Influenza Updates

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

@WHOCCFluMelb

Volume 14, Issue 1, May 2025

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 February 2025 onwards). We accept both viral isolates and/or original clinical respiratory specimen. The WHO Shipping Fund Project (SFP) is available to assist National Influenza Centres in covering the cost of shipping samples to WHO Collaborating Centres. **For most countries, the WHO SFP can only support one shipment in 2025 and it is therefore recommended that countries ship 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 Enquiries@influenzacentre.org
- 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 Influenza Vaccine Consultation.

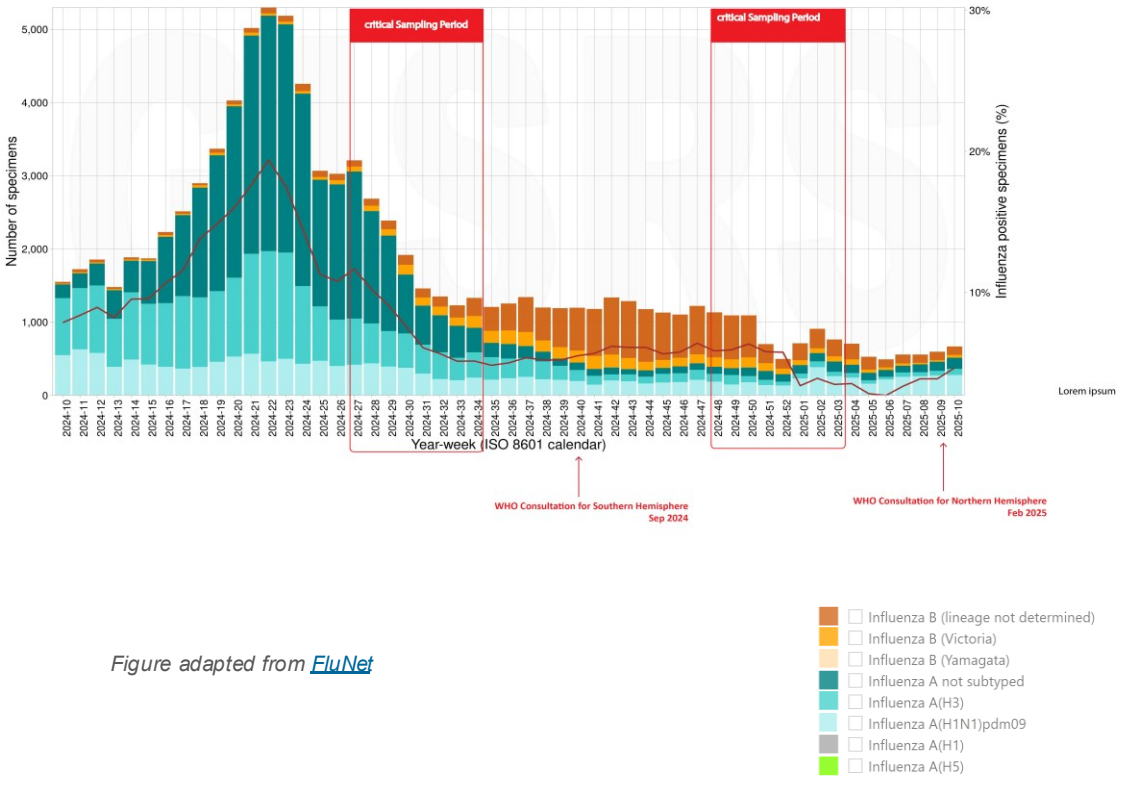


Figure adapted from FluNet

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 2025-2026 vaccine announced

The WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2025-2026 was announced in London, United Kingdom on 28 February 2025. The WHO made the following recommendations:

It is recommended that **trivalent** vaccines for use in the 2025-2026 influenza season (Northern Hemisphere winter) contain the following recommendations:

Egg-based vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Croatia/10136RV/2023 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus

Cell– or recombinant-based vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/District of Columbia/27/2023 (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 2025-2026 Northern Hemisphere influenza season:

Egg-, cell- or recombinant-based Vaccines

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

Contribution of National Influenza Centres to the vaccine

We thank everyone who has sent us influenza samples prior to the WHO influenza vaccine Consultation in February 2025. Your viruses provided essential data on recently circulating strains and helped to inform the choice of recommended vaccine strains.

