16th Australian Influenza Symposium

13-14 November 2025

Peter Doherty Institute for Infection and Immunity
Melbourne

Welcome

The WHO Collaborating Centre for Reference and Research on Influenza welcomes you to the **16th Australian Influenza Symposium 2025** at the Doherty Institute for Infection and Immunity, Melbourne, Victoria. We would especially like to thank all of the speakers for agreeing to present their work at the Symposium. Finally, we wish to acknowledge the following:

Symposium Organising Committee:
WHO Collaborating Centre for Reference and Research on Influenza:

- Prof. Ian Barr
- Prof. Patrick Reading
- Ms Symone Mercuri
- Ms Vishma Varsani
- Ms Katie Milne

Travelling scholars program by SK Bioscience, South Korea

WHO Collaborating Centre for Reference and Research on Influenza
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The Royal Melbourne Hospital
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We are especially thankful for the financial support from:

Australian Government
Department of Health, Disability and Ageing

Acknowledgement of Country:
In the spirit of reconciliation, the WHO Collaborating Centre for Reference and Research on Influenza, VIDRL and the Doherty Institute, acknowledges the Traditional Custodians of country throughout Australia and their connections to land, sea and community. We pay our respect to their Elders past and present and extend that respect to all Aboriginal and Torres Strait Islander peoples today.

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Social Media

- Social media is permitted at AIS
- WHO CC Melbourne's Twitter handle is @WHOFluCCMelb, LinkedIn is WHO Collaborating Centre for Reference and Research on Influenza and Blue sky is whofluccmelb.bsky.social
- AIS event hashtag is #AIS2025Melbourne
- Please do not include any talks/slides speakers specifically request NOT be included in social media

Program Day 1

Thursday, 13 November 2025		
9:00	Meeting opening and logistics: Ian Barr, WHO CC, Doherty Institute, Melbourne, VIC	
9:10	Opening remarks	
Plenary Session 1 | **Chair: Patrick Reading, WHO CC, Doherty Institute, Melbourne,**		
09:15	Andy Bowman, Ohio State University, USA	The Udder Story: H5N1 Pathogenesis, Transmission Paradox, and Cross-Immunity
09:45	Erik Karlsson, Institut Pasteur Cambodia, Cambodia	A New A/H5N1 Reassortant Genotype Infecting Poultry, Humans, and Big Cats in the Greater Mekong Subregion
10:15	Emily Martin, University of Michigan, USA	Innovations in Cohort Studies for Respiratory Virus Response
10:45	*Morning tea*	
Plenary Session 2 | **Chair: Jodie McVernon; Doherty Institute & Uni. Melbourne**		
11:15	Ben Cowling, Hong Kong University, Hong Kong SAR	Repeated influenza vaccination effects in a randomised placebo-controlled trial
11:40	Nikki Moreland, Auckland Uni., Auckland, NZ	Evolving Applications of Serology: From tracking SARS-CoV-2 exposure to exploring post-pandemic immunity gaps in Aotearoa New Zealand
12:00	Bette Liu, NCIRS, Sydney, NSW	COVID-19 vaccine effectiveness and impact on mortality in Australia
12:20	Shidan Tosif, RCH, MCRI, Melbourne	The Victorian RSV Program Journey: Lessons from Early Implementation
12:40	Thomas Williams, University of Edinburgh, Scotland	Maternal RSV vaccination program in the UK Title to be confirmed (PRE-RECORD)
13:00	*Lunch*	
Abstracts Session 3 Virology | Chair: Marios Koutsakos & Adam Wheatley, Uni Melbourne		
13:45	Ahmed Quadeer, University of Melbourne DMI	Inferring effects of mutations on SARS-CoV-2 transmission from genomic surveillance data
14:00	Saira Hussain, WHOCC Doherty Institute, Melbourne	Development of a novel long-acting pan-antiviral to influenza
14:15	Callum Lay, ACDP, CSIRO, Geelong	Analysis of H5NX Avian influenza diffusion, evolution and recombination in South-East Asia
14:30	Lara Schwab, University of Melbourne	Antigenic evolution of the influenza B virus hemagglutinin over 81 years
14:45	Maddy Belfrage, ACDP, CSIRO, Geelong	Antigenic characterisation of Australian H7 highly pathogenic avian influenza virus under immunological pressure
15:00	Rebecca Rockett, Westmead Hospital, Sydney	Novel methods to rapidly perform genomic epidemiology on a broad spectrum of respiratory pathogens
15:15	*Afternoon tea*	
Plenary Session 4 and Panel discussion | Chair & Moderator: Michelle Wille, WHO CC, Doherty Institute		
15:45	Jenna Hassall & Lauren Kutzner, Australian Centre for Disease Control, Canberra	National summary of the 2025 respiratory season and the Australian Respiratory Surveillance Report
16:10	Oliver Eales, University of Melbourne	Real-time situational assessment of respiratory virus epidemics in Australia and New Zealand over winter 2025
Roundtable: Should we focus on ameliorating the effects of the big 3 respiratory viruses (seasonal influenza, RSV and SARS-CoV-2) instead of worrying about the next pandemic, now that we have mRNA vaccines?		
16:30	Discussion Panel members	Andy Bowman, Erik Karlsson, Nikki Moreland, David Speers, Emily Martin.
17:30	**Day 1 concludes: Drinks and finger food in foyer.**	

Program Day 2

Friday, 14 November 2025		
Plenary Session 5 Industry – Commercial & product updates **| Chair: Ian Barr, WHO CC, Doherty Institute**		
08:30	Upasna Varma, GSK, Melbourne	Options for co-administration of the AS01E-adjuvanted respiratory syncytial virus (RSV) prefusion F protein (adjuvanted RSVPreF3) vaccine with other adult vaccines: a review of existing data
08:50	Keith Chappel, Uni Queensland, Brisbane	The Molecular Clamp Platform: A broadly applicable solution to the manufacture of multipathogen subunit vaccines
09:10	Merrin Tulloch, AstraZeneca, Australia	Live Attenuated Influenza Vaccine: Southern Hemisphere Nasal Spray Flu Vaccine for 2026
09:30	Najwa Ejje, Sanofi Australia	Combination COVID-19 and Influenza Vaccines: Development Landscape and Potential Public Health Implications
09:50	Jules Bayliss, Sequris Australia	The ABC of Flu Vaccines: Consideration for Innovation and Public Health
10:10	Tor Beiring, Sorensen University of Copenhagen	DAN-RSV: RSVpreF Vaccine for preventing cardiorespiratory hospitalisation
10:30	*Morning tea*	
Plenary Session 6 | Chair: Siobhan St George, Department of Health, Disability and Ageing, Canberra		
11:00	David Speers, Pathwest, WA	Human metapneumovirus, the other respiratory paramyxovirus, incidence and genomic diversity during a pandemic era in Western Australia
11:20	Avram Levy, Pathwest, WA	Evolving Capacity and Challenges in Wastewater Surveillance for Respiratory Viruses
11:40	Annette Fox, WHO CC, Melbourne, Victoria	The first Australian Influenza Controlled Human Infection Study (CHIM): Immune Correlates of Viral Clearance and Symptoms
12:00	Arutha Kulasinghe, Uni Queensland, Brisbane	Viral Cartography: Understanding the impact of severe COVID on multiple organ systems
12:20	*Lunch*	
Abstracts Session 7 Epidemiology | Chair: Freya Shearer Uni Melb. & Craig Dalton, Uni Newcastle		
13:00	Jules Bayliss, Seqirus, Melbourne	Relative Effectiveness of Cell-Based Versus Egg-Based Quadrivalent Influenza Vaccines Across Paediatric Populations During the 2023-24 Influenza Season in the United States and Public Health Impact on Australia."
13:15	Julian Carlin, University of Melbourne	Cost-effectiveness of immunising interventions to reduce respiratory syncytial virus disease burden in infants in Australia
13:30	Jenny Herz, Biointelect, Sydney	Australia's new incubator for vaccine and infectious disease innovation
13:45	Zubair Akhtar, Kirby Institute, Sydney	Epidemiology of respiratory syncytial virus (RSV) within a New South Wales-based multi-centre health district between 2018-2024 in Australia
14:00	David Muscatello, UNSW, Sydney	Are known influenza or COVID-19 infections documented in Australian hospital databases**?**
14:15	Janaki Amin, Health Protection NSW, NSW Ministry of Health	The NSW 2024 RSV immunisation program: targeted effectiveness and population level impact.
14:30	*Afternoon tea*	
Plenary Session 8 | Chair: Ben Cowling, Hong Kong University, Hong Kong SAR China		
15:00	Emily Martin, University of Michigan, USA	Seek and You Will Find: Co-Circulating Viruses in Epidemiology and Effectiveness Studies
15:30	Andy Bowman, Ohio State University, USA	Hogging the Flu? Surveillance and Immune Gaps at US Swine Exhibitions
16:00	Closing comments	Ian Barr
16:05	**Australian Influenza Symposium concludes**	

Abstracts

Day 1	Plenary Session 1
9:15	**The Udder Story: H5N1 Pathogenesis, Transmission Paradox, and Cross-Immunity**
Speaker	Andy Bowman, Ohio State University, USA

Authors
Natalie Tarbuck[1], Cody Warren[2], Andrew Bowman[1]
Affiliations
1. The Ohio State University, Department of Veterinary Preventive Medicine
2. The Ohio State University, Department of Veterinary Biosciences

Abstract
The emergence of highly pathogenic avian influenza (HPAI) A(H5N1) in U.S. dairy cattle, initially highlighted by widespread viral nucleic acid detection in retail milk surveillance, represents a significant shift in our understanding of influenza A virus host range, specifically revealing a strong tropism for the bovine mammary gland. We investigated the pathogenesis and transmission of the B3.13 genotype in lactating dairy cattle. Experimental studies demonstrated that intramammary (IM) inoculation with an extremely low dose (10 $TCID_{50}$) was sufficient to establish robust infection, high-titer viral shedding in milk (peaking 10^8 $TCID_{50}$/mL), and clinical mastitis, consistent with severe outcomes observed on farms. However, despite the low infectious dose and high shedding, we were unable to recapitulate transmission via contaminated milking equipment or close contact under experimental conditions. This critical finding challenges current transmission hypotheses and suggests that unidentified agent, host, or environmental cofactors are necessary for the efficient spread observed in the field.

Given the continued spread and risk of endemicity, we assessed the impact of pre-existing immunity on clinical disease and viral replication. Dairy cows naturally exposed to the B3.13 genotype (April 2024) and naïve controls were experimentally re-infected via the IM route with low or high doses of homologous (B3.13) or heterologous (D1.1) viruses. Naïve controls infected with either genotype developed fever and significant reductions in milk yield, shedding high titers of infectious virus. In contrast, re-infected cows showed restricted viral replication, with limited or no infectious virus recovered, despite detection of viral RNA. Homologous (B3.13) re-infection provided complete protection against clinical disease at both doses. However, heterologous (D1.1) challenge still induced fever, transient morbidity, and gross mammary lymph node pathology, comparable in some respects to naïve controls. These findings indicate that prior H5N1 exposure effectively restricts the shedding of infectious virus, likely reducing transmission potential, but partial immunity against evolving heterologous strains may still permit clinical disease and tissue pathology, underscoring the urgency for continued viral surveillance.

