Influenza Updates

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

@WHOCCFluMelb

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WHO Recommendations for the Southern Hemisphere 2025 Influenza Vaccines

The WHO Consultation on the Composition of Influenza Vaccines for the Southern Hemisphere 2025 was held in Melbourne, Australia between 23-27 September 2024.

Following the Consultation, the WHO made the following recommendations:

The WHO recommends that **trivalent** vaccines for use in the 2025 southern hemisphere influenza season contain the following:

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 culture-, recombinant protein- or nucleic acid-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.

The recommendation for the B/Yamagata lineage component of quadrivalent influenza vaccines remains unchanged from previous recommendations:

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

More details about the recommendations can be found here. Recommendations

AIVC recommendation for the composition of influenza vaccine for Australia in 2025

The Australian Influenza Vaccine Committee (AIVC) met on 9 October 2024 to recommend the composition of the influenza virus vaccines for 2025 and the committee has accepted the WHO recommendation. The full statement is available here.

Contribution of National Influenza Centres to the vaccine recommendations

We thank everyone who has sent us influenza samples prior to the Consultation. Your viruses provide essential data on recently circulating strains and help 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 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.

Centre Training, Activities and Awards

We welcomed **Abdul Ahad** and **Nazish Badar** from National Institute of Health, Pakistan from 24 -28th June 2024 for training in bioinformatics. **Clyde Dapat, Xiaomin Dong,** and **Steven Edwards** from the Centre coordinated the training, which covered topics such as quality assessment of sequence data, genome assembly for influenza virus and respiratory syncytial virus (RSV), genome annotation, and phylogenetic analysis.

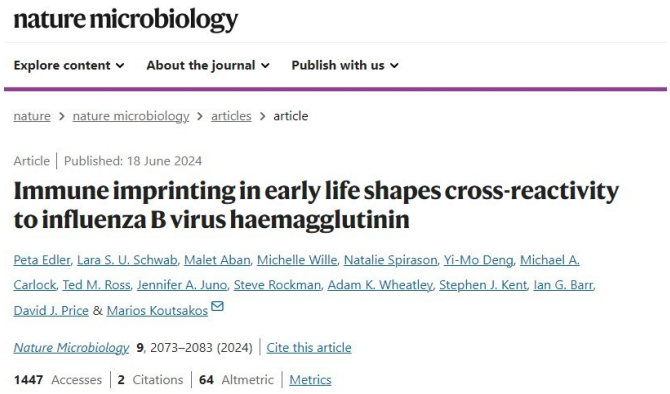
Clyde Dapat and **Yi-Mo Deng** conducted the International Workshop on Influenza Virus and RSV Genome Sequencing' in Pune, India, between 3-7 June 2024. The workshop, co-hosted by the ICMR - National Institute of Virology, Pune and the WHO Collaborating Centre for Reference and Research on Influenza, Melbourne, was held at the ICMR - National Institute of Virology, Pune and attended by 13 participants from WHO SEARO countries including Bangladesh, Bhutan, India, Indonesia, Nepal, and Sri Lanka. Participants received training in PCR, library preparation, next-generation sequencing using Nanopore technology, and bioinformatics analysis on whole genome sequence data.

The RSV surveillance team from our Centre, consisting of **Xiaomin Dong, Steven Edwards, Yi-Mo Deng, Clyde Dapat, Paul Whitney,** and **Ian Barr,** won The Catton Prize for Impact in Public Health in the 2024 Doherty Institute Internal Awards.

Featured Research Article

'Immune imprinting in early life shapes cross-reactivity to influenza B virus haemagglutinin' Featuring **Malet Aban, Michelle Wille, Natalie Spirason, Yi-Mo Deng, and Ian Barr** from our Centre

Published in *Nature Microbiology* in August 2024, this collaborative study reveals that early-life exposure to influenza B virus (IBV) significantly influences the immune system's response to future IBV infections. By analyzing haemagglutination-inhibition titres from 1,451 samples collected between 1992 and 2020, the researchers found that early IBV exposure creates immunological biases, leading to stronger immune responses to IBV strains similar to those encountered during childhood. This lineage-specific cross-reactivity is supported by serological evidence, highlighting the long-term impact of early-life influenza exposures on immune responses and suggesting potential implications for future vaccine strategies.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Article | Published: 18 June 2024