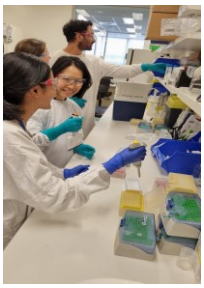
In this context, we would like to acknowledge the contribution and critical role played by WHO National Influenza Centres and other submitting laboratories in providing influenza samples and associated data to WHO Collaborating Centres, not only for the purposes of analysis and surveillance, but also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

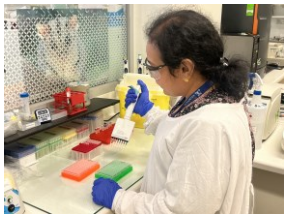
Trainings and visitors at the Centre

The Centre hosted **Hytham Saber**, the Technical Officer – National Influenza Networks from the **WHO South East Asian Office (SEARO)** between 8-15 February 2025. Hyatham gave a fantastic talk about his new role at SEARO as well as influenza surveillance in SEAR countries, and spent the week working with Centre staff to gain a deeper understanding of the work performed at the Melbourne WHO CC.

The Centre hosted **Regis Grailhe** and **Quentin Olivier** from **Institut Pasteur Korea** between 17-21 February 2025. They worked with Ian Barr and Harry Stannard from the Centre on a collaborative project to establish an improved tool for live imaging of mice and ferrets.

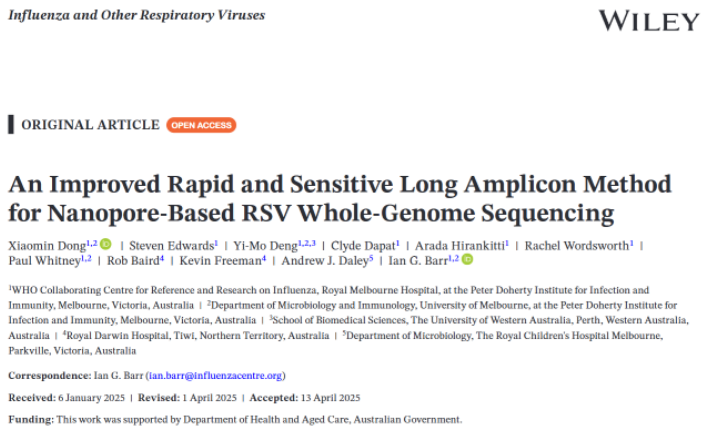
The Centre hosted **Natchaya Khiadsang and Wandee Meechalad** from **the National Influenza Centre (NIC),at the National Institute of Health, Thailand** between 10-14 March 2025. They were trained by Saira Hussain, Ashwin Muraleetharan and Clyde Dapat from the Centre in genotypic and phenotypic assays relevant to antiviral testing in influenza viruses.





The Centre hosted **Narcisse Joseph** from the **University Putra Malaya, Malaysia** between 7- 18 April 2025. She was trained by Yi-Mo Deng and Clyde Depart from the Centre in molecular techniques, including NGS, RT- PCR and bioinformatics for influenza and other viruses.

Featured Publication



Influenza and Other Respiratory Viruses

WILEY

ORIGINAL ARTICLE OPEN ACCESS

An Improved Rapid and Sensitive Long Amplicon Method for Nanopore-Based RSV Whole-Genome Sequencing

Xiaomin Dong[1,2] | Steven Edwards[1] | Yi-Mo Deng[1,2,3] | Clyde Dapat[1] | Arada Hirankitti[1] | Rachel Wordsworth[1] | Paul Whitney[1,2] | Rob Baird[4] | Kevin Freeman[4] | Andrew J. Daley[5] | Ian G. Barr[1,2]

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Funding: This work was supported by Department of Health and Aged Care, Australian Government.

Dong X, Edwards S, Deng YM, Dapat C, Hirankitti A, Wordsworth R, Whitney P, Baird R, Freeman K, Daley AJ, **Barr IG.** An Improved Rapid and Sensitive Long Amplicon Method for Nanopore-Based RSV Whole-Genome Sequencing. Influenza Other Respir Viruses. 2025 May;19(5):e70106. doi: 10.1111/irv.70106. PMID: 40296507; PMCID: PMC12037990.