Day 1	Plenary Session 1
9:45	**A New A/H5N1 Reassortant Genotype Infecting Poultry, Humans, and Big Cats in the Greater Mekong Subregion**
Speaker	Erik Karlsson, Institut Pasteur Cambodia, Cambodia

Authors
Erik Albert Karlsson[1]
Affiliations
1. Virology Unit, Institut Pasteur du Cambodge

Abstract
Highly pathogenic avian influenza (HPAI) A/H5N1 viruses have circulated endemically in poultry across the Greater Mekong Subregion for nearly two decades, periodically spilling over into humans and other mammals. Between 2023 and 2025, Cambodia and Vietnam have detected multiple human and animal infections linked to a novel reassortant clade 2.3.2.1e genotype, underscoring the ongoing viral evolution occurring within an endemic ecosystem.
In Cambodia, 33 laboratory-confirmed human infections were detected between February 2023 and October 2025, 17 of which occurred in 2025. Fourteen deaths were reported, corresponding to an overall case-fatality rate of 42.4% (47.1% in 2025). All cases had direct or indirect exposure to sick or dead poultry, with no evidence of human-to-human transmission. In Vietnam, sudden mortality among tigers, lions, and a leopard at two zoological facilities during August and September 2024 was confirmed to result from A/H5N1 infection. Whole-genome sequencing of viruses

from seven tigers and one leopard revealed a monophyletic cluster with minimal genetic divergence and near identity to poultry isolates from a concurrent farm outbreak, indicating a single-source feedborne exposure with limited or no onward transmission. One human H5N1 infection was also detected in Vietnam during this period.
Genomic analysis revealed that the viruses belonged to a novel reassortant genotype derived from regionally endemic clade 2.3.2.1e viruses that had acquired gene segments through two reassortment events from clade 2.3.4.4b and low-pathogenic avian influenza viruses. Mammalian-associated markers, including PB2 E627K, HA T156A, HA S110N, and PB1 H99Y, were detected in poultry, human, and felid sequences, suggesting enhanced polymerase activity and altered receptor binding affinity in mammalian hosts.
These findings highlight the continued diversification and persistence of A/H5N1 in the Greater Mekong Subregion and the recurrent spillovers that occur at the animal–human interface. The detection of a single reassortant genotype across poultry, felids, and humans illustrates the interconnected nature of viral evolution in shared ecological landscapes and reinforces the need for integrated One Health surveillance to identify and contain emerging strains before they achieve broader mammalian adaptation or sustained transmission.

Day 1	Plenary Session 1
10:15	**Innovations in Cohort Studies for Respiratory Virus Response**
Speaker	Emily Martin, University of Michigan, USA

Day 1	Plenary Session 2
11:15	**Repeated influenza vaccination effects in a randomised placebo-controlled trial**
Speaker	Ben Cowling, Hong Kong University, Hong Kong SAR

Author
Ben Cowling[1]
Affiliations:
1. World Health Organization Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, The University of Hong Kong, Hong Kong Special Administrative Region, China

Abstract
Antibody responses to influenza vaccination vary between people and in the same person over time. In observational studies, prior vaccination is associated with some of this variation: antibody responses often seem hampered in repeat vaccinees compared with those not recently vaccinated. It is unclear how much this effect arises from confounders or reflects a true blunting of responses by pre-existing antibodies. It is also unclear how much responses vary among people with similar vaccination histories and pre-vaccination antibody titers – and whether each person responds consistently to different vaccine components or to the same component in different years. To answer these questions, we established the DRIVE-I study, a randomized, placebo-controlled trial of repeated influenza vaccination in healthy adults 18-49 years old in Hong Kong. We analyzed hemagglutination inhibition (HAI) and neutralization titers (FRNT) at 0, 30 and 182 days after vaccination. We found that vaccine-induced antibody boosts were smaller in people with higher pre-vaccination titers, but prior vaccination reduced the boost beyond this “antibody ceiling” effect: for the same pre-vaccination titer, each prior vaccination reduced peak post-vaccination titers to some vaccine strains by up to 1.7 $\log_2$ units (95% CrI 1.5-2.0), contributing to higher titers in non-repeat compared with repeat vaccinees for up to a year after vaccination. These results show that prior vaccination is associated with reduced vaccine responses (and post-vaccination titers for some strains in some years) after accounting for differences in pre-vaccination titers between repeat vaccinees and first-time vaccinees.

Day 1	Plenary Session 2
11:40	**Evolving Applications of Serology: From tracking SARS-CoV-2 exposure to exploring post-pandemic immunity gaps in Aotearoa New Zealand**
Speaker	Nikki Moreland, Auckland Uni., Auckland, NZ

Authors
Nikki Moreland[1], Reuben McGregor[1], Natalie Lorenz[1], Lauren Carlton[1], Alex James[2], Michael Baker[3], Richard Charlewood[4]

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Abstract
New Zealand (NZ) followed an elimination strategy during the COVID-19 pandemic, avoiding major health impacts of SARS-CoV-2 with stringent border controls, intermittent lock-downs and other non-pharmaceutical interventions. Immunological enquiry complemented these efforts including our development of sensitive and specific serological assays to detect Sars-Cov-2 antibodies. These assays enabled estimation of past infections, including asymptomatic and undiagnosed cases, and contributed to NZ's science-led response. A nationwide serosurvey of nearly 10,000 donors in late 2020 revealed an exceptionally low seroprevalence (0.103%), confirming minimal community transmission and validating the success of the elimination strategy. Building on this foundation we have since applied these assays to investigate antibody half-life, vaccine induced responses in both NZ and Fiji and most recently to post-pandemic immune dynamics and shifts in susceptibility to respiratory pathogens. Following the easing of restrictions, notable surges in infections such as respiratory syncytial virus (RSV) and Group A *Streptococcus* have been observed. Ongoing work is examining how waning immunity and "immunity gaps" caused by reduced exposure during the pandemic may have contributed to these trends. This illustrates how serological surveillance can evolve from pandemic response to broader population-level monitoring and provide insights for preparedness of future respiratory disease threats.

Day 1	Plenary Session 2
12:00	**COVID-19 vaccine effectiveness and impact on mortality in Australia**
Speaker	Bette Liu, NCIRS, Sydney, NSW

Authors
Bette Liu [1]

Abstract
As the severe acute respiratory coronavirus 2 (SARS-CoV-2) evolves, monitoring of COVID-19 vaccine effectiveness and vaccine impact on disease-specific outcomes is needed to inform public health decision-making. This presentation will outline monitoring of COVID-19 vaccine effectiveness against COVID-19 mortality in the whole Australian population aged 65+ years since 2022, including recent estimates of the effectiveness of the JN.1 COVID-19 vaccine and the changing impact of vaccination.

Day 1	Plenary Session 2
12:20	**The Victorian RSV Program Journey: Lessons from Early Implementation**
Speaker	Shidan Tosif, RCH, MCRI, Melbourne

Authors
Shidan Tosif[1,2,3,] Alissa McMinn1, Nigel Crawford[1,2,3]
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1. SAEFVIC, Infection and Immunity, Murdoch Childrens Research Institute, Parkville, Victoria, Australia
2. Department of Immunisation, Royal Childrens Hospital Melbourne, Parkville, Victoria, Australia
3. Department of Paediatrics, University of Melbourne, Parkville, Victoria, Australia

Abstract
Respiratory syncytial virus (RSV) remains one of the leading causes of hospitalisation in infants and young children. With the recent availability of long-acting monoclonal antibodies and maternal vaccines, Australia is entering a new era of RSV prevention. This presentation outlines Victoria's approach to implementing RSV program and will highlight the lessons learned from initial rollout phases.

Day 1	Plenary Session 2
12:40	**RSV Maternal Vaccination: the UK Experience**
Speaker	Thomas Williams, University of Edinburgh, Scotland

Authors

Thomas Williams[1]
Affiliations
1. Department of Child Life and Health, University of Edinburgh, United Kingdom.
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Abstract
In August/September 2024, the United Kingdom rolled out universal maternal vaccination for respiratory syncytial virus (RSVpreF), with all pregnant women at 28 weeks or more of gestation eligible. At the same time, we launched the BronchStop study, a multicentre, test-negative, case-control study to analyse the vaccine effectiveness of maternal RSVpreF vaccination against the primary outcome of hospitalisation for RSV-associated acute lower respiratory infection (ALRI) in infants. Included patients were infants with ALRI born after Aug 12, 2024 (Scotland), and Sept 1, 2024 (England), and therefore had mothers eligible for maternal vaccination, who were admitted to 30 hospital sites across the UK from Sept 30, 2024, to Jan 20, 2025, and tested for RSV. Infants were followed up until hospital discharge or death as an inpatient. Primary vaccine effectiveness of maternal RSVpreF vaccination against RSV-associated hospitalisation was calculated with the use of a conditional logistic regression adjusted by site, calendar month of hospital attendance for the infant, age, preterm birth, and sex. We included 537 mother–infant pairs in our analysis, in whom there were 391 RSV-positive infant cases (median age 1·63 months [IQR 0·94–2·26]) and 146 RSV-negative infant controls (1·41 months [0·77–2·03]).We found that the adjusted effectiveness of maternal RSVpreF vaccination for preventing infant hospitalisation was 58% (95% CI 28–75) for infants whose mothers were vaccinated at any time before delivery and 72% (48–85) for infants whose mothers were vaccinated more than 14 days before delivery (39 [11%] of 357 RSV-positive cases vs 43 [33%] of 129 RSV-negative controls). In my talk I will describe the conduct of the study, future plans for the BronchStop Collaboration, and challenges to increasing the uptake of maternal RSVpreF in a UK setting.

Day 1	Plenary Session 3
13:45	**Inferring effects of mutations on SARS-CoV-2 transmission from genomic surveillance data**
Speaker	Ahmed Quadeer, University of Melbourne DMI

Authors
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[4]Department of Microbiology and Immunology, University of Melbourne, at The Peter Doherty Institute for Infection and Immunity, Melbourne, Victoria, Australia.
[5]Department of Physics and Astronomy, University of Pittsburgh, USA.
[6]Department of Computational and Systems Biology, University of Pittsburgh School of Medicine, USA.
*Passed away on July 6, 2025
Abstract
New and more transmissible variants of SARS-CoV-2 have arisen multiple times over the course of the pandemic. Rapidly identifying mutations that affect transmission could facilitate outbreak control efforts and highlight new variants that warrant further study. Here [1], we develop an analytical path integral model that infers the transmission effects of mutations from genomic surveillance data. Applying our model to SARS-CoV-2 data across many regions, we find multiple mutations that substantially affect the transmission rate, both within and outside the Spike protein. The strongly selected mutations we infer for SARS-CoV-2 are supported by experimental evidence regarding their effects on neutralizing antibody escape, T cell/immune evasion, replication/infectivity, cell entry, and structure/cleavage (**Figure 1**). Importantly, our model detects lineages with increased transmission even at low frequencies. As an example, we infer significant transmission advantages for the Alpha, Delta, and Omicron variants shortly after their appearances in regional data, when their local frequencies were only around 1-2%. Our model thus facilitates the rapid identification of variants and mutations that affect transmission from genomic surveillance data.

