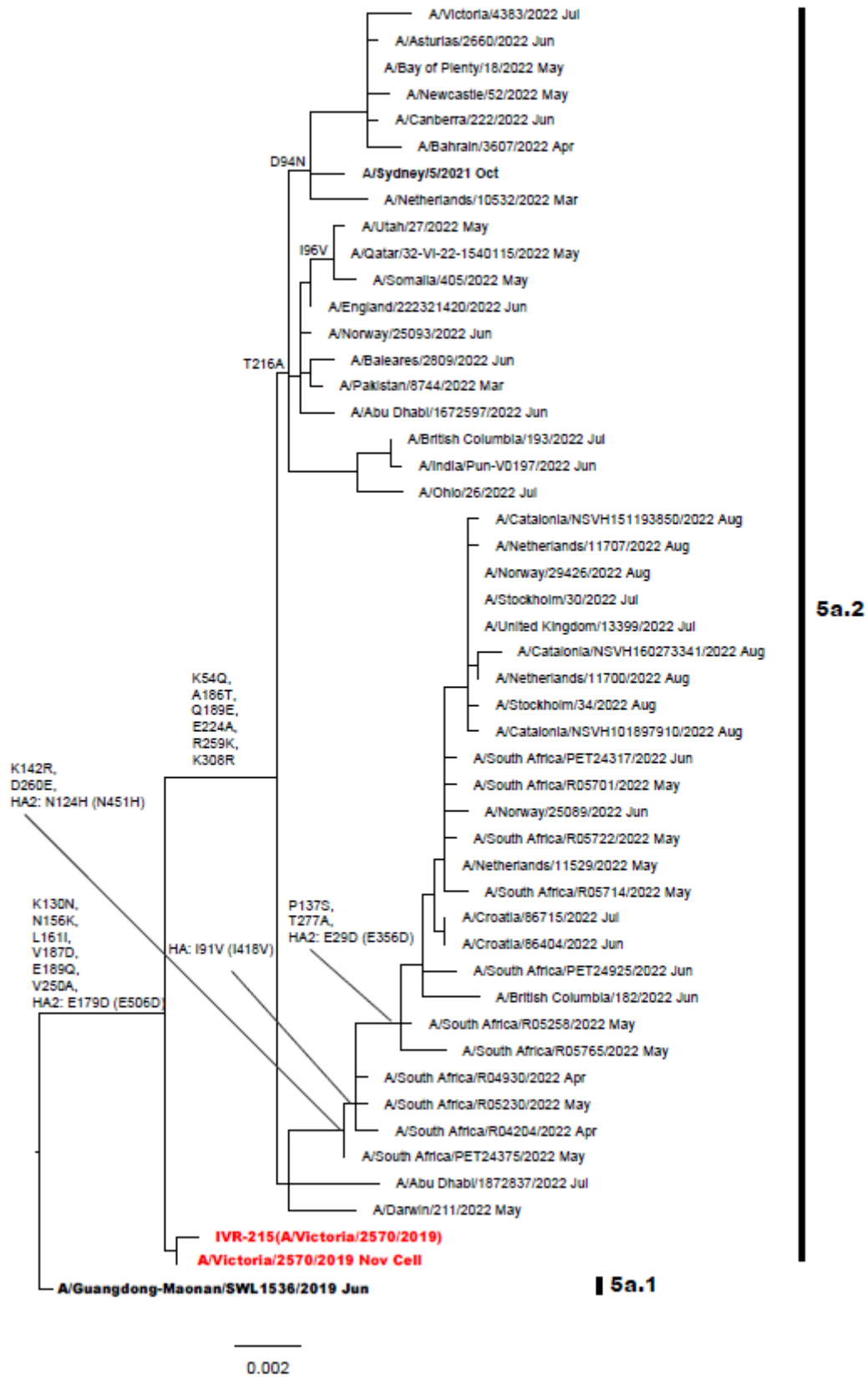
### Influenza A(H1N1)pdm09 viruses

A(H1N1)pdm09 viruses have circulated in many parts of the world. Since 1 February 2022 viruses have been characterized from Europe, North America, parts of Central and South America, southern, east and west Africa, the Middle East, the Indian subcontinent, Japan, Australia and New Zealand.