Immune imprinting in early life shapes cross-reactivity to influenza B virus haemagglutinin

Peta Edler, Lara S. U. Schwab, Malet Aban, Michelle Wille, Natalie Spirason, Yi-Mo Deng, Michael A. Carlock, Ted M. Ross, Jennifer A. Juno, Steve Rockman, Adam K. Wheatley, Stephen J. Kent, Ian G. Barr, David J. Price & Marios Koutsakos

Nature Microbiology 9, 2073–2083 (2024) | Cite this article

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Edler P, Schwab LSU, Aban M, Wille M, Spirason N, Deng YM, Carlock MA, Ross TM, Juno JA, Rockman S, Wheatley AK, Kent SJ, Barr ĮG, Price DJ, Koutsakos M. Įmmune imprinting in early life shapes cross-reactivity to in ụenza B virus haemagglutinin. Nat Microbiol. 2024 Aug;9 (8):2073-2083. doi: 10.1038/s41564-024-01732-8. Epub 2024 Jun 18. PMĮD: 38890491.

NEW APPOINTMENTS

It is with great pleasure we announce the appointment of our new Director and our new Head of Epidemiology.

Dr. Patrick Reading was recently appointed as the Centre Director. Patrick has been working at the Centre for over 15 years, primarily coordinating laboratory capacity building for National Influenza Centres and other diagnostic laboratories. He also heads a virology research laboratory at the University of Melbourne.

Dr. Jessica Miller has also joined the Centre as the Head of Epidemiology. Jessica comes with over 10 years of experience working with multinational real-world data. She has expertise in designing and conducting secondary linked data studies to measure the impact of risk factors, identify high-risk populations, and inform clinical practice in areas of childhood health, infectious diseases, immunology, HIV, COVID-19, and antimicrobial resistance.

Recent activities at the Centre (1 May — 30 September 2024)

Below is a summary of surveillance activities at the Centre during this recent reporting period.

Samples received:

The Centre received 8416 influenza samples from the laboratories and institutions listed below between 1 May — 30 September 2024.

AUSTRALIA: CANBERRA HOSPITAL, 4CYTE PATHOLOGY, ICPMR WESTMEAD, PRINCE OF WALES HOSPITAL, THE CHILDREN'S HOSPITAL AT WESTMEAD, ROYAL DARWIN HOSPITAL, PATHOLOGY QUEENSLAND, PUBLIC & ENVIRONMENTAL HEALTH, FORENSIC AND SCIENTIFIC SERVICES, QUEENSLAND CHILDREN'S HOSPITAL, ROYAL BRISBANE HOSPITAL, SA PATHOLOGY, HOBART PATHOLOGY, ROYAL HOBART HOSPITAL, AUSTRALIAN CLINICAL LABS (ACL) , ALFRED HOSPITAL, AUSTIN PATHOLOGY, MELBOURNE PATHOLOGY, MONASH MEDICAL CENTRE, ROYAL CHILDREN'S HOSPITAL, ROYAL MELBOURNE HOSPITAL, VICTORIAN INFECTIOUS DISEASES REFERENCE LABORATORY, PATHWEST LABORATORY MEDICINE (QEII)

CAMBODIA: INSTITUT PASTEUR DU CAMBODGE

COOK ISLANDS: TE MARAE ORA MINISTRY OF HEALTH

FIJI: CENTRE FOR DISEASE CONTROL

INDIA: NATIONAL INSTITUTE OF VIROLOGY, PUNE

INDONESIA: NATIONAL HEALTH BIOLOGY LABORATORY

MALAYSIA: NATIONAL PUBLIC HEALTH LABORATORY, MINISTRY OF HEALTH

NEPAL: NATIONAL PUBLIC HEALTH LABORATORY

NZ: INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH LIMITED

PHILIPPINES: RESEARCH INSTITUTE FOR TROPICAL MEDICINE

SAMOA: TUPUA TAMASES MEAOLE HOSPITAL

SINGAPORE: NATIONAL PUBLIC HEALTH LABORATORY

SOLOMON ISLANDS: NATIONAL REFERRAL HOSPITAL

SOUTH AFRICA: NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES

SRI LANKA: MEDICAL RESEARCH INSTITUTE

TAHITI: INSTITUT LOUIS MALARDÉ

THAILAND: NIC, NATIONAL INSTITUTE OF HEALTH

TONGA: LABORATORY SERVICE VAIOLA HOSPITAL TONGATAPU

Isolation of viruses in eggs:

The Centre undertakes primary isolation of selected viruses in eggs to obtain potential vaccine strains. From 1 May — 30 September 2024, 5 A(H1N1)pdm09, 4 B/Victoria viruses and 4 A(H3N2) viruses were successfully isolated in eggs at the Centre.

Recent activities at the Centre (1 May — 30 September 2024) continued

Antigenic analysis
3033 viruses analysed by haemagglutination inhibition (HI) assay

Antiviral drug susceptibility
2157 viruses analysed by neuraminidase inhibition (NAI) assay

Sequencing
2322 viruses analysed

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 lineage undetermined	B/Victoria	A(H1N1)pdm09	A(H3N2)	B lineage undetermined	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria
Australia	1150	1205	14	106	717	666	2	62	849	1001	115
Brunei	9	44	0	3	9	44	0	3	11	19	7
Cambodia	5	0	0	22	5	19	0	22	4	15	8
Cook Island					6	0	0	0			
Fiji	13	8	0	0	15	8	0	0	15	5	0
India	17	2	0	2	17	2	0	2	1	1	2
Indonesia	0	4	0	2	3	4	0	2	2	3	2
Nepal	0	2	0	0	6	2	0	0	0	2	0
New Zealand	80	42	0	9	102	90	0	9	34	18	6
Papua New Guinea	0	0	0	4							
Philippines	1	5	0	0	1	7	0	0	1	7	0
Samoa					10	0	0	0	0	2	0
Singapore	49	22	0	26	50	35	0	26	2	1	0
Solomon Islands									1	0	0
South Africa	26	2	0	10	26	2	0	10	26	2	6
Sri Lanka	11	1	0	5	12	10	0	5	22	15	6
Tahiti	2	5	0	1	14	5	0	1	12	4	1
Thailand	6	7	0	6	6	7	0	6	6	7	2
Timor-Leste	17	77	0	0	19	77	0	0	13	38	0
Tonga	11	0	0	0	11	0	0	0	13	0	0
	1397	**1426**	**14**	**196**	**1029**	**978**	**2**	**148**	**1012**	**1140**	**155**

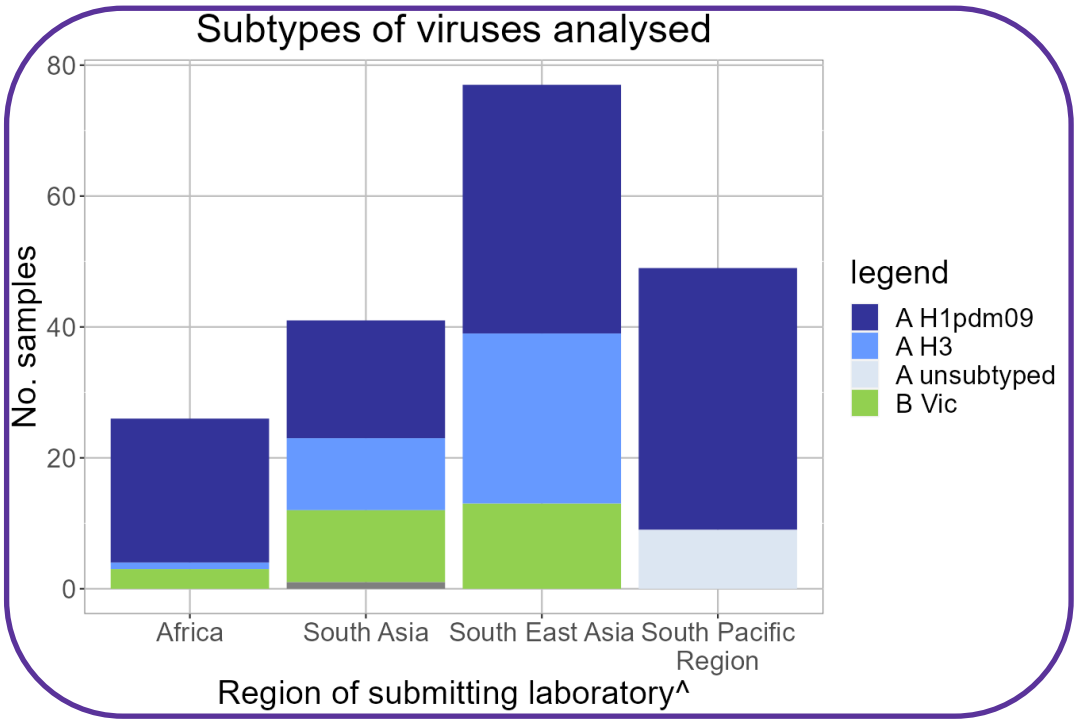
* *Subtypes and lineages are based on analysis of HA and in some cases confirmed by genetic analysis of NA.*

