Influenza Updates

The newsletter of the WHO Collaborating Centre for Reference and Research on Influenza in Melbourne

@WHOCCFluMelb

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Preparation for the upcoming influenza season

Winter and the influenza season is fast approaching over the next few months across many Southern Hemisphere countries. This means that any sample you are able to send to us will be vital in our continued surveillance efforts.

With this in mind, please note the following points:

- Please send us your samples (ideally March 2023 onwards) as soon as possible after collection, as they are most useful when they have been collected recently
- We accept both viral isolates and/or original clinical specimens
- We need to receive samples by the end of August at the very latest (and preferably earlier) in order to process them in time for the Consultation.
- The WHO Shipping Fund Project (SFP) is available to assist National Influenza Centres in covering the cost of shipping samples to WHO Collaborating Centres up to four times per year. It is recommended that one of the shipments be in July to mid-August. If you have any questions about shipping samples or would like information about accessing the WHO Shipping Fund, please contact us at *whoflu@influenzacentre.org*.

Timing for sending samples to a WHO Collaborating Centre

Number of specimens positive for influenza by subtype

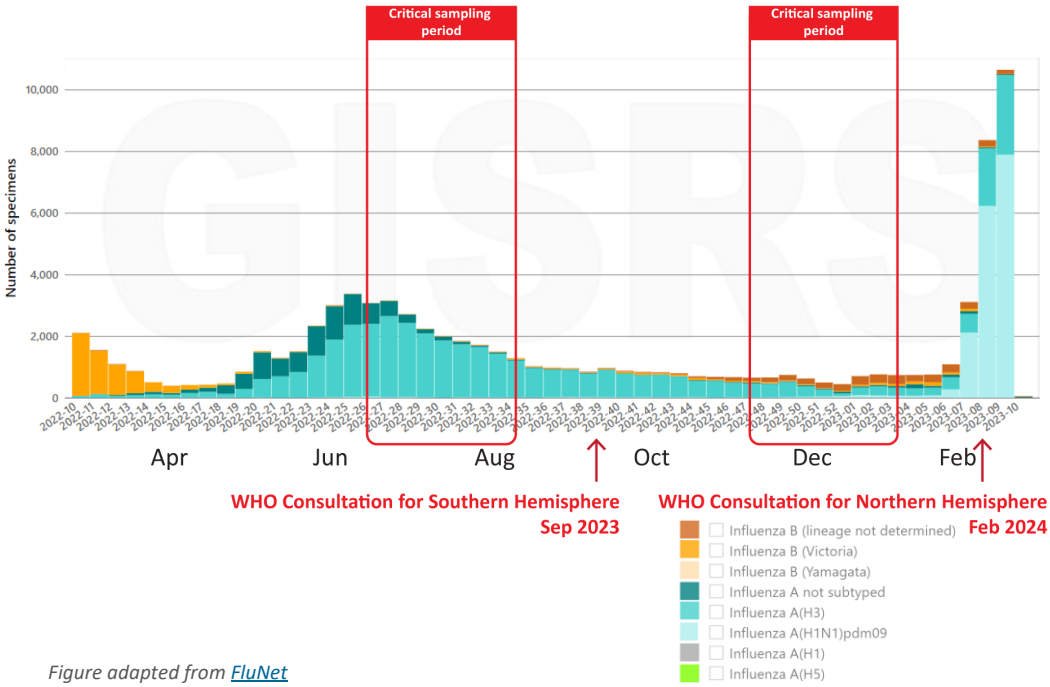


Figure adapted from FluNet

WHO Collaborating Centre for Reference and Research on Influenza
VIDRL

Doherty Institute

The University of Melbourne

The Royal Melbourne Hospital

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

Recommendations for Northern Hemisphere 2023-2024 vaccine announced

The WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2023-2024 was held in Geneva, Switzerland on 24 February 2023. Following the Consultation, WHO made the following recommendation:

It is recommended that **quadrivalent** vaccines for use in the 2023-2024 Northern Hemisphere influenza season contain the following:

Egg-based:

- an A/Victoria/4897/2022 (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– or recombinant protein-based:

- an A/Wisconsin/67/2022 (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 composition of trivalent influenza vaccines is recommended to include the A(H1N1)pdm09, A(H3N2), and the B Victoria lineage viruses.

