BREATHING INFECTION

Unravelling respiratory riddles in South Eastern Sydney

A thesis submitted for the degree of Master of Philosophy (Applied Epidemiology) of The Australian National University

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2023-2024

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Originality Statement

"I hereby declare that this submission is my own work and to the best of my knowledge it contains no material previously published or written by another person, or substantial proportions of material which have been accepted for the award of any other degree or diploma at the Australian National University or any other educational institution, except where due acknowledgement is made in the thesis. The work was undertaken from February 2023 to October 2024 as part of the degree Master of Philosophy (Applied Epidemiology), The Australian National University.

Any contribution made to the research by others, with whom I have worked with is explicitly acknowledged in this thesis. I also declare that the intellectual content of this thesis is the product of my own work, except to the extent that assistance from others in the project's design and conception or in style, presentation, or linguistic expression is acknowledged."

Signed:  Dated: 26/10/2024

Eunice Stiboy

"Vaccines and antibiotics have made many infectious diseases a thing of the past; we've come to expect that public health, and modern science can conquer all microbes. But nature is a formidable adversary."

- Dr. Tom Frieden.

"Epidemiology is like a science of detective work- finding the source of diseases, the clues to their spread, and the methods for stopping them."

- Dr. William Foege.

Acknowledgements

So many individuals have contributed to my journey, and I am deeply grateful to each of them.

Firstly, I would like to acknowledge the traditional custodians of the lands on which I have lived, worked, and learned during my Master of Philosophy (Applied Epidemiology) (MAE). Sovereignty was never ceded, and this always was, and always will be, Aboriginal land. My field placement projects took place on the lands of the Bidjigal and Gadigal peoples of the Eora nation, whose beautiful landscapes have provided me with peace, renewal, and inspiration. The Australian National University (ANU), located on the lands of the Ngunnawal and Ngambri peoples, has offered me invaluable learning opportunities and the chance to build lasting relationships, for which I am deeply grateful.

I extend my heartfelt thanks to my field supervisors, Dr Vicky Sheppeard and Dr Anthea Katelaris at South Eastern Sydney Local Health District (SESLHD) Public Health Unit (PHU), and my academic supervisors, Anna Glynn-Robinson and Dr Amy Parry. I could not have asked for more formidable, wise and empowered women to lead me through this journey. Thank you for your invaluable guidance, encouragement, patience and honest opinions throughout the two years. Vicky, I promise my grammar will never be the same!

To my colleagues at SESLHD PHU, your support, expertise and passion for public health have made my time here truly rewarding. I will never recover from the surplus of baked goods. It has been nothing short of a pleasure to work with every single one of you, both before and during the MAE.

I am also grateful to those who generously shared their expertise: Standish Rigava, Danielle Ferraro, Kirsty Hope, Zoe Baldwin, Professor Greg Dore, Heather Valerio, Shane Tillerkeratne and members of the Public Health Infectious Disease Network in New South Wales.

To my fellow MAE 2023 cohort, thank you for sharing this journey with me. Your camaraderie, laughter, support and invaluable advice have made this experience extraordinary. The MAE social committee, the awards night, endless social activities, lunchtime sports and all our shared moments have been highlights of my time in the program. The Nutbush will forever live on.

Finally, to my partner, Samuel. As I complete my second master's degree, I reflect with deep gratitude on your unwavering support and the way you've opened my eyes to

boundless possibilities. Your encouragement has empowered me to strive for my best and has been a cornerstone of my success. Thank you for believing in me, showing me that dreams do come true, and helping this girl from the country move closer to realising her career aspirations can be a reality. Your steadfast belief and love have contributed to making this achievement possible.

Thesis Summary

This thesis is presented in seven chapters. Chapter one outlines the field placement and projects meeting the degree requirements. Chapters two through to five describe the projects I completed to meet the core requirements of the MAE. Chapter six focuses on the teaching activities I undertook during the MAE. Chapter seven presents additional public health work conducted during my MAE. The numbering of figures, tables and references restart in each chapter.

Abbreviations

ANSTO	Australian Nuclear Science and Technology Organisation
ANU	Australian National University
ARI	Acute Respiratory Infections
CDIC	Communicable Disease and Immunisation Conference
DC	Decompensated cirrhosis
ESCAIDE	European Scientific Conference on Applied Infectious Disease Epidemiology
HBV	Hepatitis B virus
HCC	Hepatocellular carcinoma
LGA	Local government area
MAE	Master of Philosophy (Applied Epidemiology)
NCIMS	Notifiable Conditions Information System
NSW	New South Wales
PaCH	Population and Community Health
PHU	Public Health Unit
SESLHD	South Eastern Sydney Local Health District
TB	Tuberculosis
WHO	World Health Organization

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Abstract

This thesis presents four projects and public health activities from my field placement at the South Eastern Sydney Local Health District's (SESLHD) Public Health Unit (PHU), fulfilling the competencies for my Master of Philosophy (Applied Epidemiology) (MAE) at the Australian National University.

In early 2023, I participated in the investigation of a tuberculosis (TB) outbreak in Sydney, which underscored the value of genomic sequencing and informed my evaluation of TB contact data quality in the state Notifiable Conditions Information System (NCIMS) against local clinic records. This evaluation revealed deficiencies in NCIMS data, and I was able to review the points at which contacts dropped out of the screening pathway.

In January 2024, the PHU responded to an outbreak of *Legionella pneumophila* serogroup 1 in 15 people who had visited the Sydney central business district (CBD), for which I was the lead epidemiologist. I coordinated outbreak management team meetings, produced situation reports, maintained a case line list, and collaborated with the Ministry of Health to perform geocoding and mapping.

As part of the post-pandemic response, I conducted an evaluation of the District's existing Acute Respiratory Infections (ARI) report. This assessment focused on the report's timeliness, usefulness, and readability. Following the evaluation, I rebuilt the report using R statistical software and based on the World Health Organization's (WHO) guidelines for respiratory surveillance, to enhance the report's utility and relevance post-pandemic. This included developing workplace instructions and introducing automation to increase efficiency.

My final project examined factors associated with delayed hepatitis B (HBV) diagnosis in SESLHD using linked population-based data. The findings provided evidence to inform local policy and prevention activities.

Additionally, I engaged in various public health activities, including teaching epidemiology, participating in seasonal arbovirus control, touring the Australian Nuclear Science and Technology Organisation (ANSTO) for biopreparedness activities, developing a new reporting format for acute respiratory disease outbreaks in aged care facilities, establishing a local R club, creating outbreak documentation templates, managing infectious disease cases, and participating in field work including *legionella* sampling, cruise ship inspections, and a sex on premises site visit. These experiences enriched my understanding of applied epidemiology and contributed to public health operations and decision-making.

Chapter I

Introduction to field placement and summary of experience

Tamarama beach on a winter's day located within SESLHD

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Overview

I commenced my MAE field placement at the South Eastern Sydney Local Health District (SESLHD) Public Health Unit (PHU) in Randwick, Sydney in February 2023. I was fortunate to already be working as an epidemiologist and public health nurse within the PHU prior to undertaking the MAE. This provided a foundation of experience and workplace familiarity to ensure I capitalised on the learning opportunities available when I commenced the MAE. SESLHD is one of the largest local health districts in metropolitan NSW, covering Sydney's central business district, the eastern beaches of Bondi down to Cronulla and The Royal National Park. SESLHD covers the local government areas of City of Sydney (partially), Waverley, Woollahra, Randwick, Bayside, Georges River and Sutherland Shire.

The PHU is part of the Population and Community Health (PaCH) Directorate and is responsible for surveillance, prevention, and control of communicable disease in SESLHD, as well as managing environmental health issues. Activities include:

- Providing advice on guidelines for preventing disease spreading from person to person and from animals to people
- Managing cases, contacts, and outbreaks of communicable diseases,
- Coordination of community and school-based vaccination programs within SESLHD
- Monitoring and responding to disease outbreaks within SESLHD
- Planning for pandemics and biosecurity threats
- Disease surveillance
- Exotic mosquito surveillance
- Cruise ship surveillance

SESLHD has provided me the opportunity to apply field epidemiology skills while learning about public health practice and the operations of a local public health unit in NSW. I have been able to experience and contribute to the core functions of the PHU, including routine surveillance, responding to public health threats, using evidence to help inform local policies, and daily functions of the infectious diseases team. As part of this experience, I have achieved the competencies for the MAE Program (*Table 1*).