Genetically characterized viruses had haemagglutinin (HA) genes that belong to phylogenetic clade 6B.1A.5a (5a), characterized by HA1 amino acid substitutions N129D, T185I and N260D, which grouped in two major subclades: 5a.1 defined by HA amino acid substitutions D187A and Q189E in antigenic site Sb and 5a.2 defined by amino acid substitutions in the receptor binding site and antigenic site Sa (Fig. 2).

Subclade 5a.2 viruses collected after January 2022 have further diversified with additional HA1 amino acid substitutions (K54Q, A186T, Q189E, E224A, R259K and K308R), some of which are located in antigenic site Sb. There are a number of emerging subgroups, such as viruses with HA1 substitutions K142R and P137S, both of which are in antigenic site Ca, and another defined by T216A (Fig. 2).

**Fig. 2. A phylogenetic tree for the HA genes of representative subclade 6B.1A.5a.2 viruses.**



A phylogeny of 5a.2 viruses collected after January 2022 was rooted to the previously recommended 5a.1 vaccine virus (A/Guangdong-Maonan/SWL1536/2019) and followed by the A/Victoria/2570/2019 5a.2 cell culture- and egg-propagated vaccine viruses.

The antigenic characteristics of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) assays with post-infection ferret antisera (Table 1). HI results for viruses with collection dates after January 2022 showed that the majority of 5a.1 viruses were recognized well by antisera raised against the previous vaccine virus (egg- and cell culture-propagated A/Guangdong-Maonan/SWL1536/2019-like 5a.1 viruses). Viruses in subclade 5a.2 were recognized poorly by these 5a.1 antisera. Ferret antisera raised against cell culture- and egg-propagated A/Victoria/2570/2019 vaccine viruses recommended for the NH 2021-2022 and 2022-2023, and the SH 2022 seasons, recognized 5a.2 viruses well despite substitutions at known antigenic sites compared with the vaccine viruses. These ferret antisera recognized 5a.1 viruses poorly. However, a pool of sera from adults who had received the SH 2022 egg-based vaccine generally showed good recognition of both 5a.1 and 5a.2 viruses, though a subgroup of 5a.2 viruses that have HA1 K142R and P137S substitutions was recognized less well (Table 1).

**Table 1. HI assay of recently circulating A(H1N1)pdm09 viruses.**

Reference viruses	Virus passage details		Clade		Post-infection ferret antiserum						Human serum pool	
					E4		S3, MDCK1		E4			E3
					Guang/SWL1536	Vic2455	Togo881	MDCK1	Vic2570	Vic2570		Syd5
A/Guangdong-Maonan/SWL1536/2019	E4	5a.1	<u>1280</u>	2560	2560	<80	<80	<80	80	320		
A/Victoria/2455/2019	MDCK3	5a.1	1280	<u>1280</u>	1280	<80	<80	<80	80	640		
A/Togo/881/2020	S3, MDCK2	5a.1	2560	2560	<u>2560</u>	<80	80	160	160	640		
A/Victoria/2570/2019	MDCK1	5a.2	80	80	<80	<u>320</u>	320	320	320	160		
A/Victoria/2570/2019	E6	5a.2	80	80	<80	1280	<u>1280</u>	1280	1280	<b>640</b>		
A/Sydney/5/2021	E3	5a.2	<80	80	<80	2560	1280	<u>2560</u>	640	640		
<b>Test viruses</b>												
A/Sydney/894/2022	MDCK1	5a.2	<80	<80	<80	1280	1280	1280	1280	320		
A/Perth/184/2022	MDCK1, MDCK1	5a.2	<80	<80	<80	640	1280	1280	1280	320		
A/Canberra/222/2022	MDCK1	5a.2	<80	<80	<80	1280	1280	2560	320	320		
A/Darwin/488/2022	SIAT2	5a.2	<80	<80	<80	640	1280	1280	1280	320		
A/South Africa/R05765/2022	MDCK1, MDCK1	5a.2	<80	<80	<80	640	640	640	80	80		
A/South Africa/R05258/2022	MDCK1, MDCK1	5a.2	<80	<80	<80	1280	1280	1280	1280	160		
A/South Africa/R04994/2022	MDCK1, MDCK1	5a.2	<80	<80	<80	1280	1280	2560	160	160		
A/South Africa/R03645/2022	MDCK1, MDCK1	5a.2	<80	<80	<80	1280	1280	2560	160	160		
A/Sydney/877/2022	MDCK1	5a.1	1280	2560	2560	<80	<80	80	640	640		
A/Sydney/866/2022	MDCK1	5a.1	2560	2560	2560	<80	80	80	640	640		
A/Sydney/869/2022	MDCK1	5a.1	2560	2560	2560	<80	<80	80	640	640		
A/South Africa/R05655/2022	MDCK1, MDCK1	5a.1	1280	1280	1280	<80	<80	<80	320	320		
A/South Africa/R05558/2022	MDCK1, MDCK1	5a.1	1280	2560	1280	<80	<80	80	320	320		
A/South Africa/R05539/2022	MDCK1, MDCK1	5a.1	1280	2560	1280	<80	<80	80	640	640		