The recommendations for the Northern Hemisphere 2023-2024 vaccine remain largely the same as the recommendations for the 2023 Southern Hemisphere vaccine, except the A(H1N1)pdm09 component was changed from A/Sydney/5/2021 to A/Victoria/4897/2022. More details about the most recent recommendations can be found here.

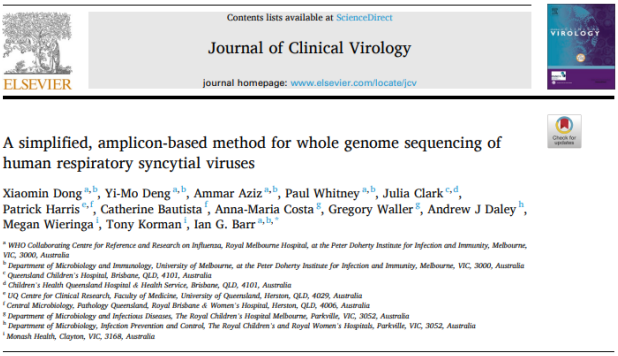
Contribution of National Influenza Centres to the vaccine recommendations

We thank everyone who has sent us influenza samples prior to the February 2023 influenza vaccine Consultation. Your viruses provide essential data on recently circulating strains and help to inform the choice of recommended vaccine strains.

We are especially pleased that the most recently added A (H1N1)pdm09 virus in the vaccine recommendation, A/Victoria/4897/2022 (egg), was originally submitted to our Centre by the **Royal Melbourne Hospital**, Victoria, Australia.

In this context, we would like to acknowledge the contribution and critical role played by WHO National Influenza Centres and other submitting laboratories in providing influenza samples to WHO Collaborating Centres, not only for the purposes of analysis and surveillance, but also for the provision of potential vaccine candidates. Please continue to send us your samples. The need for constant surveillance remains as the influenza virus continues to circulate and evolve.

Featured Research Articles


Contents lists available at ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

A simplified, amplicon-based method for whole genome sequencing of human respiratory syncytial viruses

Xiaomin Dong [a,b], Yi-Mo Deng [a,b], Ammar Aziz [a,b], Paul Whitney [a,b], Julia Clark [c,d], Patrick Harris [c,f], Catherine Bautista [f], Anna-Maria Costa [g], Gregory Waller [g], Andrew J Daley [h], Megan Wieringa [i], Tony Korman [i], Ian G. Barr [a,b,*]

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[i] Monash Health, Clayton, VIC, 3168, Australia

Dong X, Deng YM, Aziz A, Whitney P, Clark J, Harris P, Bautista C, Costa AM, Waller G, Daley AJ, Wieringa M, Korman T, Barr IG. A simplified, amplicon-based method for whole genome sequencing of human respiratory syncytial viruses. J Clin Virol. 2023 Apr;161:105423. doi: 10.1016/j.jcv.2023.105423. PubMed Link.

'A simplified, amplicon-based method for whole genome sequencing of human respiratory syncytial viruses '

Featuring Xiaomin Dong, Yi-Mo Deng, Ammar Aziz, Paul Whitney, and Ian Barr from the Centre

Published in the Journal of Clinical Virology last month, this article describes the development of a rapid and simplified amplicon-based one-step multiplex reverse-transcription polymerase chain reaction for whole genome sequencing of both types of human respiratory syncytial virus (RSV).

This assay produces robust results while being simple to set up. The sample preparation is easily scalable, and is also relatively inexpensive. Therefore, this assay will be a valuable addition to existing next generation sequencing methodology for the whole genome sequencing of RSV.

15th Australian Influenza Symposium—SAVE THE DATE

We are pleased to announce that the 15th Australian Influenza Symposium will be held on 2-3 November 2023 at the Peter Doherty Institute for Infection and Immunity.

Further information (including registration details) will be communicated at a later date.

If you have any questions regarding the Symposium, please email *symposium@influenzacentre.org*.

Training at the Centre and visits to regional laboratories

We welcomed Ms Angella Margaret Manele from the National Referral Hospital Molecular Laboratory in Honiara, Solomon Islands, and Mr Jeffery Kalomar from the Villa Central Hospital Molecular Laboratory in Port Villa, Vanuatu, from 27 February—17 March for a training program in collaboration with VIDRL.

During their time at the Centre, both undertook training in techniques relevant to PCR for the detection of influenza virus in clinical samples.

We hope the skills gained from this training stand them in good stead.