Major Competencies

Table 1: Summary of projects and core competencies of the MAE program

Competency	Chapter 2 Outbreak investigations: TB and *Legionella*	Chapter 3 Respiratory infections surveillance report	Chapter 4 Analysis of Hepatitis B delayed diagnosis	Chapter 5 TB contact data evaluation	Chapter 6 Teaching field epidemiology	Chapter 7 Additional PH activities
Investigation of an acute public health problem						
Analysis of a public health dataset						
Evaluate a surveillance or health information system						
Design and conduct an epidemiological study						
Literature review						
Report to a non-scientific audience						
Conference presentation						
Peer-reviewed publication						
Teaching field epidemiology						

Investigation of an acute public health problem or threat

Genomic Sequencing Identifies Tuberculosis Outbreak in Inner City Sydney Boarding House, Sydney, Australia 2022

In 2023, I was part of a team investigating a tuberculosis cluster in a Sydney boarding house. We identified 91 contacts and uncovered a fourth case linked to the cluster. I presented the findings at the NSW TB Conference and the Communicable Disease and Immunisation Conference (CDIC) in 2023.

Where the cooling water drifts: an outbreak of *Legionella pneumophilia* serogroup 1 in the central business district of Sydney, 2024

In summer 2024, I investigated a *Legionella* outbreak in Sydney's central business district with 15 cases, including 14 hospitalisations, linked to a contaminated cooling water system. The investigation emphasised the need for stricter cooling water system regulations and timely international reporting. I presented this investigation at CDIC and will present at ESCAIDE in Sweden in November 2024.

Analysis of a public health dataset

Evaluation and review of the South Eastern Sydney Local Health District Acute Respiratory Infections Report

The SESLHD Public Health Unit transitioned from separate influenza and COVID-19 reports to a combined weekly Acute Respiratory Infections (ARI) report post-pandemic. I led an evaluation incorporating stakeholder feedback, to redesign the report format. The new version integrates WHO guidelines, additional data sources, descriptive data analysis, and automated processes for greater efficiency, and improved data interpretation.

Evaluation of a surveillance or health information system

Enhancing TB Contact Screening: An evaluation of surveillance systems in South Eastern Sydney Local Health District

This evaluation assessed the quality and completeness of TB contact data in SESLHD, revealing 100% completion but identified data quality issues suggesting more efficient surveillance systems are needed. The findings highlight the need for a better understanding of TB contact data and development of more user friendly and efficient data collection systems.

Design and conduct and epidemiological study

Factors associated with delayed diagnosis of hepatitis B in South Eastern Sydney Local

Health District

Using linked health data, this study analysed factors associated with delayed hepatitis B (HBV) diagnosis, focusing on demographic and clinical variables. Results identified associations of late diagnosis with age, sex, and the year of diagnosis of decompensated cirrhosis (DC) or hepatocellular carcinoma (HCC), while associations with local government area (LGA) and country of birth were not significant.

Minor Competencies

Literature review search strategy

A targeted literature search and synthesis of relevant information was undertaken for each project. The search was conducted as part of the outbreak of tuberculosis in a boarding house and the search strategy and results are detailed in *Chapter II*.

Report to a non-scientific audience

The pertussis (whooping cough) contact letters (*Appendix I*) for the Public Health Unit (PHU) were reviewed and revised to provide advice and information to pertussis contacts in various exposure settings. Additionally, a media release for the *Legionella* outbreak was drafted, with both documents tailored to ensure comprehension at a basic literacy level (*Appendix II*).

Peer-reviewed publication

A manuscript has been submitted to *Western Pacific Surveillance and Response* for my outbreak report of TB in a boarding house. A late-stage draft has also been completed for the investigation of the *Legionella pneumophilia* serogroup 1 outbreak in the Sydney central business district 2024 for planned submission to *Communicable Diseases Intelligence*.

Teaching of topics in field epidemiology

I developed and delivered a teaching exercise on "*Tuberculosis contact tracing in low-incidence settings*", along with participation in cohort-led Lessons from the Field exercises and local R club sessions. Additionally, I led education sessions on Excel data and hepatitis D that were provided to the PHU Infectious Disease Team.

Conference presentations

I had the opportunity to present my work at more than one conference, this is detailed in *Table 2*.

Table 2: Conference presentations undertaken during the MAE

Conference	
NSW Tuberculosis Conference, March 2023	Oral presentation on the TB outbreak (10 minutes + 5 minutes of questions)
Communicable Disease and Immunisation Conference, June 2023	Oral presentation on the TB outbreak (10 minutes + 5 minutes of questions)
Communicable Disease and Immunisation Conference, June 2024	Oral presentation on the *Legionella* outbreak (6 minutes + 4 minutes of questions)
European Scientific Conference on Applied Infectious Disease Epidemiology, November 2024	Oral poster presentation on the *Legionella* outbreak (3 minutes + 5 minutes of questions)

Course work

I successfully completed the following courses as part of the program requirements administered by the Australian National University (ANU).

POPH8913 Analysis of Public Health Data

POPH8914 Issues in Applied Epidemiology

POPH8915 Research Design and Methods

POPH8916 Outbreak Investigation

POPH8917 Public Health Surveillance

Additional field placement activities

In addition to the activities related to the core program requirements, I also took part in the following activities and projects detailed in *Table 3* and *Table 4*. These activities are also detailed in *Chapter: VII*.

Table 3: Summary of workshop and conference attendance throughout the MAE program.

Conference and workshop attendance
New South Wales Tuberculosis Conference, 16-17 March 2023
Communicable Disease and Immunisation Conference, 19-21 June 2023
SESLHD Eliminating Hepatitis C Workshop, 18 July 2023
Urban Insights Walk for Homelessness Awareness Week, 9 August 2023
South Asia Field Epidemiology and Technology Network (SAFETYNET) Scientific Conference, 11-15 September 2023
New South Wales Health Infectious Disease Workshop, 13-14 November 2023
New South Wales Arborvirus Workshop, 11-12 December 2023
New South Wales Tuberculosis Conference, 3 May 2024
OzFoodNet Face to Face open sessions meeting, 14 May 2024
Centre for Research Excellence Tuberculosis Symposium 30-31 May 2024
Communicable Disease and Immunisation Conference, 11-13 June 2024
European Scientific Conference on Applied Infectious Disease Epidemiology, 20-22 November 2024

Table 4: Additional public health activities undertaken during the MAE

Other activities
Participated in routine seasonal arbovirus control and surveillance activities
Assisted a cruise ship vessel inspection
Revised and produced a monthly Residential Aged Care Facility (RACF) Acute Respiratory Infections (ARI) outbreak report
Supported *Legionella* environmental sampling
Attended Australian Nuclear Science and Technology Organisation tour
Participated in Infectious Disease Network Lunch and Learn Sessions: CDIC presentations
Completed the Nurse Immunisation Course
Participated in multijurisdictional outbreak investigation (MJOI) of *shigellosis*

Appendix I

Example pertussis contact letter

South Eastern Sydney Local Health District

[Click here to enter Name]
[Click here to enter Address]

NSW GOVERNMENT

Ref: NCIMS XXXXXXX

Whooping cough (pertussis) exposure

Dear XXX

You/your child have been in contact with a confirmed case of whooping cough (pertussis).

What is whooping cough?
Whooping cough is a very contagious bacterial infection. You can get whooping cough from infected people who cough or sneeze near you. Whooping cough can be a very serious illness in babies. Older children and adults can get whooping cough too and pass it on to babies.

People most at risk of severe disease are:
- Infants <6 months of age
- Pregnant women in the last month of pregnancy (because they could infect their newborn)

If you/your child develops symptoms, please contact your family doctor as soon as possible. Take this letter with you to the doctor.

What are the symptoms?
Symptoms can take up to 3 weeks to develop after contact with whooping cough.

Whooping cough usually begins like a cold, with a blocked or runny nose, mild fever, tiredness, and a cough. The cough can become worse and last many months.

Older children and adults may only have a cough that won't stop. The first sign of the illness in small babies may be pauses in normal breathing (apnoea).

What should you do if you have symptoms?
Your doctor can arrange testing (the best test to use is a throat swab) and treatment if needed. You do not need to get tested if you do not have symptoms.

A person with whooping cough can give it to other people for 3 weeks after the coughing begins. A person can no longer give whooping cough to other people after a course of antibiotics. Your doctor can prescribe the correct antibiotic and dose.

How is whooping cough prevented?
Vaccinating babies on time at 6 weeks, 4 and 6 months of age gives them the best protection. Immunity can fade over time which means boosters are required. Booster doses are given at 18 months and 4 years of age, in high school, and during each pregnancy.
If you/your child has whooping cough, you should keep them home from school, childcare and away from small babies and pregnant women until they have had at least five days of antibiotics.

It is important to check that your child is fully up to date with their immunisations against whooping cough. If in doubt, please ask your doctor to check.