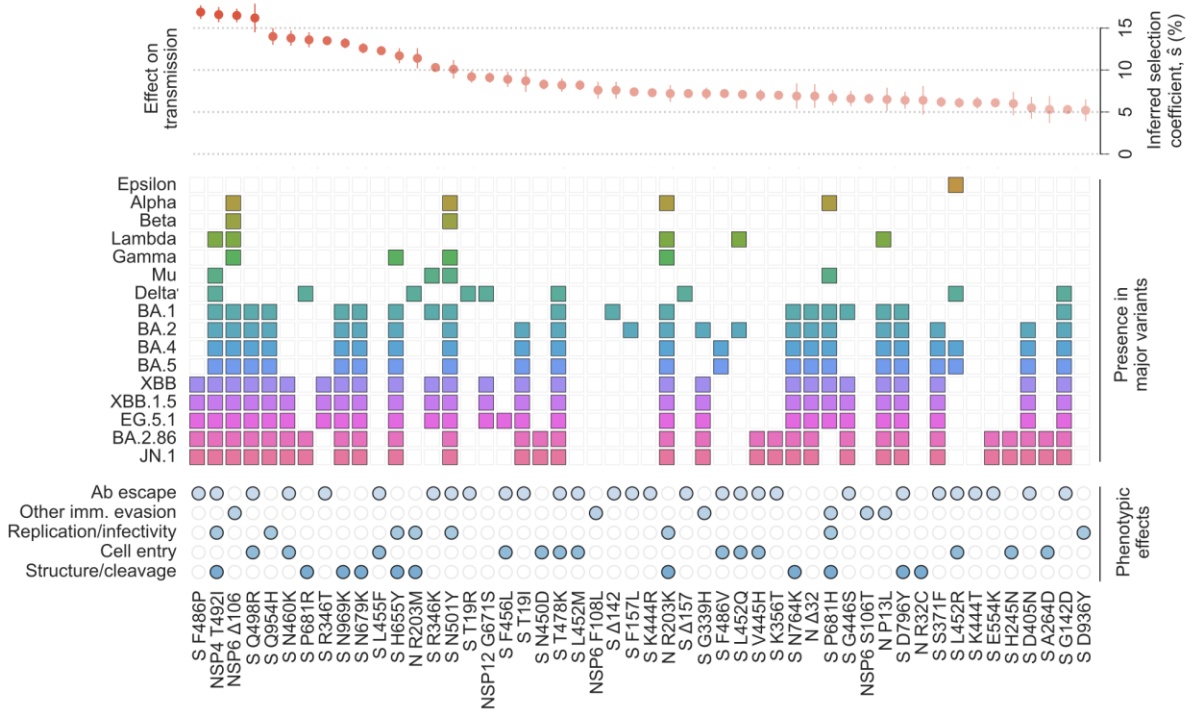

Figure 1: Top 50 mutations/deletions inferred to increase SARS-CoV-2 transmission the most. The top panel shows their inferred selection coefficients, the middle panel shows the major variants in which they are observed, and the bottom panel shows their phenotypic effects reported in the literature.
[1] Lee, B. et al. Inferring effects of mutations on SARS-CoV-2 transmission from genomic surveillance data. *Nature Communications* 16, 441 (2025).

Day 1	Plenary Session 3
14:00	**Development of a novel long-acting pan-antiviral to influenza**
Speaker	Saira Hussain, WHOCC Doherty Institute, Melbourne

Authors
Saira Hussain[1,2], Charley McKenzie Kludas[2], Ashwin Muraleetharan[1], Paul Jones[3], Wen-Yang Wu[3], Francesca Mercuri[2], Betty Jin[3], Peter Jenkins[3], Jennifer McKimm-Breschkin[2], Lorena Brown[2], Ian Barr[1,2], Kanta Subbarao[2]
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[3] AusBio Ltd. Melbourne VIC, Australia
Abstract
Antiviral drugs can be used as first-line countermeasures against emerging pandemic influenza strains while vaccine development is underway. Widespread reduced susceptibility to licensed antivirals such as oseltamivir and the adamantanes has previously occurred, highlighting the need to develop novel drugs. We tested a new compound MD-X from Aus Bio Ltd, which has a modular structure and a dual mode of action. This compound possesses an effector domain that creates an acidic microenvironment mimicking the low pH found inside the endosome. This domain induces an irreversible pH dependent conformational change in the haemagglutinin and prevents attachment of the virus. The acidic effector domain has been linked to a zanamivir anchoring domain to facilitate attachment to virions via the neuraminidase (NA). The anchor not only provides proximity for the effector domain, but also suppresses the enzymatic activity of the NA that prevents spread of progeny virions, like a traditional NA inhibitor (NAI). The compound showed efficacy in the low nanomolar (nM) range *in vitro* 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 influenzas A(H3N8) and A(H5N1), respectively, and also against viruses showing reduced susceptibility to current drugs, oseltamivir and baloxavir. *In vitro*, the compound showed superior inhibition when compared to oseltamivir and zanamivir. Mice infected with a lethal challenge were completely protected from mortality and clinical signs, except some weight loss, when the compound was administered 25 days before or 48 hours after infection. MD-X

shows promise as an effective influenza antiviral for prophylaxis after a single dose and could fill a gap in our pandemic response.

Day 1	Plenary Session 3
14:15	**Analysis of H5NX Avian influenza diffusion, evolution and recombination in South-East Asia**
Speaker	Callum Lay, ACDP, CSIRO, Geelong

Authors
Callum Le Lay[1], Edna Felipe, Vicky Stevens[1], Pat Mileto[1], Kelly Davies[1], Ivano Broz[1], Matthew Neave[1], Frank Wong[1]
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2. Bureau of Animal Industry, Philippines

Abstract
We analyzed 504 gene segment sequences of highly pathogenic avian influenza (HPAI) H5NX viruses collected in the Philippines through outbreak investigations and active surveillance between 2017 and 2023. Ninety complete hemagglutinin (HA) genomes were included in the primary dataset, of which 64 also contained neuraminidase (NA) segments and 33 were complete across all eight gene segments. Phylogenetic analysis revealed two distinct epidemic waves: the first caused by clade 2.3.4.4e (H5N6) circulating locally from 2017 to 2021, and the second by clade 2.3.4.4b (H5N1) comprising two outbreak clusters detected during 2022–2023.

The 2.3.4.4e lineage persisted with a largely stable genome constellation, except for a 2020 sub-clade that acquired divergent polymerase complex and matrix segments. Subsequent 2.3.4.4b viruses retained conserved internal gene constellations, showing limited reassortment and no direct exchange with the earlier endemic 2.3.4.4e lineage.

This study expands the available genomic data for the Philippines more than fifteenfold and highlights the country's role as a regional interface for avian influenza transmission. The results provide a foundation for improved genomic surveillance, reassortment tracking, and regional risk assessment of HPAI in Southeast Asia.

Day 1	Plenary Session 3
14:30	**Antigenic evolution of the influenza B virus hemagglutinin over 81 years**
Speaker	Lara Schwab, University of Melbourne

Authors
Lara Schwab[1], Ruopeng Xie[2,3], Ellie Reilly[1], Malet Aban[4,] Shu Hu[2,3], Natalie Spirason[4], Yi-Mo Deng[4,] Randy Suryadinata[5,6], Matthew Gartner[1], Kanta Subbarao[1,4,] Karen Laurie[7,] Steve Rockman[7], Stephen Kent[1,8,] Adam Wheatley[1,] Ian Barr[4], Vijaykrishna Dhanasekaran[2,3], Marios Koutsakos[1]
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4. WHO Collaborating Centre for Reference and Research on Influenza, Doherty Institute, Australia
5. Department of Respiratory Medicine, Royal Children's Hospital, Parkville, Australia
6. Infection and Immunity, Murdoch Children's Research Institute, Royal Children's Hospital, Australia
7. Seqirus Ltd, Parkville, Victoria, Australia
8. Melbourne Sexual Health Centre and Department of Infectious Diseases, Alfred Hospital and Central Clinical School, Monash University, Melbourne, Victoria, Australia

Abstract
Background: Influenza B viruses (IBV) were first identified in humans over 80 years ago and contribute to seasonal epidemic outbreaks. Although IBV evolves at a lower rate than Influenza A virus (IAV), antigenic changes in IBV haemagglutinin (HA) constantly accumulate, resulting in the need for annual vaccine updates. The evolutionary processes that drive IBV HA mutations are not fully resolved.

Methods: We applied antigenic cartography using haemagglutination inhibition (HAI) data from 50 ferret antisera and 253 IBV isolates (1940-2021) and integrated it with phylogenetic analyses of >400 IBV HA sequences. Pairing antigenic and amino acid sequence data, we identified antigenic cluster-defining mutations in the HA. We evaluated the fitness effects of cluster-defining mutations in air-liquid-interface (ALI) human airway cell cultures from the upper and lower respiratory tract. We also evaluated how population immunity influences IBV HA mutations, by performing HAI assays of human sera against IBV mutants with cluster defining mutations.
Results: We found that IBV HA followed a continuous genetic diversification which was accompanied by punctuated antigenic changes, resulting in appearance of 13 antigenic clusters over the last 81 years. These clusters did not follow a linear path in antigenic space, and were mainly driven by <10 positions near the receptor binding (136, 150, 162-167 and 203). These residues formed complex epistatic networks and re-appeared during 81 years of viral evolution, highlighting the impact of mutation recycling. Several mutations generated a permissive backbone via epistatic interactions on which immune escape emerged without a replicative fitness cost.
Conclusion: We deciphered the molecular basis of IBV antigenic evolution and identified important similarities and differences with that of A/H3N2. Our work will help to predict the emergence of new antigenic variants and will inform on future vaccine designs.

Day 1	Plenary Session 3
14:45	**Antigenic characterisation of Australian H7 highly pathogenic avian influenza virus under immunological pressure**
Speaker	Maddy Belfrage, ACDP, CSIRO, Geelong

Authors
Madeline Belfrage[1], Vicky Stevens[1], Frank Y. K. Wong[1] and Jasmina M. Luczo[1]
Affiliations
[1]CSIRO, Australian Centre for Disease Preparedness, Geelong, Victoria, Australia
Abstract
H7 high pathogenicity avian influenza viruses (HPAIVs) pose a significant threat to avian health. H7 HPAIV outbreaks have severely impacted the Australian poultry industry and have resulted in significant socioeconomic losses, as exemplified by the 2024 and 2025 H7 HPAIV outbreaks.
Avian influenza viruses (AIV) evolve antigenically to evade the host immune response. Antigenic drift describes the accumulation of substitutions in antigenic epitopes that result in immune escape. The AIV surface glycoproteins, hemagglutinin (HA) and neuraminidase (NA) are the primary targets of the host immune response and antigenic drift is monitored to inform the evolution of AIV lineages.
In this study, we characterised the antigenic drift of A/chicken/NSW/2012 H7N7 HPAIV HA and NA under immunological pressure. H7N7 HPAIV was incubated with increasing concentrations of homologous chicken polyclonal antisera or naïve chicken serum before passaging in embryonated chicken eggs. Viral genetic diversity was monitored by next generation sequencing to determine changes in regions encoding antigenic epitopes followed by antigenic characterisation to understand the impact of these changes.
Sequencing revealed that the immune escape virus had substitutions in antigenic sites A, B and D of the HA glycoprotein and substitutions in variable segments I and VII of the NA glycoprotein. The antigenic characteristics of the parental and immune escape viruses were compared using hemagglutinin inhibition assay. A loss in haemagglutination inhibition titre was observed for the immune escape virus, suggesting that the immune escape virus had evolved to evade inhibition by homologous antisera more effectively than the parental virus.
Given the continued threat H7 viruses pose to Australia's poultry industry, this data informs the antigenic architecture of Australian H7 AIVs, the development of vaccines, and helps us forecast the antigenic drift of H7 AIVs.