Patrick Reading participated in the joint national and international influenza surveillance review (Sentinel Surveillance & Laboratory assessment) from 5-9 March 2023 in Male, Republic of the Maldives. The review was coordinated by WHO SEARO.

He was the team lead for assessment of the National Influenza Laboratory at Indira Gandhi Memorial Hospital to identify the areas and provide recommendations for strengthening in order to be recognised as a National Influenza Centre by WHO. Other members of the laboratory assessment team were influenza experts from India, Sri Lanka and Bhutan.

Upcoming meetings and conferences

Communicable Diseases & Immunisation Conference 2023

'Adapting to a new landscape for infectious disease prevention and control'

Monday 19 to Wednesday 21 June 2023
Perth Convention and Exhibition Centre, WA

Public Health Association AUSTRALIA
Communicable Diseases network AUSTRALIA
PHLN Public Health Laboratory Network

#CDIC2023

Communicable Diseases & Immunisation Conference 2023

Monday 19th—Wednesday 21st of June 2023
Perth Convention and Exhibition Centre, WA

For information on the conference (including registration details and program), please click here.

Farewell and good luck

It is with sadness but good wishes that we announce the departure of several staff members from the Centre. We thank Paulina, Sook Kwan, Ammar, and Melanie for their significant contributions to the Centre, and wish them all the very best for their future.

Dr Paulina Koszalka had been a Medical Scientist with the Antivirals and Animal Influenzas group for around 9 months, prior to which she was a Ph. D student under the supervision of Kanta Subbarao, Vijaykrishna Dhanasekaran (Monash University), Stephen Turner (Monash University), and Aeron Hurt (Roche). She has now taken on a position as a Post-Doctoral researcher at Monash University.

Ms Sook Kwan Brown had been a Medical Scientist for 13 years, most recently as part of the Antivirals group. She has now taken on a position as a Medical Scientist with Seqirus.

Dr Ammar Aziz had been a Bioinformatician with the Centre for around 3 years. He has now taken on a position as a Bioinformatician with VIDRL.

Dr Melanie Duncan had been a Post-Doctoral researcher with the Antivirals and Animal Influenzas group for a year. She has now taken on a position as a Research Support Officer at the Children's Cancer Institute.

Recent activities at the Centre (1 January — 30 April 2023)

Below is a summary of surveillance activities at the Centre during this current reporting period. We anticipate that the next few months will be an increasingly busy time for the Centre as the Southern Hemisphere influenza season commences.

Samples received: The Centre received 3045 influenza samples from the laboratories and institutions listed below during the period 1 January—30 April 2023.

AUSTRALIA: Canberra Hospital, 4Cyte Pathology, The Children's Hospital at Westmead, Prince of Wales Hospital, Westmead Hospital, John Hunter Hospital, Royal Darwin Hospital, Queensland Children's Hospital, Sullivan Nicolaides Pathology, SA Pathology, Royal Hobart Hospital, Australian Clinical Labs (Geelong), Alfred Hospital, Austin Pathology, Australian Clinical Labs, Monash Medical Centre, Royal Children's Hospital, Royal Melbourne Hospital, St Vincent's Hospital, VIDRL, PathWest Laboratory Medicine (QEII)