For more information see www.health.nsw.gov.au/Infectious/whoopingcough/Pages/default.aspx
Yours sincerely

Name
Title

Public Health Unit
Locked Mail Bag 81, Randwick NSW 2031

02 9382 8333
SESLHD-PublicHealthEnquiry@health.nsw.gov.au

Chapter II

Investigation of an acute public health problem

Section 1 Genomic sequencing identifies tuberculosis outbreak in inner city boarding house, Sydney, Australia, 2022

Section 2 Where the Cooling Towers Drift: An outbreak of *Legionella pneumophila* serogroup 1 in the central business district of Sydney, Australia, 2024

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Abbreviations

AFB	Acid fast bacilli
COPD	Chronic obstructive pulmonary disorder
CXR	Chest x-ray
DNA	Deoxyribonucleic acid
ED	Emergency department
IGRA	Interferon-Gamma Release Assay
LTBI	Latent Tuberculosis Infection
NSW	New South Wales
PCR	Polymerase chain reaction
PHU	Public Health Unit
SESLHD	South Eastern Sydney Local Health District
SNP	Single nucleotide polymorphism
SVH	St Vincent's Hospital
TB	Tuberculosis
TST	Tuberculin skin test

Prologue

Introduction

In December 2022 the South Eastern Sydney Public Health Unit (PHU) was notified by the New South Wales (NSW) Tuberculosis (TB) Program of genomically clustered *Mycobacterium tuberculosis* isolates from two smear-positive TB patients diagnosed three months apart. Initial investigations found the TB smear-positive patients lived in the same boarding house but were not known to each other.

My Role

Although this outbreak was recognised prior to me commencing the MAE, most of the follow-up and contact investigations took place in the first months of my placement (2023). Under the guidance of my field supervisors, I was responsible for maintaining and collecting case and contact information, contact follow-up, and documentation of findings. I collaborated with the local TB clinic, who led the investigation, to maintain a central line list of contacts for follow-up and liaised regularly with the team to ensure the data were kept up to date. In March 2023 I conducted a site visit to perform an environmental investigation and interviewed the facility manager to obtain further information on cases and their movements in the facility. From the site visit I drew a floor plan and mapped case and contact locations to try and determine transmission pathways. I used other health databases to search for additional contact details of contacts who had been lost to follow up and attempted to reach them for follow-up. I liaised with TB services in other districts to collect outcomes of contact screening, performed descriptive analysis and collated tables and figures to summarise the outbreak investigation. I also conducted a literature review to understand the use of genomic sequencing techniques to detect outbreaks and transmission events of TB, and to contextualise this piece of work.

Lessons Learnt

I enjoyed greatly my participation in this outbreak investigation. This was my first experience with a TB investigation and contact follow-up, and I found it a welcome challenge to learn of the complexities of TB diagnoses and risk assessments. I learnt about the roles and responsibilities of the local TB services, PHU and NSW TB program when investigating a large contact group such as this. The investigation exposed me to the importance of routine genomic sequencing as a means of cluster identification. I also developed a greater understanding and appreciation of the challenges and barriers when performing contact follow-up. Throughout this investigation I was in awe of the

knowledge and expertise of the local TB clinic nurses and those who work primarily in the field of TB. I valued the opportunity to learn from these professionals to enhance my knowledge of TB and how they cover so many areas of TB control that would often go unnoticed by the public.

Public Health Impact

This outbreak demonstrated the value of routine genomic sequencing to identify clustering and local transmission of TB, leading to targeted public health investigation. It also displayed the importance of robust outbreak investigation using a multi-disciplinary team, with broad screening and multiple follow-up strategies in multi-dwelling buildings or other complex exposure sites. Unrecognised transmission of TB in Australia poses a significant risk to the maintenance of low-TB incidence and adds to the prevalence of TB infection [latent tuberculosis infection (LTBI)]. Contact investigation and robust outbreak management are essential elements for control in low-incidence settings.

Acknowledgements

I would like to express my sincere gratitude to the local chest clinic CNC Standish (Stan) Rigava, for their invaluable guidance, patience, and knowledge during this investigation. The knowledge gained in TB throughout this experience has been truly invaluable. Working closely with the local chest clinic has deepened my understanding of TB prevention, diagnosis, and treatment strategies. I am grateful for the work contributed by the wider team in this investigation and the opportunity to contribute to this piece of work and to continue learning within the TB field. Despite my best efforts I am sure I will continue to be baffled and amazed by this fascinating bacterium.

Abstract

Objective

In 2022 the New South Wales (NSW) TB Program were notified of genomically clustered *Mycobacterium tuberculosis* isolates from two smear-positive tuberculosis (TB) patients diagnosed three months apart. Investigations found they resided in the same boarding house. We investigated this cluster and conducted active case finding among contacts to prevent ongoing transmission.

Methods

We conducted a site visit to understand transmission risk, reviewed patient histories, performed a risk assessment, and conducted onsite TB contact screening, including interferon-gamma release assay (IGRA) testing. Long-term residents were also screened via chest x-rays. Past residents were referred to local TB services. TB disease or infection was defined as per the NSW Health Tuberculosis Control Guidelines and TB cases were considered part of the outbreak if they had resided at the boarding house during the exposure period.

Results

We identified four residents with TB disease, three of which were genomically linked to the outbreak. We determined the exposure period in the boarding house as January 2021 to September 2022. All residents and staff were considered contacts requiring screening. Of the 91 contacts identified, 37 (41%) completed screening. Sixteen (48%) of 33 current residents attended the onsite clinic. Of 37 screened contacts, we found one resident with TB disease (patient number four), three residents and one staff member with TB infection.

Discussion

This outbreak highlights the role of genomic sequencing in detecting TB transmission. The first three patients were infectious for prolonged periods prior to diagnosis, likely facilitating transmission in the boarding house communal areas. In multi-dwelling buildings with TB exposures, contact screening of all residents may be required when prolonged exposures are found. If low TB incidence countries are to progress to elimination, investment in routine genomic sequencing and robust public health investigation should be commonplace in TB management guidelines and policies.

Introduction

Tuberculosis (TB) is an illness caused by the bacteria *Mycobacterium tuberculosis*, typically affecting the lungs.[1] It spreads through the air when individuals with pulmonary

TB cough, sneeze, or spit, and infection can occur by inhaling just a small number of these bacteria.[1] Australia has one of the world's lowest incidence rates of TB and has maintained this status through excellent TB control over the last three decades, despite its proximity to some of the highest incidence countries in the world.[2] In 2018 Australia reported 1,438 TB notifications representing a rate of 5.8 per 100,000 people with 89% of those cases reported in people who were born overseas.[2] In the four years between 2015-2018 the most frequently reported countries of birth for people with TB disease diagnosed in Australia were India, Vietnam, the Philippines, China and Nepal.[2]

In 2022, the rate of TB in New South Wales (NSW) was 6.5 per 100,000 people, with these notifications comprising 41% of the total notifications in Australia.[3] The majority (91%) of the notified 528 TB patients reported being born overseas.[3] The most frequently reported countries of birth were India and Nepal.[3] Notification rates by country of birth varied from 104.7 per 100,000 for those born in Nepal to 0.9 per 100,000 people for those who were born in Australia.[3]

During 2016, NSW Health introduced routine whole genome sequencing (WGS) for all *Mycobacterium tuberculosis* isolates, which has allowed for the surveillance of circulating strains, detection of genotypic drug susceptibility, differentiation of TB endogenous re-lapse from exogenous re-infection, inference of transmission pathways and cluster detection to guide public health responses, as well as detection of laboratory cross contamination.[4, 5] Routine WGS has also the potential to allow for better targeting of contact tracing interventions and prevention strategies.[5]

With Australia being a country of low incidence for TB, transmission amongst the general population is expected to be uncommon, with most incident TB generated by reactivation of TB infection [latent tuberculosis infection (LTBI)] acquired overseas.[6, 7] Local transmission is occasionally recognised, but is unexpected and usually occurs in households, health care facilities, or congregate settings such as prisons or facilities for people experiencing homelessness.[8] The low incidence of locally acquired TB can lead to reduced awareness of the risk and result in delayed identification of transmission, which may have significant epidemiological and public health impact.[6] A comprehensive understanding of local epidemiology and transmission is crucial in low-incidence countries, as detailed by the World Health Organization's Framework towards TB elimination in low-incidence countries.[8] The framework outlines the requirement for tailored approaches to contain local outbreaks with rigorous contact investigations and outbreak management being essential elements for control of TB in low-incidence settings.[8]

We report an outbreak of TB in a boarding house in inner-city Sydney, NSW, Australia that was detected via routine WGS.

Methods

In November 2022 the South Eastern Sydney Local Health District's (SESLHD) Public Health Unit (PHU) and the chest clinic at St Vincent's Hospital (SVH) were notified by the NSW Health TB Program of genomically clustered *M. tuberculosis* isolates from two tuberculosis patients with a single nucleotide polymorphism (SNP) difference on routine WGS. At time of notification for each patient, it was apparent that these two patients shared the same residential address, a boarding house in inner-city Sydney, but were not known to one another or identified during individual patient follow-up, when prompted about boarding house exposures.

