Annual Report 2025

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

Contents

About the Centre

The WHO Collaborating Centre for Reference and Research on Influenza at the Victorian Infectious Diseases Reference Laboratory (VIDRL) in Melbourne is part of the World Health Organisation Global Influenza Surveillance and Response System (WHO GISRS). The network was established in 1952 to monitor the frequent changes in influenza viruses with the aim of reducing the impact of influenza through the use of vaccines containing currently circulating strains. Together with WHO Collaborating Centres in Atlanta, Beijing, London and Tokyo, the Centre is responsible for analysing influenza viruses currently circulating in the human population in different countries around the world. The Centre in Melbourne was first designated as a Collaborating Centre in 1992, the third such Centre in the world.

Terms of Reference

Under its designation as a WHO Collaborating Centre for Reference and Research on Influenza, the Centre's Terms of Reference (for 2024-2028) are:

1. To obtain, isolate and preserve representative viruses from outbreaks and sporadic cases of influenza, and characterise their antigenic, genetic and drug sensitivity properties as requested by the WHO.
2. To collect epidemiological information on the prevalence of influenza, especially in countries and areas in the Region, under WHO's leadership.
3. To exchange information and materials (including viruses and antisera) with other WHO Collaborating Centres for Influenza, with Essential Regulatory Laboratories and with Veterinary Laboratories to assist WHO in developing recommendations on viruses to be included in seasonal and potential pandemic influenza vaccines (according to the Pandemic Influenza Preparedness Framework requirements).
4. Under WHO's coordination, to provide training and laboratory support to WHO National Influenza Centres and other laboratories, especially those in the developing world, in specialised techniques for diagnosis, isolation and characterisation of influenza viruses, according to their needs.
5. Under WHO's leadership to undertake research to improve the detection, prevention and treatment of influenza as prioritized by the WHO Research Agenda for influenza.

Governance

The Centre is supported by the Australian Government Department of Health and Aged Care through a funding agreement between the Commonwealth and Melbourne Health, and reports directly to the Department as well as to WHO.

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Highlights of 2025

Surveillance

In 2025 the Centre received a total of **14,056 samples** from 44 laboratories and 22 countries, of which **99.5% were tested**.

Hosting the 16th Australian Influenza Symposium

The Centre hosted a very successful symposium with over 200 registrants from biomedical, clinical and public health sectors.

Novo Nordisk Grant

A research team, including staff from the Centre, was awarded a new collaborative grant of EUR 2,499,882 from The Novo Nordisk Foundation to continue the further preclinical development of a novel long-acting pan-influenza

Onshore and Offshore Training

Centre staff travelled to Vietnam and Malaysia to deliver training and support, as well as hosting trainees from Thailand, Malaysia, Philippines, Fiji and South Africa at the Centre.

Research, publications and grants

The Centre further developed its research program during 2025, with Centre staff involved as authors on **48 papers** in peer-reviewed journals.

Director’s report

I present the 2025 Annual Report of the WHO Collaborating Centre for Reference and Research on Influenza. The Centre has continued to fulfil its commitments to the WHO, National Influenza Centres in the region, and to the Commonwealth Government, as well as participating in training and research activities.

In 2025 Australia experienced its highest recorded influenza season to date, with over 500,00 laboratory-confirmed cases nationwide (source: NINDSS). The Centre also received and processed over 14,000 influenza samples from laboratories in Australia and in 21 other countries. Overall, influenza A(H1N1) pdm09 accounted for the majority of viruses characterised at the Centre in 2025. An unusual late surge of A (H3N2) viruses from October onward extended the typical influenza season to the end of the year, while influenza B activity remained consistently low. The Centre continued to assess the antigenic and genetic properties of the viruses received, noting an increase in genetic diversification within the HA genes of the A/H1, A/H3, and B/Victoria lineage viruses. Additionally, routine testing was performed to determine the sensitivity of influenza viruses to neuraminidase inhibitors and to the polymerase inhibitor baloxavir marboxil.

During 2025 the Centre continued to work on isolation of cell-based and egg-based viruses for vaccine production. For trivalent egg-based vaccines, one of the three prototype strains recommended for the 2025-2026 Northern Hemisphere and for the 2026 Southern Hemisphere influenza vaccines were derived at the Centre.

Highly pathogenic avian influenza A(H5Nx) viruses continued to circulate in 2025, with A(H5N1) clade 2.3.4.4b viruses detected in wild birds, poultry, and mammals in all continents except Australia. Overall, the Centre continues to monitor influenza viruses with pandemic potential, seeks to obtain new viruses as they are detected, and confirms that methodologies are established to allow for their detection and characterisation at the Centre.

Centre staff participated in in-person training in several countries, including in Vietnam and Malaysia. In addition, we hosted visitors from Thailand, Malaysia, Philippines, Fiji and South Africa at the Centre for training in serologic and molecular techniques. Centre staff also contributed to a total of 48 original research papers, reviews, and reports. In 2025, research at the Centre was supported by grants from a variety of sources, including the NHMRC (MRFF), the Cumming Global Centre for Pandemic Therapeutics, Novo Nordisk Foundation and NIH (USA) for work on influenza and SARS-CoV-2.

We are very grateful to Dr Chuan Lim, the Acting Director of VIDRL, and to many other members of VIDRL staff, especially Matthew Killen, Dallas Wilson, Ann Cornish, and Claudine Rensburg for their support of the Centre’s work at every level during 2025. The continuing support and counsel of the Office of Health Protection in the Australian Government Department of Health, Disability and Ageing are deeply appreciated.

Finally, I would like to thank all the staff and students of the Centre for their excellent work through 2025. It is a privilege to work with the Centre staff and I look forward to working with our partners in 2026 and onwards.

Prof Patrick Reading
Centre Director

Surveillance

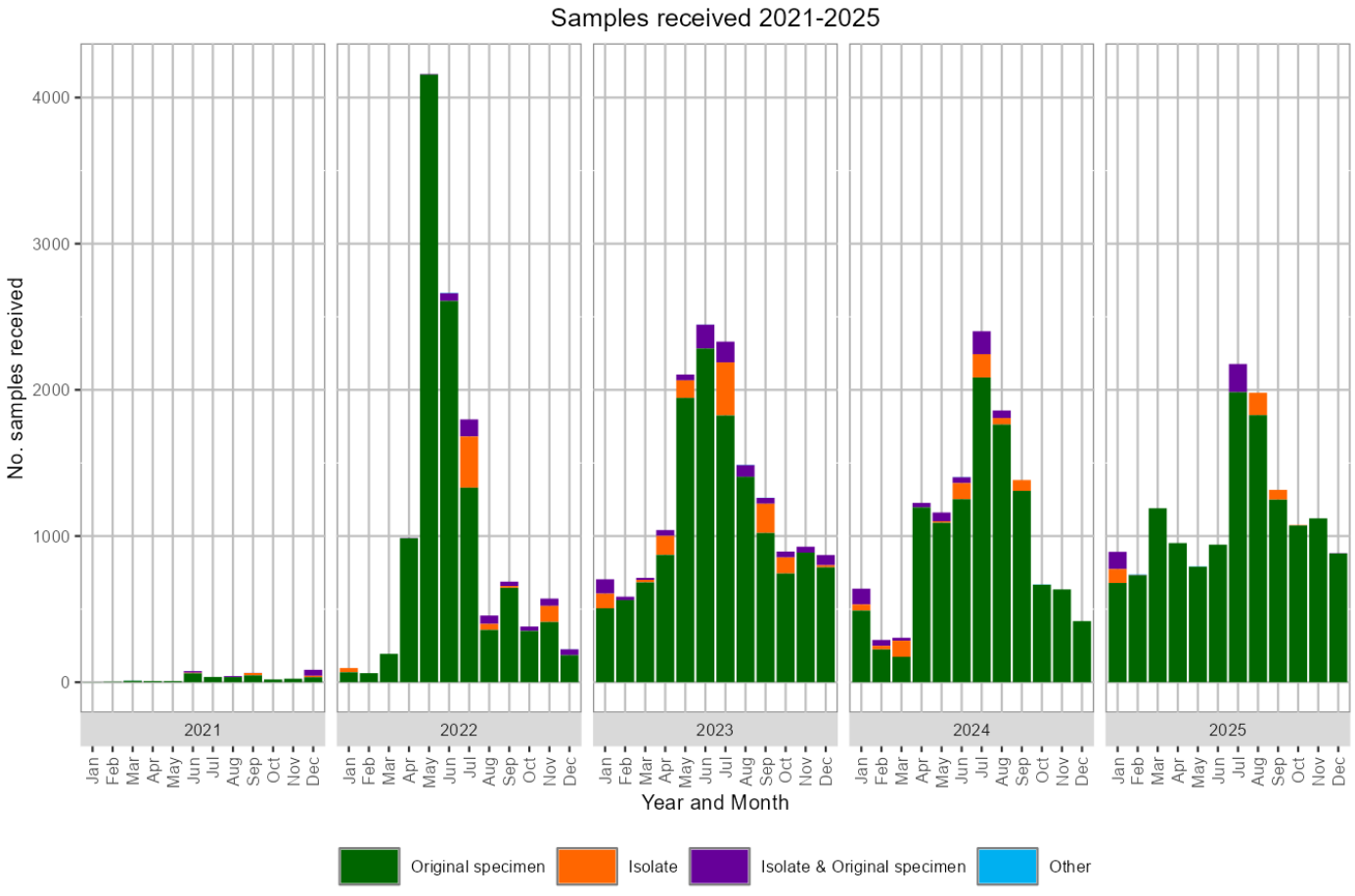
Introduction

The WHO Collaborating Centre for Reference and Research on Influenza (WHO CCRRI) at the Doherty Institute in Melbourne conducts human influenza surveillance for the WHO by analysing influenza samples submitted by WHO National Influenza Centres (NICs) and other laboratories. There are four other such Collaborating Centres around the world, the others being in Atlanta, Beijing, London and Tokyo. Most of the samples received at the Centre in Melbourne are provided by laboratories in the Asia-Pacific region.

Twice a year (once each for the Northern and Southern Hemispheres), based on data and advice from the five Collaborating Centres and other experts, the WHO makes recommendations on suitable influenza strains to be included in the next seasonal vaccine.

There are two types of influenza virus, type A and type B, which cause significant disease in humans. Two glycoproteins, the haemagglutinin (HA) and the neuraminidase (NA), protrude from the surface of the virus and are used to classify type A viruses into subtypes. There are 18 distinct HA subtypes and 11 NA subtypes of influenza A viruses that exist in nature, usually in wild birds. Influenza B viruses are not classified into subtypes, but rather into lineages based on the genetic and antigenic characteristics of their HA glycoproteins. The B/Victoria lineage currently circulates in humans whereas the B/Yamagata lineage has not been detected since March 2020. Currently, the main influenza viruses circulating in the human population are influenza A(H1N1)pdm09, influenza A(H3N2) and influenza B viruses.

Figure 1. Samples received by the Centre, 2021-2025.



Receipt of Influenza Viruses

During 2025, the Centre received 14,056 clinical specimens and/or virus isolates from 44 laboratories in 22 countries (Figures 1 and 2, Table 1). This is more than the number of samples received by the Centre during 2024 and is consistent with the high number of influenza infections during the 2025 influenza season in Australia. Of samples received by the Centre for which the age of the patient was known, the largest number were from subjects aged between 0-4 years (Figure 3). Of samples received, 5749 samples came from Australian general practitioner-based surveillance systems (Table 2).

Isolation and analysis of viruses

Original clinical specimens received by the Centre can be genetically analysed through sequencing or real-time reverse-transcription (RT)-PCR. Additionally, they are required for virus isolation in eggs or qualified cell lines, which may serve as potential vaccine strains. For more extensive analyses, the viruses present in the clinical specimens are cultured and isolated in Madin-Darby canine kidney (MDCK) cells.

Of the 14,056 samples received, 13,989 (99.5%) were tested in cell culture and/or analysed by RT-PCR or sequencing. Of the samples tested, 46.5% were identified as A(H1N1)pdm09, 21.1% were A(H3N2), 12.2% were A unsubtyped, and 17.1% were B/Victoria viruses (Table 2). Samples for which a positive cell culture result was obtained with sufficient titre were further analysed by haemagglutination inhibition (HI) assay. For reporting purposes, subtypes and lineages are based on antigenic analysis of the HA and, in some cases, are confirmed by genetic analysis of the HA gene (Table 3).

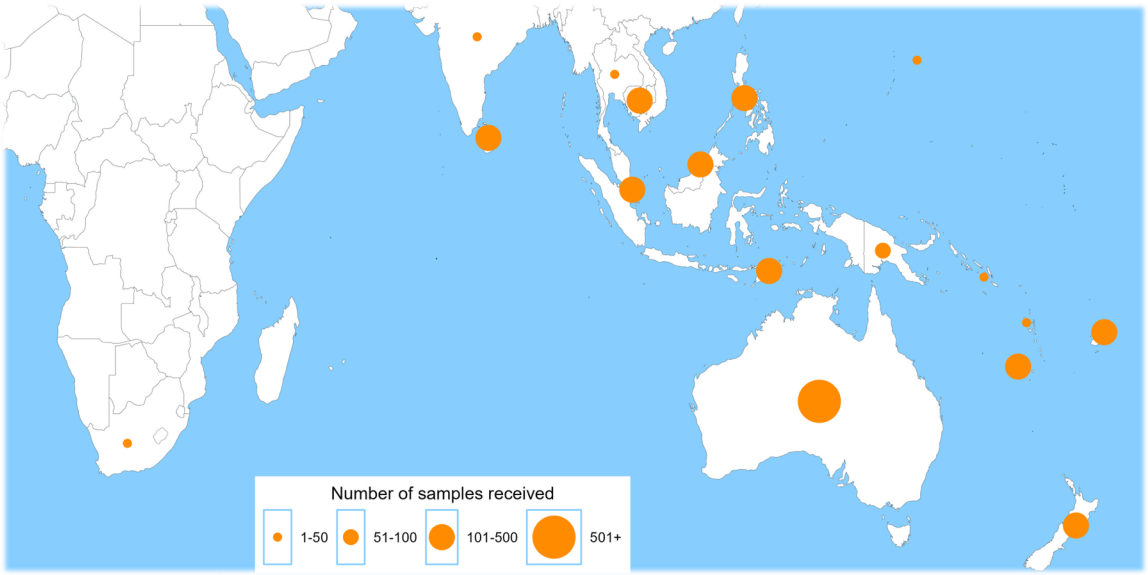


Figure 2. Geographic spread of laboratories submitting viruses to the Centre in 2025.

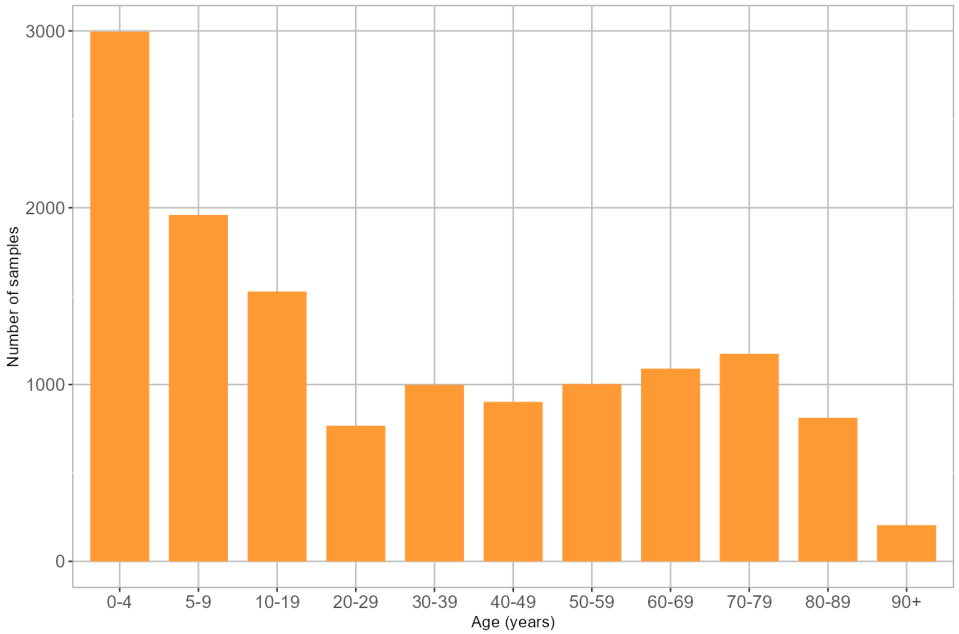


Figure 3. Age distribution of patients from whom samples were received at the Centre in 2025, where the patients age was recorded.

Table 1. Samples received by the Centre in 2025, by country.

Country	Samples received				% Samples tested
	Specimens	Isolates	Specimen + Isolate	Other (eg. RNA/DNA/ tissue)	
AUSTRALASIA					
Australia	11900	0	132	4	99.40%
New Zealand	46	152	0	0	100%
SOUTH EAST ASIA					
Brunei	325	0	0	0	100%
Cambodia	2	108	0	0	100%
Philippines	123	0	5	0	100%
Singapore	3	0	156	0	100%
Thailand	35	10	0	0	100%
Timor-Leste	248	0	0	0	100%
SOUTH ASIA					
Bhutan	50	0	0	0	100%
India	0	49	0	0	100%
Nepal	55	0	0	0	100%
Sri Lanka	115	0	0	0	100%
SOUTH PACIFIC					
Cook Islands	5	0	0	0	100%
Fiji	189	0	0	0	100%
Kiribati	1	0	0	0	100%
New Caledonia	199	0	0	0	100%
Papua New Guinea	59	0	0	0	100%
Samoa	3	0	0	0	100%
Solomon Islands	30	0	0	0	100%
Tahiti	20	0	0	0	100%
Vanuatu	2	0	0	0	100%
AFRICA					
South Africa	7	0	23	0	100%
TOTAL	13417	319	316	4	99.50%

Table 2. Samples received from general practitioner-based surveillance systems, namely the Australian Sentinel Practices Research Network (ASPREN) and the hospital-based Influenza Complications Alert Network (FluCAN), in 2025.

	No. samples received	No. isolates recovered*	Viruses analysed by HI assay*
Australian Sentinel Practices Research (ASPREN) Network	568	314	313
Influenza Complications Alert Network (FluCAN)	5181	2523	2460
TOTAL	**5749**	**2837**	**2773**

** These numbers do not include samples from which isolates were recovered but did not have sufficient haemagglutination titres to be tested by HI assay.*

Table 3. Samples successfully isolated and analysed by cell culture and/or RT-PCR assay at the Centre in 2025, by country.

Country	Samples tested by cell culture and/or RT-PCR assay				
	A(H1N1) pdm09	A (H3N2)	A unsubtyped	B/Victoria	B lineage undetermined
AUSTRALASIA					
Australia	5533	1966	1575	1865	362
New Zealand	36	48	0	112	0
SOUTH EAST ASIA					
Brunei	104	90	0	18	1
Cambodia	55	34	0	21	0
Philippines	15	34	0	23	8
Singapore	58	56	0	42	0
Thailand	14	15	0	16	0
Timor-Leste	32	87	0	35	0
SOUTH ASIA					
Bhutan	3	8	0	11	0
India	10	25	0	13	0
Nepal	5	28	3	9	0
Sri Lanka	36	26	0	17	3
SOUTH PACIFIC					
Cook Islands	4	0	0	1	0
Fiji	13	153	0	11	2
Kiribati	0	0	0	0	0
New Caledonia	84	93	0	9	0
Papua New Guinea	9	2	0	7	0
Samoa	3	0	0	0	0
Solomon Islands	0	30	0	0	0
Tahiti	5	2	5	7	1
Vanuatu	0	0	0	2	0
AFRICA					
South Africa	2	27	0	1	0
TOTAL	6021	2739	1577	2220	377

Antigenic Analysis of Influenza Isolates

Background

The antigenic properties of influenza virus isolates are analysed using the HI assay, in which viruses are tested for their ability to agglutinate red blood cells in the presence of ferret antisera previously raised against reference viruses. A number of A (H3N2) viruses are also analysed antigenically using a microneutralisation assay known as the Focus Reduction Assay (FRA-MN). Subtypes are assigned based on analysis of the HA and, in some cases, are confirmed by genetic analysis of the NA gene.

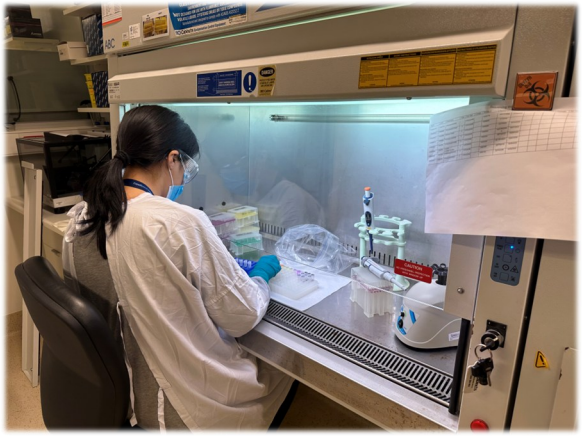


Figure 4. Influenza subtypes and lineages of samples received in 2025 and characterised by antigenic analysis.

Antigenic analyses in 2025

A total of 13,985 of the samples received at the Centre in 2025 were cultured and isolated in MDCK cells. The largest proportion of viruses were A (H1N1) pdm09 viruses (52.6%), followed by A (H3N2) viruses (28.5%), and B/Victoria viruses (18.6%) (Figure 4). Predominance of A(H3N2) was observed in Africa, South Asia, South East Asia and in the South Pacific region followed by A(H3N2) then B/Victoria. In Australasia, A(H1N1)pdm09 viruses predominated, followed by A(H3N2)and then B/Victoria (Figure 5).

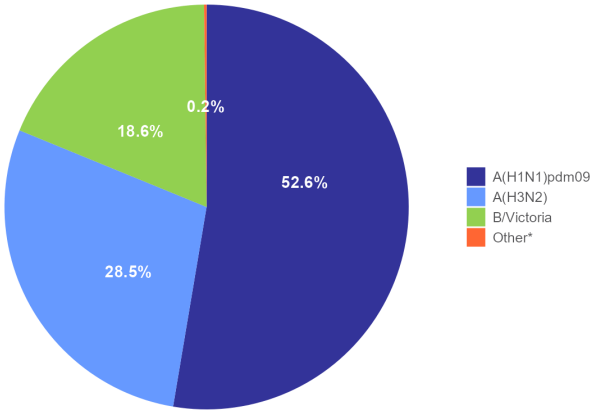
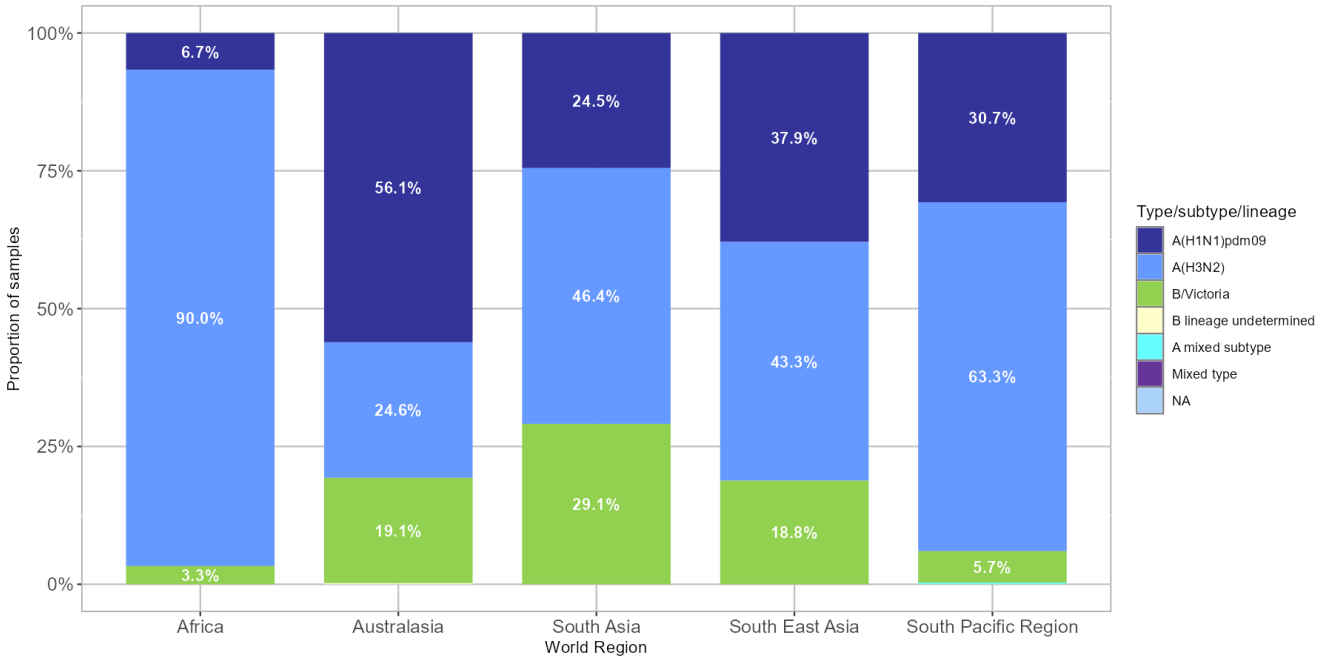


Figure 5. Antigenic characterization of influenza virus subtypes and lineages by global region in 2025.