Day 1	Plenary Session 3
15:00	**Novel methods to rapidly perform genomic epidemiology on a broad spectrum of respiratory pathogens**
Speaker	Rebecca Rockett, Westmead Hospital, Sydney

Authors
Rebecca J Rockett[1,2], Tanya Golubchik[1,2] Kingsley King-Gee Tam[1,2], Winkie Fong[1,2], Carl J E Suster[1,2], Kerri Basile[1,2,3], Vitali Sintchenko[1,2,3], and Jen Kok[1,2,3]
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Abstract

The ability to rapidly sequence the genomes of respiratory pathogens has revolutionised molecular epidemiology—enhancing our understanding of disease transmission, pathogen evolution, antimicrobial resistance, and potential reductions in vaccine effectiveness. However, sequencing protocols often vary between organisms, frequently requiring pathogen-specific culture or whole genome amplification. These laboratory complexities limit the rapid application of genomics across the wide array of respiratory pathogens, especially during surges in viruses such as respiratory syncytial virus (RSV), human metapneumovirus (hMPV), and coronavirus disease 2019 (COVID-19), as well as bacterial pathogens like *Bordetella pertussis*, *Mycoplasma pneumoniae*, and *Chlamydia pneumoniae*.

One proposed solution is the use of hybridisation-based approaches to enrich nucleic acids from target genomes using biotinylated probes that tile across the genomes of interest. These probe-based techniques have long been used in human genomics to selectively sequence genes associated with tumourigenesis and resistance to cancer therapies. Hybridisation offers several advantages over amplification-based methods: probes require less homology with the target sequence and do not interact with each other, enabling simultaneous capture of millions of bases.

In this study, we demonstrate the utility of capture-based methodologies to streamline genomic workflows and enable rapid genomic epidemiology for Influenza, COVID-19, hMPV, *B. pertussis*, and *M. pneumoniae*, while also highlighting implementation challenges and innovations.

We utilised both commercial and custom hybridisation panels to conduct genomic epidemiology studies following surges in Influenza A (n=180, 2022), hMPV (n=120, 2024), *B. pertussis* (n=255, 2024), and *M. pneumoniae* (n=322, 2024). Whole genome recovery rates were 75% (117/157), 90% (108/120), 61% (146/241), and 39% (124/322), respectively, from specimens confirmed positive by PCR. Recovery correlated with pathogen load, with whole genome recovery from specimens with PCR cycle threshold (Ct) values <25 reaching 90% (103/114), 93% (70/75), 69% (116/169), and 62% (78/126), enabling laboratories to better target sequencing efforts.

Additional predictors of genome recovery were identified, particularly for bacterial pathogens, including nucleic acid extraction purity and challenges in balancing capture pools to prevent high-load samples from dominating sequencing outputs. Despite these barriers, hybridisation-based techniques successfully identified mutations conferring antimicrobial resistance, with high concordance to phenotypic susceptibility and PCR-based detection. Furthermore, these methods enabled phylogenomic analyses, including genotyping, quantification of viral reassortment, and co-detection.

This presentation will demonstrate how hybridisation-based capture methods can expand the use of genomics for a broader range of respiratory pathogens, supporting both technical innovation and public health response.

Day 1	Plenary Session 4
15:45	**National summary of the 2025 respiratory season and the Australian Respiratory Surveillance Report**
Speaker	Jenna Hassall & Lauren Kutzner, Australian Centre for Disease Control, Canberra

Authors

Jenna Hassall[1], Lauren Kutzner[1], Caitlin Trenorden[1] , Siobhan St George[1]

Affiliations

1. Viral Respiratory Diseases Epidemiology and Surveillance Section, interim Australian Centre for Disease Control, Australian Government Department of Health, Disability and Ageing

Abstract

The Australian Respiratory Surveillance Report draws on data from 9 surveillance systems, 5 sentinel laboratories and 2 national registers to describe acute respiratory infection trends in Australia. Using these data, we present a national summary of COVID-19, influenza and respiratory syncytial virus (RSV) in 2025 to date.

Community helpline calls for influenza-like illness (ILI) were consistent with historical trends until June, when ILI call rates exceeded those at the same time in 2023–2024. In contrast, self-reported fever and cough symptoms among community survey participants remained largely consistent with historical trends. In 2025, COVID-19 notifications declined about 32% from 2024. The winter peak occurred in June, consistent with 2024 and 2023. COVID-19 notification rates were highest in adults aged 70 years and over, and notification trends were similar across jurisdictions. Influenza notifications rose 18% from 2024, driven by elevated interseasonal activity, a prolonged June–August peak and slower decline in notifications than prior seasons. Influenza notification rates were highest in children aged 0–14 years, with all jurisdictions experiencing high notification rates from June–August, despite variation at other times. There has been a higher proportion of influenza B notifications this season than in 2024, particularly among children aged 5–19 years. In 2025, RSV notifications have been comparable to 2024 but higher than 2023. RSV notifications peaked in July, two months later than previous years, though trends were notably different across jurisdictions. RSV notification rates were highest in children aged 0–4, but there were 32% fewer notifications in those aged under 8 months than in 2024 and 27% fewer than in 2023, which may indicate impact of the national vaccination program.
At sentinel general practice sites, ILI consultations mirrored influenza notification trends, and the most commonly detected respiratory pathogens in those tested were rhinovirus and influenza. At sentinel hospitals, severe acute respiratory infection (SARI) admissions peaked across June and July, driven by a high number of influenza admissions during winter. Despite increased SARI admissions in 2025, the proportion admissions who died was not different from 2024.
At sentinel laboratories, SARS-CoV-2 positivity peaked in January with a smaller second peak in June, as in 2024. The SARS-CoV-2 recombinant lineage XEC dominated in early 2025, then shifted to NB.1.8.1. Influenza positivity peaked in July and declined more steeply than influenza notifications. Most influenza A(H1N1) and B/Victoria lineage isolates tested matched 2025 vaccine components; however, only 80% of A(H3N2) isolates were antigenically similar. RSV positivity peaked in August 2025, later than in notifications this season and in 2024.
Death registrations indicate COVID-19 remains the leading cause of respiratory infection deaths (2023–2025). Between January–July deaths involving COVID-19 (both due to and with) were lower than 2023–2024, deaths involving influenza were higher, and deaths involving RSV lower than 2024. Immunisation data shows COVID-19 vaccine coverage fell to 11%, while influenza vaccine coverage was 31%, both lower than in previous years. Over 130,000 maternal Abrysvo doses have been administered and nirsevimab uptake reached 20% among infants.
Overall, the 2025 respiratory season has had a moderate to high impact on the community and health care services, highlighting the need for improved vaccine uptake and continuous improvement of surveillance and reporting, including the Australian Respiratory Surveillance Report, to guide interventions.

Day 1	Plenary Session 4
16:05	**Real-time situational assessment of respiratory virus epidemics in Australia and New Zealand over winter 2025**
Speaker	Oliver Eales, University of Melbourne

Abstract
Case time-series — which are used to monitor epidemic activity — often exhibit substantial noise, and day-of-the-week effects that can limit visual interpretation of trends in the data. Statistical methods can quantify and account for different sources of noise, allowing meaningful trends in case time series (and their uncertainty) to be inferred and future trends to be predicted. From 16 May–3 October 2025 the Australia–Aotearoa Consortium for Epidemic Forecasting and Analytics (ACEFA), produced weekly situational assessments of respiratory virus activity across all eight Australian states and territories and New Zealand. This was the first year of nationwide reporting, following a pilot Situational Assessment Program in Victoria over winter 2024.
Weekly analyses were performed on case time series for SARS-CoV-2, RSV and influenza. Past and current trends — including real-time estimates of the growth rate, reproduction number, and doubling/halving times — were inferred for each pathogen using a statistical model. For influenza, type/subtype data were incorporated where available, using a statistical model that accounts for the distinct dynamics of influenza subtypes, to simultaneously infer trends for each influenza subtype. Multiple forecasting teams developed and used models to predict the short-term future trends in cases. Each team's forecasts were combined into an ensemble forecast that was included in weekly reports. In this presentation I will provide an overview of ACEFA's 2025 Situational Assessment Program and plans for future seasons.

Day 1	Roundtable discussion
16:30	**Should we focus on ameliorating the big 3 (seasonal influenza, RSV, SARS-CoV-2) instead of worrying about the next pandemic now that we have mRNA,?**
Panel	• Andy Bowman • David Speers • Emily Martin • Erik Karlsson • Michelle Wille • Nikki Moreland

Day 2	Plenary Session 5
8:30	**Options for co-administration of the AS01E-adjuvanted respiratory syncytial virus (RSV) prefusion F protein (adjuvanted RSVPreF3) vaccine with other adult vaccines: a review of existing data**
Speaker	Upasna Varma, GSK, Melbourne

Presented by: Upasna Varma
Authors
Nicolas Lecrenier[1], Frithjof Kosfeld[1], Kayhan Binazir[2], Paulia Kwo Ton Ge Jua[1], Hiwot Amare Hailemariam[1], Amulya Jayadev[3], Vicky Cárdenas[4]
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Abstract
Background: RSV disease in adults has been identified as a significant health concern. The adjuvanted RSVPreF3 vaccine is approved for the prevention of RSV-related lower respiratory tract disease (RSV-LRTD) in ≥60-year-olds in >65 countries and for 50–59-year-olds at increased risk for RSV-LRTD in most of these countries. Co-administration of vaccines allows immunisation against several diseases at a single healthcare provider (HCP) visit, with better management of healthcare resources as well as improved vaccine uptake. This review aims to consolidate available clinical data and national recommendations on co-administration of adjuvanted RSVPreF3 vaccine with other vaccines, providing an overview of immunogenicity, reactogenicity, and safety.
Methods: Co-administration of the adjuvanted RSVPreF3 vaccine with other adult vaccines was identified in 6 clinical trials (Table).[1-6] National recommendations on co-administration of the adjuvanted RSVPreF3 vaccine with other routine vaccines were obtained from relevant national recommendation websites/publications.
Results: In total, 4,599 participants, including 2,299 who received co-administered vaccines, were vaccinated across the 5 completed trials (Table).[1-5] Immune responses against RSV-A, RSV-B, and 27 antigens from 5 vaccines were non-inferior or without clinically relevant interference when the vaccines were coadministered versus sequential administration (SA).[1-5] No clinically meaningful differences in solicited local and systemic adverse events (AEs), unsolicited AEs, serious AEs or potential immune-mediated diseases were observed between co-administration and SA. The most common solicited local and systemic AEs were injection-site pain and myalgia/fatigue. Different national recommendations are currently in place, from no co-administration to co-administration with selected vaccines or with any other adult vaccines.
Conclusions: In most cases, the immunogenicity of the co-administered antigens was preserved, with a clinically acceptable safety profile, supporting the co-administration of the adjuvanted RSVPreF3 vaccine with other adult vaccines, which is recognised by several national recommendations. This review provides a summary of data supporting HCPs in their recommendation to routinely co-administer the adjuvanted RSVPreF3 vaccine with other currently licensed adult vaccines, which can enhance vaccination coverage and reduce healthcare resource use.
Acknowledgements Funding: GSK. Encore abstract from ESCMID Vaccines 2025