Epidemiological investigation

Epidemiological investigation was undertaken by the SVH chest clinic in accordance with the NSW TB control guidelines.[8] The boarding house was contacted and notified of the exposure in the building; boarding house details and a list of residents who stayed in the boarding house during the exposure period were obtained. We undertook an inspection of the boarding house to assess transmission risk. The boarding house manager was interviewed to determine staff and resident movements within the building.

Boarding house screening

Based on preliminary investigation, one of the patients reported that a relative who had previously lived with her in the boarding house had been diagnosed with pulmonary TB after leaving Australia. Investigations into this patient found their symptom onset was approximately April-May 2021. Based on these findings' investigation dates were extended back to January 2021 (to include a margin of uncertainty).

We conducted a risk assessment to determine the screening strategy. We determined that all residents, staff, and visitors (resided at the boarding house for ≥7 days) of the boarding house warranted contact tracing and screening for TB infection for the period of January 2021 to September 2022 (when the second case was admitted to hospital).

Contact tracing

Identified contacts were screened for TB symptoms[8] and TB infection via a single interferon-gamma release assay (IGRA) as it was more than 8 weeks since last exposure to an infectious patient. Residents identified as long term (defined as living in the boarding house for more than 2 years) were considered higher risk and offered a chest x-

ray (CXR) in addition to IGRA testing.

At the time of investigation, residents and staff of the boarding house were offered screening at a one-off clinic held at the boarding house. We recorded any history of TB symptoms, previous TB exposures, TB vaccine, and demographic details including country of birth and duration of residence/work in the boarding house from people who attended screening. Blood for IGRA testing was collected onsite, and long-term residents were given a referral for a CXR that could be conducted nearby. Current residents/staff who did not attend the on-site clinic were referred to the local chest clinic.

Past residents and staff were contacted via phone to notify the potential TB risk, obtain TB risk history, and referred to their nearest chest clinic for screening. The NSW TB Program provided support by facilitating use of a call centre, initially set-up for COVID-19. Past residents were attempted to be called in two rounds of calls on different dates, with up to three calls each round. Contact attempts were made via email where available. If phone contact was made, the contact was informed of their exposure to TB, screened for symptoms, and recommended screening. Contacts were sent written information on the exposure and referred to their local chest clinic for follow up. Contacts in other health districts in NSW were referred to their local chest clinic, and contacts who were in other states or territories were notified to their jurisdictional TB program for follow up.

Laboratory methods

WGS was performed on all culture-positive isolates by the Mycobacterium Reference Laboratory NSW. Briefly, deoxyribonucleic acid (DNA) was extracted from pure cultures by an inhouse method, and a library constructed using Nextera XT (Illumina, CA). Sequencing was performed on an Illumina NextSeq500 (Illumina, San Diego, California) with a 150bp paired-end protocol using NextSeq 500/550 v2 Kits. Analysis was performed after samples passed quality control (QC) and mapped against reference genome of *M. tuberculosis* H37RV.[3] Clustering was defined as isolates having 12 or less SNPs.

Findings from the outbreak were presented at the NSW TB Conference along with presentations to Prince of Wales and St George Hospital Infectious Disease grand rounds.

Results

We identified 94 people living or working in the boarding house during the period of

interest from January 2021 to September 2022. No visitors were identified during the exposure period. This included three people with TB disease (active TB) identified at the start of the investigations. During the contact investigations, a fourth resident with TB disease (patient four) was diagnosed during routine investigations they were having at the time, bringing the total number of TB patients in the building to four (4%) of 94 people (*Table 1.1*).

Table 1.1 Summary of tuberculosis screening results for the whole cohort of residents and staff within the boarding house (n = 94)

	Current residents	Past residents	Staff	Total n (%)
TB disease (Active TB)	3	1	-	**4 (4%)**
Positive IGRA	3	-	1	**4 (4%)**
Screening negative	17	14	1	**32 (34%)**
Not screened - Unable to contact	-	22	-	**22 (23%)**
Not screened – Contacted but declined screening	7	1	3	**11 (12%)**
Not screened – Contacted but did not attend/lost to follow up	5	16	-	**21 (22%)**
Total	**35**	**54**	**5**	**94 (100%)**

TB disease patients

We identified four people with active, fully susceptible, TB in this outbreak (*Table 1.2*).

Patient 1: A female in her 20's, was born in a low incidence country and presented to the hospital emergency department (ED) in July 2022, with a four-month history of weakness, weight loss, fever, chills, and non-productive cough. At the time of presentation, she was breathless and had a persistent cough that prohibited her from walking the few metres from the bed to the door of her room in the boarding house. She also reported resting in the stairwell of the boarding house to catch her breath and wait for her cough to resolve when going to her room on the third floor. Her sputum samples on admission were 3+ positive on microscopy for acid fast bacilli (AFB) and culture positive for *Mycobacterium tuberculosis*. She had no known co-morbidities; however, she did report a previous TB exposure during her childhood. However, we considered her infection to likely be from a more recent exposure to her relative patient 3.

Patient 2: A female in her 50's, who was also born in a low incidence country, was admitted to hospital in September 2022 with abdominal pain along with a six-week history of weight loss, nausea and vomiting, iron deficiency and a 'smoker's cough' of unknown duration. She had a previous diagnosis of diabetes. After initial investigations she underwent a CXR which showed abnormalities. Her sputum sample was 2+ positive on microscopy for AFB and positive on culture for *M. tuberculosis*.

WGS results indicated a single SNP difference between *M. tuberculosis* isolates from patients 1 and 2.

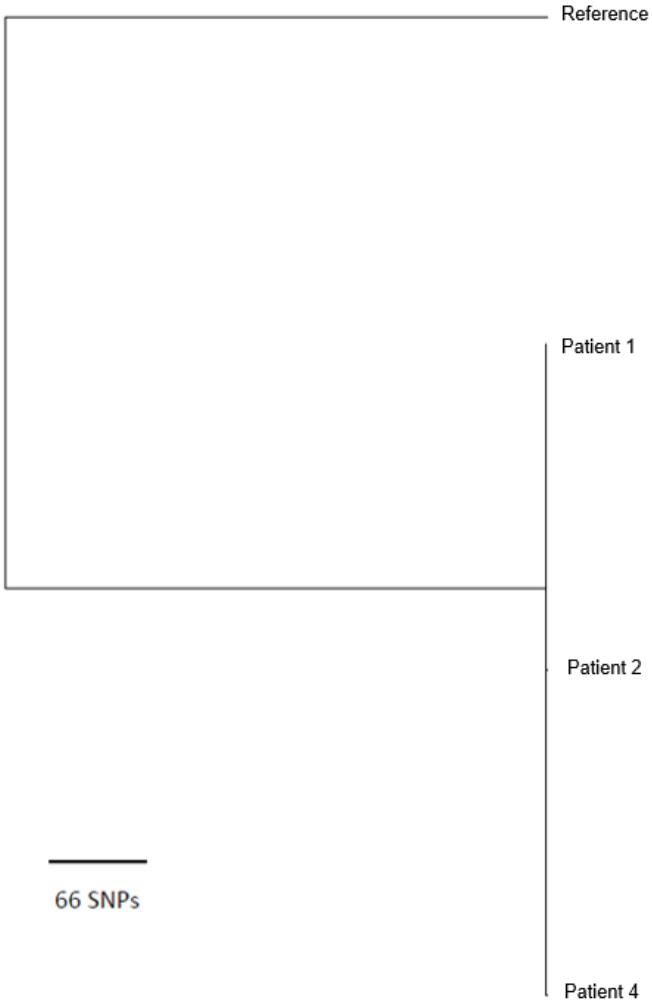
Patient 3: A male in his 20's, who was born in a low incidence country was diagnosed with TB outside of Australia. Patient 1, his relative, reported he had onset of cough from approximately April or May 2021. He reported that a CXR he received on return to his home country that showed cavities. He was tested for COVID-19 while in Australia but did not seek review of his symptoms. Patient 3 lived in the boarding house from January 2020 to August 2021. We consider patient 3 the likely primary patient in this outbreak.

Patient 4: An Australian born male, in his 70's was identified as a resident contact in the building. He reported a history of a previous TB exposure in 2019 with a borderline tuberculin skin test (TST) at the time. He completed treatment for TB infection in 2019. Whilst the patient was asymptomatic, routine imaging for chronic obstructive pulmonary disorder (COPD) follow-up in November 2022 showed changes, and he was investigated further. Initially TB sputum and culture were negative, however bronchoscopy specimens from December 2022 were AFB microscopy and culture positive. WGS showed his M. tuberculosis isolate was genomically linked to isolates from patients 1 and 2.

An isolate from patient 3 was not available for genomic sequencing. A phylogenetic tree summarising the genomic sequencing is shown in *Figure 1.1.*

The genomic sequencing results from isolates of patients 1 and 2 were the results which triggered the outbreak investigation. Both patients were interviewed, and patient 1 reported that her relative, patient 3, who previously lived in the boarding house had returned to their home country 11 months earlier in August 2021, where he had been diagnosed with TB disease.