CAMBODIA: Institut Pasteur du Cambodge

FIJI: Center for Communicable Disease Control

INDIA: National Institute of Virology

PHILIPPINES: Research Institute for Tropical Medicine

SAMOA: Tupua Tamases Meaole Hospital

SINGAPORE: National Public Health Laboratory

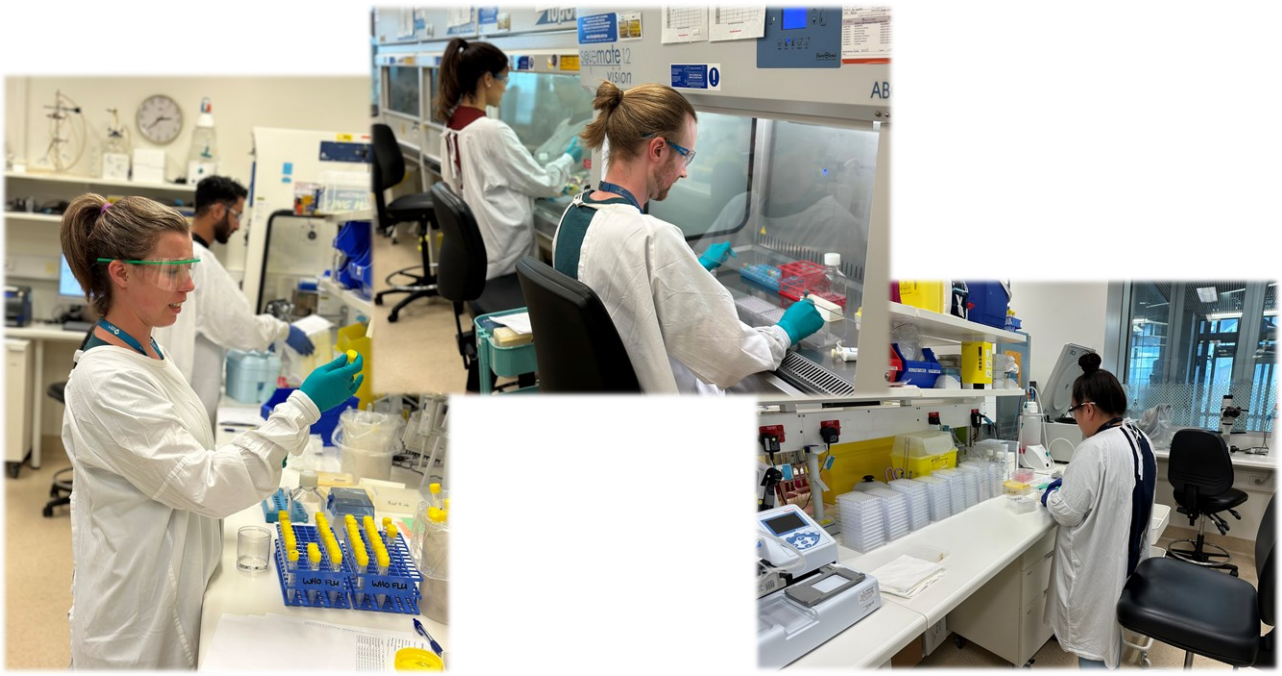
SRI LANKA: Medical Research Institute

THAILAND: Thai National Influenza Center

TONGA: Laboratory Service Vaiola Hospital

TUVALU: Princess Margaret Hospital

Isolation of viruses in eggs:
The Centre undertakes primary isolation of selected viruses in eggs to obtain potential vaccine strains. From 1 January to 30 April 2023, 5 A(H3N2) viruses were successfully isolated in eggs at the Centre.



Antigenic analysis
1236 viruses analysed by haemagglutination inhibition (HI) assay

Antiviral drug susceptibility
641 viruses analysed by neuraminidase inhibition (NAI) assay

Sequencing
264 viruses analysed
262 HA genes
260 NA genes
200 MP genes
62 NS genes

Country of submitting laboratory	No. of viruses analysed by HI assay*			No. of viruses tested by NAI assay*			No. of viruses sequenced by NGS or Sanger sequencing		
	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria
Australia	328	194	260	130	106	93	52	48	61
Cambodia	2	30	36	2	30	35	2	4	13
Fiji	154		51	79		25	17		
India	12	5	3	12	5	3	5	5	2
Malaysia	2	3	37		3	20		2	
Philippines	3	8	4	3	7	3	2	8	2
Singapore	13	44	11	13	35	11			1
Thailand	1	14	4	1	7	4	1	8	3
Tonga			6			4			2
Tuvalu	11			10			12		
Total	**526**	**298**	**412**	**250**	**193**	**198**	**98**	**82**	**84**