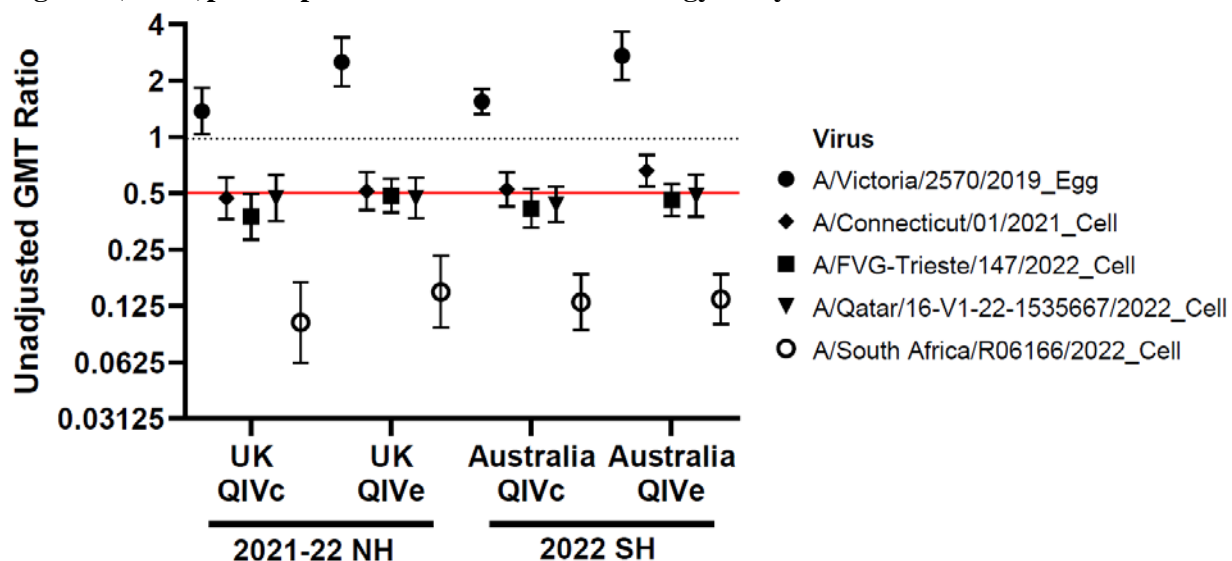
Human serology studies used three serum panels from adults (18-64 years) and elderly adults ( $\geq 65$  years) who had received egg-based quadrivalent inactivated vaccines (standard or adjuvanted) or cell culture-based quadrivalent inactivated vaccine formulated for the SH 2022 season. SH 2022 egg-based 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-based vaccines contained antigens from 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 (B/Yamagata lineage)-like viruses.

Four serum panels from children (6 months to 17 years) and adults (18-64 years) who had received egg-based quadrivalent inactivated vaccines or cell culture-based quadrivalent inactivated vaccine formulated for the NH 2021-2022 season were also used. 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; NH 2021-2022 cell culture-based 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 virus antigens.