Figure 1.1 Maximum likelihood phylogenetic tree of tuberculosis genomes sequenced from 3 case-patients in this outbreak. All isolates belong to the European American lineage. Reference isolate used in mapping is M. tuberculosis H37Rv)



Contact tracing and screening for TB disease

There were 91 residents and staff during the exposure period who required contact screening, 54 (58%) were past residents, 35 (36%) were current residents and 5 (5%) staff. There were 23 (25%) long-term residents in the cohort, duration of stay in the boarding house was unavailable for six (7%) contacts. Of the 91 residents and staff identified, 69 (76%) were able to be contacted either by the onsite communications, phone, or email. Twenty-two (24%) contacts were unable to be contacted. From the 69 contacts we were able to contact 37 (54%) completed screening.

Of the 69 residents and staff contacted, screening was not completed in 32 (46%) contacts: 21 (30%) were lost to follow-up, two (10%) of whom were considered high-risk; and 11 (16%) declined to be screened, 6 (55%) of whom were considered high-risk contacts. Of the 37 contacts who completed screening 20 (54%) residents attended the onsite clinic, 13 (35%) attended an NSW Health chest clinic and 4 (11%) were referred interstate. One (3%) contact was diagnosed with TB disease (patient 4). Four (11%) contacts returned a positive IGRA and 32 (87%) returned a negative IGRA. Of the 32 that returned a negative IGRA, two (6%) were symptomatic with a normal CXR and two (6%) were asymptomatic with an abnormal CXR. These four contacts were placed on CXR surveillance. A summary of the contact follow-up is shown in *Figure 1.2*.

The four IGRA positive residents and staff are described in *Table 1.2.* Three are current long-term residents at the boarding house and were born in Australian with no known prior TB exposure or screening history. They were all asymptomatic and had normal CXRs. One reported going into the room of patient 2 on several occasions whilst she was unwell. The other two residents did not have any known direct exposure to any of the patients. The fourth IGRA positive contact is a staff member of the boarding house. They were born in a high TB burden country, were asymptomatic, and had a normal CXR. A timeline of active and latent patients is summarised in *Figure 1.3.*

The environmental investigation identified the boarding house consisted of five floors including a communal rooftop. The staircase was narrow and had a landing halfway between each floor. Each floor consisted of individual studio apartments with shared bathrooms and toilets on each floor. The corridors were narrow and poorly ventilated. There was a communal laundry located on the rooftop that was utilised by all residents. A floorplan was collated based on the site visit and it was determined that the three residents with latent TB infection each resided on the same floor as a TB disease patient. Patients 1 and 2 changed rooms several times during their stay within the facility.

Figure 1.2 Flow chart showing the results of the contact follow up for the 91 contacts identified during the investigation (n = 91)

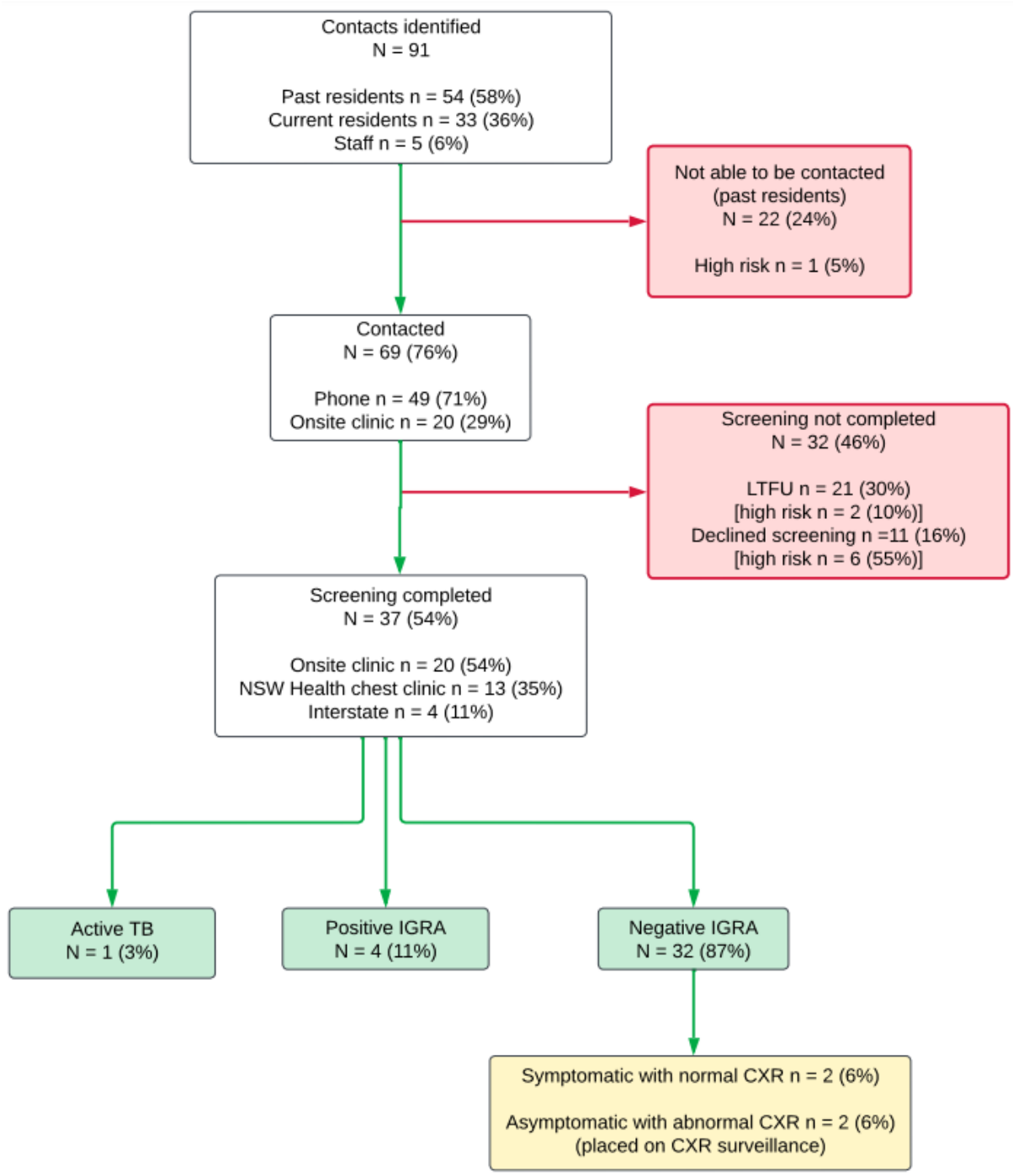


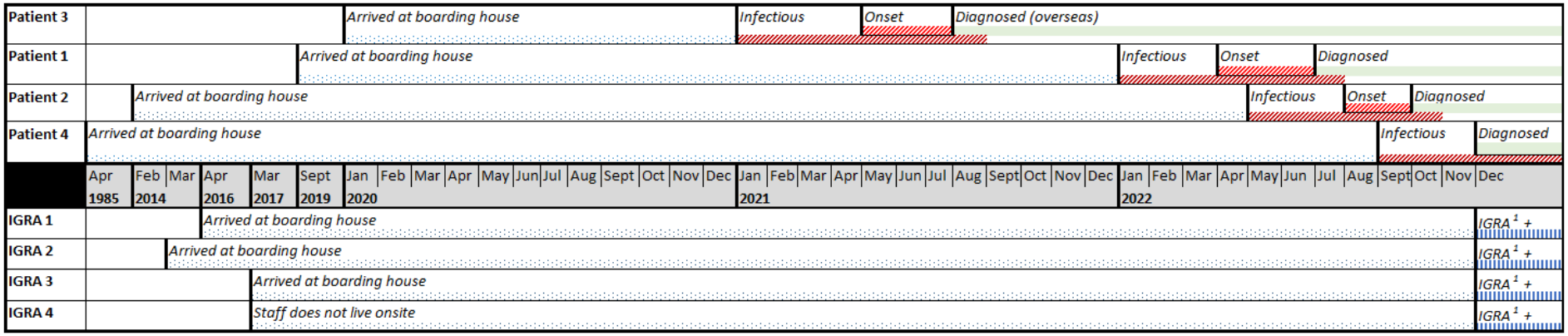
Table 1.2 Summary of tuberculosis disease patients and latent tuberculosis infection contacts who were identified during contact screening of the boarding house (n = 8)

Tuberculosis disease patients				
	Patient 1	*Patient 2*	*Patient 3*	*Patient 4*
Sex	F	F	M	M
Onset	April 2022	August 2022	~May 2021	Asymptomatic