Table: Description of the 6 identified clinical trials on co-administration of the adjuvanted RSVPreF3 vaccine

Clinical trial	Co-administered vaccines	N participants	Age	Reference
Phase 3 open-label, multi-country study NCT04841577	Adjuvanted RSVPreF3 vaccine FLU-QIV	Co-ad: 442 Control: 443	≥60 YOA	1. Chandler R, et al. Clin Infect Dis 2024:ciad786
Phase 3 open-label, multi-country study NCT05586797	Adjuvanted RSVPreF3 vaccine FLU-aQV	Co-ad: 523 Control: 522	≥65 YOA	2. Clark R, et al. Clin Infect Dis 2024;79:1088–98
Phase 3 open-label study in the US NCT05559476	Adjuvanted RSVPreF3 vaccine FLU-qIV-HD	Co-ad: 516 Control: 513	≥65 YOA	3. Buynak R, et al. Infect Dis Ther 2024;13:1789–1805
Phase 3 open-label, multi-country study NCT05879107	Adjuvanted RSVPreF3 vaccine PCV-20	Co-ad: 553 Control: 557	≥60 YOA	4. Leroux-Roels I, et al. ESCMID

					2025;PS073/07983
Phase 3 open-label, multi-country study NCT05966090	Adjuvanted RSVPreF3 vaccine RZV	Co-ad: 265 Control: 265	≥50 YOA	5.	Dennis P, et al. EuGMS 2024;LB35
Phase 3 open-label, multi-country study NCT06374394	Adjuvanted RSVPreF3 vaccine COVID-19 mRNA vaccine	Ongoing: data not published yet	≥50 YOA	6.	https://clinicaltrials.gov/study/NCT06374394

FLU-QIV, seasonal quadrivalent influenza vaccine; **FLU-aQIV**, adjuvanted FLU-QIV; **FLU-QIV-HD**, high-dose FLU-QIV; **PCV-20,** 20-valent pneumococcal conjugate vaccine; **RZV,** adjuvanted recombinant zoster vaccine; **COVID-19 mRNA,** COVID-19 messenger ribonucleic acid; **YOA,** years of age

Day 2	Plenary Session 5
8:50	**The Molecular Clamp Platform: A broadly applicable solution to the manufacture of multipathogen subunit vaccines**
Speaker	Keith Chappel, University of Queensland

Abstract

Background: Respiratory syncytial virus (RSV), human metapneumovirus (hMPV) and parainfluenza virus 3 (PIV3) are medically important causes of respiratory tract infections. Combined these three viruses cause more severe disease and hospitalisations than influenza viruses. After more than 5 decades of unsuccessful research and development, vaccines have recently been approved for the prevention of lower respiratory tract disease caused by RSV, however vaccines for hMPV and PIV3 remain in early-stage development.

Objective: Vicebio seeks to develop easy to administer multi-pathogen vaccines to protect against respiratory viruses.

Methods: The second-generation molecular clamp platform, facilitates production of pre-fusion stabilized glycoproteins for RSV, hMPV and PIV3, and a diverse array of fusion glycoproteins from other viral families. The bivalent vaccine against RSV and hMPV (VXB-241) entered a phase I clinical trial in Q3 2024, with an interim readout planned for Q2 2025. The trivalent vaccine including RSV, hMPV and PIV3 (VXB-251), is on track to enter a phase I clinical trial in Q4 2025.

Results: Lead candidate subunit vaccines for RSV, hMPV and PIV3, have completed pre-clinical development and demonstrated all of which have demonstrated, high yield production using a universal manufacturing process and have shown to be highly stable in liquid formulation at 2-8°C. Head-to-head evaluation in mouse immunogenicity studies has demonstrated molecular clamp stabilised antigens are able to elicit a neutralising immune response that was superior or equivalent to the best-in-class comparator antigens for either RSV, hMPV and PIV3.

Conclusion: Vicebio's proprietary molecular clamp platform streamlines the production of multi-pathogen vaccines in ready-to-use, liquid-stable formulations, and thereby simplify administration while providing reliable protection against respiratory

Day 2	Plenary Session 5
9:10	**Live Attenuated Influenza Vaccine: Southern Hemisphere Nasal Spray Flu Vaccine for 2026**
Speaker	Merrin Tulloch, AstraZeneca, Australia

Authors

Merrin Tulloch[1]

Affiliations

1. AstraZeneca, 66 Talavera Road, Macquarie Park NSW 2113

Abstract

The Live Attenuated Influenza Vaccine is an intranasal needle free influenza vaccine. It has been available in the northern hemisphere since 2003, and will be supplied in the southern hemisphere for the first time in 2026. This presentation will discuss the composition, administration and immune responses to LAIV; safety profile; overseas experiences including vaccine effectiveness; and planned introduction to Australia next year.

Day 2	Plenary Session 5
9:30	**Combination COVID-19 and Influenza Vaccines: Development Landscape and Potential Public Health Implications**
Speaker	Najwa Ejje, Sanofi Australia

Authors
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Abstract
The convergence of COVID-19 and influenza presents unique challenges to global public health systems. This presentation explores the development of combination vaccines targeting both pathogens simultaneously, addressing the overlapping seasonality patterns and cumulative disease burden.
Sanofi's approach to combination vaccine combines established high-dose or recombinant influenza vaccines (Fluzone HD, Flublok) with a recombinant spike protein COVID-19 vaccine adjuvanted with Matrix-M. This strategy leverages proven platforms with evidence of improved protection versus standard-of-care influenza vaccines while addressing COVID-19 vaccine hesitancy through a profile designed to minimize side effects.
Current strain selection processes differ substantially between influenza and COVID-19. For combination vaccines, alignment of strain selection timing becomes critical, as delays in influenza strain selection beyond February could impact vaccine manufacturing timelines, potentially reducing vaccine availability and coverage.
Respiratory virus epidemiology continues to evolve, and the public health value of combinations likely derives from improved vaccination coverage rates and reduced barriers to vaccination. Rational, science-based decisions around strain selection processes are critical as combination respiratory vaccines advance through development. Broader discussions of their impact including on cardiovascular and other non-respiratory outcomes may be warranted, building on established evidence for influenza vaccination.

Day 2	Plenary Session 5
9:50	**The ABC of Flu Vaccines: Consideration for Innovation and Public Health**
Speaker	Jules Bayliss Sequris

Day 2	Plenary Session 5
10:10	**DAN-RSV: RSVpreF Vaccine for preventing cardiorespiratory hospitalisation**
Speaker	Tor Beiring -Sorensen University of Copenhagen

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Abstract

Background: Respiratory syncytial virus (RSV) can cause serious illness in older adults. The bivalent RSV prefusion F protein–based vaccine (RSVpreF) has been shown to prevent RSV-associated respiratory illness, but data from randomized trials with regard to its effect on outcomes involving hospitalization are limited. Methods: In this pragmatic, open-label trial with individual randomization, participants who were 60 years of age or older were assigned in a 1:1 ratio to receive the RSVpreF vaccine (the RSVpreF group) or no vaccine (the control group) during the 2024–2025 winter season. Baseline and outcome data were collected with the use of national registries. The primary end point was hospitalization for RSV-related respiratory tract disease. Secondary end points included hospitalization for RSV-related lower respiratory tract disease and hospitalization for respiratory tract disease from any cause. The prespecified criterion for success for the primary end point and RSV-related secondary end points was a minimum vaccine effectiveness of greater than 20%. Results: Of 131,379 participants who underwent randomization, 131,276 were included in the intention-to-treat population. During follow-up, hospitalization for RSV-related respiratory tract disease occurred in 3 of 65,642 participants in the RSVpreF group and in 18 of 65,634 participants in the control group (0.11 events vs. 0.66 events per 1000 participant-years; vaccine effectiveness, 83.3%; 95% confidence interval [CI], 42.9 to 96.9; P=0.007 for minimum effectiveness of >20%). The RSVpreF group also had fewer hospitalizations for RSV-related lower respiratory tract disease than the control group (1 vs. 12; vaccine effectiveness, 91.7%; 95% CI, 43.7 to 99.8; P=0.009 for minimum effectiveness of >20%), as well as fewer hospitalizations for respiratory tract disease from any cause (284 vs. 335; vaccine effectiveness, 15.2%; 95% CI, 0.5 to 27.9; P=0.04 for vaccine effectiveness of >0%). The incidence of serious adverse events was similar in the two groups. Conclusions: Among adults 60 years of age or older, the RSVpreF vaccine reduced the incidence of hospitalization for RSV-related respiratory tract disease as compared with no vaccine. (Funded by Pfizer; European Union Clinical Trials number, 2024-516600-42-00; DAN-RSV ClinicalTrials.gov number, NCT06684743.). Disclosures: This study was supported by Pfizer.

Day 2	Plenary Session 6
11:00	**Human metapneumovirus, the other respiratory paramyxovirus, incidence and genomic diversity during a pandemic era in Western Australia**
Speaker	David Speers, Pathwest, WA

Authors

David Speers[1,2,] Kritu Panta[1,3], Binit Lamichhane[1], Chisha Sikazwe[1,3,] David Foley[1,2,4]

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Abstract

In 2001, a previously unidentified paramyxovirus was found responsible for infections in children admitted to hospital with symptoms similar to those for respiratory syncytial virus (RSV). This agent was named human metapneumovirus (hMPV) to distinguish it from others in the Metapneumovirus genus of avian origin. hMPV is now recognized as a major cause of upper and lower respiratory infection.

Non-pharmaceutical interventions during the SARS-CoV-2 pandemic disrupted respiratory virus seasonality. We examined the seasonality and incidence of hMPV in Western Australia before, during and after the pandemic. Further to this, whole-genome sequencing of selected hMPV-positive samples was performed over this period using a tiled-amplicon approach to examine the influence of the pandemic interventions on hMPV diversity and the impact of the subsequent removal of these interventions.

There are several vaccine candidates for hMPV under development, including the use of attenuated strains, mRNA and vector-based platforms, and subunit vaccines, and there is the prospect for bivalent RSV/hMPV vaccines.

Understanding the genomic diversity, particularly within the immunodominant F protein, will be critical to antigen selection for optimal cross-neutralising antibody responses and thus the efficacy of these candidate vaccines.

Day 2	Plenary Session 6
11:20	**Evolving Capacity and Challenges in Wastewater Surveillance for Respiratory Viruses**
Speaker	Avram Levy, Pathwest, WA

Authors
Avram Levy
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2. Adjunct Associate Professor, School of Biomedical Sciences, University of Western Australia.