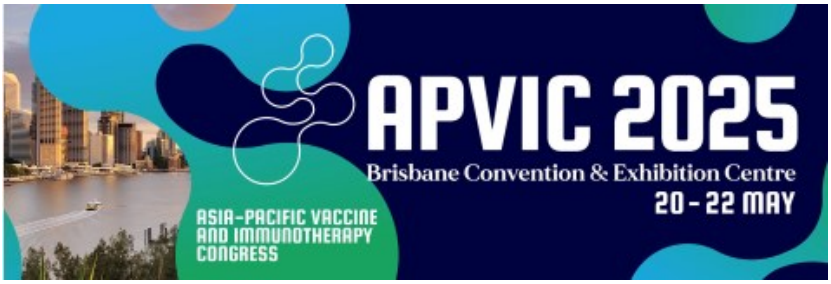
Xiaomin, Steven, Yi-Mo, Clyde, Arada, Rachel, Paul and **Ian** from the Centre published an article tilted "An Improved Rapid and Sensitive Long Amplicon Method for Nanopore-Based RSV Whole-Genome Sequencing". This article describes the development of a long amplicon-based WGS protocol using a one-step multiplex RT-PCR assay and rapid barcoding. Using 135 RSV-positive clinical samples from Australia they showed that this method achieved a 85.9% success rate for WGS, with improved turnaround times and excellent results for samples with cycle threshold (Ct) values below 30. They concluded that this new method is effective for performing RSV WGS using the ONT platform, offering a simpler and faster alternative to existing methods.

Recent Webinars

SEARO hosted a webinar titled "Strengthening Collaboration between WHO Collaborating Centers (WHO CCs) and National Influenza Centers (NICs) in the Southeast Asia Region" on 25 March 2025. **Patrick Reading** from the Centre gave a talk titled "What we do at the WHO Collaborating Centre for Reference and Research on Influenza (WHO CCRRI), Melbourne". The meeting was also attended by several staff from the Centre.

SEARO hosted an Information Sharing Meeting for sear NICs on 29 April 2025. This meeting discussed "Best practices in specimen management: Strengthening specimen management for influenza surveillance". **Katie Milne** and **Heidi Peck** from the Centre gave a talk on "Influenza sample referral to the WHO Collaborating Centre for Reference and Research on Influenza (WHO CCRRI), Melbourne". The meeting was also attended by several staff from the Centre.

Upcoming conferences



Registration link: APVIC 2025

XIXth Negative-strand RNA Virus Meeting

June 22-27, 2025

Montpellier, France

Registration link: NSV 2025

Registration link: 11th International Symposium on Avian Influenza

Registration link: IMRP

Recent activities at the Centre (1 January — 30 April 2025)

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 **3734** influenza samples from the laboratories and institutions listed below during the period 1 January—30 April 2025.

AUSTRALIA: Canberra Hospital, Westmead Hospital, The Children's Hospital at Westmead, Royal Darwin Hospital, Princess Alexandra Hospital, Queensland Health Forensic and Scientific Services, Queensland Children's Hospital, SA Pathology, Hobart Pathology, Royal Hobart Hospital, Australian Clinical Labs, Austin Pathology, Monash Medical centre, Alfred Hospital, Royal Children's Hospital, Royal Melbourne Hospital, VIDRL, Dorevitch Pathology, Pathwest QEII Medical Centre