Symptoms	Cough 10 weeks Fever Night sweats Weight loss	Cough unknown duration Iron deficiency Weight loss Nausea & vomiting	Undefined respiratory symptoms	Asymptomatic
Lab Results	Sputum microscopy (3+) and culture positive for AFB	Sputum microscopy (2+) and culture positive for AFB	Reported to have cavities on imaging	Bronchoscopy microscopy, PCR and culture positive for AFB
Diagnosis	July 2022	October 2022	~August 2021 (overseas)	December 2022
Risk factors	Childhood exposure to TB; brother recent TB	Diabetes	Childhood exposure to TB	COPD Previous unrelated TB exposure 2019*
COB	Low incidence country	Low incidence country	Low incidence country	Australia
Contacts with positive IGRA on screening				
	Contact 1	***Contact 2***	***Contact 3***	***Contact 4***
Sex	M	M	F	M
Arrival in boarding house	April 2016	March 2014	March 2017	Staff does not live onsite
Symptoms	Asymptomatic	Asymptomatic	Asymptomatic	Asymptomatic
Lab Results	IGRA positive CXR negative	IGRA positive CXR negative	IGRA positive CXR negative	IGRA positive CXR negative
Diagnosis	December 2022	December 2022	December 2022	December 2022
Previous risk factors	Nil	Nil	Nil	Born and lived in high burden country
COB	Australia	Australia	Australia	High incidence country

** TB infection treated. AFB = Acid Fast Bacilli, PCR = Polymerase Chain Reaction, COPD = Chronic Obstructive Pulmonary Disorder, IGRA = interferon-γ gamma release assay, CXR = Chest X-ray, COB = Country of Birth*

Figure 1.3 Time course of tuberculosis disease and tuberculosis infection patients in the boarding house (n = 8)



[1]*IGRA = interferon-γ gamma release assay.*

Discussion

We present an outbreak of four TB disease patients and four TB infection contacts residing within the same boarding house in inner-city Sydney. Patients 1, 2 and 3 were symptomatic for long-periods of time prior to diagnosis, facilitating transmission, most likely in the building's communal areas. The identification of this outbreak has highlighted the importance and value of routine genomic sequencing of TB isolates in confirming a TB outbreak in a low incidence setting such as Australia. We have also demonstrated the value of mass contact screening and the broad contact screening that should be considered when transmission has occurred in a residential building.

A major strength in the identification of this outbreak was the routine application of genomic sequencing, which was able to detect genomic relatedness between patient isolates. This then allowed for prompt and targeted public health investigation and follow-up. Strong collaboration between the local chest clinic, the PHU, NSW TB Program, and pathology service, and early formation of an outbreak management team, were crucial in coordination of the outbreak investigation.

The local chest clinic which conducted the patient interviews, had established a working relationship with the manager at the boarding house, who assisted in facilitating the distribution of risk communications to current residents and establishing the onsite clinic within a week of the investigation commencing. This ensured residents at the boarding house were provided with convenient options for screening rather than relying on them to present to a chest clinic, enhancing our ability to promptly conduct contact follow up and screening.

Whilst there were many strengths to this investigation, there were also limitations. Despite intensive contact investigation efforts, we were still unable to contact a large proportion of contacts identified. We suspect that many of the former temporary residents were not able to be contacted as they had returned overseas. There were also a considerable number of contacts who we contacted, made aware of their exposure, but did not complete screening. This meant we may have missed identifying all TB infection patients associated with this outbreak. We were unable to know the reasons why contacts did not complete screening, and whether this stemmed from health system or patient factors. This suggests further work is required to understand the reasons why people do not complete screening for TB if we are to increase screening completion rates and maintain a low incidence of TB in Australia. While TB testing and treatment are free in public clinics in NSW, irrespective of eligibility for government-funded health

care, anecdotally a few contacts that had attempted screening were deterred from completion when they were referred to private pathology services and asked to pay a fee. In addition, some temporary residents may have been concerned that TB testing would impact immigration visas.[9, 10]

We were unable to elicit the exact transmission pathways from either the WGS (due to the limited SNP differences) or the patient epidemiology, due to some patients having multiple exposures to infectious patients. One of the key questions left unanswered from this outbreak is the possibility of more than one chain of transmission among the known patients. Knowing how TB was transmitted between the patients would have assisted in providing a more precise risk stratification of people in the facility. Another limitation is that we were not able to know whether the people with positive IGRA tests were linked to this exposure. While three out of the four people with positive IGRA tests had no known history of prior TB exposure, another source cannot be ruled out, as none had received prior screening for TB disease. The fourth TB infection patient was born in a high burden country for TB, so we were unable to ascertain if their TB infection was a result of exposure from the boarding house or from their country of birth.

Despite the limitations of our investigation, the value of routine genomic sequencing of *M. tuberculosis* for public health investigations is beneficial and considered the gold standard in the assessment for transmission and strain relatedness.[11] The identification of closely related strains allows for detection of clusters that may indicate recent transmission and require more intensive public health investigation and follow up.[11] The usefulness of routine WGS was demonstrated in this investigation as clustering was only identified after genomic sequencing results were notified, which then expanded our contact and active case finding investigation. Although we were unable to determine the exact transmission pathways of this outbreak, when more genomic diversity is present genomic sequencing has the potential to suggest the direction of transmission.[5] Despite our investigation displaying the utility of routine genomic sequencing for TB program development and control, results should be interpreted along with epidemiological or clinical information.[5, 12]

Outbreaks of TB pose a significant risk to communities and if left without intervention, they add to the incidence of TB disease and prevalence of TB infection, threatening the maintenance of low-TB incidence and increasing the risk of local transmission.[13] Therefore, contact investigation and robust outbreak management are essential elements for TB control in low-incidence settings.[8] When local transmission is suspected, or an outbreak identified, a coordinated and prompt response based on a multi-

disciplinary approach is required.[14] A risk assessment to prioritise contact follow up based on the infectiousness of the index patient and intensity of exposure should be considered, especially in multi-dwelling buildings or other complex exposure sites.[15] This approach to the risk assessment and epidemiological investigation helps optimise resources, which are often stretched in TB programs.[13]

Conclusion

This outbreak has demonstrated the value of routine genomic sequencing to identify clustering and local transmission of TB, leading to targeted public health investigation. We have shown the importance of robust outbreak investigation using a multi-disciplinary team, with broad screening and multiple follow-up strategies in this boarding house environment where residents did not necessarily know each other. Despite intensive contact tracing efforts, we were not able to complete screening for a substantial proportion of contacts, suggesting that methods to improve TB contact screening completeness should be explored. If low TB incidence countries are to progress to elimination, investment in routine genomic sequencing and robust public health investigation should be commonplace in TB management guidelines and policies.

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Appendix I

Literature review search strategy

I conducted a literature review to contextualise the role of whole genomic sequencing to detect outbreaks of TB in low incidence settings

Specifically, the objectives of my search were to:

Assess how routine genomic sequencing contributes to identify transmission clusters and guiding public health investigations.

Determine the role of genomic sequencing in enhancing contact and active case finding during TB outbreaks.

Explore the integration of genomic sequencing with traditional epidemiological and clinical data to improve outbreak management and TB control in low-incidence settings.

Research question

What is the role of routine genomic sequencing of *Mycobacterium tuberculosis* isolates in detecting TB outbreaks in low-incidence settings?

Search strategy

The search strategy included the following terms:

(tuberculosis OR "*Mycobacterium tuberculosis*") to capture studies on the disease

- AND ("low incidence settings" OR "low burden") to capture geographical regions of low-incidence TB
- AND (outbreak* OR "Disease Outbreaks" OR transmi* OR "disease transmission") to identify studies describing outbreaks, or transmission events.
- Preference was also given to studies that mentioned genomic sequencing or building transmission.