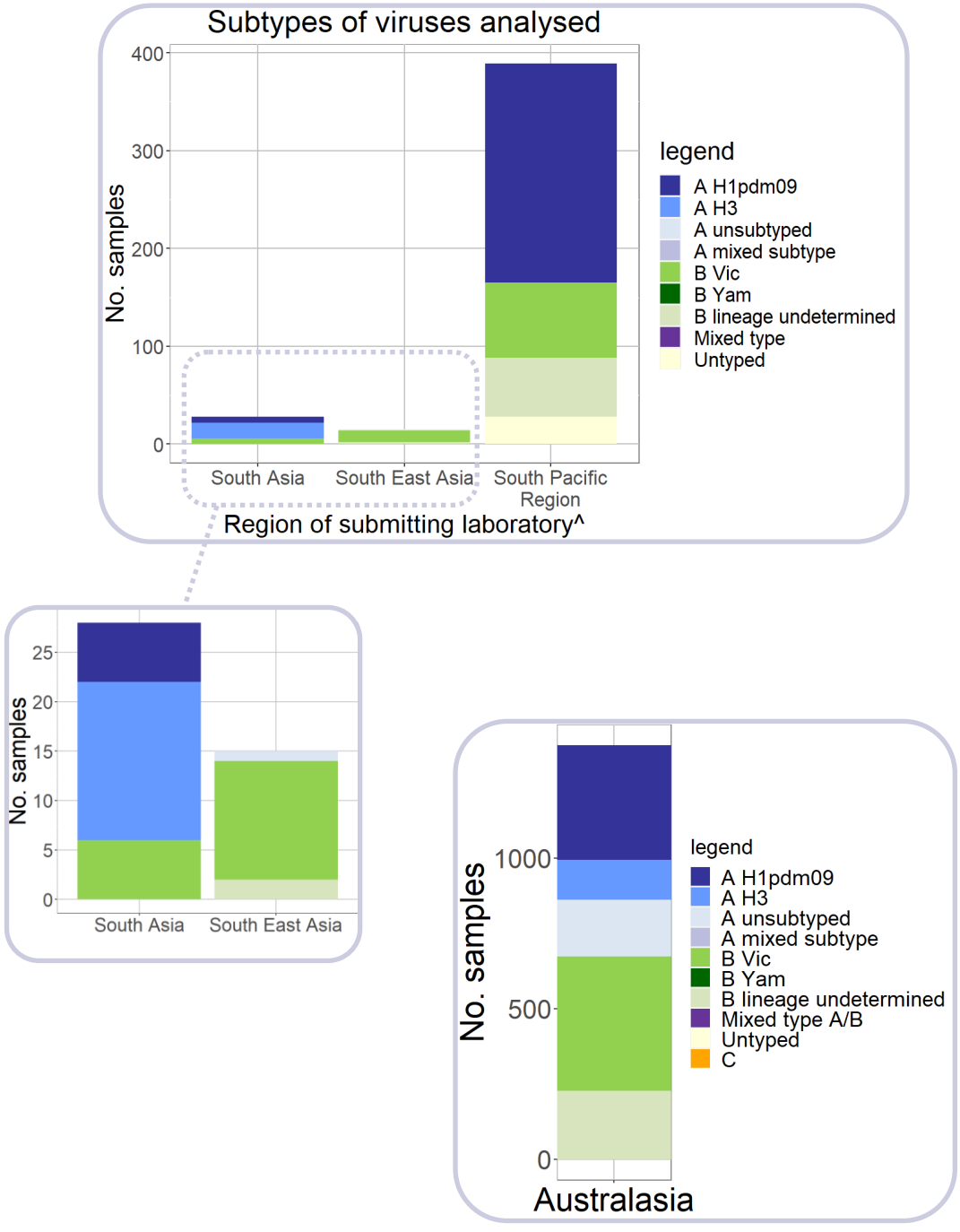
**Subtypes and lineages are based on analysis of HA and in some cases confirmed by genetic analysis of NA.*

Surveillance update: Virus activity 1 January—30 April 2023

The data below are results for viruses collected or sampled between 1 January and 30 April 2023 that have been analysed at the Centre as of 3 May 2023.

Virus types/subtypes[†]
The type and subtype/lineage of 1808 viruses have been determined.