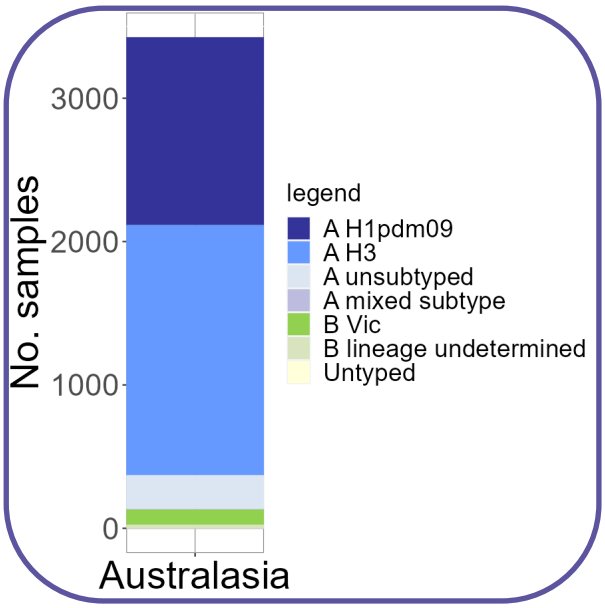
Surveillance update: Virus activity 1 May—30 September 2024

The data below are results for viruses collected between 1 May and 30 September 2024 that have been analysed at the Centre as of 2 October 2024.

Virus types/subtypes*
The type and subtype/lineage of 3455 viruses have been determined.

46.1% A(H1N1)pdm09
47.1% A(H3N2)
6.5% B/Victoria





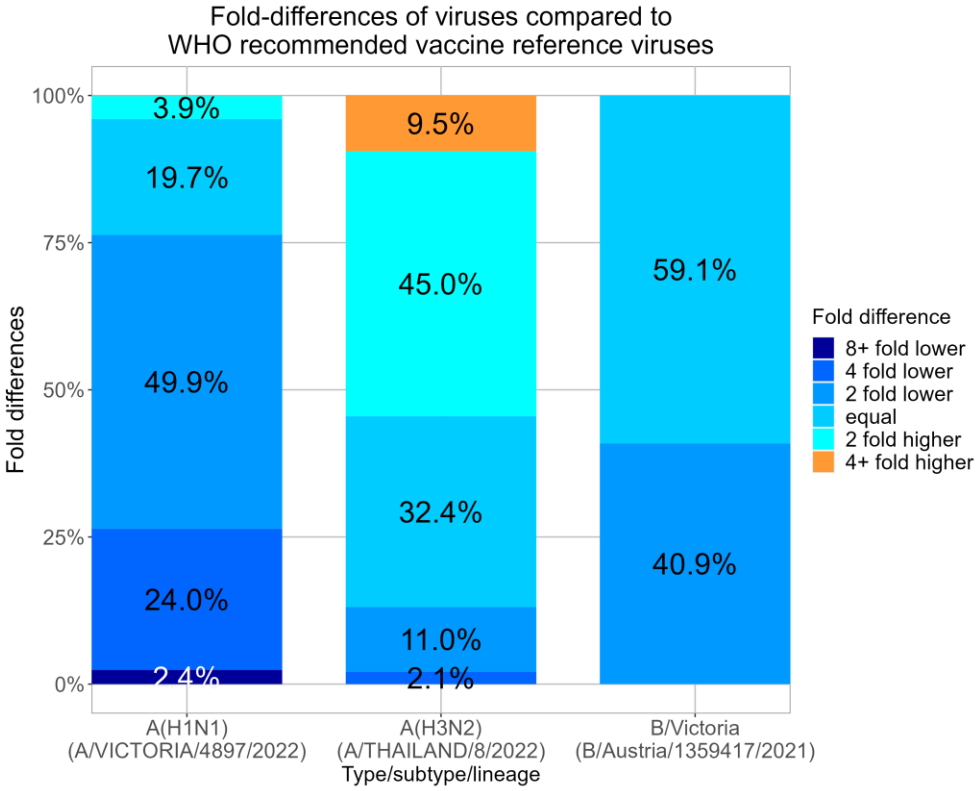
**Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.*