BRUNEI: National Virology Reference Laboratory

CAMBODIA: Institut Pasteur du Cambodge

COOK ISLANDS: Te Marae Ora Ministry of Heath

INDIA: National Institute of Virology

KIRIBATI: Ministry of Health and Medical Services

NEPAL: National Public Health Laboratory

NEW CALEDONIA: Centre Hospitalier De Nouvelle Caledonie

PHILIPPINES: Research Institute for Tropical Medicine

SAMOA: Tupua Tamases Meaole Hospital

SINGAPORE: National Public Health Laboratory

SOLOMON ISLANDS: National Referral Hospital

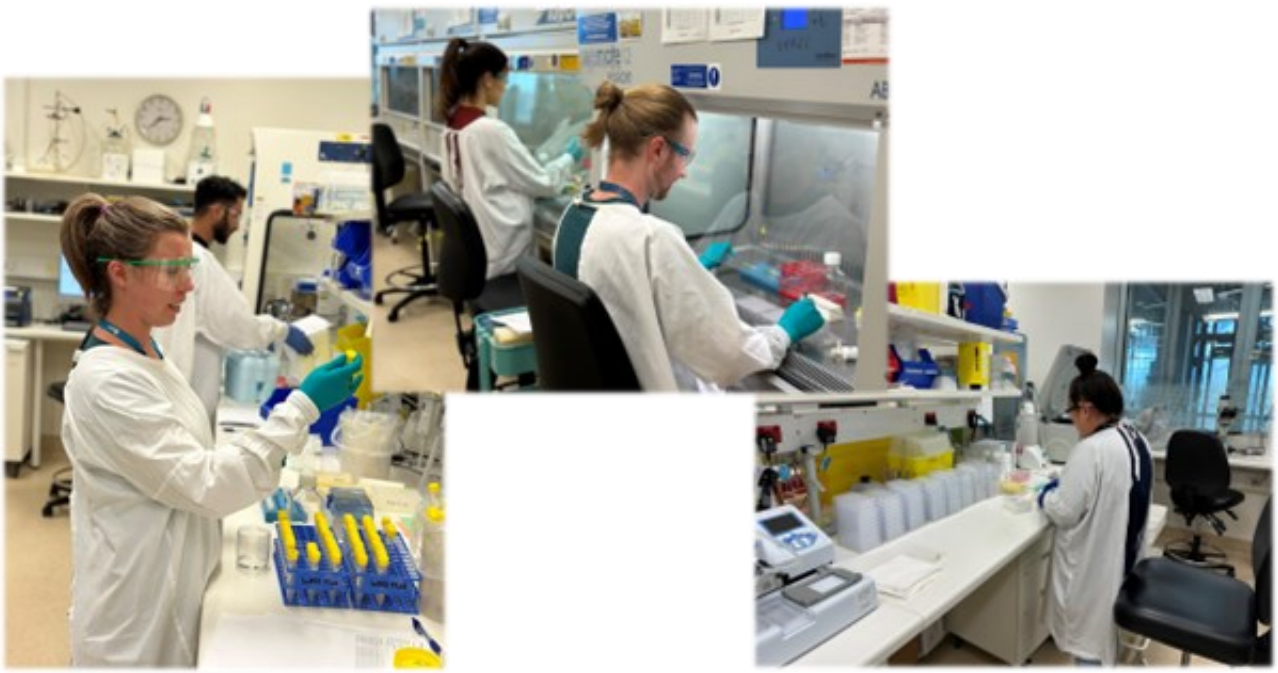
SRI LANKA: Medical Research Institute

TAHITI: Institut Louis Malarde

THAILAND: National Institute of Health

TIMOR-LESTE: Laboratorio Nacional Da Saude

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 2025, 7 A(H3N2) and 2 viruses A(H1N1) were successfully isolated in eggs at the Centre.



Recent activities at the Centre (1 January — 30 April 2025) continued

Antigenic analysis
1560 viruses analysed by haemagglutination inhibition (HI) assay

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

Sequencing
862 viruses analysed
861 HA genes
862 NA genes
745 MP genes
148 NS genes