33.8% A(H1N1)pdm09
8.2% A(H3N2)
30.0% B/Victoria



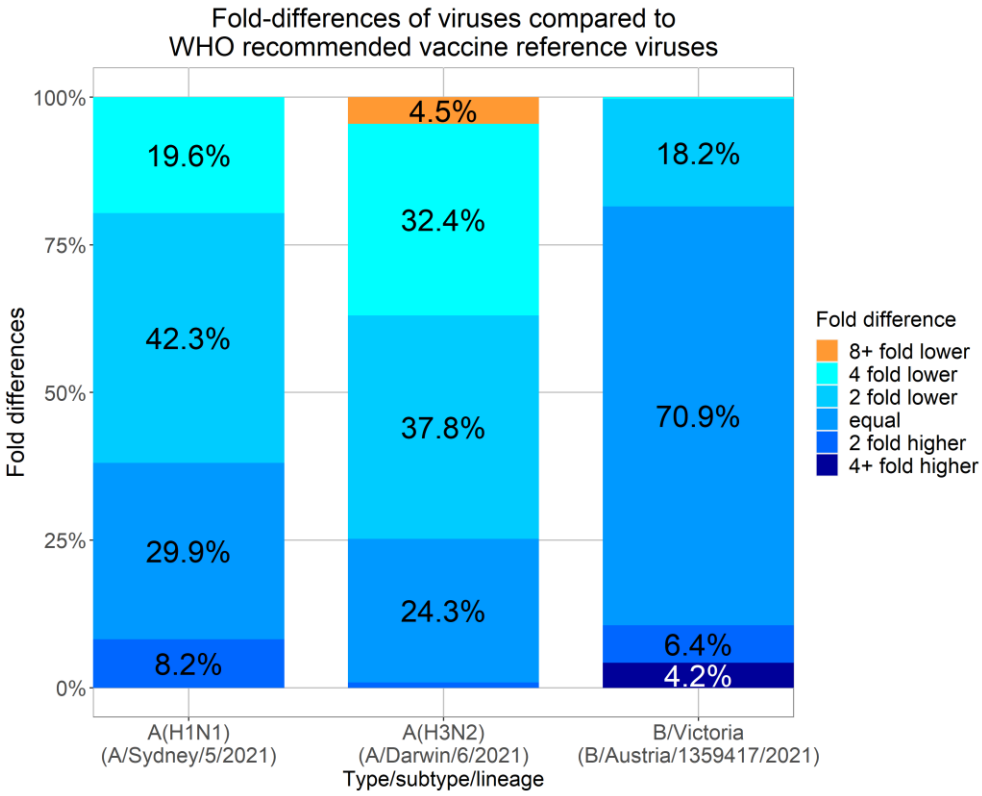
[†] *Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.*

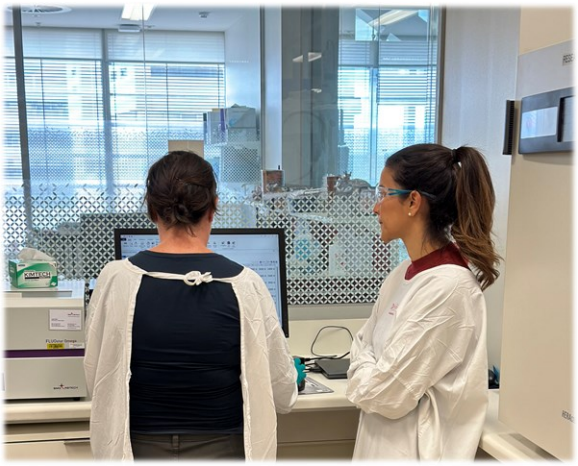
^The Pacific region comprises countries in Polynesia, Melanesia, and Micronesia.

Antigenic analysis*

A total of 566 viruses were tested using the haemagglutination inhibition (HI) assay.

Viruses were identified as low-reactors if their titre against reference antiserum was at least 8-fold lower than the titre of the reference virus. All A(H1N1)pdm09 and B/Victoria viruses were antigenically similar to their respective reference strains. A small proportion (4.5%) of A (H3N2) viruses were low reactors to the reference strain, A/Darwin/6/2021.