Genetic Analysis of Influenza Viruses

Background

A subset of all influenza viruses analysed at the Centre undergo genetic analysis by sequencing of viral genes. Determining the amino acid sequence of antigenic regions of the HA and NA glycoproteins provides a sensitive method to examine how these glycoproteins are evolving in circulating influenza viruses. Routine genetic sequencing of the matrix protein (MP) and non-structural protein (NS) genes is also performed. The Centre also routinely sequences the full genomes of a smaller subset of viruses.

Viruses selected to undergo sequencing include those that exhibit evidence of antigenic drift by HI assay, as well as viruses that are generally representative of samples received by the Centre based on geography and date of collection. Sequence data are used to compare viruses from different parts of the world and help to inform the selection of vaccine strains.

Next generation sequencing (NGS) techniques are now routinely employed at the Centre for efficient and cost-effective whole genome sequencing of viruses, and/or selected influenza virus genes. NGS is performed at the Centre using either Illumina or Oxford Nanopore Technologies (ONT) platforms.

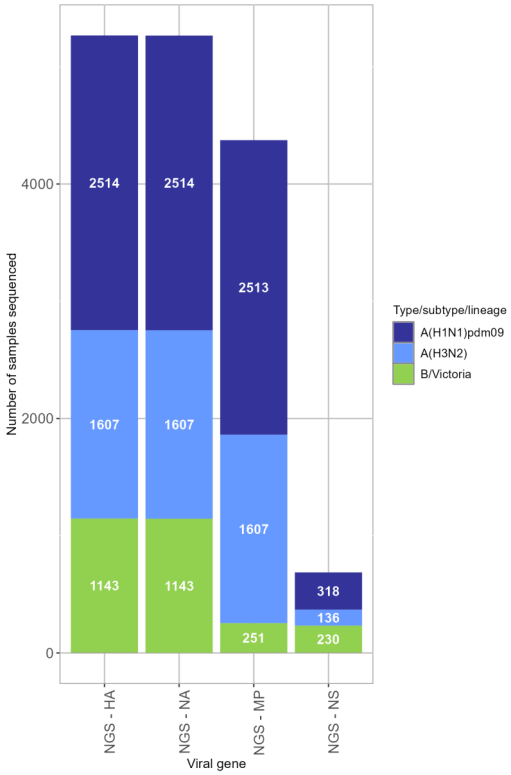


Figure 6. Sequencing of viruses received at the Centre in 2025.

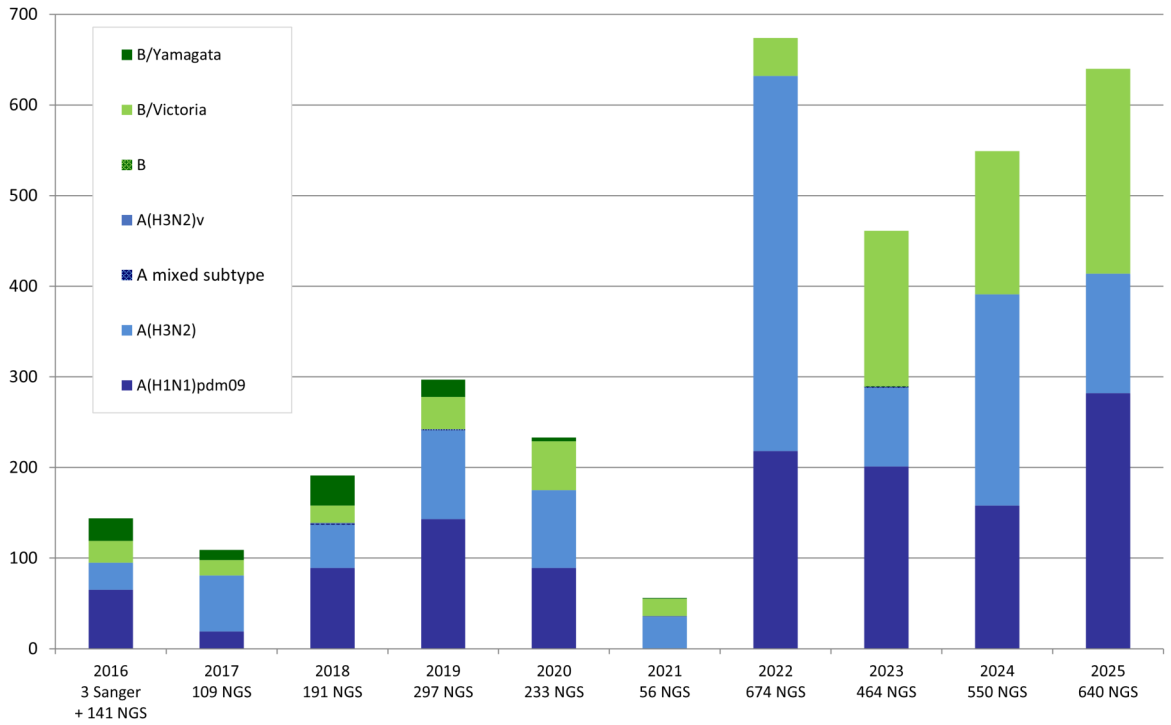
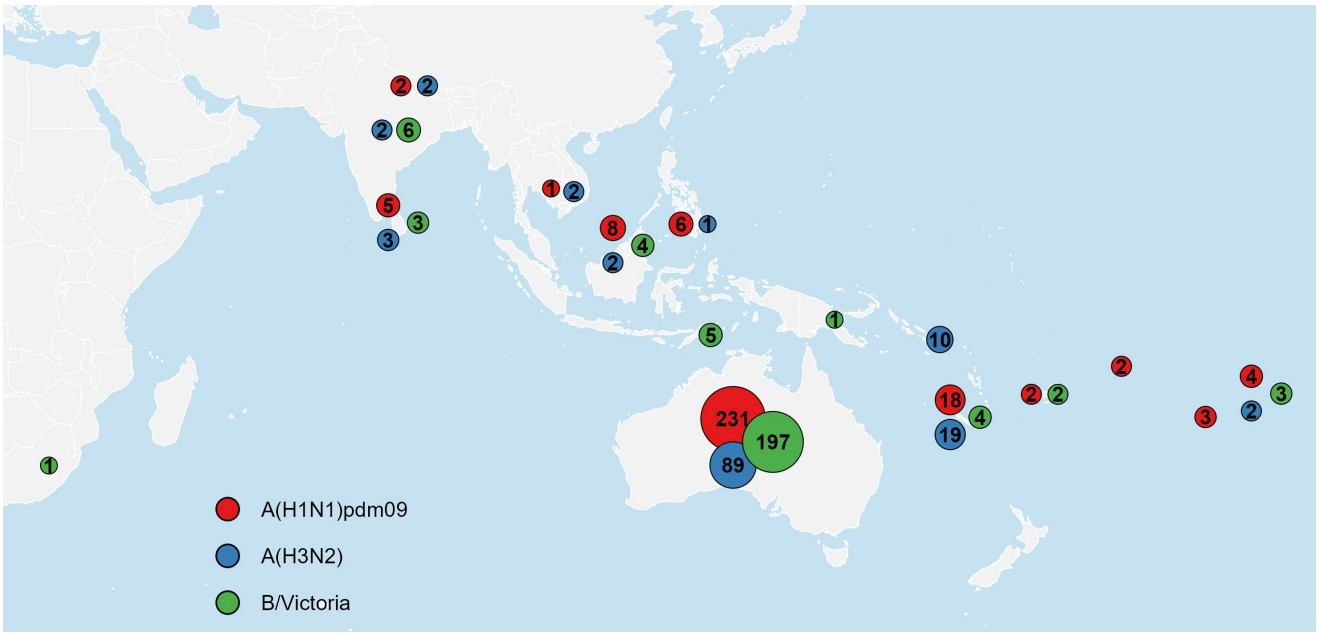


Figure 7. Number of viruses analysed by full genome sequencing from 2016-2025 using Sanger sequencing and/or NGS (Illumina or ONT).

Sequencing in 2025

In 2025, 5263 HA, 5263 NA, 4370 MP and 684 NS genes from 5238 human viruses received at the Centre were analysed by NGS (Figure 6). Of these viruses, full genome sequencing was performed on 640 viruses using NGS techniques (Figures 7 and 8). Viruses were selected for these analyses because they were representative of the viruses received and/or because they displayed unusual properties during antigenic analysis.

Figure 8. Geographic spread of submitting laboratories and numbers of viruses analysed by full genome sequencing using NGS techniques at the Centre in 2025.



Background

Virus sequences generated at the Centre are shared with the global influenza community through the EpiFlu™ database, a publicly accessible international repository of influenza virus sequences developed by the Global Initiative on Sharing All Influenza Data (GISAID) (http://www.gisaid.org).

Sequences submitted in 2025

A total of 17,292 gene sequences from 4192 human influenza viruses were deposited with GISAID in 2025 (Table 4). The largest number of these sequences were of HA and NA genes, followed by MP and PA genes. Full genomes of 335 influenza viruses (142 A(H1N1)pdm09 viruses, 89 A(H3N2) viruses and 104 B/Victoria viruses) were also represented in the Centre's submissions (data not shown).

Table 4. Genetic sequences submitted to GISAID by the Centre in 2025.*

Gene / Type/ Subtype/ Lineage	HA	NA	MP	NS	PB1	PB2	PA	NP	Total
A(H1N1)pdm09	2322	2311	2275	200	149	197	2134	199	9787
A(H3N2)	1019	1012	974	99	90	92	953	99	4338
B/Victoria	851	846	154	148	115	118	801	134	3167
Total	4192	4169	3403	447	354	407	3888	432	17292

**Numbers include all sequences submitted to GISAID during 2025, which includes viruses received in previous years and viruses sequenced for reference and research purposes*

Surveillance Results by Influenza Subtype or Lineage

Viruses were analysed by comparison with reference viruses recommended by WHO for the 2025 Southern Hemisphere vaccines. Using the HI assay, viruses were identified as low-reactors if their titre with the reference antiserum was at least 8-fold lower than the homologous titre of the reference virus. Results of sequencing analysis of the HA gene are also described in the following sections.

Influenza A(H1N1)pdm09

Antigenic analysis

A total of 3804 A(H1N1)pdm09 isolates were analysed by HI assay in 2025. A small percentage of viruses (0.44%) received from the Australasia region were antigenically dissimilar (i.e. low reactors) to the cell-grown vaccine A/Victoria/4897/2022 (Figure 9,10, Table 5). All viruses from Africa, East Asia, South Asia and the South Pacific region displayed similar antigenic properties to the reference strain.

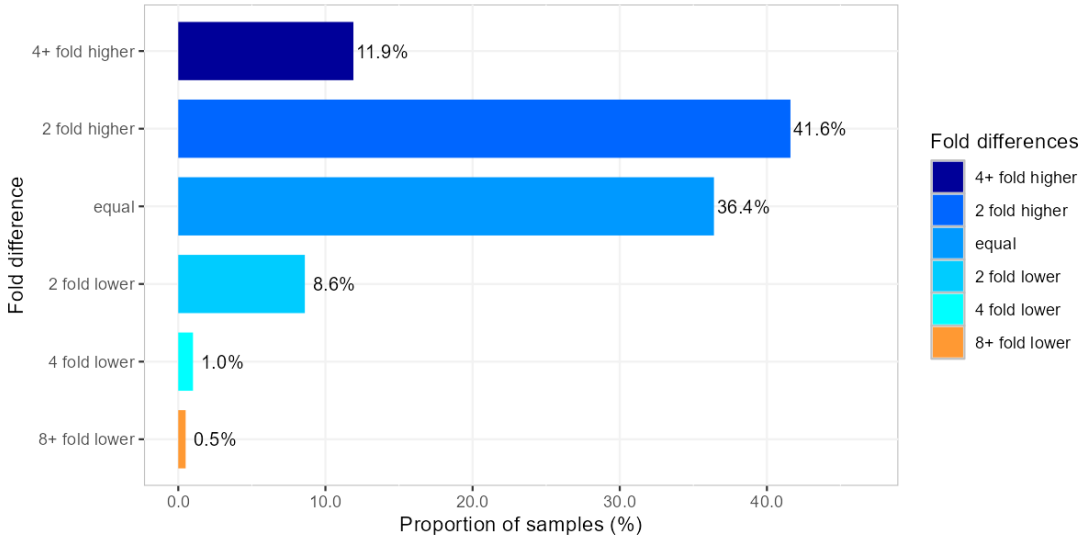
Haemagglutinin gene sequencing

Sequencing was performed on a total of 2322 HA genes. Phylogenetic analysis showed that the majority of A(H1N1)pdm09 viruses received at the Centre during 2025 belonged to subclades C.1.9.3 and D.3.1. While the 2024-2025 vaccine strain A/Victoria/4897/2022 belongs to subclade D, the emergence of these variants informed the selection of A/Missouri/11/2025, a subclade D.3.1 virus, as the vaccine strain for 2026.

Table 5. Antigenic characterisation of A(H1N1)pdm09 viruses analysed at the Centre compared to the A/Victoria/4897/2022 reference virus.

	A(H1N1)pdm09 reference strain: A/VICTORIA/4897/2022-LIKE	
Region	**Like**	**Low reactor (%)**
Africa	2	0
Australasia (AUS + NZ)	3392	15 (0.44 %)
South Asia	37	0
South East Asia	251	0
South Pacific Region	107	0
TOTAL	3789	15 (0.39 %)

Figure 9. Summary of fold differences in HI titres of A(H1N1)pdm09 viruses analysed at the Centre compared to the A/ Victoria/4897/2022 reference virus.



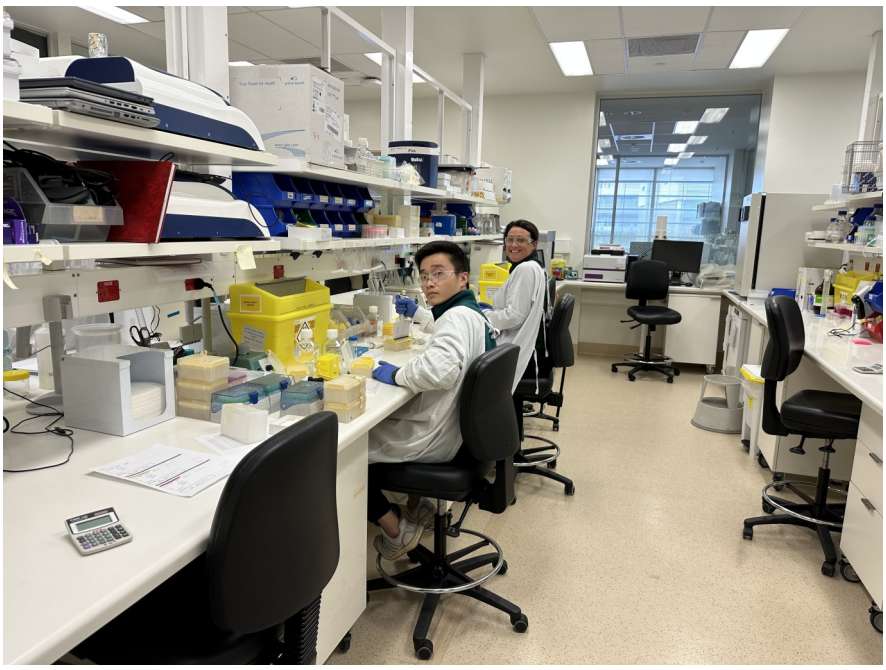
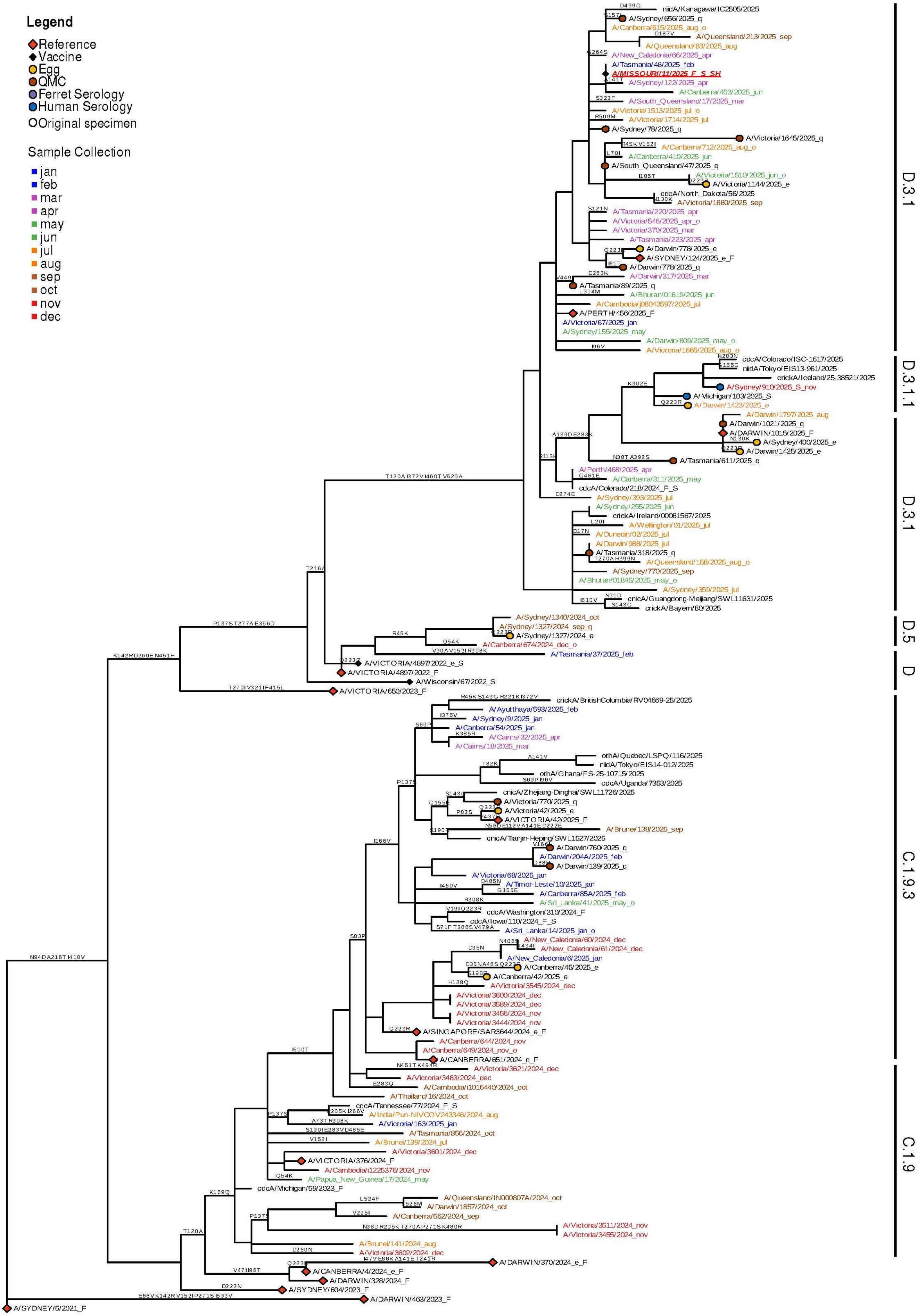


Figure 11. Phylogenetic tree of representative HA genes of A(H1N1)pdm09 viruses received by the Centre during 2025.



Influenza A(H3N2)

Antigenic analysis

Due to evolutionary changes, some contemporary A(H3N2) viruses have acquired NA proteins that can bind sialic acid receptors on red blood cells, complicating analysis of viruses using conventional HI assays. To prevent this interference, oseltamivir carboxylate is added to the assay to selectively inhibit NA activity. The focus reduction microneutralisation assay (FRA-MN), represents an additional assay for antigenic characteristisation of A(H3N2) and other viruses that is performed at the Centre.

A total of 1901 A(H3N2) isolates were analysed by HI assay against a like strain of the cell-grown recommended vaccine strain for the 2025 Southern Hemisphere (A/District of Columbia/27/2023). In these assays, 7.4%, 74%, 8.1%, 47.3% and 47% % of viruses received from Africa, Australasia, South Asia, South East Asia and the South Pacific Region, respectively, were antigenically dissimilar (i.e. low reactors) to the reference strain (Table 6).