Abstract
Wastewater surveillance was broadly adopted for respiratory viruses post-COVID, proving complementary to existing disease surveillance systems while adding powerful new population-level insights. Applications evolved from qualitative trend analyses to quantitative pathogen load estimates and viral characterisation for lineage distribution and source attribution. With the technology now proven and wastewater recognised as a uniquely representative sample type, opportunities exist for integrated, multi-pathogen surveillance systems that are cost-effective, scalable, and capable of supporting real-time health response across sectors. However, considerable technical, logistical, and interpretive challenges remain.
This talk will outline current capacity in wastewater-based surveillance with a focus on respiratory pathogens, highlighting lessons from implementation and considering strategies to address persistent bottlenecks. Emphasis will be placed on translating wastewater-derived data into actionable intelligence and on building sustainable systems to inform health risk decision-making

Day 2	Plenary Session 6
11:40	**The first Australian Influenza Controlled Human Infection Study (CHIM): Immune Correlates of Viral Clearance and Symptoms**
Speaker	Annette Fox, WHO CC, Melbourne, Victoria

Authors
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Abstract
Correlates of protection are needed to advance vaccine development, particularly when efficacy trials are not feasible, such as for vaccines targeting future pandemic viruses. Controlled Human Infection Model (CHIM) studies are considered to be a valuable option for establishing such correlates because pathogen exposure can be precisely controlled and standardised across participants. However, the outcomes selected and the extent to which experimental inoculation reflects natural exposure may influence how immune responses mediate or correlate with protection. Here we present preliminary results of the first Australian FluCHIM in the context of previous influenza CHIM (FluCHIM) studies that identify different correlates of protection depending on their design.
The primary objective of our FluCHIM study was to determine influenza attack rates following intranasal challenge with 10^6 $TCID_{50}$ of a recombinant A/Texas/71/2017 (H3N2) virus. Exploratory analyses examined correlations between immune responses, virus shedding and symptoms. Eleven healthy adults aged 18-50 years with baseline serum hemagglutination inhibition (HAI) antibody titres ≤ 1:40 against challenge-like virus were

inoculated between May – June 2025. Nasopharyngeal swabs were collected daily for seven days post-inoculation; blood and nasal lining fluid were collected on days 0, 3, 7, 14, 56, and 168 to assess influenza hemagglutinin (HA) and neuraminidase (NA)-reactive antibody and B-cell responses.
Ten participants (91%) shed influenza RNA on more than one day; seven had a Modified Jackson Score of ≥6 (symptomatic), while three remained below this symptom threshold. Six of the ten participants with viral shedding had a ≥4-fold rise in HAI titres consistent with seroconversion. The remaining participant reported symptoms and met seroconversion criteria but did not shed viral RNA. Whole-blood flow cytometry demonstrated mean fold-rises by day 7 of 3.2 (range 1.1-8.1) for plasmablasts, and 3.0 (range 0.8-9.1) for activated CD8+ T cells, which were associated with an antibody response and symptoms, respectively. Pre-challenge NA inhibiting (NAI) antibody titres correlated weakly with the duration of infectious virus shedding but not with other outcomes. Only two participants demonstrated increases in serum NAI antibody titres, along with rises in peripheral blood NA-reactive B cells, whereas increases in HA-reactive B cells were more commonly seen across the challenge cohort.
These findings improve our understanding of systemic correlates of protection, while highlighting the need to integrate mucosal immunity, and its association with protection, into future FluCHIM studies to refine models relevant to emerging pandemic threats.

Day 2	Plenary Session 6
12:00	**Viral Cartography: Tracing Influenza's Cellar Imprint**
Speaker	Arutha Kulasinghe, Uni Queensland, Brisbane

Author
Arutha Kulasinghe
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Abstract
Background: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) which emerged in late 2019 has spread globally, causing a pandemic of respiratory illness. A better definition of the host response to SARS-CoV-2 infection is required to understand viral pathogenesis and to validate putative COVID-19 biomarkers that have been proposed in clinical studies.
Methods: Here, we used spatial transcriptomics, proteomics and H&E assessments of formalin-fixed paraffin-embedded tissue to generate an in-depth picture of the pulmonary, cardiac and brain transcriptional landscape of COVID-19 with contrasts to pandemic H1N1 influenza and uninfected control patients.
Results: Host transcriptomics showed a significant upregulation of genes associated with inflammation, type I interferon production, coagulation and angiogenesis in the lungs of COVID-19 patients compared to non-infected controls. SARS-CoV-2 was non-uniformly distributed in lungs with the areas of high viral load associated with an increased type I interferon response. Strikingly, the interferon-associated gene *IFI27*, previously identified as a useful blood biomarker to differentiate bacterial and viral lung infections, was significantly upregulated in the lungs of COVID-19 patients compared to patients with influenza.
Conclusion: Collectively, these data demonstrate that spatial transcriptomics is a powerful tool to identify novel gene signatures within tissues, offering new insights into the pathogenesis of SARS-COV-2 to aid in patient triage and treatment.

Day 2	Plenary Session 7
13:00	**Relative Effectiveness of Cell-Based Versus Egg-Based Quadrivalent Influenza Vaccines Across Paediatric Populations During the 2023-24 Influenza Season in the United States and Public Health Impact on Australia."**
Speaker	Jules Bayliss, Seqirus, Melbourne

Authors
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Abstract
Background: Egg-adaptive mutations occurring during egg-based influenza vaccine manufacturing can alter the antigenicity of the vaccine virus, contributing to reduced effectiveness. Previous studies have demonstrated improved effectiveness of cell-based (QIVc) versus standard-dose, egg-based (QIVe) quadrivalent influenza vaccines in the 2017-18 to 2019-20 and 2022-23 seasons in the United States. In Australia, QIVc was first registered in 2020 has been licensed for children and adults ≥6 months since 2023. Here, we report relative vaccine effectiveness (rVE) for the 2023-24 season in children aged 6 months to 17 years in the United States.
Methods: We used linked data combining electronic health records, medical and pharmacy claims, and laboratory tests from multiple sources in the United States. A retrospective test-negative design was applied among children aged 6 months to 17 years vaccinated with either QIVc or QIVe in 2023-24, who had an influenza test obtained within 7 days of an acute respiratory or febrile illness. rVE was estimated using a doubly robust logistic regression analysis for all children, younger children aged 6 months to 8 years, and older children aged 9 to 17 years.
Results: The dataset included 60,990 vaccinated and influenza-tested paediatric patients, of whom 7,194 (11.8%) received QIVc and 53,796 (88.2%) received QIVe. QIVc was significantly more effective than QIVe in preventing test-confirmed influenza in the full paediatric population, with an estimated rVE of 19.6% (95% CI: 13.6–25.3%). Consistent rVE results were observed across both paediatric age subgroups.
Conclusions: This study demonstrates superior effectiveness of QIVc compared to QIVe in preventing test-confirmed influenza in paediatric populations during the 2023-24 season in the United States. Substantial influenza burden could be prevented by use of cell-based instead of egg-based influenza vaccines in the paediatric population.

Day 2	Plenary Session 7
13:15	**Cost-effectiveness of immunising interventions to reduce respiratory syncytial virus disease burden in infants in Australia**
Speaker	Julian Carlin, University of Melbourne

Authors
Julian B. Carlin[1], Adrian J. Marcato[1], Yingying Wang[2], Robert Moss[2], Kylie S. Carville[1, 3], Xinghui Chen[1, 2], Victoria L. Oliver[2], Violeta Spirkoska[1], Patricia T. Campbell[1], David J. Price[1, 2], Natalie Carvalho[2], Jodie McVernon[1, 3]
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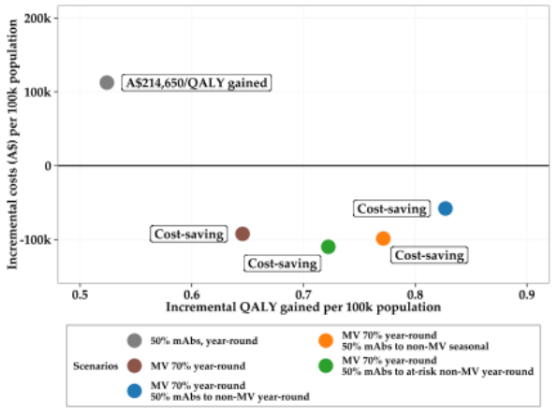
Abstract
Two immunising products are emerging to prevent the burden of respiratory syncytial virus (RSV) in infants: long-lasting monoclonal antibodies (mAbs) and maternal vaccines given during pregnancy (MV). We assessed the potential cost-effectiveness of programs involving each product, to help inform policy decisions related to their implementation in Australia.
We developed an individual-based dynamic transmission model of RSV infection, linked to a clinical pathways model and cost-effectiveness model. We modelled key scenarios exploring varying eligibility and coverage of immunisation

products for at-risk and not-at-risk populations, in addition to sensitivity analyses of immunisation characteristics, program costs, and the impact of potential under-ascertainment of RSV burden. We estimated the cost-effectiveness of each program from a health system perspective, with results presented as incremental cost-effectiveness ratios in terms of cost per quality-adjusted life year gained (QALY).

We found a combined program in which administration of MV during pregnancy is supplemented with a birth-dose of mAbs for newborns born without protection from MV is likely to be cost-saving, compared to the status quo of no MV or mAbs delivered. This program averted on average 41% of infant hospitalisations per year and reduced QALY losses by 33%.

Programs combining infant immunisation products are likely to significantly reduce the burden of RSV disease in Australia, and be cost-saving. However, their estimated impact and cost-effectiveness is strongly dependent on key assumptions i) the consistency and completeness of ascertainment of disease burden over time; ii) the cost of a hospitalisation and immunising dose; iii) the efficacy and durability of protection of the modelled products, and; iv) the timing and coverage of the immunisation delivery.



Day 2	Plenary Session 7
13:30	**Australia's new incubator for vaccine and infectious disease innovation**
Speaker	Jenny Herz, Biointelect, Sydney

Authors
Leanne Hobbs[1], Jennifer Herz[12]
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1. Biointelect Venture, Biointelect Pty LTD
2. Biointelect Pty LTD

Abstract
Australia produces world-class research, yet faces persistent translational challenges that limit commercialisation and real-world impact. Systemic barriers include strong research output but low commercialisation outcomes, limited collaboration between research institutions and industry, under-support for SMEs to access funding, infrastructure, and expertise, funding skewed toward early discovery, fragmented and complex funding schemes, and insufficient training in commercialisation and product development requirements[1]

Vaccines and infectious diseases - areas in which Australia's scientific capability is internationally recognised - exemplify these challenges, particularly as not all infectious disease interventions present compelling returns on investment for the private sector. Since 2000, more than 600 vaccine-related technologies have been patented and over 100 clinical trials have been conducted in Australia, yet only a single vaccine has reached market[2]. Most projects remain concentrated at Technology Readiness Levels (TRLs) 2–5, with few advancing beyond proof-of-concept.

Despite Australia's established strengths in infectious disease research and immunology, this potential has not been fully realised through successful translation and commercialisation. With the growing threat of antimicrobial resistance and lessons from recent pandemics, infectious disease preparedness and vaccine development have become global priorities. Strengthening translation will be critical to ensure Australian research delivers tangible health impact locally, regionally, and globally.