Databases searched

The search was conducted across multiple databases to ensure comprehensive coverage of existing literature. The databases included:

- SCOPUS
- PubMed
- MedLine

Methods

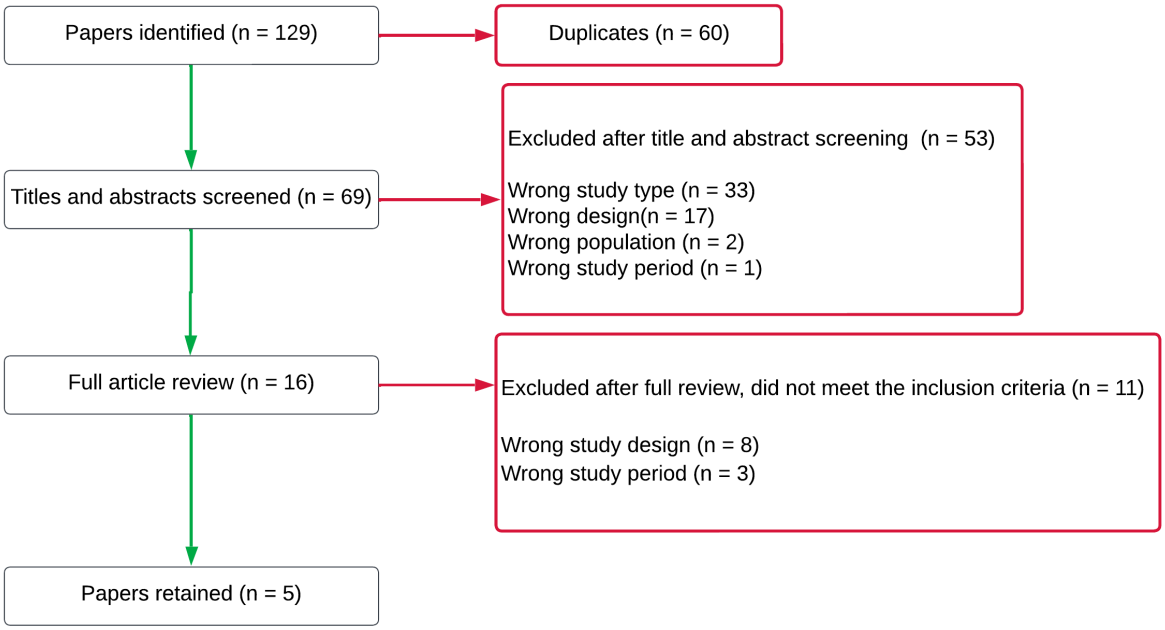
The search was limited to English language papers published between 2013 to 2023. Articles were excluded if the study type or design did not align with the objectives such as papers that focused on basic epidemiology, cost-effectiveness or descriptive studies

without exploring the role of genomic sequencing. Studies conducted in high-burden settings or non-outbreak settings were excluded as they did not address low-incidence scenarios or outbreak dynamics. Articles that mentioned genomic tools in passing without evaluating their role in detecting or managing outbreaks were excluded. Articles that were general reviews or commentaries on TB control without presenting new findings, case studies, or insights relevant to low-incidence settings were also excluded. Articles were screened by title, abstract, and full text were necessary.

Results

The search of the three databases returned 129 articles. Sixty were duplicates. Sixty-nine articles had their abstract and titles screened and 16 were retained for full article review. A further 11 were removed after full article review as they did not meet the inclusion criteria. Five studies met the inclusion criteria and directly addressed the research objectives, providing insights into the role of WGS in low-incidence TB outbreak detection and management. The findings from these papers were used to inform the discussion section of the report, emphasising the importance of genomic sequencing as a complementary tool to traditional TB control methods.

Figure 1.4 Literature review database search strategy



Chapter II – Section 2

Where the cooling water drifts: An outbreak of Legionella pneumophilia serogroup 1 in the central business district of Sydney, Australia, 2024

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Abbreviations

CBD	Central business district
CDC	Centres for Disease Control and Prevention
cfu/mL	Colony-forming units per millilitre
CWS	Cooling water systems
FASS	Forensic and Analytical Science Service
HCC	Heterotrophic colony count
HDU	High dependency unit.
ICU	Intensive care unit
Illumina	Illumina DNA Prep
LD	Legionnaires' disease
Lp1	Legionella pneumophila serogroup 1
NIR	National Incident Room
NSW	New South Wales
QIAGEN	DNeasy UltraClean Microbial Kit
RMP	Risk management plan
SABS	Safety Alert Broadcast System
SBT	Sequence-based typing
SESPHU	South Eastern Sydney Public Health Unit
SNP	Single Nucleotide Polymorphism

Prologue

Introduction

In January 2024 the South Eastern Sydney Public Health Unit (PHU) was alerted to four people with a confirmed diagnosed of *Legionella pnuemophilia* serogroup 1. The four cases did not reside within SES Local Health District (LHD), but they all had visited the Sydney central business district (CBD) during their exposure period.

My Role

When we began investigating this outbreak, I was the only epidemiologist rostered on at the time. The outbreak occurred during a period of low activity over the Christmas and New Year holiday period. As a result, I was the lead epidemiologist for this outbreak. I was responsible for coordinating outbreak management team meetings and distributing agendas and minutes for these meetings. I produced regular situation reports, maintained a case line list and collaborated with the One Health Branch at the Ministry of Health to perform geocoding and mapping of case locations, walking routes and environmental investigation areas. I also drafted a media release outlining the initial investigations of the outbreak.

Lessons Learnt

This outbreak provided an invaluable learning experience. One of my key accomplishments was quickly mastering geocoding and mapping software, despite having no prior experience. Adapting to new tasks was crucial, particularly since I had no background in *Legionella* or its control. A significant lesson I learned was the importance of organisation—collaborating with multiple internal and external stakeholders presented challenges in data sharing and coordination. Finding fast, effective solutions became essential. One of the more complex aspects involved translating environmental health fieldwork into electronic records for epidemiological analysis, something I had to navigate without prior experience in environmental investigations. Managing data from several contributors while maintaining a single source of truth was another challenge. Additionally, learning about *Legionella* risk management plans, cooling water system registration, and numbering significantly contributed to improving the accuracy of data collection.

Public Health Impact

This outbreak demonstrated the potential impact of construction dust on contamination of nearby cooling water systems in the Sydney CBD. We suspect that dust and debris from an adjacent construction site may have contributed to ongoing contamination of a

cooling water system (CWS), even after initial disinfection. Construction activities have been previously documented to increase the risk of *Legionella* proliferation. This ongoing contamination could have extended the exposure risk despite the prompt environmental interventions described in this outbreak. This outbreak has highlighted the importance of enhanced monitoring and cleaning protocols for CWS during periods of nearby construction.

Acknowledgements

I would like to sincerely thank Kirsty Hope and Zoe Baldwin (previous MAE scholars, now working in the NSW Ministry of Health) who were such a wonderful support during this outbreak, in assisting with outbreak management, geocoding and mapping, I will be forever grateful and will always remember this outbreak fondly. Thank you to Dr Karen Chee and Dr Mark Ferson for your patience and guidance throughout this outbreak. Thank you to Misha Klingstrom for answering all my environmental health questions and to the wider environmental health team at SESPHU for being such a fabulous team to work with!

Abstract

Objective

Legionnaires' disease (LD) causes severe pneumonia. Outbreaks are infrequent in Australia, with cooling water systems (CWS) regulated to reduce risk. In summer 2024, a *Legionella pneumophila* serogroup 1 (Lp1) outbreak was detected in visitors to the Sydney central business district (CBD). We investigated to identify cases and control the source.

Methods

Case-patients were detected through routine laboratory notifications and classified as per surveillance case definitions. Case-patients were also identified following a public health alert. Case-patients were interviewed to determine symptoms, and environmental exposures 2-10 days prior to symptom onset. We mapped exposures sites and used a 500m radius buffer to identify overlapping areas for investigation. CWS in shared exposure areas were inspected and tested for *Legionella*. Historical results from routine CWS testing were reviewed. Genomic sequencing was performed on environmental and patient isolates. Clinician and public alerts were issued, and CBD building managers were requested to maintain CWS.

Results

The investigation identified 15 legionellosis case-patients: two had Lp1 positive sputum cultures, 14 were hospitalised, and six required intensive care. All case-patients visited the CBD between 12-26 December 2023. Between 3-12 January 2024, 166 CWS across 118 CBD sites, plus three water fountains were tested. Lp1 was cultured from one CWS. Genomic sequencing from five environmental and two clinical isolates showed a probable link. The positive CWS was decontaminated but continued to have Lp1 detected, below the reportable limit, possibly due to ongoing dust contamination, necessitating additional maintenance.

Weeks later, a case-patient diagnosed in Europe who had visited key exposure locations in the CBD between 21-23 December 2023 was epidemiologically linked to the outbreak.

Conclusion

Our investigation indicates a contaminated CWS may have been the source of this outbreak, potentially precipitated by nearby construction. Given the CWS was contaminated with levels below the reported limit, this emphasises the importance of strengthening regulations to reduce Lp1 outbreak risk, and timely reporting under International Health Regulations to identify additional outbreak cases.