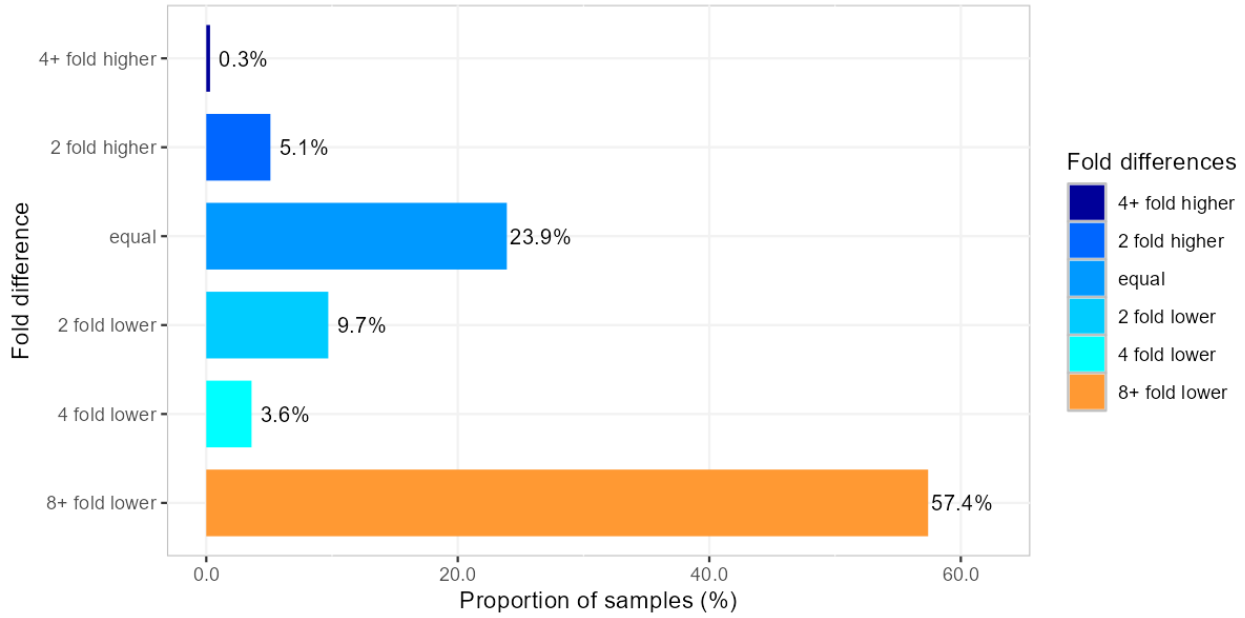
Haemagglutinin gene sequencing

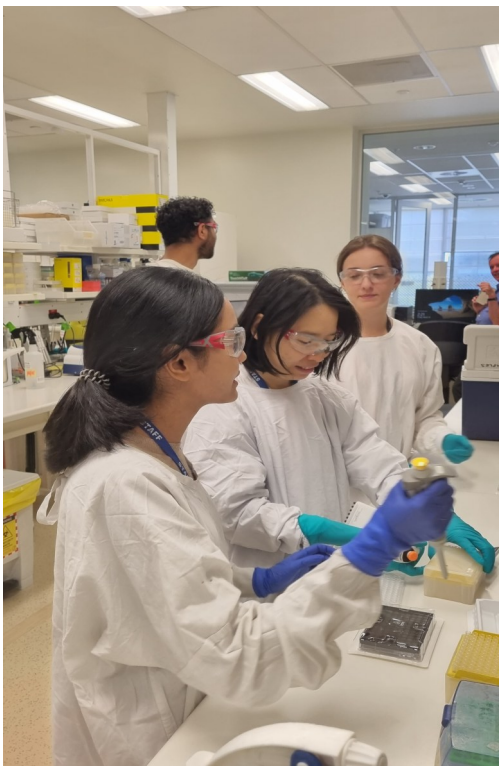
Following sequencing of a total of 1019 HA genes from A(H3N2) viruses, phylogenetic analyses revealed that most circulating viruses belong to subclade K (Figure 13). Consequently, the A(H3N2) strain recommended for the 2026 Southern Hemisphere vaccine was updated to A/Singapore/GP20238/2024, a subclade J.2.4 virus, likely to provide better protection against subclade K viruses.

Table 6. Antigenic characterisation of A(H3N2) viruses analysed at the Centre compared to cell-grown A/District of Columbia/27/2023-like reference viruses.

	A(H3N2) reference strain: A/District of Columbia/27/2023-like	
Region	**Like**	**Low reactor (%)**
Africa	25	2 (7.4%)
Australasia	389	1105 (74%)
South Asia	34	3 (8.1%)
South East Asia	88	79 (47.3%)
South Pacific Region	94	82 (47%)
TOTAL	**630**	**1271 (67%)**

Figure 12.A. Summary of fold differences in titres of A(H3N2) viruses analysed at the Centre by HI assay compared to the cell-grown A/District of Columbia/27/2023-like reference viruses.





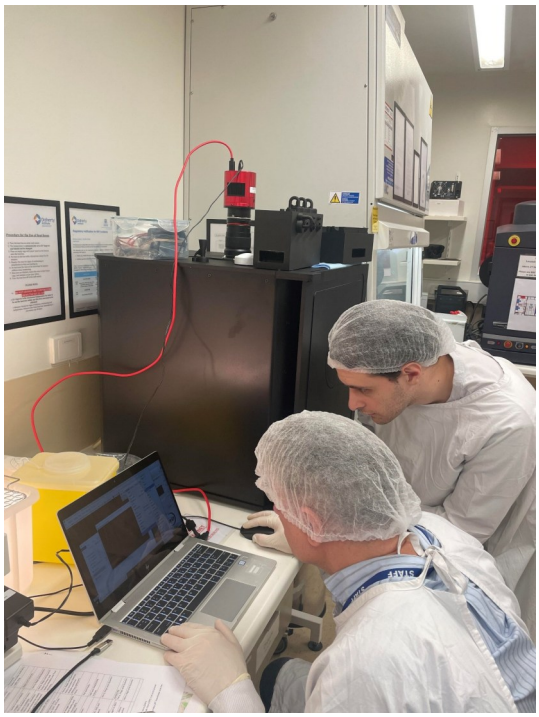
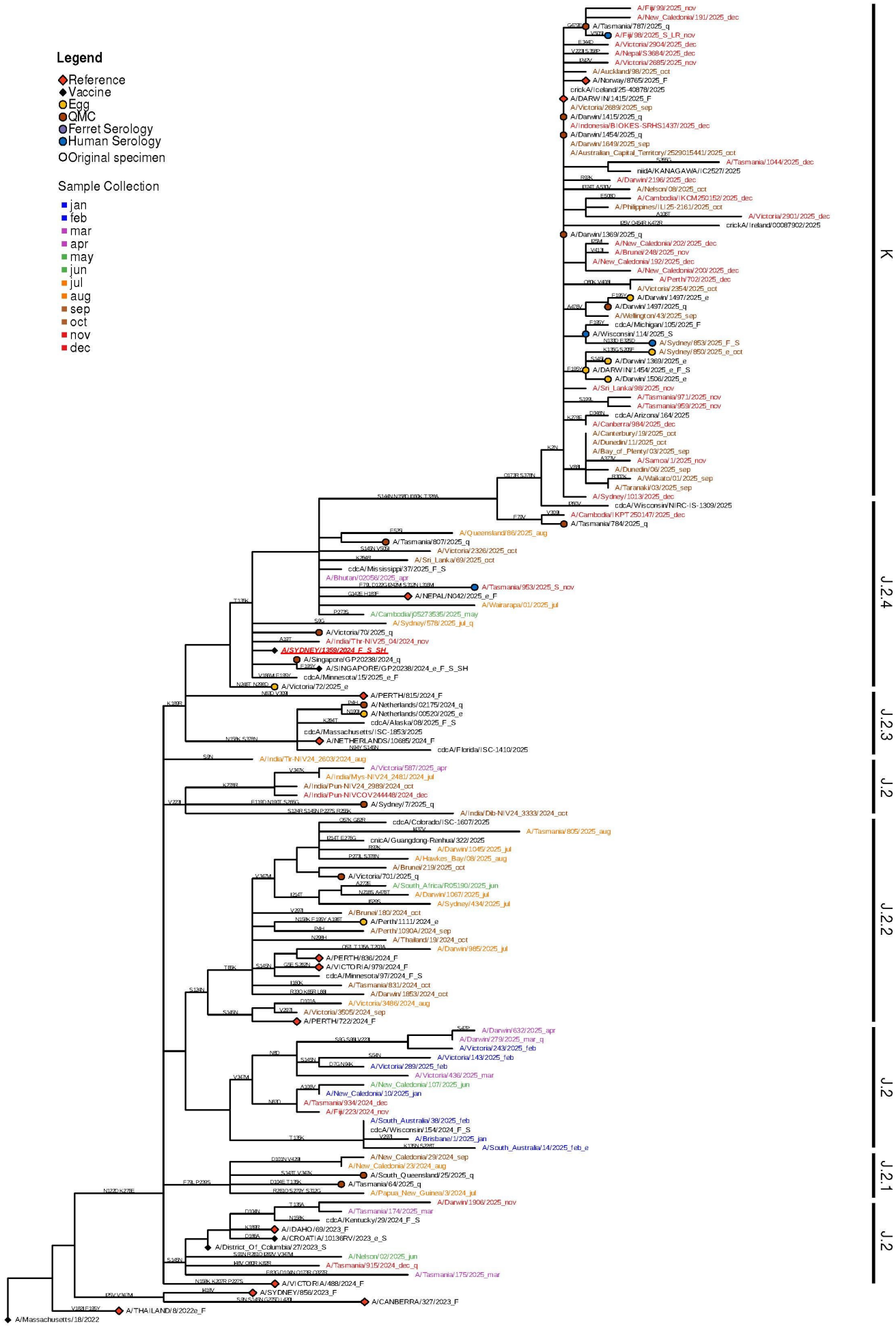


Figure 13. Phylogenetic tree of representative HA genes of A(H3N2) viruses received by the Centre during 2025.



Influenza B/Victoria

Introduction

Until recently, two antigenically and genetically distinct lineages of influenza B virus circulated in humans — the B/Victoria/2/87 lineage (represented by the 2022 vaccine strain, B/Austria/1359417/2021), and the B/Yamagata/16/88 lineage (represented by the 2022 vaccine strain B/Phuket/3073/2013). Until 2001, B/Victoria lineage viruses had been restricted to Asia where they tended to alternate in predominance with the B/Yamagata lineage. In 2002, the B/Victoria lineage became the predominant influenza B lineage in most parts of the world. This trend was reversed in 2003 and 2004 when the B/Yamagata lineage predominated. Since then, both lineages co-circulated, with alternating cycles of predominance every few years until 2020. However, no B/Yamagata lineage viruses with collection dates after March 2020 have been detected globally, and the Centre did not receive any samples containing B/Yamagata viruses in 2025.

Antigenic Analysis

A total of 1313 B/Victoria lineage isolates were analysed by HI assay in 2025. When these viruses were tested against the cell-grown recommended vaccine strain for the 2025 Southern Hemisphere (B/Austria/1359417/2021). There were 26 (1.98%) viruses detected from the Australasian region that were antigenically dissimilar (i.e. low reactors) to the reference strain. (Figure 14, Table 7).

Haemagglutinin gene sequencing

A total of 851 HA genes from B/Victoria-lineage viruses were sequenced. Phylogenetic analyses indicate that most circulating viruses belonged to subclades C.5.6 and C.5.7. The recommended vaccine strain for the 2025 Southern Hemisphere (B/Austria/1359417/2021) belongs to subclade C.5 (Figure 15).

Table 7. Antigenic characterisation of B/Victoria-lineage viruses received at the Centre during 2025 compared to the B/Austria/1359417/2021 reference virus.

	B/Victoria lineage reference strain: B/Austria/1359417/2021	
Region	**Like**	**Low reactor (%)**
Africa	1	0
Australasia	1098	26 (2.31%)
South Asia	43	0
South East Asia	125	0
South Pacific Region	20	0
TOTAL	**1287**	**26 (1.98%)**

Figure 14. Summary of fold differences in HI titres of B/Victoria-lineage viruses analysed at the Centre compared to B/ Austria/1359417/2021 reference virus.

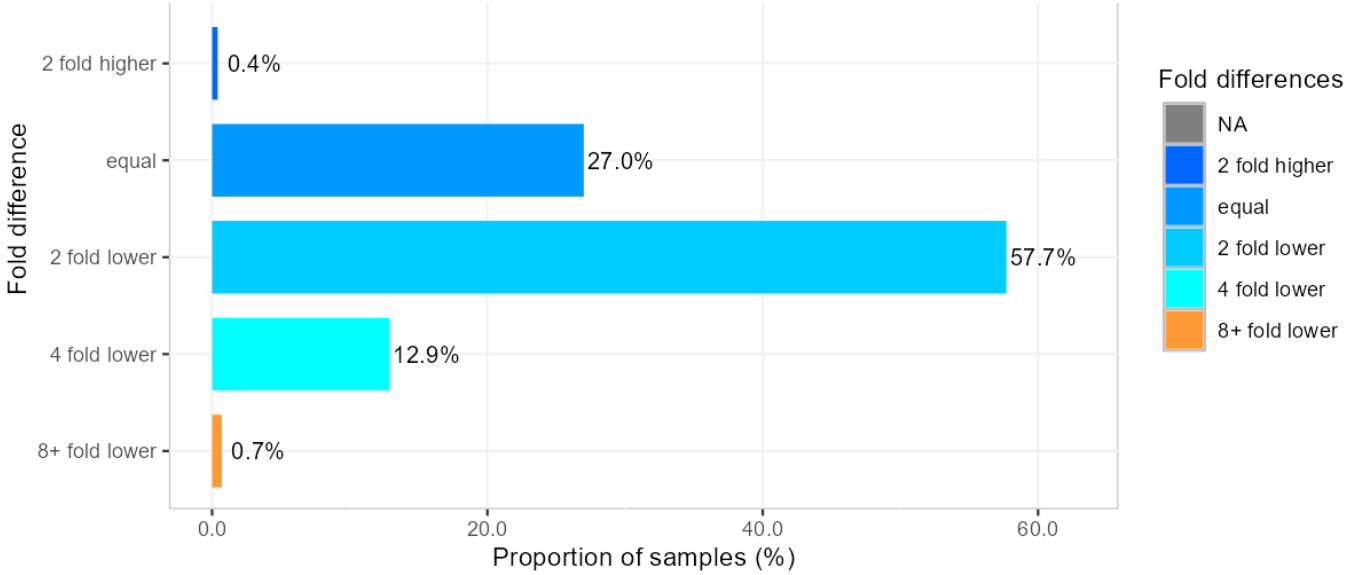
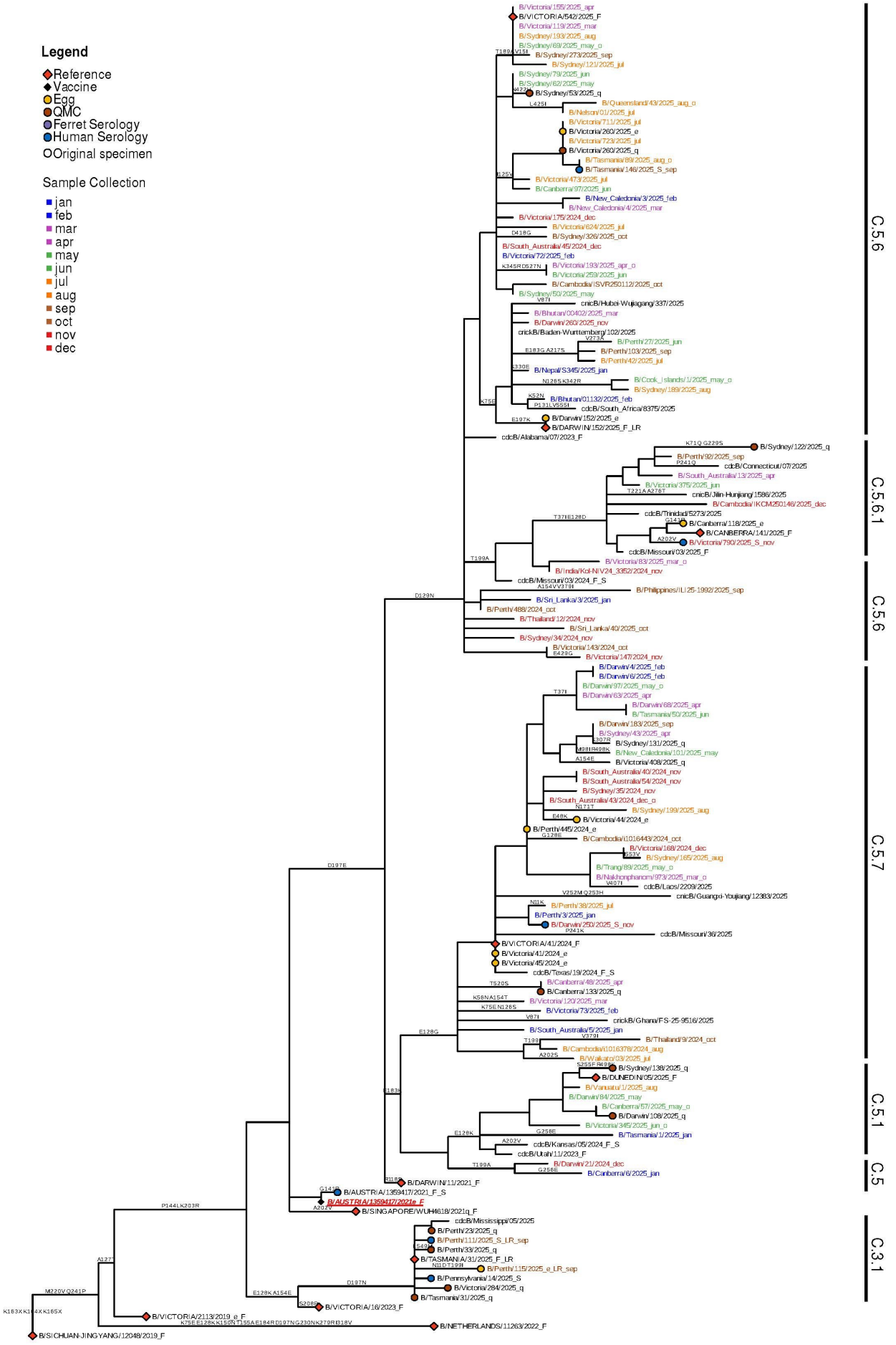


Figure 15. Phylogenetic tree of representative HA genes of B/Victoria viruses received by the Centre during 2025.



Antiviral Drug Resistance Testing

Sensitivity to Neuraminidase Inhibitors (NAIs)

Background

As influenza viruses continually undergo genetic change, their potential to develop resistance to antiviral drugs is an ongoing concern. To detect the emergence of drug-resistant influenza strains that could present future treatment challenges, viruses are tested for their sensitivity to the currently used neuraminidase inhibitors oseltamivir (Tamiflu), zanamivir (Relenza), laninamivir and peramivir. Laninamivir is not currently approved in Australia but is used in Japan. The Centre has routinely tested and reported the sensitivity of viruses to all four NAIs using the neuraminidase inhibition assay (NAI assay) since 2012. Viruses are routinely screened by an automated NAI assay using a Tecan EVO 200 liquid-handling robot.

The sensitivity of viruses to NAIs is measured according to the concentration of drug required to inhibit 50% of NA activity (IC50). The relationship between the IC50 value and the clinical effectiveness of a NAI against a given virus is not well understood. Further studies would be required to determine whether a virus with an elevated IC50 is clinically resistant.

Table 8. Viruses received by the Centre in 2025 and tested by NAI assay, by country.

	Type/subtype/lineage			
Country	**A(H1N1)pdm09**	**A(H3N2)**	**B/Victoria**	**TOTAL**
Africa				
South Africa	0	25	1	26
Australasia				
Australia	1510	263	307	2080
New Zealand	35	38	110	183
South East Asia				
Brunei	59	78	3	140
Cambodia	53	32	19	104
Philippines	5	32	5	42
Singapore	58	54	42	154
Thailand	12	14	14	40
Timor-Leste	6	60	2	68
South Asia				
Bhutan	3	5	11	19
India	10	22	11	43
Nepal	1	20	8	29
Sri Lanka	20	14	11	45

*Table 8. Continued below**

Country	A(H1N1)pdm09	A(H3N2)	B/Victoria	TOTAL
South Pacific				
Cook Islands	4	0	1	5
Fiji	7	120	3	130
New Caledonia	79	88	3	170
Papua New Guinea	5	2	2	9
Samoa	2	0	0	2
Tahiti	4	2	2	8
Vanuatu	0	0	2	2
TOTAL	1873	869	557	3299

Antiviral resistance analyses in 2025

NAI assays were used to analyse 3299 viruses for reduced inhibition by the NAIs (Tables 8 and 9). Viruses showing reduced or highly reduced inhibition to one or more NAIs underwent further analysis to determine the presence of amino acid substitutions in the NA protein associated with the reduction of inhibition by NAIs.

A total of 39 viruses (all A(H1N1)pdm09) had highly reduced inhibition (HRI) by one or more of the NAIs. These viruses were sequenced to determine the presence of amino acid substitutions in the NA protein that were associated with reduced inhibition by NAIs (Table 10). For example, it is well established that the substitution of histidine (H) to tyrosine (T) at position 275 (H275Y) of the NA protein of A(H1N1)pdm09 viruses results in reduced inhibition by oseltamivir, and the same is seen for the equivalent H273Y mutation in B viruses.

Table 9. Neuraminidase inhibitor sensitivity of viruses received by the Centre in 2025.

Type/Subtype/ Lineage	No. tested	Oseltamivir		Peramivir		Laninamivir		Zanamivir	
		RI*	HRI*	RI*	HRI*	RI*	HRI*	RI*	HRI*
A(H1N1)pdm09	1873	5 (0.27%)	39 (2.08%)	3 (0.16%)	39 (2.08%)	1 (0.05%)	0	2 (0.11%)	0
A(H3N2)	869	0	0	0	0	0	0	0	0
B/Victoria	557	0	0	0	0	0	0	0	0
TOTAL	3299	5 (0.15%)	39 (1.18%)	3 (0.09%)	39 (1.18%)	1 (0.03%)	0	2 (0.06%)	0

** Based on IC50, the NAI sensitivity of each strain is classified as the following: Normal inhibition = IC50 values are within or close to the median IC50 of type/subtype-matched viruses tested at the Centre during the past year. Reduced inhibition (RI) = IC50 values are 10- to 100-fold above the median value of viruses with normal inhibition (5- to 50-fold for influenza B viruses). Highly reduced inhibition (HRI) = IC50 values are greater than 100-fold above the median value of viruses with normal inhibition (above 50-fold for influenza B viruses).*

Table 10. Characteristics of viruses received by the Centre during 2025 with highly reduced inhibition by NAIs.

Type/Subtype/ Lineage	Country of submitting laboratory	NAI(s) with highly reduced inhibition (marked with *)				
		Oseltamivir	Peramivir	Laninamivir	Zanamivir	Mutations detected
A(H1N1)pdm09	Thailand	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	New Caledonia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Singapore	*	*			H275Y

Table 10. Characteristics of viruses received by the Centre during 2025 with highly reduced inhibition by NAIs (Continued).

Type/Subtype/ Lineage	Country of submitting laboratory	NAI(s) with highly reduced inhibition (marked with *)				
		Oseltamivir	Peramivir	Laninamivir	Zanamivir	Mutations detected
A(H1N1)pdm09	Singapore	*	*			H275Y
A(H1N1)pdm09	Singapore	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	New Caledonia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y
A(H1N1)pdm09	Australia	*	*			H275Y

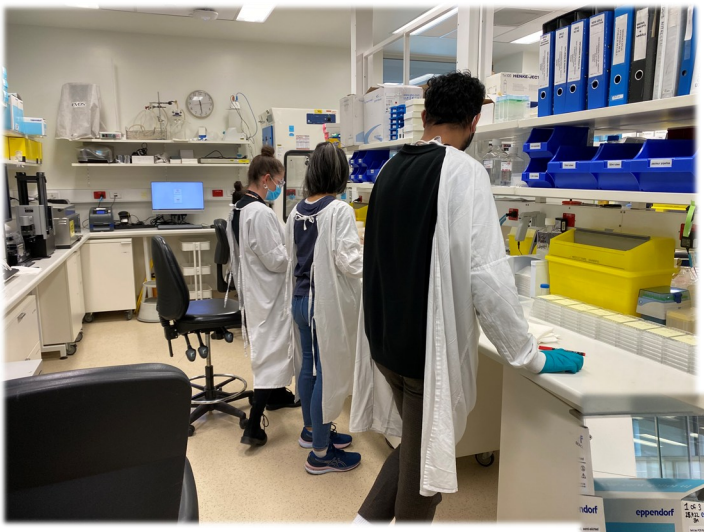
Resistance to Baloxavir Marboxil

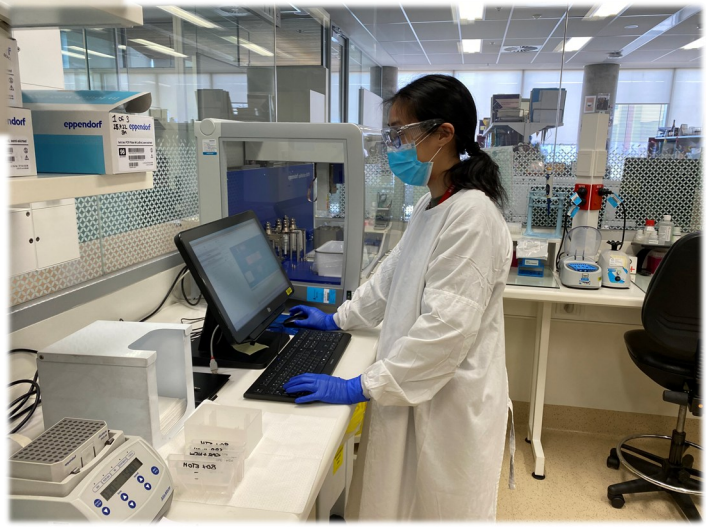
Background

Baloxavir marboxil (XofluzaTM) is an antiviral drug that has had regulatory approval for use in the treatment of influenza in Japan and the USA since 2018, and in Australia since 2020. Baloxavir acts by inhibiting the PA endonuclease of influenza A and B viruses, thereby preventing viral replication in host cells. As part of its antiviral drug resistance surveillance program, the Centre has developed a biological assay to detect and monitor circulating influenza viruses for reduced susceptibility to baloxavir.