[1] Department of Industry, Science and Resources. (2025). Strategic examination of R&D: discussion paper consultation findings and analysis. Australian Government.
[2] Biointelect. (2024). Australia's Vaccine Value Chain Conference. [Unpublished presentation]. Biointelect Pty Ltd.

The inaugural Australian Vaccine Value Chain Conference (AVVCC24), which convened over 215 key opinion leaders across academia, industry, government, and investors, reinforced these findings[3]. Its outputs called for stronger national coordination, clearer roles and accountabilities, greater engagement of end users across the whole value chain, and the establishment of public–private partnerships to accelerate translation, commercialisation, and equitable access.

In response, the Medical Research Future Fund has funded, under the BiomedTech Incubator Grant Opportunity, *Biointelect Venturer (BV)*. BV is a new national, virtual incubator dedicated to accelerating vaccines, vaccine-related technologies and immunotherapies for the prevention of infectious diseases. Over four years, BV will deploy $25 million in direct SME and spinout support to address the translational "valley of death" at TRLs 2–6, where traditional grants rarely apply and private capital is not yet engaged. Beyond funding, BV provides structured support in translational planning, regulatory and clinical strategy, non-clinical studies, and early-phase trials, complemented by expert mentorship, project consultants, targeted masterclasses, and facilitated access to investors and enabling infrastructure. This integrated model is designed to convert early breakthroughs into investment-ready opportunities and attract follow-on funding. By supporting technologies with strong commercial potential as well as those with clear global health benefit, BV ensures that investments deliver societal value while building a sustainable pipeline of innovation.

BV aligns with several recent national policy priorities and strategies1 , which emphasise sovereign capability, pandemic preparedness, preventive health, community engagement and more coordinated national investment. By addressing translational gaps and integrating AVVCC insights, BV aims to bridge the valley of death between discovery and market, enhance sustainability of innovation, and ensure Australian breakthroughs deliver both societal and global health benefits.

Day 2	Plenary Session 7
13:45	**Epidemiology of respiratory syncytial virus (RSV) within a New South Wales-based multi-centre health district between 2018-2024 in Australia**
Speaker	Zubair Akhtar, Kirby Institute, Sydney

Authors

Akhtar, Z.[1], Notaras, A.[1], Tawfiq, E.[1], Kunasekaran, M.[1], MacIntyre, C.R.[1], Rawlinson, W.[2,3], Walker, G.[2,3]

Affiliations

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Abstract

Background: RSV epidemiology in Australia is unclear given recent advances in diagnostic testing, COVID-19 interventions and under-recognition in older adults. Data is needed to inform new RSV vaccine use.

Methods: We analysed laboratory data from all viral respiratory RT-qPCR diagnostic tests conducted at NSW Health Pathology in the South-Eastern Sydney and Illawarra Health Service from 2018-2024. Panel and descriptive analyses were used to report annual RSV testing and detection by age group, care setting, and co-infection with other respiratory viruses using Stata v.18.

Results: Of 370,126 unique episodes tested for RSV, there were 13,293 (3.6%) detections across all age groups (Table 1). Public health measures for COVID-19 significantly impacted RSV circulation in 2020, with detections near-absent in the winter season (June-August), and an off-season epidemic occurring in the summer. Annual testing and detection peaked in 2022, and was considerably higher compared to pre-pandemic years (testing 6.3-fold and detection 3.4-fold higher than 2019, respectively). Across the study period, incidence was highest in children <5 years (1,613 per 100,000 population). Among older adults (≥60 years age), the prevalence was 125 per 100,000. Testing was primarily performed in outpatients (71%), of which emergency departments were the most frequent care setting (49%). Of all detections, 2,713 (20.4%) had co-infections, with the most commonly co-detected viruses being rhinovirus (37%) and bocavirus (17%).

Conclusion: RSV testing increased from 2022 due to expanded respiratory screening, RSV becoming a notifiable disease, and COVID-19 epidemics. Multiplex RT-qPCR testing increased RSV detection, but testing bias exists, with

[3] Department of Health, Disability and Ageing. (2025) National Health and Medical Research Strategy 2026-2036. Australian Government.

children tested more than adults. Continued surveillance across age groups is essential to assess new immunization strategies' impact.

Table 1. Annual RSV testing, detection, within the SESIHS, 2018-2024

RSV test and results		<1 year	1-5 years	6-18 years	19-50 years	51-60 years	61-70 years	>70 years	Total
2018-2024 (n=370,126)	Tested (%)	15,899 (4.3)	42,494 (11.5)	25,700 (6.9)	81,232 (21.9)	28,893 (7.8)	39,461 (10.7)	136,447 (36.9)	370,126
	Detections (%)	2,905 (18.3)	5,530 (13)	605 (2.4)	1,204 (1.5)	392 (1.4)	579 (1.5)	2,078 (1.5)	13,293 (3.6)
2018 (n=14,519)	Tested (%)	1,144 (7.9)	2,368 (16.3)	1,080 (7.4)	2,352 (16.2)	1,077 (7.4)	1,666 (11.5)	4,832 (33.3)	14,519
	Detections (%)	316 (27.6)	395 (16.7)	41 (3.8)	63 (2.7)	28 (2.6)	69 (4.1)	255 (5.3)	1,167 (8.0)
2019 (n=22,794)	Tested (%)	1,338 (5.9)	3,081 (13.5)	1,600 (7.0)	3,994 (17.5)	1,768 (7.8)	2,616 (11.5)	8,397 (36.8)	22,794
	Detections (%)	318 (23.8)	413 (13.4)	46 (2.9)	63 (1.6)	36 (2.0)	81 (3.1)	300 (3.6)	1,257 (5.5)
2020 (n=14,687)	Tested (%)	809 (5.5)	1,965 (13.4)	1,035 (7.1)	3,494 (23.8)	1,215 (8.3)	1,513 (10.3)	4,656 (31.7)	14,678
	Detections (%)	199 (24.6)	383 (19.5)	28 (2.7)	53 (1.5)	13 (1.1)	21 (1.4)	63 (1.4)	760 (5.2)
2021 (n=12,463)	Tested (%)	1,158 (9.3)	2,711 (21.8)	787 (6.3)	1,584 (12.7)	727 (5.8)	1,122 (9.0)	4,374 (35.1)	12,463
	Detections (%)	151 (13.0)	253 (9.3)	18 (2.3)	26 (1.6)	9 (1.2)	33 (2.9)	114 (2.6)	604 (4.9)
2022 (n=143,511)	Tested (%)	3,266 (2.3)	13,077 (9.1)	8,574 (6.0)	42,029 (29.3)	12,701 (8.9)	15,463 (10.8)	48,403 (33.7)	143,513
	Detections (%)	601 (18.4)	1,721 (13.2)	235 (2.7)	632 (1.5)	155 (1.2)	157 (1.0)	461 (1.0)	3,962 (2.8)
2023 (n=100,63	Tested (%)	3,306 (3.3)	11,449 (11.4)	6,859 (6.8)	18,452 (18.3)	7,243 (7.2)	11,209 (11.1)	42,120 (41.9)	100,638
	Detections (%)	551 (16.7)	1,469 (12.8)	127 (1.9)	241 (1.3)	90 (1.2)	139 (1.2)	496 (1.2)	3,112 (3.1)
2024 (n=61,512)	Tested (%)	4,878 (7.9)	7,843 (12.8)	5,765 (9.4)	9,327 (15.2)	4,162 (6.8)	5,872 (9.5)	23,665 (38.5)	61,512
	Detections (%)	769 (15.8)	896 (11.4)	111 (1.9)	126 (1.4)	61 (1.5)	79 (1.4)	389 (1.6)	2,431 (4.0)

Tested = Test numbers (Test numbers/ Total tests, %); Detections = Tested positive (Tested positive/Total tests, %).

Day 2	Plenary Session 7
14:00	**Are known influenza or COVID-19 infections documented in Australian hospital databases?**
Speaker	David Muscatello, UNSW, Sydney

Authors

David Muscatello[1]

Affiliations

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Abstract

Introduction

Influenza and COVID-19 are major causes of severe acute respiratory infections in Australia. This record linkage study aimed to determine the proportion of notified influenza and COVID-19 infections recorded in administrative hospital datasets, what other diagnoses are used and what factors are associated with the infection not being recorded.

Methods

This was a descriptive and logistic regression analysis of inpatient admissions from the PEARL probabilistic record linkage database of emergency department, infection notification, hospitalisation and death records. It includes a cohort of all patients with an acute respiratory infection-like diagnosis presenting to an emergency department (ED) participating in the NSW Emergency Department Data Collection, 1 January 2005 – 28 February 2023. Dual infections (n=189) were excluded and the first inpatient episode was used for principal diagnosis analysis, if >1 episode.

Results

During the study period, there were 37,928 inpatients with notified influenza from presentations to 174 hospitals, and 36,307 with notified COVID-19. Among influenza inpatients, 6.8% had ICU admission and 2.9% died. For COVID-19, 8.4% had ICU admission and 6.1% died.

For influenza infections, 21.3% of the ED presentations with inpatient admission had influenza or influenza-like illness recorded as a principal ED diagnosis and, for COVID-19, 78.1% had COVID-19 or coronavirus recorded. Other common ED diagnoses were fever or non-specific infection, pneumonia, and breathing problems. For influenza, 59.4% had an influenza principal admission diagnosis and 75.8% had influenza among any diagnoses. For COVID-19, 11.2% had a COVID-19 principal admission diagnosis and 92.9% had COVID-19 among any diagnoses. Pneumonia was the most common other principal admission diagnosis for both infections.

After adjusting for available confounders, the factors most strongly associated with influenza *not* being recorded in any admission diagnosis were age 15-44 years, lower urgency at ED triage, absence of a virus-specific ED diagnosis, briefer hospital stay, being tested prior to ED arrival, and presenting earlier in the study period. For COVID-19, results were similar but also included not arriving by ambulance and not receiving intensive care. Presentation during the Omicron variant period (from December 2021) was strongly associated with absence of a COVID-19 diagnosis.

Conclusions

Disease surveillance and research relying on hospital records in Australia will underestimate the incidence of outcomes of influenza and COVID-19 infections. Young adults, persons tested prior to hospital arrival and lower urgency or less complex cases are likely to be under-represented. Influenza capture has improved over time and COVID-19 was best recorded earlier in the pandemic.