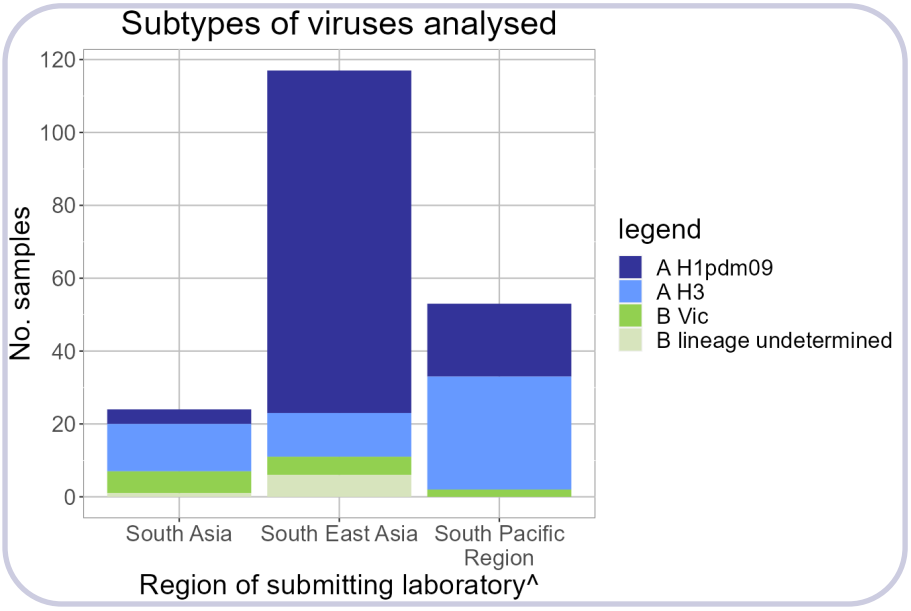
Country of submitting laboratory	No. of viruses analysed by HI assay*			No. of viruses tested by NAI assay*			No. of viruses sequenced by NGS (ONT or Illumina)				
	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria	B lineage undetermined	A unsubtyped
Australia	733	237	164	395	103	36	382	126	89	10	2
Brunei	0	2	0	24	4	0	5	3	0	0	
Cambodia	15	26	19	15	26	18	9	17	19	0	
Cook Islands	3	0	0	3	0	0	3	0	0	0	
India	9	14	7	9	14	7	4	13	7	0	
Nepal	2	6	4	0	5	4	3	6	4	0	
New Caledonia	56	40	0	56	40	0	25	20	0	0	
Philippines	1	0	2	1	0	2	6	1	15	0	
Samoa	2	0	0	2	0	0	3	0	0	0	
Singapore	38	20	20	38	20	20	0	4	0	0	
Sri Lanka	9	12	4	9	11	4	14	17	6	1	
Tahiti	4	2	3	4	2	2	4	2	3	0	2
Thailand	6	7	7	6	7	7	6	6	7	0	
Timor-Leste	16	66	4				9	6	3	0	
Total	**894**	**432**	**234**	**562**	**232**	**100**	**473**	**221**	**153**	**11**	**4**

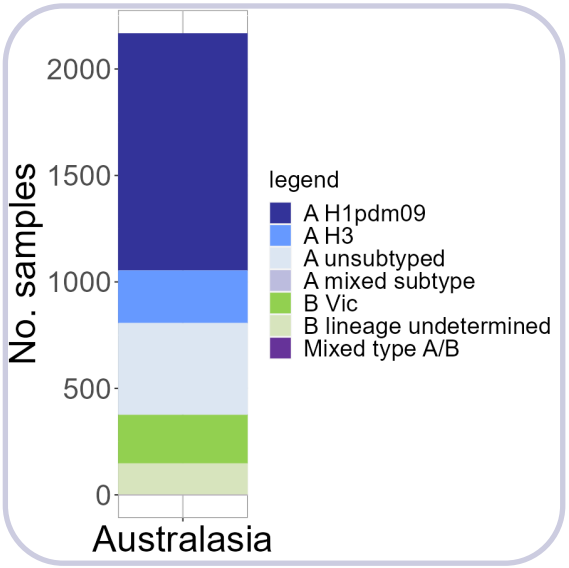
**Subtypes and lineages are based on analysis of HA and in some cases confirmed by genetic analysis of NA.*

The data below are results for viruses collected or sampled between 1 January and 30 April 2025 that have been analysed at the Centre as of 5 May 2025.

Virus types/subtypes†
The type and subtype/lineage of 2036 viruses have been determined.