Screening for baloxavir resistance in 2025

A large proportion of viruses received at the Centre are sequenced by next generation sequencing (NGS) using a 4-gene multiplex assay (HA, NA, PA, MP) and a smaller proportion by whole genome sequencing (Figures 6 and 7). In 2025, 2610 A(H1N1)pdm09, 1331 A(H3N2) and 1011 B/Victoria-lineage viruses were screened for known substitutions in the PA gene associated with reduced susceptibility to baloxavir marboxil (these substitutions are indicated in the WHO influenza antiviral PA marker tables)[1]. Mutations associated with reduced susceptibility to baloxavir are commonly found in the I38 position of the PA endonuclease, with the PA-I38T shown to have clinical impact [2,3,4] . However, no substitutions associated with resistance to baloxavir were detected (Table 11). Previously, when a genetic marker associated with resistance to baloxavir has been detected (such as the PA-A37T substitution, detected in a small number of viruses in 2024), these viruses, along with a subset of temporally and geographically representative viruses, are further characterised using a phenotypic assay known as the Influenza Replication Inhibition Neuraminidase-based assay (IRINA).





1. https://cdn.who.int/media/docs/default-source/influenza/laboratory---network/quality-assurance/antiviral-susceptibility-influenza/pa-marker-who-table_28-11-2025_updated.pdf?sfvrsn=5307d6fe_4

2. *Uehara T, Hayden FG, Kawaguchi K, Omoto S, Hurt AC, De Jong MD, Hirotsu N, Sugaya N, Lee N, Baba K, Shishido T, Tsuchiya K, Portsmouth S, Kida H. 2020. Treatment-Emergent Influenza Variant Viruses With Reduced Baloxavir Susceptibility: Impact on Clinical and Virologic Outcomes in Uncomplicated Influenza. J Infect Dis 221:346-355.*

3. *Sato M, Takashita E, Katayose M, Nemoto K, Sakai N, Fujisaki S, Hashimoto K, Hosoya M. 2021. Detection of Variants With Reduced Baloxavir Marboxil and Oseltamivir Susceptibility in Children With Influenza A During the 2019-2020 Influenza Season. J Infect Dis 224:1735-1741.*

4. *Takashita E, Fujisaki S, Morita H, Nagata S, Miura H, Kishida N, Nakamura K, Shirakura M, Sato A, Akimoto M, Sugawara H, Mitamura K, Abe T, Ichikawa M, Yamazaki M, Watanabe S, Odagiri T, Hasegawa H, Influenza Virus Surveillance Group of J. 2026. Baloxavir susceptibility of seasonal influenza viruses during the first seven seasons of clinical use in Japan, 2017/18 to 2023/24. Euro Surveill 31.*

Table 11. Viruses screened for mutations associated with reduced susceptibility to baloxavir by NGS during 2025.

	Next generation sequencing						
Country / Type/subtype/ lineage	A(H1N1)pdm09	A(H3N2)	B/Victoria	A unsubtyped	B lineage undetermined	MIXED A/B	Influenza C
Australasia							
Australia	2404	915	869	17	17	2	1
New Zealand	19	48	23	0	0	0	0
South East Asia							
Brunei	29	48	8	0	1	0	0
Cambodia	18	22	20	0	0	0	0
Indonesia							
Malaysia	0	0	1	0	0	0	0
Philippines	6	9	15	0	0	0	0
Singapore	4	2	0	0	0	0	0
Thailand	14	15	11	0	0	0	0
Timor-Leste	9	6	8	0	0	0	0
South Asia							
Bhutan	3	8	11	0	0	0	0
India	4	14	7	0	0	0	0
Nepal	4	22	6	0	0	0	0
Sri Lanka	32	23	14	0	2	0	0
South Pacific							
Cook Islands	4	0	1	0	0	0	0
Fiji	8	93	3	0	0	0	0
Kiribati	0	3	0	0	0	0	0
New Caledonia	37	75	5	0	0	0	0
Papua New Guinea	7	11	3	0	0	0	0
Samoa	4	1	0	0	0	0	0
Solomon Islands	0	10	0	0	0	0	0
Tahiti	4	2	3	2	0	0	0
Vanuatu	0	0	2	0	0	0	0
Africa							
South Africa	0	4	1	0	0	0	0
TOTAL	**2610**	**1331**	**1011**	**19**	**20**	**2**	**1**

Resistance to Adamantanes

Background

The adamantane class of antiviral drugs (amantadine and rimantadine) target the viral M2 protein and were previously used to treat influenza A virus infections. They are no longer recommended for clinical use due to widespread, near universal resistance amongst circulating influenza A viruses, which is primarily associated with a serine to alanine substitution at position 31 (S31N) in the influenza A M2 protein. Our Centre continues to screen the submitted viruses which are sequenced for the S31N substitution.

Screening for adamantane resistance in 2025

Sequencing was performed on 3800 influenza A viruses, representative of samples submitted to the Centre during 2025 (Figure 12). With the exception of 3 A(H1N1)pdm09 viruses, all sequenced viruses carried the MP-S31N amino acid substitution which confers resistance to amantadines.

Figure 12. Viruses received by the Centre during 2025 and screened for adamantane resistance.

	Type/subtype/lineage			
Country	**A(H1N1)pdm09 Tested**	**A(H1N1)pdm09 Resistant**	**A(H3N2) Tested**	**A(H3N2) Resistant**
Australasia				
Australia	2315	2312	899	899
New Zealand	19	19	48	48
South East Asia				
Brunei	26	26	45	45
Cambodia	18	18	25	25
Philippines	1	1	8	8
Singapore	4	4	1	1
Thailand	14	14	14	14
Timor-Leste	8	8	5	5
South Asia				
Bhutan	3	3	7	7
India	4	4	14	14
Nepal	4	4	21	21
Sri Lanka	24	24	16	16
South Pacific				
Cook Islands	4	4	0	0
Fiji	8	8	93	93
Kiribati	0	0	3	3
New Caledonia	36	36	73	73
Papua New Guinea	7	7	11	11
Samoa	4	4	0	0
Solomon Islands	0	0	8	8
Tahiti	4	4	2	2
Africa				
South Africa	0	0	4	4
TOTAL				

Candidate Vaccine Strains

Background

The Centre works closely with the other WHO Collaborating Centres and vaccine manufacturers to ensure the suitability of candidate strains for inclusion in seasonal vaccines. Selected original clinical specimens containing potential vaccine strains are used to isolate viruses in eggs and in Qualified MDCK cells. (QMCs). Isolation of candidate vaccine strains is performed in laboratories designed for this purpose under conditions consistent with current internationally accepted regulatory requirements for influenza vaccine viruses. These isolates are then analysed by HI assay and genetic sequencing.

Isolation of viruses in eggs in 2025

In 2025, a total of 32 viruses were successfully isolated in eggs at the Centre, representing an overall isolation rate of 46% (Tables 12 and 14).

Table 12. Virus isolation in eggs at the Centre in 2025.

Type/subtype	Isolates attempted	Isolates obtained	Success rate (%)
A(H1N1)pdm09	22	11	50%
A(H3N2)	41	17	41%
B/Victoria	7	4	57%
Total	**70**	**32**	**46%**

Isolation of viruses in QMCs in 2025

In 2025, a total of 70 viruses were successfully isolated in QMCs at the Centre, representing an overall isolation rate of 54% (Tables 13 and 15).

Table 13. Virus isolation in QMCs at the Centre in 2025.

Type/subtype	Isolates attempted	Isolates obtained	Success rate (%)
A(H1N1)pdm09	42	21	50%
A(H3N2)	72	37	51%
B/Victoria	16	12	75%
Total	130	70	54%

Table 14. Potential candidate vaccine strains isolated in eggs at the Centre in 2025.

A(H1N1)pdm09
A/Canberra/42/2025
A/Canberra/45/2025
A/Victoria/42/2025
A/Darwin/778/2025
A/Sydney/124/2025
A/Darwin/1021/2025
A/Victoria/1139/2025
A/Victoria/1144/2025
A/Sydney/400/2025
A/Darwin/1425/2025
A/Darwin/1423/2025

A(H3N2)
A/Perth/1111/2024
A/Nepal/N042/2025
A/Singapore/GP20238/2024
A/Victoria/143/2025
A/Tasmania/807/2024
A/Canberra/550/2024
A/Netherlands/00520/2025
A/Victoria/72/2025
A/South Australia/14/2025
A/Tasmania/46/2025
A/Darwin/1369/2025
A/Darwin/1497/2025
A/Darwin/1506/2025
A/Darwin/1454/2025
A/Darwin/1499/2025
A/Darwin/1496/2025
A/Sydney/850/2025

B/Victoria
B/Victoria/260/2025
B/Canberra/118/2025
B/Perth/115/2025
B/Darwin/152/2025

Table 15. Potential candidate vaccine strains isolated in QMCs at the Centre in 2025.

A(H1N1)pdm09	A(H3N2)		B/Victoria
A/Canberra/651/2024	A/Singapore/NUH1188/2024	A/Darwin/708/2025	B/Tasmania/31/2025
A/Victoria/3436/2024	A/Perth/1111/2024	A/Tasmania/46/2025	B/Victoria/284/2025
A/Tasmania/868/2024	A/Tasmania/915/2024	A/Darwin/1559/2025	B/Sydney/53/2025
A/Tasmania/785/2024	A/Singapore/KK2563/2024	A/Darwin/1369/2025	B/Victoria/260/2025
A/Canberra/652/2024	A/Perth/1152/2024	A/Perth/615/2025	B/Darwin/108/2025
A/Victoria/3425/2024	A/Perth/1157/2024		B/Canberra/133/2025
A/Darwin/139/2025	A/Thailand/27/2024		B/Perth/23/2025
A/Tasmania/89/2025	A/Sydney/7/2025		B/Perth/33/2025
A/Sydney/78/2025	A/Singapore/GP20238/2024		B/Victoria/408/2025
A/Darwin/778/2025	A/Sydney/16/2025		B/Sydney/122/2025
A/Tasmania/318/2025	A/Victoria/211/2025		B/Sydney/131/2025
A/Darwin/760/2025	A/Victoria/244/2025		B/Sydney/138/2025
A/Victoria/770/2025	A/Tasmania/185/2025		
A/South QLD/47/2025	A/Darwin/279/2025		
A/Tasmania/611/2025	A/Tasmania/64/2025		
A/Sydney/352/2025	A/Victoria/257/2025		
A/Darwin/1021/2025	A/Sydney/68/2025		
A/Darwin/1028/2025	A/Victoria/317/2025		
A/Darwin/1035/2025	A/South QLD/25/2025		
A/Victoria/1645/2025	A/Victoria/699/2025		
A/Sydney/656/2025	A/Victoria/701/2025		
	A/Victoria/869/2025		
	A/Darwin/1415/2025		
	A/Darwin/1454/2025		
	A/Sydney/578/2025		
	A/Tasmania/784/2025		
	A/Tasmania/787/2025		
	A/Darwin/1497/2025		
	A/Tasmania/807/2025		

Preparation and Analysis of Vaccine Seed Viruses

The Centre exchanges candidate vaccine viruses that have been isolated in eggs and qualified MDCK cells, as well as post-infection ferret antisera raised against these and other reference viruses, with the other WHO Collaborating Centres to enable direct comparison of strains isolated in the five Centres. During 2025, 4 candidate vaccine viruses that had been received from other WHO Collaborating Centres and laboratories were passaged in eggs at the Centre (Table 16).

Selected candidate vaccine strains isolated in eggs are made available to the three laboratories that undertake virus reassortment for WHO — Seqirus, the National Institute for Biological Standards and Control (NIBSC, UK) and New York Medical College (NYMC, USA) — where they are reassorted with established egg or cell-adapted strains to produce potential vaccine seed strains. The reassortant vaccine seed viruses are returned to the Centre, where they are analysed by HI assay and genetic sequencing to ensure that key antigenic and genetic properties of the vaccine virus have been retained. The vaccine seed viruses are distributed to other WHO Collaborating Centres and vaccine manufacturers worldwide through Essential Regulatory Laboratories at the Therapeutic Goods Administration (Australia), NIBSC and the Centre for Biologics Evaluation and Research (CBER), and the Food and Drug Administration (USA). During 2025, 24 reassortant viruses were tested at the Centre (Table 16).

Table 16. Potential candidate vaccine viruses from other WHO Collaborating Centres and passaged in eggs and reassortant viruses received and tested at the Centre during 2025

A(H3N2)
Candidate Vaccine Viruses
A/Guizhou-Yilongxin/2738/2024
Reassortants received and tested:
SAN-035 (A/Canberra/69/2024)
CVR-289 (A/Victoria/800/2024)
IVR-261 (A/Idaho/69/2023)
A/Perth/722/2024 v1
IVR-277 (A/Singapore/GP20238/2024)
SVR-08 (A/Sydney/1359/2024)
SVR-11 (A/Sydney/1359/2024)
CVR-355 (A/Sydney/1359/2024)
CVR-378 (A/Sydney/1359/2024)
CVR-381 (A/Sydney/1359/2024)
A(H1N1)pdm09
Candidate Vaccine Viruses
A/Shanghai-Putuo/SWL1666/2024
A/Missouri/11/2025
A/Switzerland/6849/2025
Reassortants received and tested:
SAN-038 (A/South Australia/27/2024)
IVR-265 (A/Darwin/1191/2024)
IVR-266 (A/Singapore/SAR3644/2024)
A/South Australia/27/2024 v1

A(H1N1)pdm09 (continued)
Reassortants received and tested:
IVR-272 (A/Singapore/IMH0025/2024)
NYMC X-439 (A/South Australia/27/2024)
A/Vic22P17-4-EP2 (A/Victoria/4897/2022)
A/Vic22P18_6.0 (A/Victoria/4897/2022)
A/Vic22P19_6.0 (A/Victoria/4897/2022)
SAN-039 (A/Singapore/SAR3644/2024)
AZ_v4 383222 (A/Victoria/4897/2022)
AZ_v10 400034 (A/Victoria/4897/2022)
AZ_v12 400035 (A/Victoria/4897/2022)
CVR-344 (A/Sydney/78/2025)
CVR-351 (A/Tasmania/318/2025)
CVR-359 (A/Tasmania/318/2025)
B/Victoria
Reassortants received and tested:
BVR-26 (B/Austria/1359417/2021)

Serological Analyses

Background

Antigenic changes in circulating influenza viruses are also monitored by the extent to which they are inhibited by antibodies produced by subjects who have been immunised with current inactivated seasonal influenza vaccines. Twice a year the WHO Collaborating Centres and Essential Regulatory Laboratories in the WHO surveillance network exchange panels of sera collected from subjects pre- and post-influenza vaccination. These panels are analysed using the HI assay against the current vaccine and representative influenza strains in preparation for the biannual WHO Consultations on the Composition of Influenza Vaccines (Table 17).

Serum panel analyses in February 2025

In February, the Centre analysed serum panels from the following age groups: paediatric (3-8 years), paediatric (9-17 years), adults (18-64 years), and elderly adults (>65 years) who had received the 2024-2025 Northern Hemisphere seasonal quadrivalent inactivated egg- or cell-based, or recombinant influenza vaccine, in the USA. The Centre also analysed serum panels for paediatric (1-10 years), adults (18-64 years) and elderly adults (>65 years) that had received the 2024-2025 Northern Hemisphere seasonal quadrivalent inactivated egg-based vaccine in China, and one panel of adults (18-64 years) that had received the Northern Hemisphere seasonal quadrivalent inactivated egg vaccine in the UK.

A(H1N1)pdm09: Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a and 5a.2a.1 were analysed in HI assays using the above sera panels. When compared with responses to cell-propagated A/Wisconsin/67/2022-like vaccine reference viruses, post-vaccination geometric mean titres (GMTs) were not significantly reduced for most recently circulating viruses.

A(H3N2): Recent A(H3N2) viruses with HA genes from 2a.3a.1 subclade J.1.1, J.2, J.2.1, and J.4 were analysed in HI and virus neutralisation (VN) assays. When compared to titres against cell-propagated A/Massachusetts/18/2022-like vaccine reference viruses, post-vaccination GMTs were significantly reduced for the majority of recent viruses.

B/Victoria: Post vaccination HI GMTs against recent B/Victoria lineage viruses in the 3a.2 clade were not significantly reduced when compared to either cell or egg-propagated B/Austria/1359417/2021-like viruses.

Serum panel analyses in September 2025

In September, the Centre analysed serum panels from adults (18-64 years) and elderly (>65 years) who had received either the 2025 Southern Hemisphere seasonal quadrivalent inactivated egg or cell-based vaccine in Australia.

A(H1N1)pdm09: Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a and 5a.2a.1 were analysed in HI and VN assays using the above sera panels. When compared with responses to cell-propagated A/Wisconsin/67/2022-like reference viruses, post-vaccination GMTs were significantly reduced for some recently circulating viruses.

A(H3N2): Recent A(H3N2) viruses with HA genes from 2a.2a.1 subclades J.2, J.2.1, J.2.2, J.2.3, J.2.4 and J.2.5 were analysed in HI and VN assays. When compared to titres against cell-propagated A/District of Columbia/27/2023-like vaccine reference viruses, post-vaccination GMTs against many of the recent viruses in subclades J.2.2, J.2.3, J.2.4 and J.2.5 subclades were significantly reduced.

B/Victoria: There were no 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.

Table 17. Representative and vaccine candidate strains used for serological analyses during 2025.

FEBRUARY
A(H1N1)pdm09
A/Wisconsin/67/2022
A/Victoria/4897/2022
A/Darwin/1191/2024
A/Darwin/1868/2024
A/Victoria/3370/2024
A/Singapore/SAR3644/2024
A/Darwin/1906/2024
A/Victoria/3263/2024
A/Sydney/1356/2024
A(H3N2)
A/Massachusetts/18/2022
A/Thailand/8/2022
A/Perth/815/2024
A/Perth/836/2024
A/Samoa/34/2024
A/Fiji/295/2024
B/Victoria
B/Singapore/WUH/4618/2021
B/Austria/1359417/2021
B/Darwin/20/2024
B/Victoria/154/2024
B/South Australia/37/2024

SEPTEMBER
A(H1N1)pdm09
A/Wisconsin/67/2022
A/Victoria/4897/2022
A/Victoria/42/2025
A/Darwin/1015/2025
A/Tasmania/318/2025
A/Darwin/778/2025
A/Perth/456/2025
A(H3N2)
A/District of Columbia/27/2023
A/Croatia/10136RV/2023
A/Victoria/769/2025
A/Sydney/68/2025
A/Singapore/GP20238/2024
A/Tasmania/627/2025
A/South Africa/NCID-R05190/2025
A/Sydney/16/2025
A/Tasmania/557/2025
B/Victoria
B/Austria/1359417/2021 (Cell)
B/Austria/1359417/2021 (Egg)
B/Tasmania/31/2025
B/Victoria/399/2025
B/Canberra/118/2025
B/Bhutan/02139/2025
B/Victoria/260/2025

Recommendations on Influenza Vaccines

WHO Consultations on the Composition of Seasonal Influenza Vaccines

The antigenic, genetic, antiviral resistance and serological data generated from the Centre's surveillance activities are incorporated into detailed dossiers for use at the WHO Consultations on the Composition of Influenza Vaccines in February (for the Northern Hemisphere) and September (for the Southern Hemisphere).

The Centre Director and Deputy Director participate in preparatory teleconferences and then meet at the face-to-face Consultation with WHO, representatives from the other WHO Collaborating Centres and the four Essential Regulatory Laboratories (Center for Biologics Evaluation and Research, US Food and Drug Administration, USA; National Institute for Biological Standards and Control, UK; National Institute of Infectious Diseases, Japan; Therapeutic Goods Administration, Australia). Vaccine effectiveness estimates were also presented by the Centre's senior epidemiologist in person at the Consultation in September. Consultations are also attended by observers from the World Organisation for Animal Health (WOAH), the University of Cambridge, several WHO National Influenza Centres and other relevant organisations. In 2025 WHO made the recommendations reported below.

WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2025-2026, 28 February 2025.

The WHO recommends that trivalent vaccines for use in the 2025-2026 northern 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- or recombinant-based vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/District of Columbia/27/2023 (H3N2)-like virus;
- 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.

WHO Consultation on the Composition of Influenza Vaccines for the Southern Hemisphere 2026 26 September 2025.

The WHO recommends that **trivalent** vaccines for use in the 2026 southern hemisphere influenza season contain the following:

Egg-based vaccines

- A/Missouri/11/2025 (H1N1)pdm09-like
- A/Singapore/GP20238/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Cell– or recombinant-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Sydney/1359/2024(H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Consistent with the four previous WHO recommendations since September 2023, it remains the opinion of the WHO influenza vaccine composition advisory committee that the inclusion of a B/Yamagata lineage antigen is no longer warranted.

In addition to the overall recommendations as described above, WHO lists candidate vaccine viruses (CVVs) that may be suitable for inclusion in vaccines. These CVVs, which are listed on the WHO website, are antigenically similar to the recommended vaccine strains. In 2025, the following CVVs, which were originally isolated at the Centre in either eggs or cells, were listed by WHO as being suitable for vaccine use following the February or September meeting as indicated.

Type/Subtype/ Lineage	Egg-derived CVVs	Cell-derived CVVs
A(H1N1)pdm09		A/South Queensland/47/2025 (Sep) A/Tasmania/318/2025 (Sep)
A(H3N2)	A/Singapore/GP20238/2024 (Sep) A/Nepal/N042/2025 (Sep) A/Perth/722/2024 (Feb)	A/Singapore/GP20238/2024 (Sep) A/Sydney/68/2025 (Sep) A/Victoria/317/2025 (Sep)
B/Victoria		B/Singapore/WUH4618/2021 (Sep) B/Singapore/INFTT-16-0610/2016 (Feb) B/Singapore/INFKK-16-0569/2016 (Feb) B/Brisbane/9/2014 (Feb)

Australian Seasonal Influenza Vaccine Recommendation

Whereas the WHO makes recommendations on suitable viruses for inclusion in seasonal influenza vaccines, in individual countries the decision on the composition of vaccines is made by national or regional authorities. In Australia, the Therapeutic Goods Administration makes the decision on the advice of the Australian Influenza Vaccine Committee (AIVC). The Centre Director and Deputy Director both serve on the AIVC.