Day 2	Plenary Session 7
14:15	**The NSW 2024 RSV immunisation program: targeted effectiveness and population level impact**
Speaker	Janaki Amin, Health Protection NSW, NSW Ministry of Health

Authors

Chris Lambeth[1], Sally Ellis[1], Mareeka Hair[1], Sonya Ennis[1], Elizabeth Wilson[1], Christine Selvey[1], Janaki Amin[1,2,3]

Affiliations

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Abstract

Respiratory syncytial virus (RSV) is a common cause of respiratory tract infections with the highest rates of diagnosed infection and hospitalisation in young children. In clinical trials the long acting monoclonal antibody against RSV, nirsevimab, reduced risk of hospitalisation by nearly 80%. In March 2024, NSW Health implemented a program to immunise with nirsevimab, babies at high-risk of severe outcomes from RSV infection: premature infants <37 weeks gestation, Aboriginal and Torres Strait Islander infants and other infants with specific complex conditions. 6416 infants were immunised, an approximate coverage of 8% infants <6 months of age and 1922 (42%) of premature infants. Among premature infants the rate of RSV hospitalisations was 2.7/100,000 days at risk compared with 12.1/100,000 days at risk among unimmunised infants; demonstrating immunisation effectiveness using the screening method of 85.% (95% CI 71.9%, 92.8%). Population level impact of the program was assessed by comparing the relative rates (RR) of RSV outcomes in infants aged 0-<6 months to those in infants aged 6-<12 months in 2023, before the program began, and 2024, the intervention year. Comparison against the older age group was used to account for differences in amount of circulating RSV between the two years. For diagnosed RSV infection, the RR for 2024, 0.73 (95%CI 0.70-0.76) was significantly lower than for 2023, RR 0.91 (95%CI 0.87-0.95). Similarly for RSV hospitalisations, the 2024 RR 1.59 (95%CI 1.49-1.69) was significantly lower than for 2023 RR 1.87 (95%CI 1.75-1.99). NSW Health was able to rapidly roll out nirsevimab to high-risk infants. While the program only targeted infants most at risk of severe

outcomes and was highly effective in this group, a significant population impact was also demonstrated. This targeted strategy for RSV prevention should be considered in resource limited settings.

Day 2	Plenary Session 8
15:00	**Seek and You Will Find: Co-Circulating Viruses in Epidemiology and Effectiveness Studies**
Speaker	Emily Martin, University of Michigan, USA

Day 2	Plenary Session 8
15:30	**Hogging the Flu? Surveillance and Immune Gaps at US Swine Exhibitions**
Speaker	Andy Bowman, Ohio State University, USA

Authors
Dillon S. McBride[1], Hannah J. Cochran[1], Jacqueline M. Nolting[1], Andrew Bowman[1]
Affiliations
1. The Ohio State University, Department of Veterinary Preventive Medicine

Abstract
Zoonotic influenza A virus (IAV) transmission at US swine exhibitions presents an ongoing pandemic risk, yet active surveillance in the high-risk youth exhibitor population is lacking. To address this gap, we enrolled 711 youth participants at nine swine exhibitions during 2019-2021, collecting 700 nasal swabs and 400 serum samples. We assessed neutralizing antibody titers against eight swine-origin IAV candidate vaccine viruses (CVVs) and characterized 430 IAV strains circulating in exhibition swine. Although H3 cluster IV (clade 3.1990.4.a) became the dominant HA lineage in exhibition swine during 2020-2021, we found that the mean neutralizing antibody titers in the exhibitor cohort were low against this specific lineage. This resurgence of the 3.1990.4.a H3 lineage in swine did not correspond to an increase in reported human variant cases or a rise in antibody titers within our study samples. These results indicate relatively low seroprotection against a dominant, circulating swine IAV lineagthis high-risk population, highlighting a public health vulnerability at the swine-human interface.
Building on this pilot work, the North American Swine-exhibitor Active Longitudinal Surveillance (NASALS) cohort was established in 2021 to better examine the viral, host, and environmental factors that facilitate interspecies transmission in this frontline population. Baseline blood samples and medical histories were collected at enrolment, followed by early- and late-exhibition season blood draws each subsequent year. Serum samples (n=456) drawn from 262 participants over two years (2022-2024) were tested against six CVVs representing clades known to circulate in the U.S. swine population. This longitudinal analysis revealed that while nearly all samples (98.9%) had a neutralizing antibody response to H1 clade 1B.2.1, the geometric mean titer (GMT) was only 81.3. Additionally, only 74.8% responded to H1 clade 1B.2.2.1, with a GMT of just 26.9. Given that these clade 1B.2.2.1 viruses are actively circulating in US swine, these relatively low GMTs in a high-exposure cohort suggest a persistent immunologic gap, emphasizing the continued pandemic risk of swine-lineage IAV.

2025 Delegates

Abigail Fernando | Murdoch Children's Research Institute
Ada Yan | RMIT University
Adam Wheatley | University of Melbourne
Adam Baker | Australian Vaccine Services
Adrian Marcato | Peter Doherty Institute
Agnes Chaumont | GSK
Ahmed Abdul Quadeer | University of Melbourne
Aimee Oldham | The Royal Melbourne Hospital
Al Gomez | Interim Australian CDC
Al Gomez | Australian CDC
Alan Hampson | International Society for Respiratory Viruses
Alexandra Hinchcliff | Menzies School of Health Research
Ali Shushtarian | bioMerieux
Alissa McMinn | Murdoch Children's Research Institute
Amy Lowry | GSK
Anastasia Moisidis | CSL Limited
Andrea Parisi | NSW Ministry of Health
Andrew Bowman | The Ohio State University
Andrew Pollitt | Bass Coast Health
Andy Bean | CSIRO
Anjana Karawita | CSIRO
Anna Lucantoni | Thermo Fisher Scientific
Anne Hahn | University of Melbourne
Anne Maree Baldwin | Queensland Health
Annette Alafaci | Murdoch Children's Research Institute
Ann-Maree Catanzariti | The Therapeutic Goods Administration
AnnMarie McEvoy |
Anthony McGuire | CSL Behring
Ariful Islam | Gulbali Research Institute, Charles Sturt University
Arjun Challagulla | CSIRO
Ash Donovan | Interim CDC
Ashiyana Khairati | IPN Medical
Belinda Hengel | Kirby Institute UNSW
Ben Cowling | Hong Kong University
Bingru Wu | Deakin University
Bridie Clemens | The University of Melbourne
Caitlin Trenorden | Department of Health, Disability and Ageing
Callum Le Lay | CSIRO - ACDP
Catherine Agius | Seqirus
Celeste Donato | Doherty Institute
CHALANI WELGAMA | CSL Seqirus
Chantal Baas | Seqirus
Cheryl Freeman | Pfizer
Chinn Yi Wong | The University of Melbourne
Christine Cooper Serra | Pfizer
Christopher Hum | Cepheid
Cleve Rynehart |
Connor Daymond | University of Melbourne
Craig Dalton | HNE Health
Crissa Kyriazis | Biocelect
Cristina Triffon | Monash University
Daniel Yu | CSL Seqirus
David Speers | PathWest
David Muscatello | UNSW Sydney
Debbie Kisa | Papua New Guinea Institute of Medical Research
Deborah Cromer | UNSW
Desiree Anthony | Sanofi
Doaa Ibrahim | Seqirus
Edin Mifsud | Pfizer
Edith Rosenberg | Seqirus
Elizabeth Siu | Biomerieux
Ellie Robinson | Victorian Department of Health
Emily Hann | CSIRO/Deakin University
Emily Martin | University of Michigan School of Public Health
Emily Armstrong | AstraZeneca Pty. Ltd
Eric Lau | Deakin University
Erik Karlsson | Institut Pasteur du Cambodge
Erin Matthews | Seqirus
Esther Marton | CSL Seqirus
Fiona Jennings | Rewlin Pty Ltd
Fiona Sorbian | VACCHO
Francesca Mercuri | The University of Melbourne
Frank Beard | National Centre for Immunisation Research and Surveillance
Freya Shearer | The University of Melbourne
Gavin Smith | Programme in Emerging Infectious Diseases, Duke-NUS Medical School
Gazala Buksh | Ministry of Health and Medical Services, Fiji NIC
George Milne | UWA
George Andrakakos | Abbott
Georgia Dow | La Trobe Institute for Molecular Science
Georgia STORMONT | Dorevitch Pathology
Gregory Walker | University of New South Wales
Hannah Morgan | Monash University
Haytham Mohamed | WHO
Heidi Peck | WHO CC for Influenza
Helen Cowdery | CSL Seqirus
Helen Malliaras | CSL Seqirus

Himanshu Kaushal | ICMR-National Institute of Virology, Pune
Holly Gardner | Clinical Trial Coordinator
Ian Napier | Seqirus
Isabelle Foo | The University of Melbourne
Jacqueline Lewis | Vaccine Research Group
James McCaw | University of Melbourne
Jan Beacham | Vitality Works
Janaki Amin | Health Protection NSW
Janet Briggs | Vaccine Research Group-UOM
Janet Strachan | Department of Health Victoria
Jasmina Luczo | CSIRO Australian Centre for Disease Preparedness
Jeanetta Barker | Vaccine Research Group
Jenna Hassall | Interim Australian Centre for Disease Control
Jenny Royle | VACCHO
Jenny McKimm-Breschkin | The Doherty Institute
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Jessie Goldsmith | University of Melbourne
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John Stambas |
John Smith | Australian Vaccine Services
Julie McAuley | Doherty Institute, Melbourne University
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Karen Detering | Department of Health, Disability and Ageing
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Katherine Santos | Seqirus
Kathryn Edenborough | The University of Melbourne
Katrina Micallef | CSL Seqirus
Kaz Bellamy | Monash Health
Kerry Mullan | University of Melbourne
Kim Valentine | Sandringham Hospital
Kirsten Spann | Queensland University of Technology
Kylie Carville | VIDRL
Kylie Ainslie | University of Melbourne
Kyu Lee | University of Washington
Lara Schwab | University of Melbourne
Lauren Burmas | WHOFLU CCRI
Lauren Kutzner | Interim Australian Centre For Disease Control
Lauren Welsh | Department of Health and Aged Care
Lee Campbell | University of Sydney
Lex Leong | SA Pathology
Lien Anh Ha Do | Murdoch Children's Research Institute
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Lisa Steinberg | Seqirus
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Maha Khairbak | WHO Collaborating Centre for Reference and Research on Influenza
Mahbubur Rahman |
Malet Aban | WHO Collaborating Centre for Reference and Research on Influenza
Malvin Ooi | VC
Mante Thobejane | University of Cape Town
Marcia Lee | CSL
Marcus Robinson | Monash University
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Matthew Gartner | University of Melbourne
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Najwa Ejje | Sanofi
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Nicole Baker | Bass Coast Health
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Robert Moss | University of Melbourne
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Sandra Carlson | HNE Health
Sarah Mercier | TGA
Sarah Londrigan | University of Melbourne
Sarah Pitts | Monash Health
Sarah MILES | Dorevitch Pathology
Sarah Yallop | Doherty Institute
Sherrie Trehan | Vitality Works
Siang Tia | Tia
Simone Parkes | Biocelect
Siobhan St George | Interim Australian Centre for Disease Control
Socheata Chea | TGA
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Sophie Syddall | Seqirus
Stacey Allen | CSIRO
Stella Liong | RMIT University
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Steve Rockman | CSL Seqirus
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Vince Matassa | CSL Seqirus
Vincent Lee | Federal Government Agency or Commonwealth Entity
Violeta Spirkoska | University of Melbourne
Will Horman | Seqirus
Wing Wah (Vera) Tse | HNELHD - Health Protection (FluTracking)
Xiaomin Dong | WHO Collaborating Centre for Reference and Research on Influenza in Melbourne
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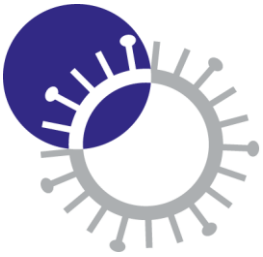

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