72% A(H1N1)pdm09
15.5% A(H3N2)
12.5% B/Victoria



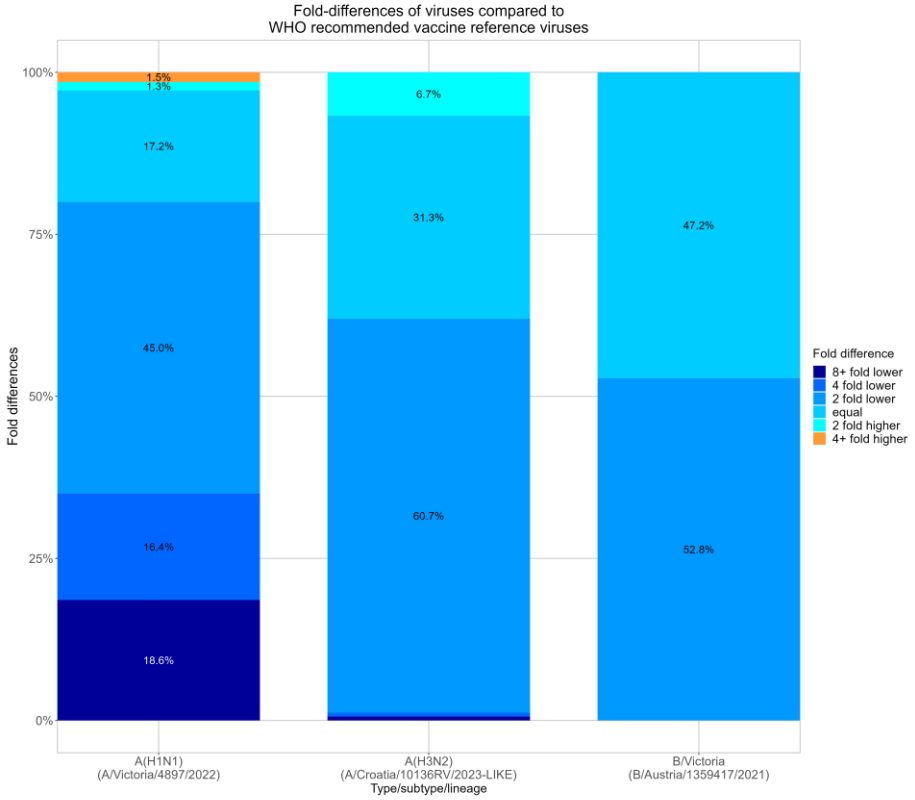


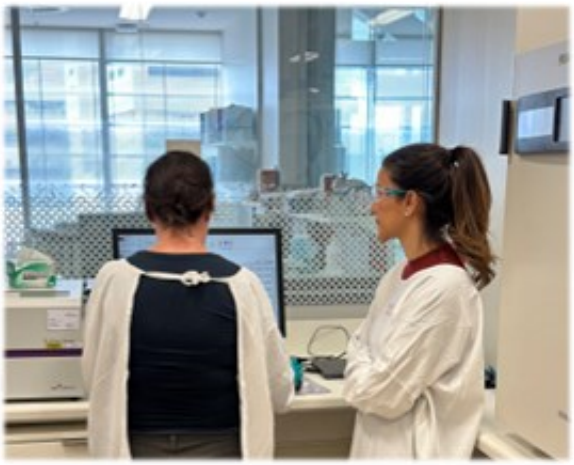
† *Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.*
^The South Pacific region comprises countries in Polynesia, Melanesia, and Micronesia.
^Australasia comprises of Australia and New Zealand.

Antigenic analysis*

A total of 1560 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(H3N2) and B/Victoria viruses were antigenically similar to their respective reference strains. A proportion (18.6%) of A(H1N1) viruses were low reactors to the reference strain A/Victoria/4897/2022.