The AIVC met on 10 October 2025 and recommended that the following viruses be used for influenza vaccines in the 2025 Southern Hemisphere influenza season:

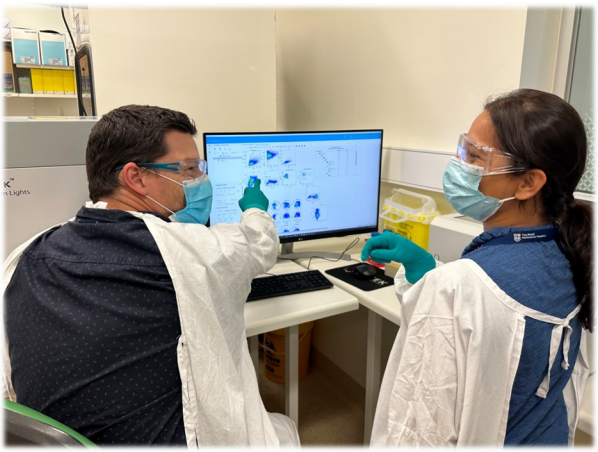
Egg-based trivalent vaccines:

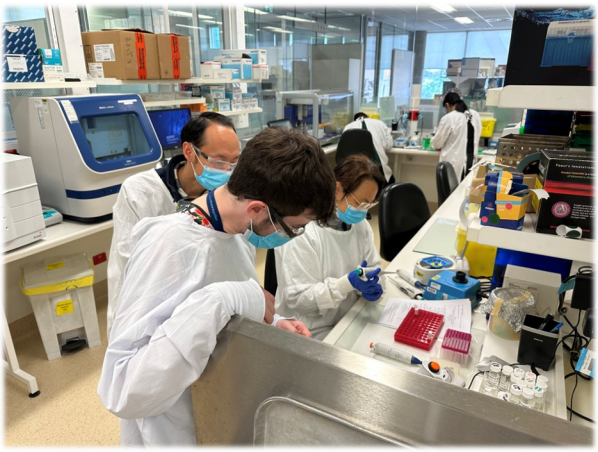
- A/Missouri/11/2025 (H1N1)pdm09-like
- A/Singapore/GP20238/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Cell- or recombinant-based trivalent influenza vaccines:

- A/Missouri/11/2025 (H1N1)pdm09-like
- A/Sydney/1359/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

The continued absence of confirmed detection of naturally occurring B/Yamagata lineage viruses after March 2020 is indicative of a very low risk of infection by B/ Yamagata lineage viruses. Consistent with the World Health Organization (WHO) recommendations since September 2023, it remains the opinion of the WHO influenza vaccine composition advisory committee that the inclusion of a B/Yamagata lineage antigen is no longer warranted. There will no longer be updated recommendations for the B/Yamagata lineage component. This position is supported by the AIVC. Further, the AIVC supports the use of trivalent influenza virus vaccines within Australia for the 2026 influenza season.





Training

Training and Support of National Influenza Centres

The Centre provides support in the form of training and advice to WHO National Influenza Centres (NICs) and other diagnostic laboratories, especially in the Asia-Pacific region. Strengthening technical capabilities and infrastructure for surveillance work in regional laboratories increases their capacity to detect and characterise circulating influenza viruses and to identify viruses with pandemic potential, thus further supporting the GISRS surveillance network. Centre staff are involved in the training of visiting scientists at the Centre, participating in regional workshops and visiting laboratories to provide direct assistance in strengthening surveillance capabilities.

Training Programs and Visits to Regional Laboratories

Patrick Reading and Michelle Wille joined a mission team to assess the two National Influenza Centres in Viet Nam at the National Institute of Hygiene and Epidemiology (NIHE) in Ha Noi and the Pasteur Institute in Ho Chi Minh City (PIHCMC), as well as the national influenza surveillance network in Viet Nam from 9 -13 June 2025 . The review included self-assessment, site visits and subsequent review of NIC functions and meetings with key ministerial stakeholders. The mission team also visited Oxford University Clinical Research Unit (OUCRU) and the Hospital for Tropical Diseases (HTD) in Ho Chi Minh City.

Jessica Miller co-facilitated a 3 day training on the WHO Pandemic Influenza Severity Assessment (PISA) in Putrajaya, Malaysia between November 25 - 27, 2025. Thirty participants from national and sub-national health departments in Malaysia, Singapore, and Brunei attended the training. The training introduced participants to the different methods used to calculate influenza severity thresholds and provided participants the opportunity to develop, present and assess their own influenza severity thresholds.

Centre-based Training

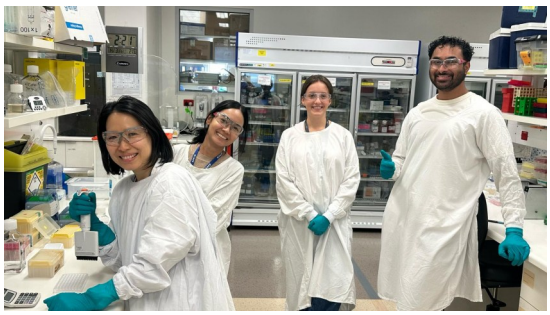
Saira Hussain, Ashwin Muraleetharan and Clyde Dapat were involved in training scientists from the National Influenza Centre (NIC) at the National Institute of Health, Thailand between 10-14 March 2025. The training focused on genotypic and phenotypic assays relevant to antiviral testing of influenza viruses.

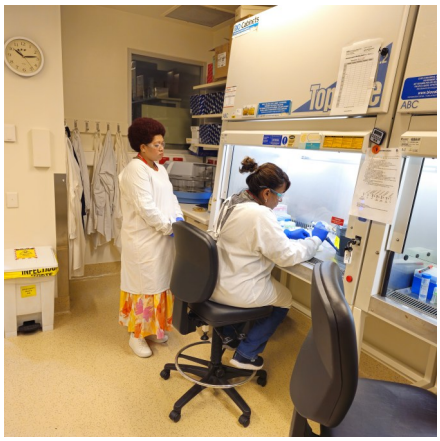
Yi-Mo Deng and Clyde Dapat were involved in training a scientist from the University Putra Malaya, Malaysia between 7-18 April 2025. The training focused on molecular techniques, including NGS, RT- PCR and bioinformatics for influenza and other viruses.

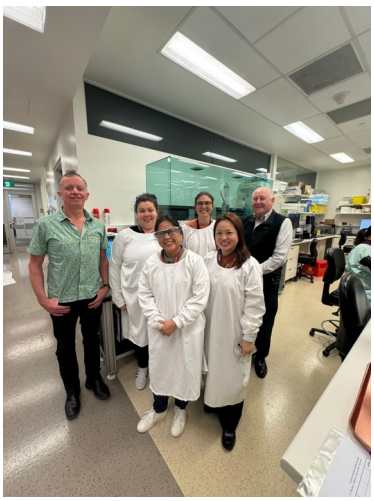
Heidi Peck, Malet Aban, Tasoula Zakis, Paul Whitney and Michelle Wille were involved in training scientists from the NIC at the Research Institute for Tropical Medicine, Philippines between 5-16 May 2025. The training covered topics such as mammalian cell culture, influenza virus isolation and influenza virus serology

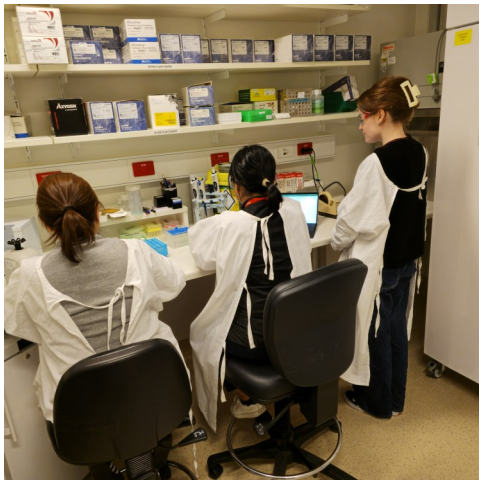
Michelle Wille, Presa Chanthalavanh and Steven Edwards were involved in molecular training for six scientists from the Pacific Island countries between 26 May - 5 June 2025 including: Fiji CDC, Labasa Hospital Fiji, Central Public Health Laboratory Papua New Guinea, Viola Hospital Tonga, Vila Central Hospital Vanuatu and Tungaru Central Hospital Kiribati. The training was performed in collaboration with colleagues at VIDRL and focussed on molecular detection and characterisation of influenza viruses.

Heidi Peck and Malet Aban were involved in training a PhD student from the National Institute for Communicable Diseases, South Africa between 21 July - 5 August 2025. The training covered topics such as laboratory methods for measuring neutralising antibodies against influenza viruses in human sera.









Research

The Centre continues to develop and expand its research interests across a range of projects, both within the Centre and with external collaborators.

Antivirals and Viral Fitness

Centre staff and students

Saira Hussain (Senior Research Scientist), Ashwin Muraleetharan, Lauren Burmas, James Barmes, Harry Stannard (PhD candidate).

Research overview

Our research mainly focuses on evaluation of the effectiveness of approved and investigational influenza antivirals, as well as the risk of the emergence of drug-resistant viruses which could spread widely amongst the community. We also study the fitness of different drug-resistant variant viruses. This information provides insights into the likelihood that such viruses could spread within the community. We are developing new tools/models for antiviral efficacy screening which are biologically relevant, low cost and reduce the number of animals used in research, as detailed below.

Collaborators

Lorena Brown, Jenny Mckimm-Breschkin, Jessica Neil, Brad Gilbertson, Matthew Gartner, Charlie-MacKenzie-Kludas, Rubaiyea Farrukee and Sarah Londrigan (University of Melbourne); Regis Grailhe (Translation Research Division, Institute Pasteur Korea); Jessica Belser (CDC); Sebastian Maurier Stroh (National University of Singapore); Larisa Gubareva (CDC); Emi Takashita (NIID, Tokyo), Andrew Mehle (University of Wisconsin); Seema Lakdawala (Emory University School of Medicine), Paul Digard (The Roslin Institute, University of Edinburgh), Elena Govorkova (St Jude's Childrens Research Hospital, US), Aus Bio Ltd. (Australia), F. Hoffmann-La Roche Ltd, SK Bioscience (Republic of Korea).

Highlights and developments 2025

Development of investigational antivirals (Pandemic Antiviral Discovery (PAD) Initiative)

The Centre's antiviral group worked to determine antiviral efficacy in vitro and in vivo (ferrets) of the Aus Bio compounds compared with licensed influenza antivirals.

For in vitro work, the group used a focus reduction assay (FRA) which they had optimised in 2024 for antiviral testing. In vitro, MD378 (the active form of the lead candidate) and a similar compound MD345 showed efficacy in the low nanomolar (nM) range against different types and subtypes of influenza viruses (seasonal influenza A(H1N1)pdm09, A(H3N2), B/Victoria-lineage, swine A(H3N2)v, low and high pathogenicity avian-origin influenza viruses A(H3N8), A(H5N1) and A(H7N9), respectively), and also against viruses showing reduced susceptibility to currently licensed drugs such as oseltamivir, baloxavir and zanamivir. The inhibitory activity was always non inferior and usually greater than oseltamivir and zanamivir. With these promising results, collaborators at the University of Melbourne commenced testing in a mouse model of influenza infection. Mice infected with a lethal dose of PR8 or mouse-adapted contemporary seasonal A(H1N1)pdm09, A(H3N2) and B/Victoria-lineage viruses were completely protected when the compound was administered intranasally as a single dose at least 25 days before or 48 hours after infection. In addition, the compound was effective in mice infected with several influenza strains including swine, LPAI and drug-resistant viruses.

Testing the lead candidate prodrug in ferrets proved challenging. In initial studies, intranasal treatment resulted in a modest reduction in viral shedding from the upper respiratory tract of ferrets infected with a contemporary A(H1N1)pdm09 strain known to replicate to high titres and to cause significant clinical signs

Antivirals and Viral Fitness (continued)

and pathology in ferrets. The group has also performed studies to investigate the antiviral efficacy of the lead compound compared to licensed drugs NAI or baloxavir using different parameters:

-Virus strains which differ in pathogenicity/replication

-Inoculation route - intranasal or contact transmission route

-Inoculation dose - moderate vs low

-Increasing drug concentration (as drug solubility protocols were optimised during the study)

-Dosing regimen - single vs multiple doses

-Time of drug delivery before or after infection

In ferrets infected with A/Perth/269/2009 A(H1N1)pdm09 virus, prophylactic administration of MD410 24 hours prior to infection resulted in significantly reduced viral shedding from the upper respiratory tract at early timepoints, as well as reduced viral loads in lower respiratory tract tissue. Therefore, single dose administration of pan-strain agnostic MD410 demonstrates promise for effective prophylaxis and may fill a gap in our pandemic responses. As the breadth of protection of the prodrug against influenza subtypes/ strains has been demonstrated successfully in mice, the group will not test the antiviral efficacy against multiple strains in ferrets, therefore reducing the overall number of ferrets required.

New Novo Nordisk Foundation Grant (2025): Researchers from the Centre, along with collaborators from the University of Melbourne, were awarded a new 2-year grant (EUR 2,499,882) from The Novo Nordisk Foundation to continue preclinical development of the novel long-acting pan-influenza antiviral drug.

Ferret Precision-Cut Lung Slices: Development of a high-throughput ex-vivo model to study influenza virus infection

Dr Saira Hussain was successful as co-investigator on a grant obtained from the Cumming Global Centre Foundation Grants in 2023 for the development of a comprehensive suite of human and animal in vitro respiratory tract models for evaluating viruses with pandemic potential. The project is led by Dr Jessica Neil, working with Prof. Kanta Subbarao and other investigators at the University of Melbourne, Monash University and the University of Adelaide. Specifically, Dr Hussain and her group have been working on developing ferret precision cut lung slices (PCLS) as a surrogate model for influenza infection and antiviral efficacy studies. PCLS are thin sections of lung tissue that retain the native lung architecture, including small airways, blood vessels, and resident cell types. The PCLS technique is now well established in the laboratory. In addition, Dr Neil and members of the Subbarao group have also established mouse and human PCLS models. Contemporary seasonal influenza A(H1N1)pdm09 and highly pathogenic avian influenza (HPAI) H5 viruses of clade 2.3.4 and 2.3.4.4 replicated well in ferret PCLS isolated from the proximal and distal regions of different lung lobes. Moreover, human seasonal A (H3N2) and B/Victoria-lineage viruses also replicated efficiently in ferret PCLS, including strains which historically do not replicate efficiently in ferret lungs in vivo. Human seasonal and HPAI H5 influenza viruses also replicated in mouse and human PCLS, with differences in replication kinetics observed between virus strains in all three models. Infectious virus titres measured from freshly prepared PCLS were similar to titres obtained from PCLS maintained in culture for >7 days, demonstrating the longevity of the slices and utility for serial passaging studies. The team also tested the efficacy of licensed antivirals in ferret and human PCLS against a A(H1N1)pdm09 virus, demonstrating a concentration-dependent reduction in virus titre with oseltamivir and baloxavir. Ferret and human PCLS offer an opportunity to assess virus infectivity and antiviral efficacy using a single donor in a system that is high throughput while still capturing much of the complexity of the lung environment.

In 2026, the Centre's antivirals group will use the newly acquired high content imaging microscopy platform, Agilent BioTek Cytation 5 to develop high throughput (96-well assays) to assess cell viability to perform antiviral efficacy screens in PCLS.

Harry Stannard (PhD): Further development of the ferret model of influenza A virus infection and its utility to explore novel therapeutic treatments

Harry Stannard began his PhD in July 2023, with his prospective thesis titled, 'Further development of the ferret model of influenza A virus infection and its utility to explore novel therapeutic treatments' under the supervision of Centre Director Prof. Patrick Reading, Dr Saira Hussain and Centre Deputy Director Prof.

Antivirals and Viral Fitness (continued)

Ian Barr. His PhD will explore multiple avenues for the improvement of the ferret model for influenza antiviral efficacy studies, with a particular focus on exploring lower respiratory tract viral load and disease kinetics using A(H1N1)pdm09, as well as A(H3N2) and B/Victoria lineage viruses. He has also worked to identify more contemporary influenza virus strains that demonstrate robust influenza disease, transmission, and lower respiratory tract (LRT) involvement in the ferret and can be used for future antiviral studies.

In 2025, collaborative studies with Dr Jessica Belser (CDC) and her team compared antiviral efficacy in ferrets following conventional liquid intranasal delivery versus aerosol inhalation (as a more biologically relevant infection route). Studies describing the outcomes of the studies have been submitted for publication and are currently under review.

Harry has also been working to establish an A(H3N2) infection and B/Victoria-lineage model in ferrets that recapitulates both the upper and LRT infection observed in humans and can be used for antiviral studies. He has made significant progress with an A(H3N2) infection in ferret lungs using different routes of infection (intranasal delivery, aerosol delivery and contact transmission) and these models will be used for antiviral efficacy studies in 2026.

In 2025, Harry also worked on setting up live imaging of influenza infection in ferrets in a collaborative project with Prof Regis Grailhe (Institute Pasteur, Korea), with the aim of developing an affordable live-imaging device to enable quantification and location of fluorescent- or bioluminescent-tagged viruses in the airways of infected animals (funded by SK Bioscience, Korea). In 2025, the Centre hosted Regis and his colleague for a week to discuss challenges and options to move forward with this project.

Roche project

Commencing in in July 2025, Dr Hussain led a project contracted by Hoffmann La-Roche to further characterise PA inhibitors in development for influenza.

Avian influenza

Centre staff

Michelle Wille

Research overview

Avian influenza viruses can pose a threat to humans via direct infection from an avian source. If the virus has the ability to replicate well in humans and transmit, there is potential that such viruses may cause an influenza pandemic. We routinely sample migratory shorebirds and resident ducks in Australia and seabirds and seals in Antarctica to determine what types of avian influenza viruses are circulating amongst avian populations and to prepare for the potential arrival of HPAI H5N1. The Centre is involved in the characterisation of viruses sampled from birds in Australia and Antarctica, including culture, sequencing and phylogenetic analysis of these viruses. Furthermore, to understand overall exposure of Australian wild birds to influenza A virus, we are also screening blood samples for antibodies against influenza A viruses. In the case of shorebirds, this will allow us to assess not only the burden of influenza locally but also provide insight into influenza exposure of these birds while at their northern breeding grounds, and during their annual migration.

Collaborators

Marcel Klaassen (Deakin University, Victoria); Frank Wong (Australian Centre for Disease Preparedness); Andrew Breed (Australian Government Department of Agriculture), Paul Eden (National Avian Influenza Wild Bird Program, Wildlife Health Australia), Meagan Dewar (Federation University).

Highlights and developments 2025

In 2025, we collected and screened 1558 paired swab and serum samples from wild Anseriformes (ducks) and Charadriiformes (shorebirds and terns) in Victoria, New South Wales, Tasmania, South Australia and Western Australia, with 14 influenza A virus detections. All samples were negative for HPAI H5N1.

A key component of our surveillance work was the continuation of our heightened surveillance from September – December, coinciding with the return of migration birds to rule out HPAI H5N1 incursion. All swab samples were negative for HPAI and none of the serum samples which were positive by ELISA were positive by HI when using a 2.3.4.4b antigen. Two samples were positive, with an H3N7 virus sequenced and found to be similar to viruses detected in arriving shorebirds in 2024. Our enhanced surveillance program was funded by Department of Agriculture, Fisheries and Forestry, administered by Wildlife Health Australia.

We conducted surveillance in Antarctica during the austral summer of 2024/25, as well as in 2025/26. During the austral summer of 2024/25, we collected 523 faecal environmental samples from penguins, seabirds and seals, all of which were negative for avian influenza. Sixteen swab samples from carcasses were positive for HPAI H5N1, and sequencing demonstrated that these viruses were of the BA2.3 genotype, and genetically most similar to HPAI H5N1 sequences generated from samples in the South Shetland Islands in the same summer. More than a thousand oral/cloacal swabs, faecal environmental samples and carcass samples have been collected in the austral summer of 2025/26, with analysis in progress. Work in Antarctica is supported by International Association of Antarctic Tour Operators, Intrepid Travel, and Hx Expeditions.

Early Recognition and Response to Influenza Infection

Centre staff

Patrick Reading

Research overview

Our research, which is undertaken at the Centre and at the University of Melbourne, investigates how the body first recognises and responds to infections with influenza and other respiratory viruses. We employ in vitro studies using human proteins and cells, as wells as in vivo studies using mouse and ferret models of infection. We are also interested in assessing novel treatment and vaccine platforms for influenza and other respiratory viruses in vitro and in animal models of infection.

Our current studies are focused on:

I. Identifying specific host proteins that are expressed in virus-infected cells and can interfere with the entry, replication and/or release of influenza and other respiratory viruses (restriction factors),

II. Understanding the similarities and differences between restriction factors expressed in humans compared to those expressed in other species susceptible to influenza virus infections, and

III. Utilizing approaches to induce host innate immunity, including an array of restriction factors, to limit the impact of subsequent infection with influenza or other respiratory viruses.

Collaborators

Gunther Hartmann and Eva Bartok (University of Bonn, Germany); Stacey Schultz-Cherry (St Jude Children's Research Hospital); Sarah Londrigan, Andrew Brooks, Justine Mintern, Sharon Lewin, Stephen Kent, Linda Wakim, Georgia Deliyannis, Carol Hartley and Joanne Devlin (The University of Melbourne), Keith Chappell, Daniel Watterson, Paul Young (University of Queensland); Ari Idris (Queensland University of Technology); Nathan Bartlett (University of Newcastle); Daniel Steinfort (Royal Melbourne Hospital).

Highlights and developments 2025

A major focus of our research is understanding and characterising particular intracellular proteins (termed restriction factors) that are expressed or induced in host cells, which can block the replication of influenza and/or other respiratory viruses. We utilise approaches to overexpress or delete putative restriction factors to determine their role in blocking virus replication and to characterise their mechanism/s of antiviral activity against influenza virus and respiratory syncytial virus (RSV).

Working with collaborators at The University of Bonn in Germany we have been using synthetic RNA molecules that target specific intracellular pattern recognition receptors to stimulate host innate immunity and to provide protection against subsequent influenza and respiratory syncytial virus (RSV) infections in vitro and in mouse and ferret models of infection. This collaboration was key to securing $AUD 54M funds for the Bonn-Cumming Pandemic Therapeutics Research Program in which Prof. Reading now acts as a co-lead (with Prof. Eva Bartok from Bonn) for one of the three work packages focussed on host-directed therapeutics.

Our group are also investigating the potential of mRNA-mediated delivery of particular restriction factors as a novel antiviral treatment. In addition to humans, we are also studying restriction factors expressed by mammalian species susceptible to influenza infections (e.g. ferrets, mink, cattle and other species) which may play a role in limiting interspecies transmission and/or driving virus evolution.

In 2024, research contributed to four peer-reviewed publications in Nature Structural & Molecular Biology, The Journal of Virology, The Journal of Biological Chemistry, Immunology Prof. Reading leads of research group at the University of *Melbourne consisting of two post-doctoral scientists, one research assistant and four Ph.D. students.*

Epidemiology

Centre staff

Jessica Miller, Tanya Diefenbach-Elstob, Jessie Goldsmith (PhD student, UoM)

Research overview

Our work primarily focuses on using surveillance data to examine fluctuations in influenza activity and vaccine effectiveness across populations and seasons. We have been working with influenza sentinel surveillance systems operating in Australia to estimate influenza vaccine effectiveness in the community and provide ongoing estimates to government and WHO. We also conduct various simulation studies and meta-analysis/meta-regression to understand the validity of study designs used to estimate vaccine effectiveness.

The team collaborates on studies exploring the validation of various data source used to capture influenza and RSV cases. This includes examining the validity of thresholds used to determine excess influenza-associated mortality (Jessie Goldsmith) and of RSV syndromic surveillance data in Victoria (Tanya Diefenbach-Elstob).