Human serology studies using these serum panels showed minor reductions in post-vaccination HI geometric mean titres (GMTs) for the majority of recently circulating, representative A(H1N1)pdm09 5a.1 viruses when compared to cell culture-propagated A/Wisconsin/588/2019-virus. However, significant reductions in HI GMTs were observed for some 5a.2 viruses with additional HA1 amino acid substitutions A186T, Q189E, T216A and E224A, notably so for those with additional amino acid substitutions P137S and K142R (e.g. A/South Africa/R06166/2022) (Fig. 3). When measured against egg-propagated A/Victoria/2570/2019, most recent A(H1N1)pdm09 viruses showed significantly reduced GMTs.



**Fig. 3. 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 receiving NH 2021-2022 egg-propagated vaccine (United Kingdom QIVe), NH 2021-2022 cell culture-propagated vaccine (United Kingdom QIVc), SH 2022 egg-propagated vaccine (Australia QIVe) and SH 2022 cell culture-propagated vaccine (Australia QIVc) were tested against the **5a.2** viruses indicated. GMT ratios and 90% confidence intervals are shown.

Of 879 A(H1N1)pdm09 viruses collected after January 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analysis, five viruses had an H275Y substitution in the neuraminidase. Of these five, four were available for phenotypic analysis and showed highly reduced inhibition by oseltamivir and peramivir, and normal inhibition by zanamivir and laninamivir. Of 607 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 February 2022 showed that viruses belonging to genetic subclade 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 predominated globally and were detected in all regions. The 2a.2 HA further diversified into 4 genetic groups containing H156Q or H156S and D53G or H156S and D53N or D53G, that circulated in different proportions in different regions. However, viruses belonging to 3C.2a1b subclade **2a.1** (HA1 substitutions G186S, F193S, Y195F and S198P) predominated in China and early in 2022 in Timor-Leste. Viruses reported from China had additional substitutions K171N and I48T in HA1.

Generally, ferret antisera raised against cell culture-propagated A/Darwin/6/2021-like viruses and egg-propagated A/Darwin/9/2021-like viruses (**2a.2**), representing the vaccine viruses for the SH 2022 and NH 2022-2023 influenza seasons, recognized recent 2a.2 viruses possessing the HA1 substitution H156S well. However, a small number of 2a.2 viruses without the H156S substitution reacted less well with these antisera. Recent 2a.1 viruses, including those with additional HA1 substitutions, were recognized well by ferret antisera raised against cell culture-propagated A/Cambodia/e0826360/2020-like viruses (**2a.1**), but were recognized less well by ferret antisera raised against 2a.2 viruses (cell culture-propagated A/Darwin/6/2021-like and egg-propagated A/Darwin/9/2021-like viruses).

Human serology studies were conducted with human serum panels from the SH 2022 season as described

above, using HI and virus neutralization (VN) assays. Geometric mean HI and VN titres against most recent representative A(H3N2) viruses from genetic groups 2a.2 and 2a.1 were not significantly reduced compared to titres against the cell culture-propagated A/Darwin/6/2021 vaccine virus. Reductions of VN GMTs were more pronounced when compared to egg-propagated A/Darwin/9/2021-like reference viruses.

Of 4,577 influenza A(H3N2) viruses collected after January 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analysis, none showed evidence of reduced inhibition by neuraminidase inhibitors. Of 3,250 A(H3N2) viruses examined for endonuclease inhibitor baloxavir susceptibility by genetic and/or phenotypic analysis, one showed evidence of reduced susceptibility to baloxavir and had an E23G substitution in the PA protein.

### **Influenza B viruses**

Globally, influenza B viruses represented 4.7% of the viruses detected since 1 February 2022, and all of those tested 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 substitution K136E and a triple amino acid deletion in HA1 (positions 162-164). The 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 belong to group 1A.3a. A small number of 1A.3 viruses continue to circulate and recent viruses detected in Kenya and the Netherlands have acquired additional substitutions K75E, E128K, T155A and G230N in HA1. The 1A.3a HA diversified into 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**). HA subgroup 3a.1 represented a small proportion of the viruses circulating in early 2022 in China. The 3a.2 HA subgroup has predominated in Africa, Asia (including China), Europe, North America, Oceania, and South America. The majority of viruses in the 3a.2 HA subgroup have the additional substitution D197E in HA1.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2) recognized the predominant 3a.2 subgroup well, but recognized other viruses less well. Ferret antisera raised against B/Sichuan-Jingyang/12048/2019-like viruses (3a.1) recognized viruses in subgroup 3a.1 well but subgroup 3a.2 viruses less well. The viruses in subclade 1A.3 that have continued to evolve were not 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).