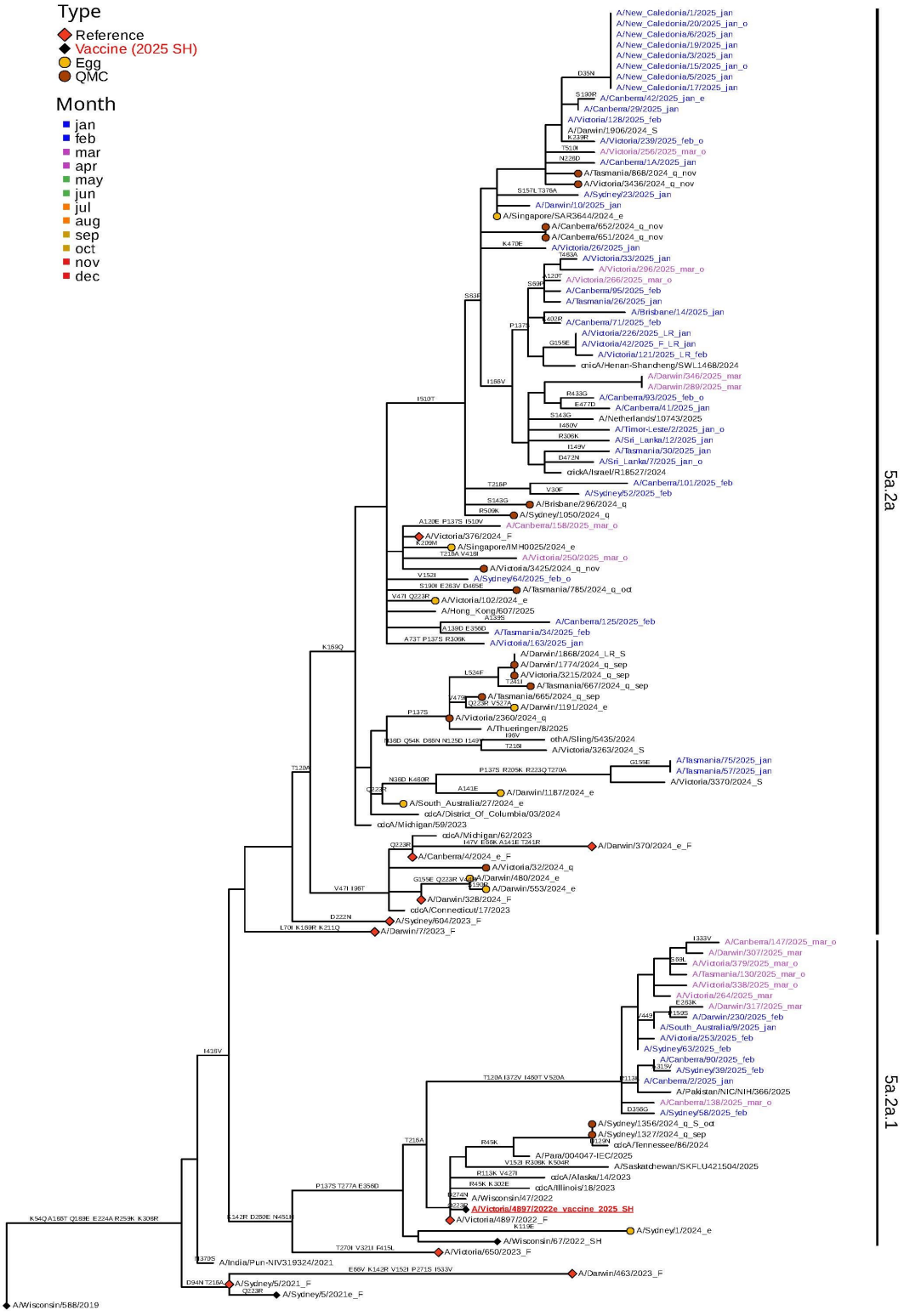




† *Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.*

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

Phylogenetic analysis shows the majority of A (H1N1)pdm09 viruses belong to the 5a.2a clade.



Antiviral drug susceptibility testing:
492 viruses tested by neuraminidase inhibition (NAI) assay

Testing for susceptibility to the antiviral drugs oseltamivir (Tamiflu), zanamivir (Relenza), peramivir, and laninamivir showed that one virus had highly reduced inhibition by one or more of these 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	362	0	1	361	1	1	363	0	0	362	1	0
A(H3N2)	98	0	0	98	0	0	98	0	0	98	0	0
B/Victoria	31	0	0	31	0	0	31	0	0	31	0	0
Total	**491**	**0**	**1**	**490**	**1**	**1**	**492**	**0**	**0**	**491**	**1**	**0**

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	Mutation detected	NAI(s) with highly reduced inhibition (marked with *)			
				Oseltamivir	Peramivir	Laninamivir	Zanamivir
A(H1N1)pdm09	A/Victoria/56/2025	Australia	H275Y	*	*		

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