The team continues to work closely with the WHO and other partners on influenza burden of disease studies and provides technical support to member states in the SEAR and WPR.

Collaborators

VE studies: Monique Chilver (University of Adelaide); Allen Cheng (Monash)

VE hospital studies: FluCAN and PAEDS collaborators (Allen Cheng, Philip Britton, Christopher Blyth, Kristine Macartney, Tom Kotsimbos) on behalf of the FluCAN investigators and PAEDS network.

VE paediatric studies: Sheena Sullivan (Monash); Patricia Campbell and Katherine Gibney (UoM); Janet Strachan (Vic DoH); Stephen Lambert (QLD DoH).

RSV validation studies: Rob Moss (UoM); Sheena Sullivan (Monash); Janet Strachan (Vic DoH); Kara Martin (Vic DoH)

Household Transmission pilot study: Adrian Marcato (UoM); Annaliese van Diemen (NEPHU, Austin Health)

The following collaborations are in the early phase and project plans are currently being formulated:

Severity studies: David Price (VIDRL); Allen Cheng (Monash)

Highlights and developments 2025

We continued to work with the Australian Sentinel Practices Research Network (ASPREN) and the Influenza Complications Alert Network (FluCAN), to evaluate the effectiveness of Australian trivalent inactivated seasonal influenza vaccines in 2025. HI assay and sequencing data generated by the Centre were used to inform VE estimates, and patient information obtained from the surveillance programmes was used to inform selection of viruses for sequencing (e.g., vaccination status). As always, all ASPREN samples were received at the Centre. In 2025, 67% of FluCAN samples were received, reflecting enhanced efforts to ensure these samples are included in the Centre's virological surveillance, and to improve the quality of vaccine effectiveness estimates possible through that network.

The epidemiology group compiled the Global Influenza Vaccine Effectiveness Reports for the 2024/2025 and 2025 influenza seasons. The reports were presented by Jessica Miller at the WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2024/2025 and at the WHO Consultation on the Composition of Influenza Vaccines for the Southern Hemisphere 2025. In addition, the Centre's epidemiology group prepared the 'Seasonal Ifluenza Activity' sections of the 'WHO Recommended Composition of Influenza Virus Vaccines' technical document for the 2024/2025 and 2025 influenza seasons which are published on the WHO website following the consultations.

Epidemiology (continued)

The group continued their work on vaccine effectiveness in various populations. Jessie Goldsmith continued to work on vaccine effectiveness in children and published a systematic review on vaccine efficacy and effectiveness by dose for children less than 9 years of age in the first year of vaccine. She continued analyses of influenza vaccine effectiveness in 2022 among children born during the COVID-19 pandemic when influenza was temporarily eliminated in Australia (2020 and 2021). This project uses linked health administrative data from Victoria and Queensland. Jessie Goldsmith continued to explore potential biases in test-negative studies and has been co-leading a systematic review and meta-analysis to understand the underlying sources of heterogeneity in vaccine effectiveness studies for COVID-19 vaccines. The group continued to work with FluCAN and the Paediatric Active Enhanced Disease Surveillance (PAEDS) collaborators to describe vaccine effectiveness in Australian sentinel hospitals.

The group also continued to describe the disease burden of influenza and RSV using hospital and unlinked routinely collected health data from Victoria and Queensland.

Jessica Miller co-facilitated a training on the WHO Pandemic Influenza Severity Assessment (PISA) in Malaysia for national and sub-national health departments from Malaysia, Singapore, and Brunei. The training introduced participants to the different methods used to calculate influenza severity thresholds and provided participants the opportunity to develop, present, and assess their own influenza severity thresholds.

Tanya Diefenbach-Elstob continued to co-lead work on RSV and the validation of RSV syndromic surveillance data in Victoria, using linked and unlinked health administrative data from the Victorian Department of Health.

Immunity to Respiratory Viruses

Centre staff and student

Annette Fox, Stephany Sanchez, Anastasia Jessica Hadiprodjo, Arada Hirankitti, Ziheng Zhu (PhD student)

Research overview

A key goal of our work is to identify strategies to improve the immunogenicity and, in turn, effectiveness of seasonal influenza vaccines. It is challenging to induce long-term immunity against highly mutable viruses such as influenza due to immune escape, and to a propensity for antibody levels to decline with successive exposures to variant influenza virus strains. We have established several human influenza cohorts to investigate how immune responses evolve through successive exposures to different vaccine strains +/- interim infections. We also initiated a controlled human challenge study to investigate correlates of protection. A range of techniques have been developed to understand whether B cell and antibody responses are induced against variant epitopes versus epitopes that are largely conserved with past strains. This includes modelling of antibody titres against a large array of viruses; flow cytometric characterization of B cell reactivity and cross-reactivity to hemagglutinins representing different strains; single cell B cell receptor sequencing and antibody production; and reverse genetics to generate viruses with mutations of selected antigenic sites.

Collaborators

Adam Kucharski (London School of Hygiene and Tropical Medicine),Barnaby Young (National Centre for Infectious Diseases (NCID) and Tan Tock Seng Hospital, Singapore), Andrew Ward (Scripps, San Diego, USA), Rogier van Doorn (Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam); Le Quynh Mai (National Institute of Hygiene and Epidemiology, Hanoi, Vietnam); Scott Boyd (Stanford University, Stanford CA, USA); Mark Thompson (Centre for Disease Control, Atlanta, USA); Derek Smith (Centre for Pathogen Evolution, Infectious Diseases Research Centre, Cambridge University, Cambridge, UK); Katherine Kedzierska (The University of Melbourne); David Price (The University of Melbourne, VIDRL); Adam Wheatley (The University of Melbourne); Ben Cowling (Hong Kong University)

Highlights and developments 2025

Study of early life imprinting of influenza immunity

In 2025, we continued to assess samples collected during a pilot study in infants and young children to understand how the type of first exposure to influenza (through infection versus vaccination) affects vaccine responses in subsequent years. These children, aged 6-60 months, were enrolled during 2019-2021 at The Royal Children's Hospital in Melbourne or the Westmead Children's Hospital in Sydney. They participated in the study for 1-3 years. Blood-draws were performed before and after vaccination each year for immunological assessment. Eight children been infected with influenza A(H3N2), but had not been vaccinated prior to enrolment, and all had antibodies against A(H3N2) at enrolment. Seven had been vaccinated in the year preceding enrolment but lacked documented prior infection; all had antibodies against A(H3N2), A(H1N1) or both at enrolment. Antibody responses against A(H3N2) virus hemagglutinin and neuraminidase were far greater among infection-primed compared to vaccination-primed children.

In the past year we have continued to characterize influenza-reactive B cells from these children using 10X genomics to assess B cell receptor gene use and transcription at the single cell level. Influenza-reactive B cells were detected and isolated using fluorescence- and oligo-tagged hemagglutinin and neuraminidase proteins (H1, H3 and N2), produced in-house. B cell receptor sequences were used to assign B cells to clones that use the same heavy and light chain variable and joining genes and have antigen recognition sequences of matching length. By investigating the clonal diversity of responses we can determine whether a large B cell response reflects expansion of a small number of B cell clones against limited epitopes or a diverse array of clones against many epitopes. B cell receptor sequences can also be used to infer whether a responding B cell has originated from naïve or memory B cell pools since the latter are often more mutated and isotype switched from IgM to IgG. Gene expression is used to identify B cells that are actively responding or have differentiated into plasmablasts that secrete antibodies resulting in antibody titre rise.

Immunity to Respiratory Viruses (continued)

To date, 47 samples from nine children have been processed for single cell sequencing. Sequences have been obtained for over 6000 influenza reactive B cells, which clustered discretely according to H1, H3 and N2 oligo-tags. Plasmablasts may bind poorly to influenza proteins because they switch from expressing cell surface antibody to secreting antibody. Therefore, in the second experiment, cells that had a plasmablast phenotype were included for sequencing even if they were not detectably HA+ or NA+. Accordingly, in the second experiment we detected expanded clones that included both antigen positive and negative cells (Figure 1A) where the latter had gene expression typical of plasmablasts (Figure 1B).

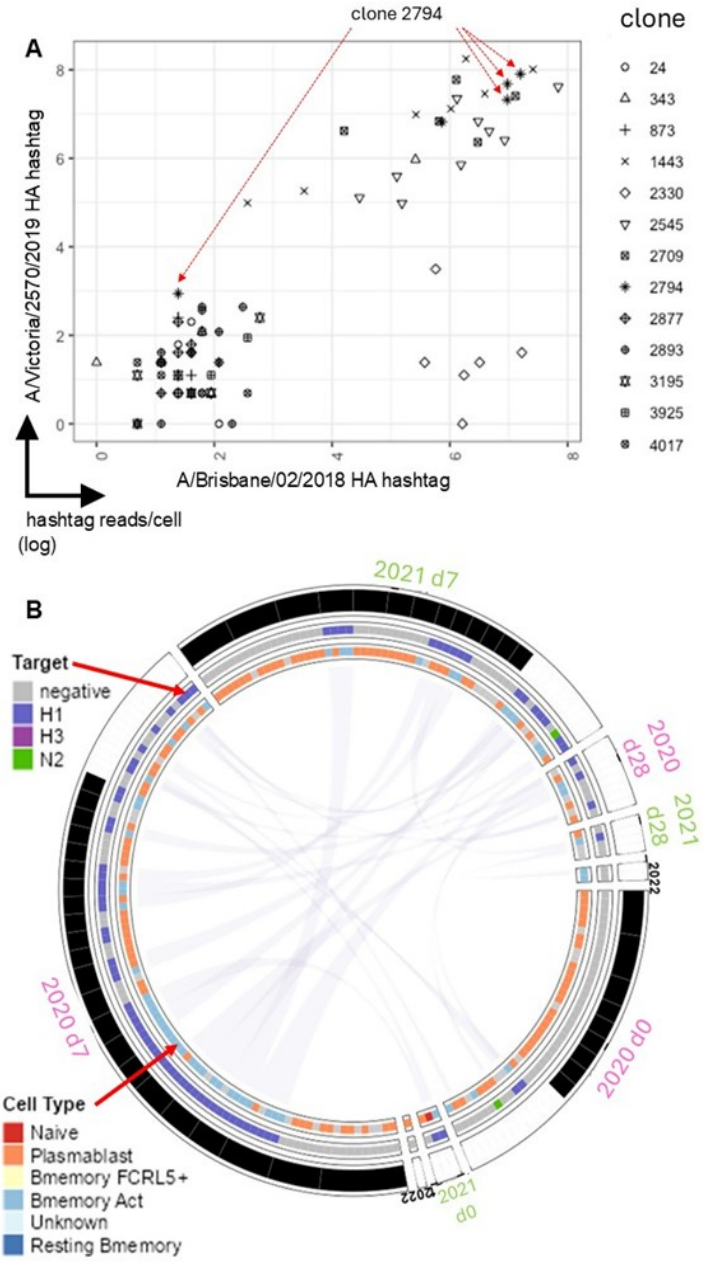


Figure 1. *Analysis of expanded clones in samples collected from one child before and after vaccination in 2020, 2021 and 2022. Panel A shows B cell reactivity against the two different H1N1 HA proteins used and includes cells belonging to clones comprising at least four cells. Each clone is represented by a different symbol (legend). Red arrows highlight a clone that contains both H1N1 HA positive and negative cells. Panel B shows the size distribution of clones at each time-point in the outer circle where white areas indicate the proportion of clones that contain only one cell and black segments indicate clones containing >1 cell. The middle circle indicates the antigen reactivity of each clone (see legend) and the inner circle indicates the cell-type based on gene expression (see legend). Shaded arcs connect clones that are shared across timepoints within the same year or across years (2020 shown in pink and 2021 in green*)

Immunity to Respiratory Viruses (continued)

We produced fifty monoclonal antibodies (mAbs) based on single cell B cell receptor/antibody sequences to further validate the antigen-reactivity of B cells based on single cell sequencing of oligos used to tag each protein , i.e. hemagglutinin (HA) and neuraminidase (NA) of A(H3N2) and HA of A(H1N1), referred to as (H3+ or N2+ or H1+). Clones were selected for mAb production based on clone size – with the largest clones being selected for each participant. To make recombinant antibodies, heavy and light chain DNA sequences were synthesized and cloned, then used to transfect mammalian cells. Antibody was purified from cell supernatants, run on a protein gel to confirm structure (Figure 2), and tested by ELISA for binding to HA and NA representing A(H3N2) and A(H1N1) vaccine strains (Figure 3). To date, the reactivity of most mAbs produced has aligned with the reactivity of the parent B cells, including 3/3 mAbs from N2+ B cells; 19/19 mAbs from H1+ B cells and 14/15 mAbs from H3+ B cells. This result establishes the validity of our protocols for characterizing influenza reactive B cells. mAbs will be further assessed to determine whether the epitopes recognized are conserved or variant across virus strains. Ultimately we hope to reveal whether antibodies are induced against new variant epitopes during successive vaccinations meaning that immunity is updated when strains change.

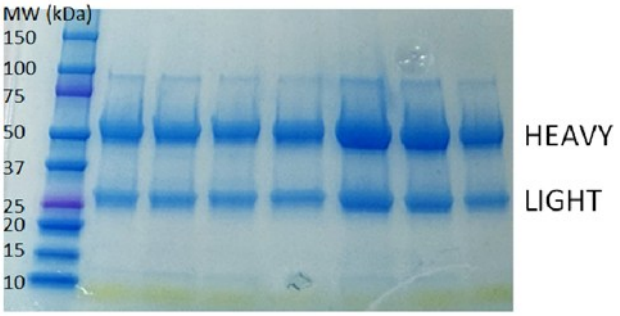


Figure 2. *Reducing gels confirm that recombinant mAbs generated from B cell receptor sequences contain heavy and light chains of the expected size.*

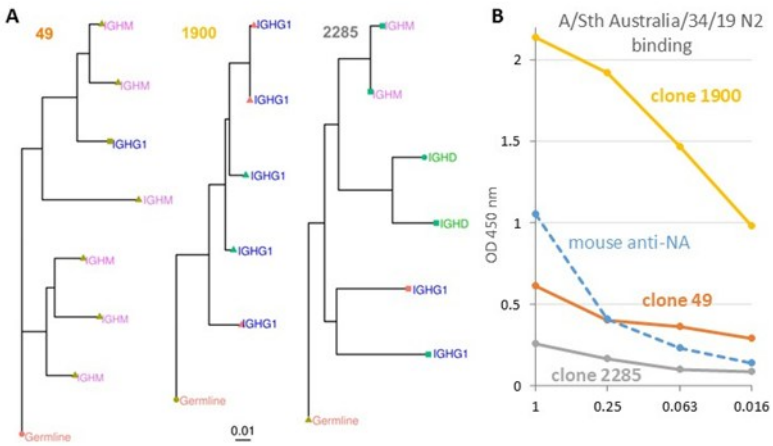


Figure 3. *N2-reactive mAbs: clone selection and analysis. (A) Phylogenetic tree of B cell receptor sequences of three different N2+ B cell clones chosen for mAb production. (B) Binding of each recombinant mAb to N2 NA protein by ELISA. A positive control mAb is also shown.*

In 2025, we commenced a similar but larger study in collaboration with Christian Medical College (CMC) Vellore, India. Mahesh Moorthy, a PhD candidate with us and Head of the Department of Clinical Virology at CMC Vellore is leading this study. We plan to enrol children aged 6 to 60 months who have not previously been vaccinated against influenza, including 100 each presenting with A(H3N2) infection, A(H1N1) infection or neither. Children will be followed for two years with blood-draws performed before and after each vaccine dose.

Immunity to Respiratory Viruses (continued)

Deep Immune Characterization Following Controlled Human A/Texas/71/2017 (H3N2) Infection of Healthy Australian Adults

The cost of randomized clinical trials, which require large sample sizes and extensive follow-up to detect relatively rare cases of symptomatic influenza, is a major impediment to influenza vaccine development. Controlled Human Infection Model (CHIM) studies are considered to be a valuable option for advancing the development of antivirals and vaccines against influenza because infection can be precisely controlled and standardized. In particular, CHIM studies can aid in the selection of candidate vaccines worthy of evaluation in a randomized clinical trial. CHIM studies may also be useful for establishing correlates of protection needed to advance influenza vaccine development.

In 2025, we collaborated with researchers at the University of Melbourne and Doherty Clinical Trials Ltd to conduct the first Australian influenza CHIM study. To identify people who are likely to be susceptible to infection we tested sera from eighty healthy adults for hemagglutination inhibition (HI) antibodies against the challenge virus, an A(H3N2) virus designated A/Texas/71/2107 (Figure 4). Eleven adults aged 21-49 years with HI titres ≤20 were inoculated intranasally with 106 TCID50 of A/Texas/71/2017 (H3N2) virus. Samples were collected as shown in Figure 4. Ten participants shed viral-RNA for ≥ 2 days of whom seven were symptomatic (Modified Jackson Score ≥6); the single participant who did not shed viral-RNA reported symptoms.

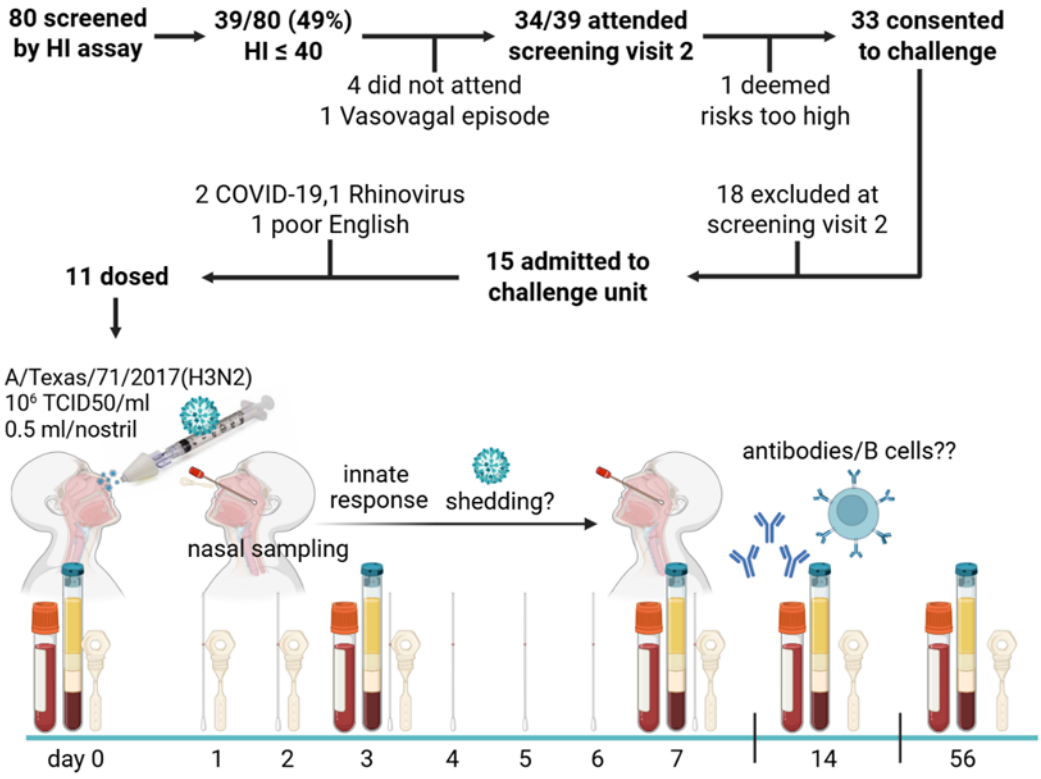


Figure 4. *Influenza CHIM participant screening and investigation schedule*

We also led studies to extensively characterize immune changes in blood and nasal lining fluid (NLF) as depicted in Figure 5. Hemagglutinin (HA) and neuraminidase (NA)-reactive antibodies were measured in sera by HI, microneutralization, and neuraminidase inhibiting (NAI) assays, and in NLF by HA- or NA-binding ELISAs. Spectral cytometry was used to measure absolute leukocyte and lymphocyte-subset counts in whole blood. To assess B cells, we produced fluorescent-tagged HA and NA proteins of challenge virus, and recently-circulating A/Darwin/6/2021 virus. These were combined with a cocktail of monoclonal antibodies to detect and characterize influenza HA or NA reactive B cells by spectral cytometry. Some of the results are also summarized in Figure 5. In brief, we demonstrate our capacity to extensively characterize immune responses induced by controlled human influenza infection including changes in T cell subsets, B cells, plasmablasts and antibodies. We also found that antibody and B cell responses following controlled intranasal

Immunity to Respiratory Viruses (continued)

inoculation were greater in the periphery compared to the mucosa, were greater against HA compared to NA, and may be skewed by memory B cells that retain affinity for past strains.

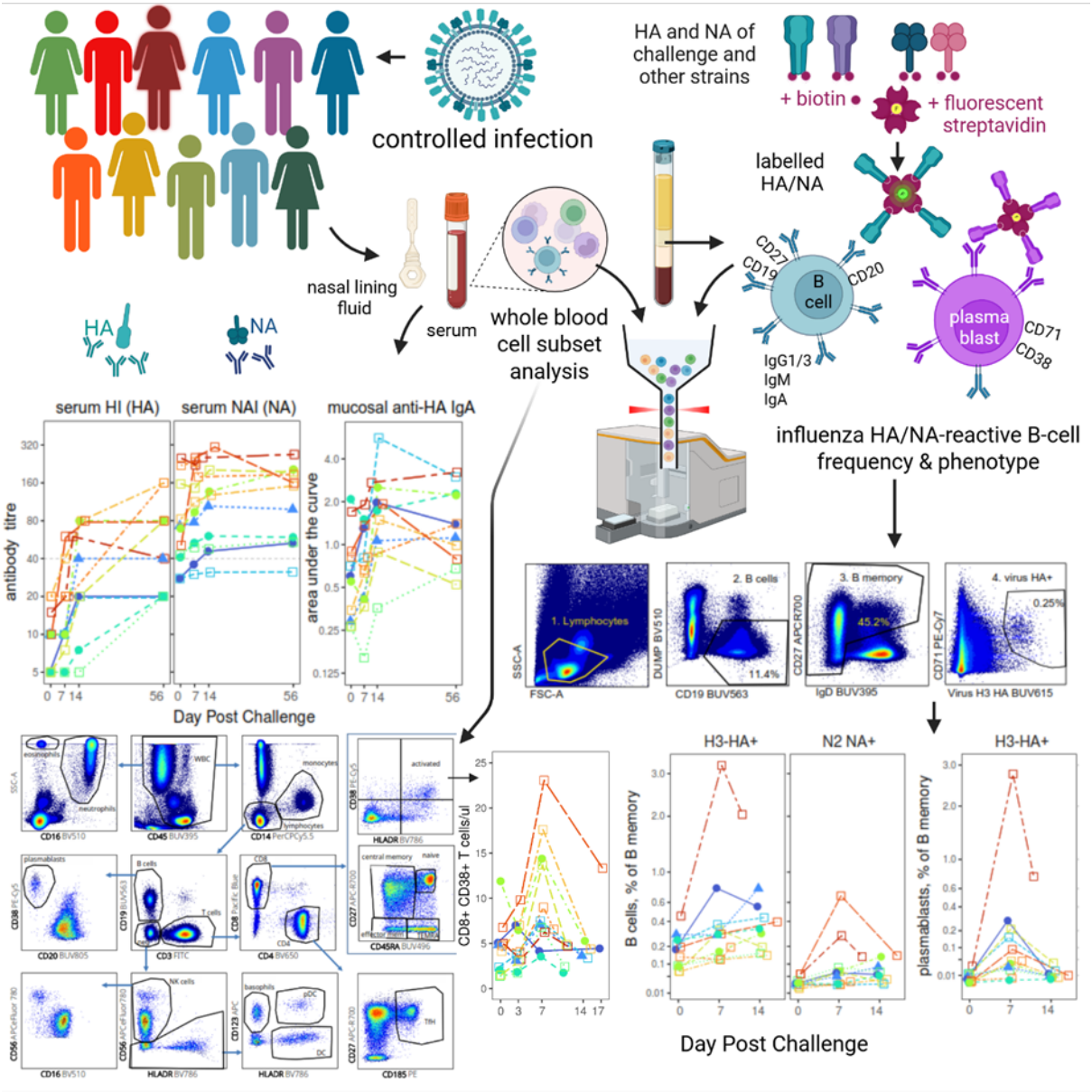


Figure 5. *Deep immunological characterization of responses to controlled infection with A/ Texas/71/2017 (H3N2) influenza virus among healthy adult volunteers.*

Collaborative Agreements

The Centre is party to two Collaborative Research and Development Agreements (CRADA) with industry bodies. As with all potential collaborations with the commercial sector, these agreements have undergone review to ensure that they support the Centre's objective of advancing global public health, have scientific merit and adhere to the principles of neutrality, transparency, independence and accountability.