Human serology studies, using the serum panels from the SH 2022 described above, did not show significant reductions in post-vaccination HI GMTs against the majority of recent representative B/Victoria lineage viruses from the 3a.2 subgroup when compared to the egg or cell culture-propagated B/Austria/1359417/2021 vaccine viruses. Significant reductions were detected with most serum panels for viruses from clade 1A.3 with additional amino acid substitutions K75E, E128K, T155A and G230N. Due to the lack of available recent viruses, human serology studies were not performed for the B/Yamagata lineage.

Of 858 influenza B/Victoria lineage viruses collected since 1 February 2022 and examined for neuraminidase inhibitor (NAI) susceptibility by genetic and/or phenotypic analysis, one had a D197N substitution in the NA and showed evidence of reduced inhibition by neuraminidase inhibitors oseltamivir and zanamivir. Of 497 B/Victoria lineage viruses examined by genetic and/or phenotypic analysis, none showed evidence of reduced susceptibility to the endonuclease inhibitor baloxavir.

### **Recommended composition of influenza virus vaccines for use in the 2023 southern hemisphere influenza season**

Influenza A(H1N1)pdm09 viruses collected since 1 February 2022 with HA genes that belonged to two

subclades, 6B.1A.5a.1 (**5a.1**) and 6B.1A.5a.2 (**5a.2**), circulated in different geographic locations. Viruses in the 5a.2 subclade continue to diversify and recently circulating viruses (represented by A/Sydney/5/2021) share substitutions in antigenic site Sb. Post-infection ferret antisera raised against the NH 2021-2022 and SH 2022 A(H1N1)pdm09 vaccine components (egg-propagated A/Victoria/2570/2019 and cell culture-propagated A/Wisconsin/588/2019 (5a.2)) recognized 5a.2 viruses well, but 5a.1 viruses poorly. However, human serology assays showed markedly reduced post-vaccination GMTs against a substantial number of recent cell culture-propagated 5a.2 viruses in most serum panels 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 February 2022 had HA genes that belonged to genetic group 3C.2a1b.2a.2 (**2a.2**). The majority of recently circulating viruses were recognized well by ferret antisera raised against 2a.2 viruses, such as cell culture-propagated A/Darwin/6/2021 and egg-propagated A/Darwin/9/2021. Human serology assays showed that post-vaccination GMTs against most recent representative A(H3N2) viruses from genetic groups 2a.2 and 3C.2a1b.2a.1 were not significantly reduced compared to titres against the cell culture-propagated A/Darwin/6/2021 vaccine virus.

All circulating influenza B viruses collected since 1 February 2022 were of the B/Victoria/2/87 lineage. Most recent viruses belonged to genetic subgroups 1A.3a.1 or 1A.3a.2 (**3a.2**), and the latter predominated. The great majority of the circulating viruses were recognized well by 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 most recent representative B/Victoria lineage viruses from genetic subgroup 3a.2 were not significantly reduced compared to titres against the cell culture-propagated B/Austria/1359417/2021 vaccine virus.

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

#### **Egg-based vaccines**

- an A/Sydney/5/2021 (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/Sydney/5/2021 (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 2023 southern hemisphere influenza season contain the following:

#### **Egg-based vaccines**

- an A/Sydney/5/2021 (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/Sydney/5/2021 (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 website<sup>4</sup>. 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<sup>5</sup>.

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](mailto: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](mailto:enquiries@nibsc.org)) website: [http://www.nibsc.org/science\\_and\\_research/virology/influenza\\_resource.aspx](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](mailto: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](mailto: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](mailto: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](mailto: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](mailto: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](mailto: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](mailto:whocc-china@cnic.org.cn), website: <http://www.chinaivdc.cn/cnic/en>).

WHO provides fortnightly [updates](#) of global influenza activity. Other information about influenza surveillance can be found on the WHO Global Influenza Programme website<sup>7</sup>.

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