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

Antigenic analysis*

A total of 3019 viruses were tested using the haemagglutination inhibition (HI) assay.

Viruses were identified as low-reactors if their titre with reference antiserum was at least 8-fold lower than the titre of the reference virus. The vast majority of A (H1N1)pdm09, A(H3N2), and B/Victoria lineage viruses were antigenically similar to their respective reference viruses.



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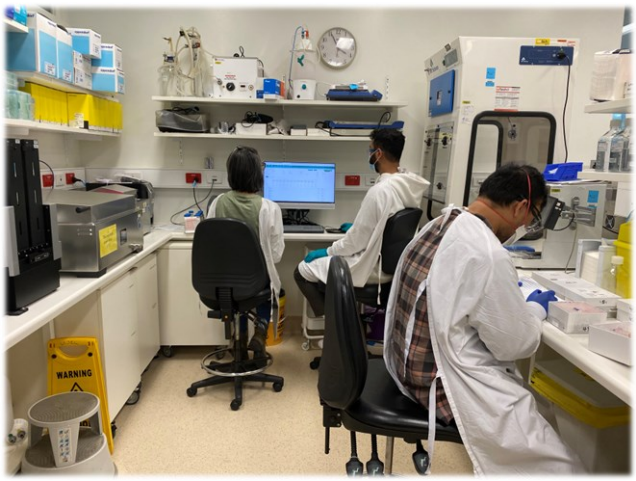
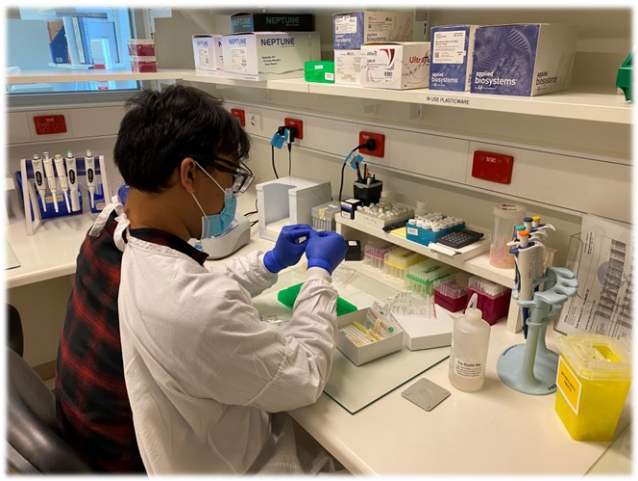
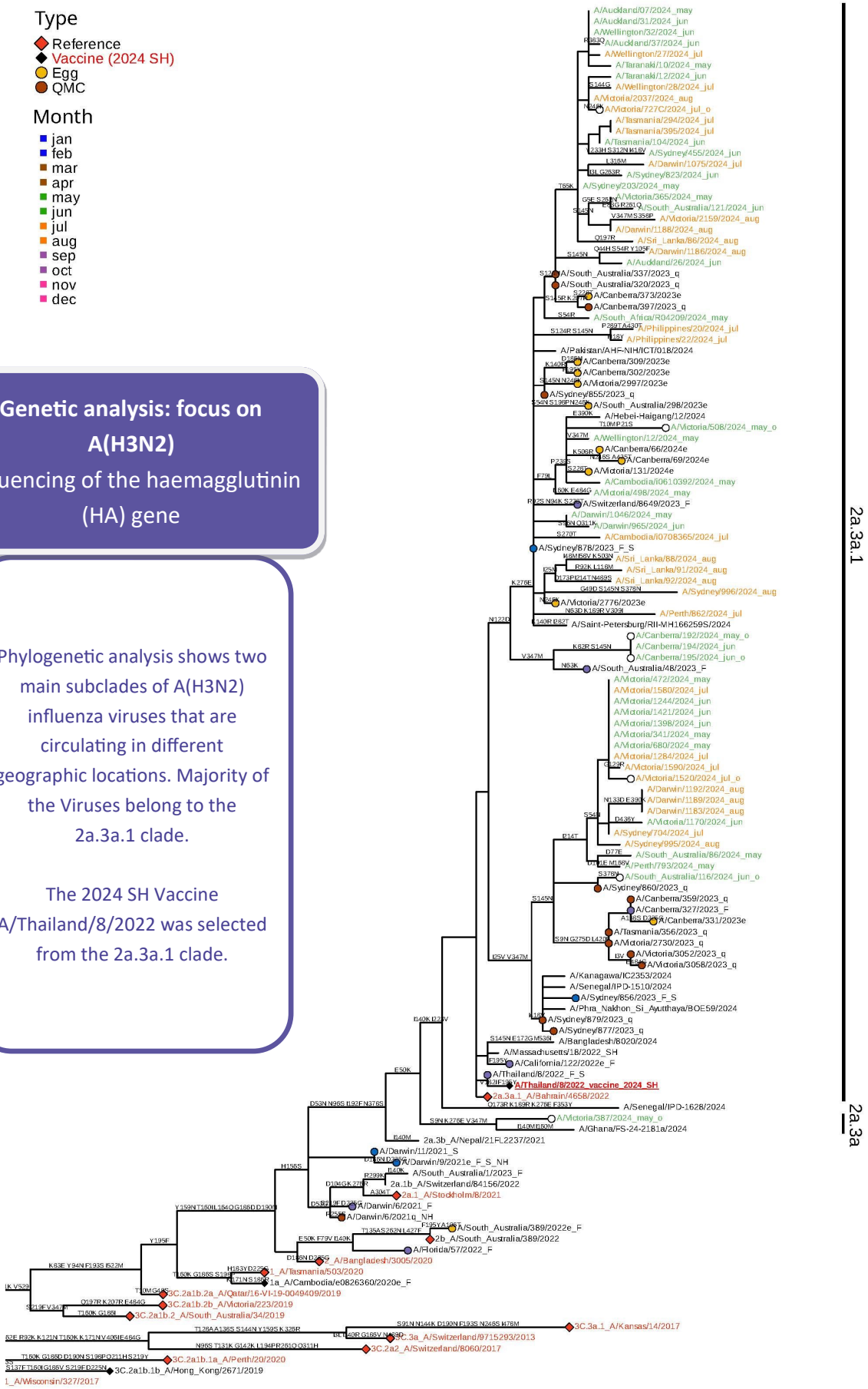




Surveillance update: Virus activity 1 May—30 September 2024 continued



Genetic analysis: focus on A(H3N2)

Sequencing of the haemagglutinin (HA) gene

Phylogenetic analysis shows two main subclades of A(H3N2) influenza viruses that are circulating in different geographic locations. Majority of the Viruses belong to the 2a.3a.1 clade.

The 2024 SH Vaccine A/Thailand/8/2022 was selected from the 2a.3a.1 clade.

Surveillance update: Virus activity 1 May—30 September 2024 continued

Antiviral drug susceptibility testing:
1328 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	599			599			605			605		
A(H3N2)	661			661			661			661		
B/Victoria	62			62			62			62		
Total	**1322**			**1322**			**1328**			**1328**		

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/Darwin/486/2024	Australia	*	*	Normal	Normal
	A/Sydney/242/2024	Australia	*	*	Normal	Normal
	A/Perth/860/2024	Australia	*	*	Normal	Normal
	A/SouthAfrica/R04202/2024	South Africa	*	*	Normal	Normal
	A/Sydney419B/2024	Australia	*	*	Normal	Normal
	A/Sudney/709/2024	Australia	*	*	Normal	Normal

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