CRADA with the International Federation of Pharmaceutical Manufacturers and Associations (IFPMA) (2012-2025)

Centre staff: Several staff are involved in this CRADA

Overview: This project aims to enhance the number and geographic range of influenza vaccine viruses isolated in eggs as candidates for reassorting and commercial influenza vaccine manufacture.

An egg isolate of A(H1N1)pdm09 derived at the Centre (A/Victoria/4897/2022) was used as the A(H1N1) pdm09 egg-derived vaccine component for the Southern Hemisphere (SH) influenza vaccine in 2025. This strain was also recommended for the Northern Hemisphere (NH) influenza vaccine for 2025-2026.

An egg isolate of A(H3N2) derived at the Centre (A/Thailand/8/2022) was used as the A(H3N2) egg-derived vaccine component for the NH influenza vaccine in 2024-2025.

An egg isolate of A(H3N2) derived at the Centre (A/Singapore/GP20238/2024) was used as the A(H3N2) egg-derived vaccine component for the SH influenza vaccine in 2026.

For the full recommendation for the NH 2024-2025 vaccine, click here.

For the full recommendation for the SH 2025 vaccine, click here.

For the full recommendation for the NH 2025-2026 vaccine, click here.

CRADA with Seqirus (formerly BioCSL) (2025-2028)

Centre staff: Several staff are involved in this CRADA

Overview: The Centre continues to isolate and evaluate various seasonal influenza virus cell isolates derived from the use a proprietary qualified Seqirus cell line (MDCK 33016PF). Virus cell isolates were evaluated as potential cell culture candidate vaccine viruses (cc-CVV) based on their antigenic properties, genetic sequence and growth properties.

Highlights and developments 2025:

A qualified cell isolate of A(H3N2) was derived at the Centre (A/Sydney/1359/2024) was a WHO approved like-strain for the A(H3N2) cell-derived vaccine component for the SH influenza vaccine in 2026. In addition, B/Singapore/WUH4618/2021 derived at the Centre was also a WHO approved like-strain for B/Austria/1359417/2021 (B/Victoria lineage)-like virus for the 2024 SH vaccine. Qualified cell isolates of B/Yamagata lineage were isolated at the Centre (B/Singapore/INFTT-16-0610/2016, B/Singapore/INFKK-16

-0569/2016,and B/Brisbane/9/2014) which were B/Phuket/3073/2013-like viruses, were available for use in the 2024 SH and the 2024-5 NH vaccines.

For the full list of candidate vaccine viruses, click here.

Research Funding and Awards

Centre staff members are Chief, Co-, or Associate Investigators in grants administered across 2025. (includes those awarded outside of 2025):

Michelle Wille was awarded a **Fellowship of The Australasian Virology Society (FAVS)** in 2025 to reflect her exceptional professional achievement and distinction in the field of virology, as well commitment to the Australasian Virology Society.

Michelle Wille co-led an enhanced surveillance packaged funded through the "Migratory shorebird and seabird surveillance fund" with AUS $114,188 from **Department of Agriculture Fisheries and Forestry and administered by Wildlife Health Australia.**

Michelle Wille was awarded a prestigious **Australian Research Council Future Fellowship** for a project entitled "Anticipating impacts and improving response to HPAI in Australia" with AUS $1,131,187 over four years (2026-2029). The fellowship is administered by the University of Melbourne. The University of Melbourne has co-invested $150,000 as an "Establishment Grant".

Jessica Miller is a Principal Investigator for the project titled "Piloting household transmission investigations (HHTIs) as an academic-public health partnership in Melbourne, Victoria to improve representativeness of surveillance during the 2026 respiratory season". The project has been awarded a total of AUS $60,000 from the **Doherty Seed Grant and the MDHS Catalyst Grant** for the 2026 period. The grant is administered by the University of Melbourne and the work will be done in collaboration between the University of Melbourne, Melbourne Health, and the North Eastern Public Health Unit at Austin Health.

Kanta Subbarao, Ian Barr and **Saira Hussain** are Co-Investigators for the EUR $2,499,882 **Pandemic Antiviral Discovery (PAD)** initiative and **the Novo Nordisk Foundation** project titled "Further development of a Novel Long-Acting Pan-Influenza Antiviral Drug" for the period 2026-2028. The grant is administered by the University of Melbourne and the Royal Melbourne Hospital.

Kanta Subbarao is a Lead Investigator **and Ian Barr** and **Saira Hussain** are Co-Investigators for the EUR $3,034,704 **Pandemic Antiviral Discovery (PAD) initiative and the Novo Nordisk Foundation** project titled "Development of a Novel Long Acting Pan-Influenza Antiviral Drug" for the period 2024-2026. The grant is administered by the University of Melbourne and the Royal Melbourne Hospital.

Kanta Subbarao and **Saira Hussain** are Co-Investigators for the AUS $587,911 **Cumming Global Centre Foundation Grants** project titled "Development of human and animal in vitro respiratory tract models for risk assessment of viruses with pandemic potential " for the period 2024-2027. The grant is administered by the University of Melbourne and the Royal Melbourne hospital.

Annette Fox is the is the project lead for the US $549,030 **NIH/NIAID via the NIAID Centers of Excellence for Influenza Research and Response (CEIRR)** grant titled 'Dissecting influenza antibody evolution through successive exposures in early life' for the period 2023-2025. The grant is administered by The Royal Melbourne Hospital and Scripps.

Harry Stanndard received the **Department of Microbiology & Immunology Travel Award** from the University of Melbourne for AUS $2000.

Highlights from the 16th Australian Influenza Symposium, 2025

The Centre hosted the 16th Australian Influenza Symposium (AIS) on 13-14 November 2025 at the Peter Doherty Institute for Infection and Immunity, Melbourne. The AIS featured an exceptional lineup of Australian and international experts who shared insights across influenza, RSV, and other respiratory viruses. The AIS had over 250 registrants including participants from Brunei, Fiji, India, Indonesia, Malaysia, Papua New Guinea and South Africa as part of the SK Biosciences (Korea) AIS Travelling Scholars Program 2025. The abstract booklet from the meeting can be here.

Research Students

PhD Candidates

Ms Jessie Goldsmith continued her PhD candidature from July 2022 at the University of Melbourne. Her project is titled, 'What can we learn about influenza as Australia's COVID-19 suppression strategy ends?', under the supervision of **Sheena Sullivan**, Katherine Gibney, and Trish Campbell.

Harry Stannard continued his PhD candidature from July 2023 at the University of Melbourne, under the supervision of **Patrick Reading, Saira Hussain** and **Ian Barr**. His thesis title is 'Further development of the ferret model of influenza virus infection and its utility to explore novel therapeutic treatments.'

Ziheng (Annie) Zhu continued her PhD candidature from September 2022 at the University of Melbourne, under the supervision of **Annette Fox, Sheena Sullivan, Stephany Sanchez,** and **Yi Liu**. Her thesis is titled, 'When and why do memory B cells dominate responses to variant influenza virus strains?'.

Josefina Gutiérrez Domínguez continued her PhD in 2022 at Universidad Austral de Chile under the supervision of Claudo Verdugo (Universidad Austral de Chile) and **Michelle Wille**. Her thesis explores changes in the virome of long-distance migratory birds.

Mahesh Moorthy continued his PhD candidature from January 2024 at the University of Melbourne, under the supervision **of Annette Fox** and **Kanta Subbarao.** His thesis title is "Impact of Prior Immunity on Influenza Vaccine Response in a Pediatric Cohort in India".

Yongyang Xia continued her PhD candidature from March 2021 at the University of Melbourne, under the supervision of **Patrick Reading**, Sarah Londrigan and Eva Bartok. Her thesis title is "Understanding restriction factors against influenza viruses and herpesviruses".

Honours student

Ted Gibson completed his Bachelor of Science Honours research project at the University of Melbourne under the supervision of **Yi-Mo Deng** and **Xiaomin Dong** from the Centre. His project focused on optimising target enrichment with hybridization capture next generation sequencing (NGS) for respiratory viruses (RSV and influenza) samples that may contain degraded RNA and therefore be of poor quality. He compared several commercial kits and custom-designed probe sets, as well as modifications to sample preparation and treatment. The methods established were tested on RSV and influenza viruses and demonstrated advantages when compared to routine amplicon-based NGS. Ted's project provided useful information for further development of in-house hybridization capture NGS approaches.

Holly Nettle completed a Bachelor of Science Honours research project with the University of Melbourne under the supervision of **Michelle Wille** and was co-supervised by Marina Alexander (Australian Centre for Disease Preparedness). Her thesis focused on the development of aptamer based "point of care" diagnostics for avian influenza viruses in wildlife.

Andre Attard commenced a Bachelor of Science Honours research project (2025-2026) with Deakin University under the supervision of **Michelle Wille** and is co-supervised by Marcel Klaassen (Deakin University) and Jasmina Luczo (Australian Centre for Disease Preparedness). His thesis is focused on characterizing the diversity of avian paramyxoviruses in Australian wild birds

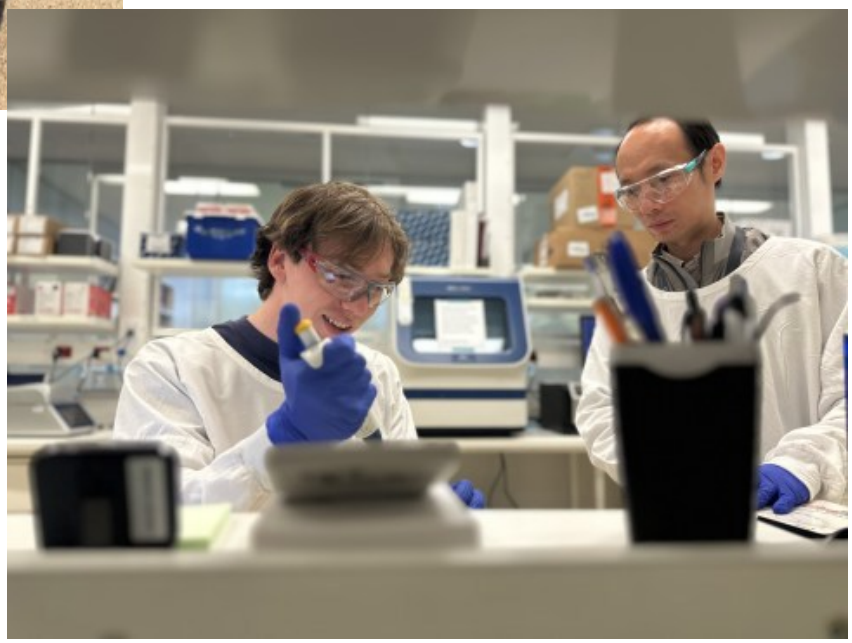
Work experience students

Zachary Hutchings from the University of Melbourne was at the Centre on 21 January 2025 as part of the VIDRL Work Experience program.

Alexander Ganino from the University of Melbourne was at the Centre on 15 May 2025 as part of the VIDRL Work Experience program.

Finn Picknell from University High school was at the Centre on 30 June - 4 July 2025 as part of the VIDRL Work Experience program.

Jamison Costello from Beaumaris Secondary College was at the Centre on 30 June - 4 July 2025 as part of the VIDRL Work Experience program.



Communications and Advisory Activities

The Centre actively contributes to the knowledge and understanding of influenza in scientific and public health domains through many different forums. Centre staff members participate in WHO meetings and workshops to support the ongoing work and growth of WHO GISRS, as well as providing advice on influenza to the Australian Government. Centre staff members publish peer-reviewed journal papers and present numerous talks and posters.

Publications and Reports

The Centre continued to build its research and surveillance profile with the publication of 48 original research papers, reviews and reports in 2025.

Centre Publications 2025

Abeykoon, A. M. H., M. Wilson, K. Subbarao, N. Geard, C. Zachreson, and **S. G. Sullivan**. "Severe Acute Respiratory Syndrome Coronavirus-2 Shedding in Exhaled Material: A Systematic Review." *Epidemiol Infect* 153 (Jun 20 2025): e75. https://dx.doi.org/10.1017/s0950268825100174.

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Presentations

Centre staff members presented talks and posters at numerous events during 2025, including national and international conferences, WHO meetings, educational lectures and research seminars.

ORAL PRESENTATIONS

Event/Institute; Location, date	SPEAKER, Title(s)
Avian Influenza in the Antarctic. Intrepid OE-5 seminars, 7 February 2025, Antarctica.	MICHELLE WILLE: Avian influenza in Antarctica
Lorne Infection and Immunity Conference,19-21 February 2025, Lorne, Victoria.	PATRICK READING: Influenza viruses – current global situation and emerging threats
BirdLife Europe Webinar, 7 May 2025, webinar.	MICHELLE WILLE: H5N1 Bird Flu: Protecting yourself and the birds you interact with
University of Melbourne Department of Veterinary Science Seminar Series, 20 May 2025, Melbourne, Victoria.	MICHELLE WILLE: Avian influenza viruses in Australia, and the HPAI threat
Centre for Innovation in Infectious Diseases and Immunology Research (CIIDIR) Fortnightly Seminar, 21 May 2025, Geelong, Victoria.	MICHELLE WILLE: Avian influenza viruses in Australia, and the HPAI threat
Centre for Infectious Diseases and Microbiology – Public Health Webinar, online, 23 May 2025.	MICHELLE WILLE: Global Updated on HPAI H5N1 and risk for incursion into Australia
Commonwealth Environmental Water Holdings/CSIRO Avian Influenza Surveillance Workship, 27 May 2025, Goolwa, South Australia.	MICHELLE WILLE: Global update on HPAI H5N1 and risk for incursion into Australia MICHELLE WILLE: Surveillance for LPAI instrumental in understanding entry and maintenance of HPAI in Australia
4th Annual CEIRR Network Meeting, 27-30 May 2025, Georgia, USA.	ANNETTE FOX: Influenza vaccine responses among young children first exposed to influenza antigens via infection versus vaccination
11th International Symposium on Avian Influenza, 24-26 June 2025, St. John's, Canada.	MICHELLE WILLE: HPAI H5N1 incursion risk and pathways into Australia
Advancing Research Priorities for Highly Pathogenic Avian Influenza H5N1 Through International Collaboration, 27 June 2025, St. John's, Canada.	MICHELLE WILLE: HPAI: Global problem, global response
Obstacles Opportunities Pathways and Synergies, 1 September 2025, Melbourne, Victoria.	HARRY STANDARD: Further development of the ferret model of influenza virus infection and its utility to explore novel therapeutic treatments
Royal Melbourne Hospital Board Meeting, 30 July 2025, Melbourne, Victoria.	PATRICK READING: Functions of the WHO Collaborating Centre for Reference and Research on Influenza in Melbourne in the Global Influenza

ORAL PRESENTATIONS (continued)	
Event/Institute; Location, date	**SPEAKER, Title(s)**
Australasian Epidemiology Association 2025, 16-18 July 2025, Tasmania.	JESSIE GOLDSMITH: Influenza vaccination for previously unvaccinated children. Are two doses better than one?
Communicable Diseases and Immunisation Conference 2025, 10-12 Jun 2024, Adelaide, South Australia.	JESSIE GOLDSMITH: Influenza vaccination for previously unvaccinated children. Are two doses better than one?
Royal Melbourne Hospital Leadership and Strategy Group Seminar, 27 August 2025, Melbourne, Victoria.	PATRICK READING: Impact of changes in the US administration of influenza surveillance and pandemic preparedness in Australia and worldwide
CDGN (communicable diseases genomics network) CoP meeting, 27 August 2025, Virtual.	YI MO DENG: Genomic surveillance at the WHO CC Melbourne
GISAID Bioinformatics Workshop, 21 September 2025, Hokkaido, Japan.	YI MO DENG: Next Generation Sequencing and Quality Checking
8th Antiviral group (AVG) and 3rd International Monitoring for Respiratory Pathogens (IMRP) meeting, 17-20th September 2025, Singapore.	IAN BARR: Overview on the Changing Landscape of Influenza Vaccines. Ian Barr also chaired panel discussions SAIRA HUSSAIN: Development of a Novel long-acting pan Antiviral to Influenza
Asia Pacific Consortium of Veterinary Epidemiology (APCOVE): Competency E Interactive Session, 18 September 2025, Australia.	MICHELLE WILLE: HPAI H5N1 and risk for incursion into Australia
Doherty Institute for Infection and Immunity undergraduate student seminar, 18 September 2025, Melbourne, Victoria.	MICHELLE WILLE: Avian Influenza: A pandemic on our doorstep
Institute for Biomedicine and Glycomics, Griffith University, 20 September 2025, Gold Coast, Queensland.	MICHELLE WILLE: HPAI H5N1 and risk for incursion into Australia
European Region Respiratory Surveillance Network webinar, 18 September 2025, Virtual.	PATRICK READING: Update on the influenza season in the Southern Hemisphere 2025
GISAID Bioinformatics Workshop, 21 September 2025, Hokkaido Japan.	YI-MO DENG: Next Generation Sequencing and Quality Checking

ORAL PRESENTATIONS (continued)	
Event/Institute; Location, date	**SPEAKER, Title(s)**
Western Port Biosphere Community Forum, 14 October 2025, Melbourne, Australia.	MICHELLE WILLE: High pathogenicity avian influenza and the threat to Australia
Australasian Virology Society: Spotlight on Viro logy in the Pacific symposium, 2 November	PATRICK READING: Molecular diagnostics in the Pacific before and after COVID-19
4th Correlates of Protection for Next Generation Influenza Vaccines, 13-14 November 2025, Vienna, Austria .	ANNETTE FOX: Influenza Vaccine responses among Young Children first Exposed to Influenza Antigens via Infection Versus Vaccination
	ANNIE CHU: A(H3N2) Antibody and B Cell Response in Repeat Compared to Naïve vaccines
RMH Research conference, 6-7 November 2025, Melbourne, Victoria.	ANNETTE FOX: Recombinant influenza vaccines may mitigate attenuation associated with repeated vaccination against A(H3N2): Results from a randomised controlled trial in healthy younger adults
	JESSICA MILLER: Influenza in Australian FluCAN and PAEDS sentinel hospitals, 2023 and 2024
	JESSIE GOLDSMITH: Invasive group A streptococcal infections in Australian adults – a descriptive cohort and cost burden study
16th Australian Influenza Symposium, 13-14 November 2025, Melbourne, Victoria.	SAIRA HUSSAIN: Development of a novel long-acting pan-antiviral to influenza
	ANNETTE FOX: The first Australian Influenza Controlled Human Infection Study (CHIM): Immune

POSTER PRESENTATIONS	
Event/Institute; Location, date	**SPEAKER, Title(s)**
13th International RSV Symposium (RSV2025) , 12-13 March 2025, Brazil.	XIAOMIN DONG: An improved rapid and sensitive long amplicon method for nanopore-based RSV whole-genome sequencing
Negative Strand Virus Meeting, 22-27 June 2025, Monpellier France.	JAMES BARNES, SAIRA HUSSAIN and PATRICK READING: Bovine myxovirus resistance protein 1 mediates antiviral activity against human and avian influenza A viruses PATRICK READING: Restriction factor SAMHD1 does not inhibit influenza a virus replication in human epithelial- or macrophage-like cells.
8th Antiviral group (AVG) and 3rd International Monitoring for Respiratory Pathogens (IMRP) meeting, 17-20th September 2025, Singapore.	SAIRA HUSSAIN: A cluster of influenza A(H3N2) viruses isolated from Tasmania with reduced susceptibility to baloxavir in 2024
RMH Research conference, 6-7 November 2025, Melbourne, Victoria.	HEIDI PECK: Circulation of and seropositivity to influenza B/Yamagata-Lineage viruses prior to and after the Covid-19 pandemic in Australia MALET ABAN: Immunity to zoonotic influenza viruses in individuals vaccinated with seasonal influenza vaccines

Committees and Advisory Groups

Centre staff members served on the following governing boards, committees and advisory groups during 2025.

Patrick Reading
Influenza and Other Respiratory Viruses, *Editorial board*

Australian Influenza Vaccine Committee (Therapeutic Goods Administration), *Member*

Peter Doherty Institute for Infection and Immunity, Global Health Capacity and Capability Building Steering Committee, *Member*

VIDRL Regional and Global Health Steering Committee, *Member*

Pacific Public Health Surveillance Network (PPHSN) Technical Working Group, *Member*

Doherty Institute for Infection and Immunity (listed stakeholder) to Intergovernmental Working Group on the WHO Pandemic Agreement (IGWG) , Advisor

WHO GISRS Pandemic Response Plan for influenza (GISRS PRPi) committee, *Member*

WHO Pandemic Influenza Vaccine Response Operational Plan (PIVR-OP) Task group , *Member*

Ian Barr

Australasian Vaccine & Immunotherapeutics Development Group, *Member*

Australian Influenza Vaccine Committee (Therapeutic Goods Administration), *Member*

Centre of Excellence for Influenza Research and Surveillance) program at St Jude Children's Research Hospital, Scientific Advisory Committee

Doherty Institute PC3 Laboratory Users Group, *Member*

Public Health Laboratory Network (Department of Health and Aged Care), *Committee member*

Influenza and other respiratory viruses, *Editorial Board*

Yi-Mo Deng

WHO Working Group for GISRS PCR detection for influenza surveillance, *Member*

Annette Fox

International Committee on Advancing Pandemic and Seasonal Influenza Vaccine Preparedness and Response. US National Academy of Medicine. 2020-2021, *Member*

Victorian Infection and Immunity Network, *Committee member*

International Society for Influenza and Other Respiratory Viruses, *Council Member*

Saira Hussain

WHO Expert Working Group for GISRS Surveillance of Antiviral Susceptibility, *Member*

Katie Milne

Medical Laboratory Quality Network, *Member*

Victorian Infectious Disease Reference Laboratory NATA Action Group, *Member*

Committees and Advisory Groups (continued)

Michelle Wille

Antarctic Wildlife Health Working Group. Expert Group for Birds and Marine Mammals. Scientific Committee for Antarctic Research, *Member*

Avian Influenza Virus AUSVETPLAN working group, *Member*

Discover Research Steering Committee for Doherty Computational Sciences Initiative, *Member*

Doherty Institute Green DISCO, *Member*

East Asian Australian Flyway Partnership Avian Disease Working Group, *Member*

eMERGE (Early and Mid-career network Committee, Peter Doherty Institute for Infection and Immunity, *Member*

Global Consortium for highly pathogenic avian influenza viruses in seabirds, *Chair*

High Pathogenicity H5N1 Avian Influenza Intersessional Group, Population and Conservation Status Working Group of the Agreement for the Conservation of Albatrosses and Petrels (ACAP), *Member*

MicroSeq Conference Organising Committee, *Member*

National Avian Influenza Wild Bird Surveillance, *Steering Committee*

Victorian Wader Study Group, *Member*

Wildlife Health Australia, *Member*

PLoS Pathogens, *Editor*

Waterbirds, *Editor*

Virology and Molecular Ecology (special issue), *Editor*

Tanya Diefenbach-Elstob

National Influenza Surveillance Committee (Department of Health and Aged Care), *Proxy*

The Computational Sciences Initiative Public Health Steering Committee, *Member*

Jessica Miller

National Respiratory Infections Surveillance Committee (previously National Influenza Surveillance Committee) (Department of Health and Aged Care), *Member*

Doherty Public Health Leadership Group*, Member*

Visitors to the Centre

The Centre was pleased to host the following visitors during 2025.