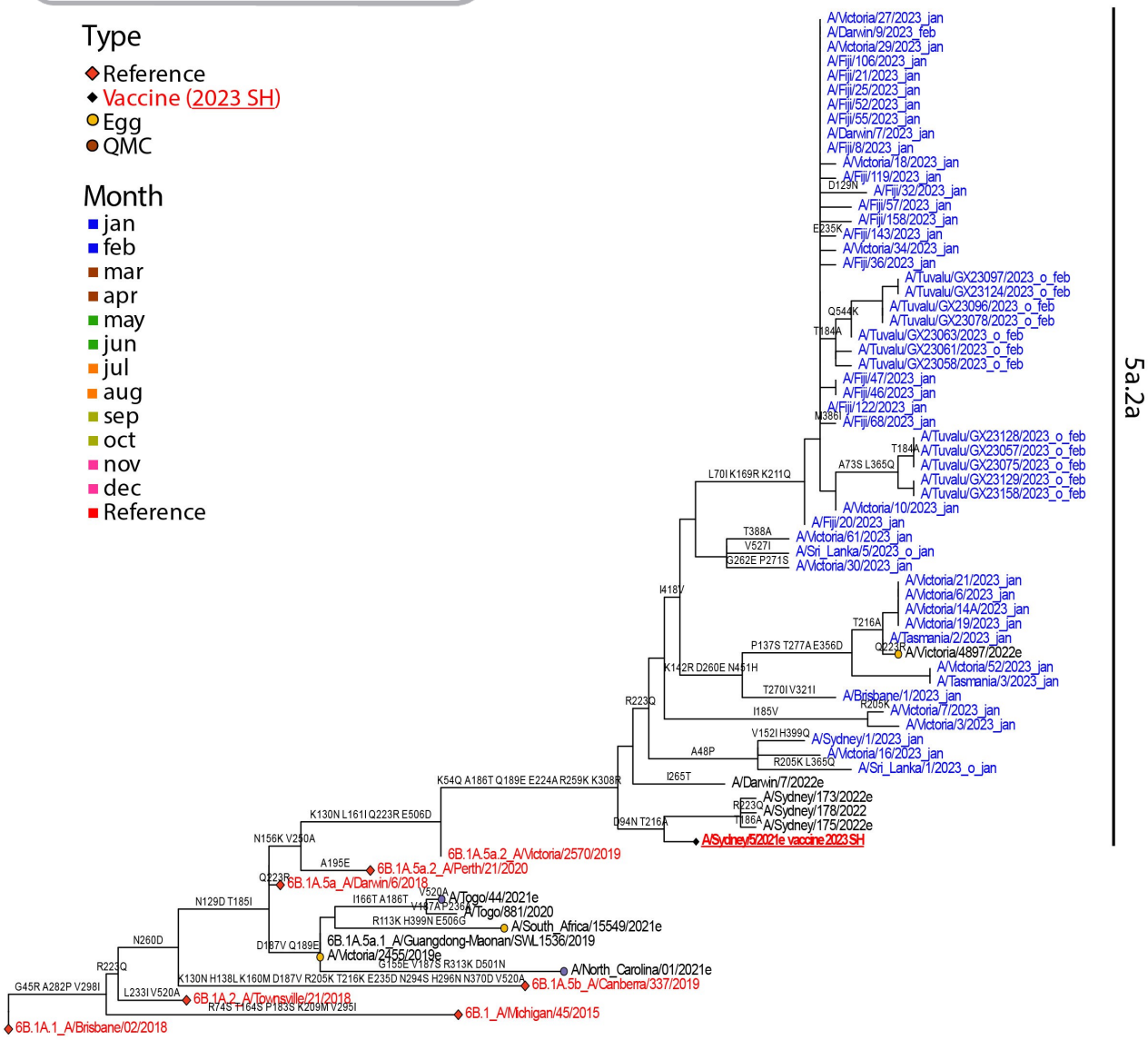




† *Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.*

Genetic analysis:
Focus on A(H1N1)pdm09
Sequencing of the haemagglutinin (HA) gene

Phylogenetic analysis shows an increasing proportion of viruses in subclade 5a.2a that do not cluster with the 2023 Southern Hemisphere vaccine strain A/Sydney/5/2021.



Antiviral drug susceptibility testing:

357 viruses tested by neuraminidase inhibition (NAI) assay

Testing for susceptibility to the antiviral drugs oseltamivir (Tamiflu), zanamivir (Relenza), peramivir, and laninamivir showed that no viruses had highly reduced inhibition by one or more neuraminidase inhibitors (NAI).

Type/subtype/ lineage	Oseltamivir			Peramivir			Laninamivir			Zanamivir		
	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition
A(H1N1)pdm09	177	1	3	178		3	181			180	1	
A(H3N2)	60			60			60			60		
B/Victoria	116			116			116			116		
Total	**353**	**1**	**3**	**354**		**3**	**357**			**356**	**1**	

Viruses with reduced inhibition by antiviral drugs in the NAI assay undergo genetic analysis of the neuraminidase gene to detect mutations associated with the functional change. The relationship between reduced inhibition and the clinical effectiveness of a neuraminidase inhibitor is not well understood. Further studies would be required to determine whether a virus with reduced inhibition in the NAI assay is clinically resistant.

Viruses with highly reduced inhibition to one or more NAI

Type/subtype/lineage		Country of submitting laboratory	NAI(s) with highly reduced inhibition (marked with *)			
			Oseltamivir	Peramivir	Laninamivir	Zanamivir
A(H1N1)pdm09	A/Victoria/380A/2023	Australia	*	*	Normal	Normal
	A/Victoria/380B/2023	Australia	*	*	Normal	Normal
	A/Victoria/380C/2023	Australia	*	*	Normal	Normal

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