Date	VISITOR and affiliation *Continued*
20 January 2025	DARWIN OPERARIO; WHO; Laboratory Technical Officer.
07 February 2025	SHALINI SINGH and GAZALA BUKSH; CDC Fiji, Visiting scientists.
10-14 February 2025	HAYTHAM MOHAMED; WHO SEARO; Technical Officer.
16-22nd February 2025	REGIS GRAILTES and QUETIN OLIVIER; Institut Pasteur Korea, collaborators.
10-14th March 2025	NATCHAYA KHIADSANG and WANDEE MEECHALAD; NIC Thailand, Visiting scientist.
07 April 2025	NARCISSE JOSEPH; University Putra Malaya, Visiting scientist.
16 April 2025	BLAIR COMLEY; Commonwealth Department of Health, Secretary.
27April - 29th May 2025	SHUJUAN CUI; Beijing CDC, Visiting scientist.
05-16 May 2025	MARIE THERESE DC. QUIMPO and MARIA NINA C. TOLEDO; Research Institute of Tropical Medicine, Visiting scientists.
26 May - 05 June 2025	MABEL VUNICAGI VANIQI; Fiji CDC NPHL, Visiting scientist. ZAHEEN SHAINAZ IBRAHIM; Labasa Hospital, Fiji, Visiting scientist. VALERIE IMANAUI-MASIN; CPHL (HIV), Papua New Guinea, Visiting scientist. LUISA VAILANU; Vaiola Hospital, Tonga, Visiting scientist. ESCAR AVOCK; Vila Central Hospital, Vanuatu, Visiting scientist. EREKANA TEINGOA; Tungaru Central Hospital, Kiribati, Visiting scientist.
17 July - 3 August 2025	URISHA NAIDO: National Institute for Communicable Diseases, Visiting student.

Visitors to the Centre (continued)

Date	VISITOR and affiliation *Continued*
29 July - 7 August 2025	LUKE BURTON: London School of Hygiene and Tropical Medicine, Visiting student.
12 August 2025	MICHEAL KIDD: Department of Health and Aged Care, Chief Medical Officer.
18-19 August 2025	RAE PEARSON: SVS Laboratories, Visiting Scientist.
21 October 2025	LU KANG, WEIXIAN SHI, JIACHEN ZHAO, AIHUA LI, Institute for Infectious Disease and Endemic Disease Control, Visiting Scientists.

Engagement in WHO activities

Event; Location, Date	Centre staff involved
WHO Northern Hemisphere TC2, virtual, 29 January 2025.	Heidi Peck, Ian Barr and Patrick Reading attended
WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2025-2026. London England, 24-29 February 2025.	Heidi Peck and Ian Barr attended and Patrick Reading attended and acted as a Temporary Advisor
WHO partnership with Collaborating Centres: Strengthening value and impact discussion, virtual, 7 April 2025.	Patrick Reading attended
Strengthening Collaboration between WHO Collaborating Centers (WHO CCs) and National Influenza Centers (NICs) in the Southeast Asia Region, webinar SEARO, 25 March 2025.	Patrick Reading gave a talk titled "What we do at the WHO Collaborating Centre for Reference and Research on Influenza (WHO CCRRI), Melbourne"
Best practices in specimen management: Strengthening specimen management for influenza surveillance, webinar SEARO, 29 April 2025.	Katie Milne and Heidi Peck gave a talk titled "Influenza sample referral to the WHO Collaborating Centre for Reference and Research on Influenza (WHO CCRRI), Melbourne"
14th Meeting of the WHO Working Group on Surveillance of Antiviral Susceptibility of Influenza Viruses for GISRS (AVWG), virtual, 10-12 June 2025.	Saira Hussain attended and presented the annual WHOCCRI Melbourne antivirals surveillance update
15th Meeting of the WHO Working Group for the Molecular Detection and Subtyping of Influenza Viruses and the use of Next Generation Sequencing, virtual, 17-19 June 2025.	Yi-Mo Deng attended and chaired the meeting
Respiratory syncytial virus sequencing considerations for an expanded Global Influenza Surveillance and Response System, 17 June 2025.	Ian Barr contributed to WHO guidelines
WHO CC forum (Western Pacific Region): Building Systems that Prevent, Detect and Respond to Public Health Threats: Genomic Surveillance, virtual, 2 September 2025.	Patrick Reading gave a talk titled "Supporting genomic surveillance for influenza and other respiratory viruses in the Asia Pacific Region"
18th Bioregional Meeting of National Influenza Centres in WHO SEARO and WPRO Regions, virtual, 9-11 September 2025.	Patrick Reading acted as Temporary Advisor and moderator for a session on "Influenza surveillance - doing more with fewer resources"

Engagement in WHO activities(count)

Event; Location, Date	Centre staff involved
18th Bioregional Meeting of National Influenza Centres in WHO SEARO and WPRO Regions, virtual, 9-11 September 2025.	Ian Barr acted as Temporary Advisor and gave a talk titled “WHO CC update on influenza activity in the Southern Hemisphere”
WHO Consultation on the Composition of Influenza Vaccines for the Southern Hemisphere in 2026 Hokkaido, Japan, 24-29 February 2025.	Yi-Mo Deng and Ian Barr attended and Patrick Reading attended and acted as Temporary Advisor . Jessica Miller attended and presented the vaccine effectiveness (VE) Report

Other Conference Participation and Professional Engagement

Centre staff members also participated in the following events as attendees and/or in other roles during 2025

Event; Location, date	Centre staff involvement
APVIC 2025, 20-22 May 2025, Brisbane, Queensland.	Ian Barr and Heidi Peck attended
CEIRR Meeting 26 May-3 June 2025, Athens Georgia.	Annette Fox attended
Negative Strand Virus Meeting, 22-27 June 2025, Monpellier France.	Patrick Reading Attended and as an invited Chair
11th International Symposium on Avian Influenza, 24-26 June 2025, St. John's, Canada.	Michellle Wille organised this conference
Bonn Cumming Annual Conference 30-3 July 2025, France.	Patrick Reading attended
BioForum - Avian influenza unmasked: Research, readiness, response, 27 August 2025, Melbourne, Victoria.	Michelle Wille and Patrick Reading where part of the panel
Emerging Respiratory Diseases Symposium, Australasian society for infectious diseases, 1-2 August 2025, Sydney, NSW.	Michelle Wille and Ian Barr where part of the panel
AIVC Recommendations for the Composition of Influenza Vaccines for Australia 8 October 2025, Canberra, ACT.	Ian Barr and Patrick Reading attended
Emergency Animal Disease Meeting (ACDP, Geelong), 12 November 2025, Geelong, Victoria.	Michelle Wille attended
MiM2025, 22 November 2025, Gold Coast, Queensland.	Michelle Wille attended
CANARIES network meeting, 30 November 2025, Cambodia.	Michelle Wille and Yi-Mo Deng attended
ANZCCART Conference, 29-31 July 2025, Brisbane, Queensland	Paul Whitney attended

Other Conference Participation and Professional Engagement continued

Event; Location, date	Centre staff involvement
NATA Accreditation Matter 30-31 July 2025, Sydney, NSW.	Katie Milne and Steven Edwards attended
PHLN Meeting 15 October 2025, Canberra.	Ian Barr attended
Medical Laboratory Quality Network (MLQN) Internal Auditors Course , 27-28 October 2025, Melbourne, Victoria.	Katie Milne Facilitated and coordinated the course
Go Viral Meeting for Respiratory Infectious Diseases, 19 July, Melbourne, Victoria	Patrick Reading was invited speaker

Community Engagement

The Director, Deputy Director and other staff members participated in requests from media representatives for interviews and comments throughout 2025.

Patrick Reading

- Was on NBN News in a discussion around “A warning has been issued about a potential surge in flu hospitalizations and deaths this winter due to a decline in vaccination rate”. Aired 21 March 2025.
- Was on Channel 9 News in a segment titled, “Warning of looming 'quad-demic' this winter as flu vaccination rates nosedive”. Aired 21 March 2025. https://www.9news.com.au/national/warning-ahead-of-flu-season-as-quaddemic-circulates/d3dc27d4-f9c2-4938-90e5-9532d432129d
- Was quoted in Shepparton News in an article titled, “Spike in flu cases sparks plea over 'dire' rate of jabs”. Published 7 May 2025. https://www.sheppnews.com.au/national/spike-in-flu-cases-sparks-plea-over-dire-rate-of-jabs/?isentiaPostId=post-1
- Was quoted on 98.9 FM in a segment titled, “Australians are being urged to get vaccinated against the flu”. Aired 7 May 2025.
- Was quoted on 2BS FM in a segment titled, “The changes in flu vaccination rates”. Aired 9 May 2025.
- Was quoted in Radio National and ABC AM radios in a segment titled, “Influenza activity in Australia”. Aired 7 May 2025.
- Was quoted in Your Life Choices, Yarrawonga Chronicle, Yass Tribune, Western Advocate and Wellington Times in an article titled, “Spike in flu cases sparks urgent call for more jabs before winter”. 7 May 2025. https://www.yourlifechoices.com.au/health/spike-in-flu-cases-sparks-urgent-call-for-more-jabs-before-winter/ https://www.wellingtontimes.com.au/story/8960278/spike-in-flu-cases-sparks-plea-over-dire-rate-of-jabs/
- Was quoted in The Chronicle and News.com.au in an article titled, “Australia records unseasonal flu surge, health experts alarmed”. 11 May 2025. https://www.thechronicle.com.au/lifestyle/health/australia-records-unseasonal-flu-surge-health-experts-alarmed/news-story/66021be5be539ede057f4b1eed600514?btr=c6ea9cc55bc91f01903a721eee269051
- Was on a news briefing by the Australian Science Media Centre in a segment titled, “ NEWS BRIEFING: How severe is this flu season shaping up to be?”. 7 May 2025. https://www.scimex.org/newsfeed/news-briefing-how-severe-is-this-flu-season-shaping-up-to-be
- Was quoted in SBS News in an article titled, “Influenza cases surge: time to get vaccinated say experts”. 7 May 2025. https://www.sbs.com.au/news/podcast-episode/influenza-cases-surge-time-to-get-vaccinated-say-experts/qc1ff2fed
- Was quoted in newsGP in an article titled, “Fresh push to turn around ‘dire’ flu vaccination rate”. 7 May 2025. https://www1.racgp.org.au/newsgp/clinical/fresh-push-to-turn-around-dire-flu-vaccination-rat
- Was quoted in Pharmacy Daily in an article titled, “Expert concern over “dire” flu vax rates”. 7 May 2025. https://pharmacydaily.com.au/news/expert-concern-over-dire-flu-vax-rates/114851
- Was quoted in Medscape Medical News in an article titled,” Australia Braces for Major Influenza, RSV, Pertussis Season”. 11 April 2025. https://www.medscape.com/viewarticle/australia-braces-major-influenza-rsv-pertussis-season-2025a10008or
- Was quoted in the Herald Sun in an article titled, ”Australia records unseasonal flu surge, health experts alarmed”. 11 May 2025. https://www.heraldsun.com.au/lifestyle/health/australia-records-unseasonal-flu-surge-health-experts-alarmed/news-story/66021be5be539ede057f4b1eed600514?btr=c6ea9cc55bc91f01903a721eee269051
- Was quoted in the Herald Sun in an article titled, ”Mum’s warning as flu cases surge” . 30 May 2025. https://www.heraldsun.com.au/health/conditions/cold-flu/mums-warning-as-flu-cases-surge/news-story/58559c48d729547a8ea3782dfe97412d?btr=386918f1c4da5ea512775e1eae744459
- Was quoted in ABC News in an article titled, “Winter flu surge across the country sees 50 per cent rise in hospital admissions amid low vaccination rates”. 18 July 2025. Winter flu surge across the country sees 50 per cent rise in hospital admissions amid low vaccination rates - ABC News

Community Engagement (continued)

- Was quoted in The MSN in an article titled, “The 'aggressive' new super-flu strain that could ruin Christmas”. 8 December 2025. https://www.msn.com/en-gb/health/other/will-this-aggressive-new-flu-virus-ruin-christmas/ar-AA1RNoch

- Was quoted in The Telegraph in an article titled, “Will this ‘aggressive’ new flu virus ruin Christmas?”. 12 December 2025. https://www.telegraph.co.uk/news/2025/12/12/will-this-aggressive-new-flu-virus-ruin-christmas/

- Was quoted in Newcastle Herald in an article titled, “'Unusual for this time of year': mutant virus spreading fast at Christmas”. 23 December 2025. https://www.newcastleherald.com.au/story/9139836/flu-surge-in-hunter-new-england-and-nsw-prompts-holiday-warning/?cspt=1767564655%7C6328024c8fe45386a5aa1c0685340e50

- Was quoted in ILLAWARRA Mercury in an article titled, “Doctors' Christmas warning: Illawarra flu cases surge back to early winter levels”. 24 December 2025. https://www.illawarramercury.com.au/story/9140613/health-alerts-rise-as-illawarra-flu-cases-increase-pre-christmas/

Ian Barr

- Was quoted in Allergy and Respiratory Republic in an article titled, “Two in three Aussies missing flu vaccination”. 12 February 2025. https://www.puffnstuff.com.au/two-in-three-aussies-missing-flu-vaccination/86282
- Was quoted in The Medical Republic in an article titled, “Two in three Aussies missing flu vaccination”. 20 February 2025. https://www.medicalrepublic.com.au/two-in-three-aussies-missing-flu-vaccination/114604
- Was quoted in CIDRAP - Center for Infectious Disease Research & Policy in an article titled, “WHO advisers swap out H3N2 strains for next Northern Hemisphere flu vaccines”. 1 March 2025. https://www.cidrap.umn.edu/influenza-vaccines/who-advisers-swap-out-h3n2-strains-next-northern-hemisphere-flu-vaccines
- Was quoted in KION News in an article titled, “Disrupted US vaccine meetings could threaten timelines, access and transparency around shots”. 28 February 2025. https://kion546.com/health/cnn-health/2025/02/28/disrupted-us-vaccine-meetings-could-threaten-timelines-access-and-transparency-around-shots/
- Wrote an article titled, “Influenza in 2025: what to expect and how to ameliorate its impact” for Respiratory Medicine Today for the April 2025 edition. https://respiratory.medicinetoday.com.au/rmt/2025/april/feature-article/influenza-2025-what-expect-and-how-ameliorate-its-impact

- Was quoted in EIN Presswire in an article titled, “AP-CHAAI Launches Virtual Think Tank to Advance Vaccine Policy and Healthy Aging Across the Asia-Pacific Region”. 12 November 2025. https://www.einpresswire.com/article/866358700/ap-chaai-launches-virtual-think-tank-to-advance-vaccine-policy-and-healthy-aging-across-the-asia-pacific-region

- Was on The Conversation Interview podcast titled, “Flu shots: how scientists around the world cooperate to choose the strains to vaccinate against each year”. 28 November 2025. https://theconversation.com/flu-shots-how-scientists-around-the-world-cooperate-to-choose-the-strains-to-vaccinate-against-each-year-270621

- Was interviewed on RTE Radio on a segment titled, “Surging Flu, vaccines and impact the flu has had on Australia”. 12 December 2025. https://www.rte.ie/radio/radio1/clips/22567794/

Michelle Wille

- Was quoted in ABC News in a forum titled, “The hunt for the next pandemic is on our shores”. 30 March 2025. https://www.abc.net.au/news/2025-03-30/next-pandemic-risk-h5n1-2-3-4-4b-bird-flu-avian-influenza/105104736?isentiaPostId=post-1
- Was interviewed by ABC for a segment on Avian Influenza. Aired 15 May 2025
- Was quoted in Winnipeg Free press in an article titled, “B.C. doctors comparing H5N1 virus that infected teen with that of Louisiana patient”. 8 January 2025. https://www.winnipegfreepress.com/arts

-and-life/life/health/2025/01/08/b-c-doctors-comparing-h5n1-virus-that-infected-teen-with-that-of-louisiana-patient

- Was quoted in SBS in an article titled, “It's killed birds, people and Australia is bracing for an outbreak. Could H5N1 get here?”. 9 January 2025. https://www.sbs.com.au/news/article/could-h5n1-avian-influenza-reach-australia/1qaju0x0x
- Was quoted in SBS Podcast in a segment titled, “Are we in danger from H5N1 Bird Flu?”. 11 January 2025. https://www.sbs.com.au/news/podcast-episode/interview-are-we-in-danger-from-h5n1-bird-flu/peqec32uj
- Was quoted in The Guardian in an article titled, “Age of the panzootic: scientists warn of more devastating diseases jumping between species”. 15 January 2025. https://www.theguardian.com/environment/2025/jan/15/age-of-the-panzootic-scientists-warn-of-more-devastating-diseases-jumping-between-species-aoe
- Was quoted in NPR in an article titled, “It's like 'dead birds flying': How bird flu is spreading in the wild”. 7 February 2025. https://www.npr.org/sections/goats-and-soda/2025/02/07/g-s1-46402/bird-flu-wild-animals-mammals-virus
- Was quoted in The Australian in an article titled, “Bird flu: do humans get it (and do I need to hard-boil my eggs)?”. 26 February 2025. https://www.theaustralian.com.au/health/diet/bird-flu-do-humans-get-it-and-do-i-need-to-hardboil-my-eggs/news-story/4681da7b7a48a33bd495a11723367178?btr=e743595702976a1e18beed2f2f8bd2b7
- Was quoted in ABC News in an article titled, “Avian influenza H5N1 in subantarctic region raise alert level for Australian islands”. 5 March 2025. https://www.abc.net.au/news/science/2025-03-05/bird-flu-infections-alert-australian-island-avian-influenza/105006040
- Was quoted in ABC News in an article titled, “Pandemic potential’ on our doorstep”. 18 May 2025. https://www.abc.net.au/news/2025-05-18/antarctica-avian-flu-h5n1-evolution-pandemic-potential/105271154
- Was quoted in Science in an article titled, “Deadly avian flu strain is spreading rapidly in Antarctica”. 13 March 2025. https://www.science.org/content/article/deadly-avian-flu-strain-spreading-rapidly-antarctica
- Was featured in Cosmos Magazine in an article titled, “Michelle is monitoring an unfolding avian catastrophe”. 17 March 2025. https://cosmosmagazine.com/nature/monitoring-avian-catastrophe/
- Was quoted in The Smithsonian Magazine in an article titled, "Avian Flu Is Rapidly Spreading Across Antarctica”.17 March 2025. https://www.smithsonianmag.com/smart-news/avian-flu-is-rapidly-spreading-across-antarctica-180986222/
- Was quoted in Medscape in an article titled, “Everything You Need to Know About Bird Flu”. 7 April 2025. https://www.medscape.com/s/viewarticle/everything-you-need-know-about-bird-flu-2025a10008ao?form=fpf
- Was quoted in CBC Lite in an article titled, “Scientists gather in St. John's to advocate for greater effort in fight against avian influenza”. 24 June 2025. https://www.cbc.ca/lite/story/1.7568810
- Was interviewed by the ABC on an article titled “Millions being spent as Australia prepares for deadly H5 strain of bird flu”. 20 October 2025. https://www.abc.net.au/news/2025-10-20/australia-prepares-for-deadly-h5-strain-of-bird-flu/105906562
- Was quoted in The Guardian in an article titled, “Expert says H5N1 virus ‘catastrophic for wildlife’ around the world”. 24 October 2025. https://www.theguardian.com/australia-news/live/2025/oct/24/australia-news-live-police-search-colleen-walker-craig-bowraville-river-labor-environment-laws-murray-watt-coalition-greens-ntwnfb?CMP=share_btn_url&page=with%3Ablock-68fac38e8f08951f69bbc093#block-68fac38e8f08951f69bbc093
- Was interviewed on ABC listen in a segment titled, “Suspected case of bird flu on Heard Island”. 24 October 2025 https://www.abc.net.au/listen/programs/radionational-breakfast/bird-flu/105936208
- Was quoted in Nature article in an article titled, “This ‘minor’ bird flu strain has potential to spark human pandemic”. 28 October 2025. https://www.nature.com/articles/d41586-025-03519-1
- Was quoted in Scientific American in an article titled, “This Overlooked Bird Flu Strain Might Be the Next Pandemic Risk”. 29 October 2025. https://www.scientificamerican.com/article/h9n2-bird-flu-virus-

could-pose-human-pandemic-risk-experts-warn/

- Was quoted in Associated Press in an article titled, “Washington resident is infected with a different type of bird flu”. 15 November 2025. https://apnews.com/article/bird-flu-infection-washington-h5n5-b8921d13aa7d96330654a960f80453c3

Jessie Goldsmith

- Was quoted in Medpage Today in an article titled, “Starting Toddlers With Two Doses of the Flu Shot Boosted Effectiveness”, 3 October 2025. https://www.medpagetoday.com/infectiousdisease/uritheflu/117783

Website and social media

The Centre website was maintained and updated throughout the year, with information provided on the progress of the influenza season and vaccine recommendations by WHO and the TGA. During 2025, the website was viewed by over 10, 000 unique users from 156 different countries. The majority of visits to the website were from Australia, followed by the USA.

Scan to access our Centre video

New staff members

Lauren Burmas

Medical Scientist

Maha Khairbak

Medical Scientist

Michelle Wille

Outreach Head and Researcher

Management and staff

Director
Prof Patrick Reading

Deputy Director
Prof Ian Barr

Outreach Head/ One Health Researcher
Michelle Wille

Quality & Regulatory Officer
Katie Milne

Administrative officer
Symone Mercuri

Laboratory Manager/ Senior Medical Scientist
Dr Paul Whitney

Data and Communications officer
Vishma Varsani

Surveillance

ANTIGENIC ANALYSIS
Head: Heidi Peck
Medical scientists:
Monica Bobbitt
Joelle Dharmakumara
Leah Gillespie
Lani Metuisela
Megan Triantafilou
Tasoula Zakis
Malet Aban
James Barnes
Maha Khairbak

GENETIC ANALYSIS
Head: Dr Yi-Mo Deng
Medical scientists:
Dr Xiaomin Dong
Steven Edwards
Hilda Lau
Olivia Lay
Presa Chanthalavanh
Natalie Spirason
Rachel Wordsworth

ANTIVIRAL DRUG SENSITIVITY
Head: Dr Saira Hussain
Medical scientist: Nikita Deshpande

BIOINFORMATICS
Manager: Dr Clyde Dapat

Vaccine development

Head: Heidi Peck
Medical scientists:
Hilda Lau
Cleve Rynehart
Jolle Dharmakumara
Sally Soppe

Research

IMMUNITY TO RESPIRATORY VIRUSES
Senior research scientist:
Dr Annette Fox

Post-doctoral researchers
Dr Stephany Sanchez

Research assistants:
Arada Hirankitti
Anastasia Jess Hadiprojo

ANTIVIRALS RESEARCH
Senior research scientist:
Dr Saira Hussain

Research assistants:
Harry Stannard
Ashwin Muraleetharan
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