Introduction

Legionellosis is a severe but uncommon form of pneumonia caused by *Legionella* bacteria.[1] In Australia *Legionella pneumophilia* serogroup 1 (Lp1) causes most outbreaks of legionellosis. *L. pneumophila* thrives in engineered water systems that can produce inhalable water aerosols, such as air conditioning cooling towers, evaporative condensers, humidifiers, decorative fountains, hot tubs and showers.[1, 2]

Air conditioning cooling towers, also known as cooling water systems (CWS) have previously been associated with outbreaks in the Sydney central business district (CBD).[3-6] In response to two significant outbreaks in the Sydney CBD in 2016, the NSW public health regulations were updated.[6, 7] Preventative measures for CWS focus on minimising the growth of the bacteria within the CWS. These measures are governed by the Public Health Act 2010 and the Public Health Regulation 2022, requiring all CWS to be equipped with a disinfection procedure that is always in operation to ensure the concentration of *Legionella* in the system is <10 colony-forming units per millilitre (cfu/mL) and the heterotrophic colony count (HCC) is <100,000 cfu/mL.[3, 8] The New South Wales (NSW) Guidelines for *Legionella* Control in CWS stipulate that each system must be assigned a distinct identifying number registered with the local government.[9] Additionally, the guidelines mandate the development of a risk management plan (RMP) and annual audits, with certificates of completion submitted to the local government authority.[9]

Monthly sampling and testing for *Legionella* and HCC are mandatory, with any results exceeding 1,000 cfu/mL for *Legionella* and 5,000,000 cfu/mL for HCC to be reported to the local government.[7, 9]

In January 2024 the South Eastern Sydney Public Health Unit (SESPHU) were notified of several Lp1 patients who had visited the Sydney CBD during their exposure period, prompting an investigation.

Methods

Clinical and epidemiological investigations

Case-patients were detected through routine laboratory notifications to local public health units. A confirmed case of Lp1 is defined in the NSW Health Legionellosis Control Guidelines[1] and requires laboratory and clinical evidence. Laboratory evidence includes isolation of *Legionella* or detection of Lp1 urinary antigen; clinical evidence includes symptoms of fever or cough or pneumonia. Where possible, sputum specimens were collected from patients and prepared for culture. Case-patients were interviewed via phone and email using the Communicable Disease Network of Australia *Legionellosis Investigation Form*,[1] to obtain information on clinical symptoms, risk factors and locations of potential environmental exposures 2-10 days prior to symptom onset *Appendix I*. Descriptive analysis was performed on case-patient's demographic and characteristic details.

Reported case-patient locations in the Sydney CBD during their exposure period, including walking and other travel routes, were geocoded in R v4.3.2, using tidygeocoder.[10] These geocoded locations were then mapped using QGIS v3.34.3.[11] Targeted environmental investigation areas were defined using case locations and walking routes. These investigation areas were modified and expanded as additional case-patients and case-patient locations were identified.

An alert was distributed, advising of the outbreak and prompting testing using the NSW Health Safety Alert Broadcast System (SABS) for hospital clinicians. An alert to general practitioners was also distributed. A media release was issued to inform the public and prompt medical review for symptomatic people who may have been in the Sydney CBD. A letter was emailed to all building managers within the CBD informing them of the outbreak investigation, reminding them of regulatory requirements for maintenance/operation and noting the possible effect of construction dust on disinfection systems.

Environmental health investigation

CWS within the investigation area were prioritised for inspection and sampling using a risk matrix of low, medium or high risk (determined by the CWS RMP). These risk classifications were based on previous noted non-compliances in an unsatisfactory audit or recent reportable *Legionella* or HCC. CWS were further prioritised for inspection and sampling based on expert knowledge of environmental health officers and local factors identified during field work. All high risk CWS within the key exposure area were

inspected and sampled, in addition to some lower-risk towers. Audit reports, cleaning, maintenance, and microbial sampling results from the three months prior to case-patient detection were also reviewed. CWS water samples were sent to the laboratory at the Forensic and Analytical Science Service (FASS) for culture.

Laboratory investigations

Environmental and clinical isolates underwent confirmatory Lp1 typing and whole genome sequencing to examine relatedness. Isolates were cultured and serotyped as previously described.[12] Genomic DNA was extracted using the DNeasy UltraClean Microbial Kit (QIAGEN) with modifications.[13] Sequencing libraries were prepared using Illumina DNA Prep (Illumina) and sequenced on the NextSeq2000 or NextSeq500 instruments. Sequencing reads were quality controlled and assembled as previously described.[14] L. *pneumophilia* sequence-based typing (SBT) was performed on the assembled genomes using legsta v0.4.0.[15] Core Single Nucleotide Polymorphism (SNP) analysis was conducted using snippy v4.3.5[16] against a SBT211 reference genome, AUSMDU00010536 (GenBank accession: CP045974.1). A core SNP phylogenetic tree was constructed IQ-TREE v1.6.7[17]running the GTR+G4 substitution model and visualised in R using ggtree v1.99.1.[18]

Results

Clinical and epidemiological investigations

There were 15 confirmed case-patients (*Table 2.1*) of legionellosis identified through notification of positive Lp1 urinary antigen tests between 28 December 2023 and 15 January 2024 who had visited Sydney CBD in their exposure period (*Figure 2.1*). Four (27%) case-patients were female and 11 (73%) were male. The age of case-patients ranged from 28 to 81 years; the median age was 66 years. Fourteen (93%) case-patients required hospital admission of whom six (43%) required high dependency or intensive care unit admission. Eight case-patients had a sputum sample collected, of which two were successfully cultured for Lp1.

All case-patients had visited the Sydney CBD between 12-26 December 2023 (*Figure 2.2*) with some patients visiting the Sydney CBD on more than one occasion during their exposure period. Fourteen (93%) of the 15 patients spent time in the CBD between 19-21 December 2023 and all visited locations in the same area of the CBD.

Table 2.1 Case-patient demographic, hospitalisation, and prevalence of legionellosis risk factors. (n= 15)

Characteristics		N (%)	Median (range)
Sex	Male	11 (73%)	
	Female	4 (27%)	
Age [years]			66 (28-81)
Hospitalisation		14 (93%)	
	HDU[1]/ICU[2]	6 (43%)	
Length of hospital stay [days]			5 (2-59)
Deaths		0 (0%)	
Risk factors	Medical conditions	11 (73%)	
	>50 years	10 (67%)	
	Smoking	2 (13%)	

HDU = High dependency unit, ICU = Intensive care unit

Figure 2.1 Epidemiological curve of Legionella pneumophila case-patients by date of symptom onset, with exposures in the Sydney CBD between 12-26 December 2023. (n= 15)

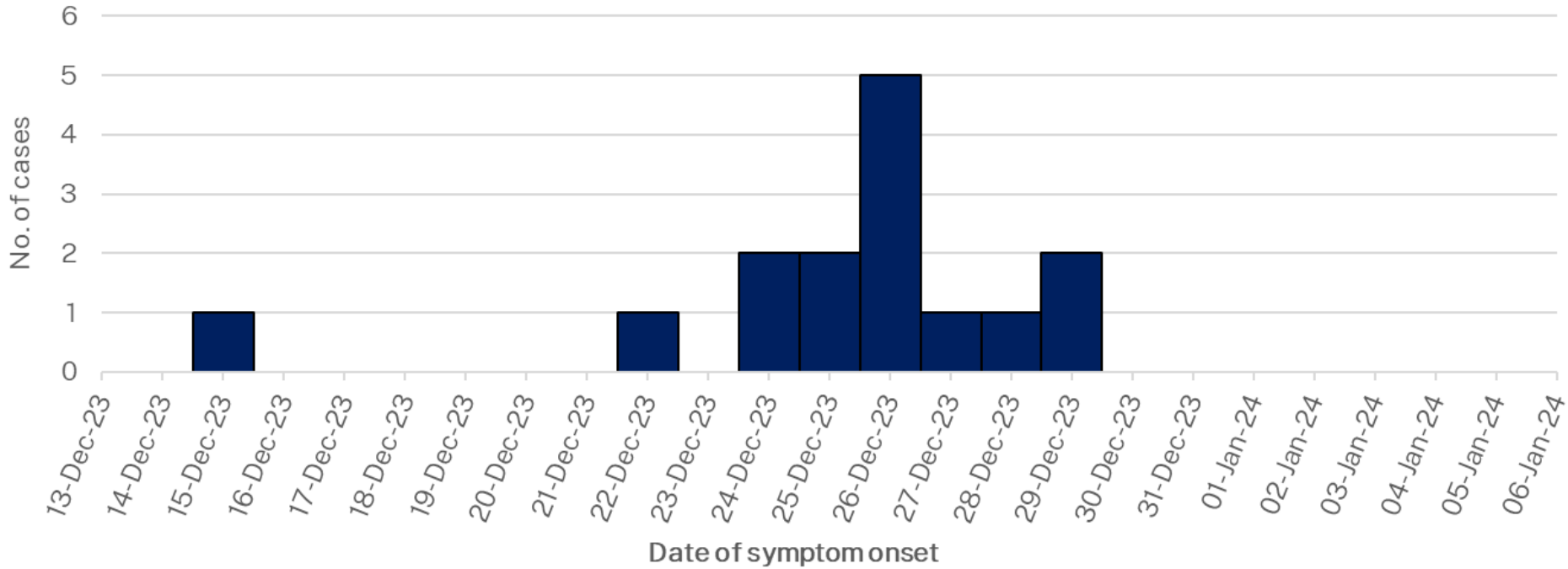
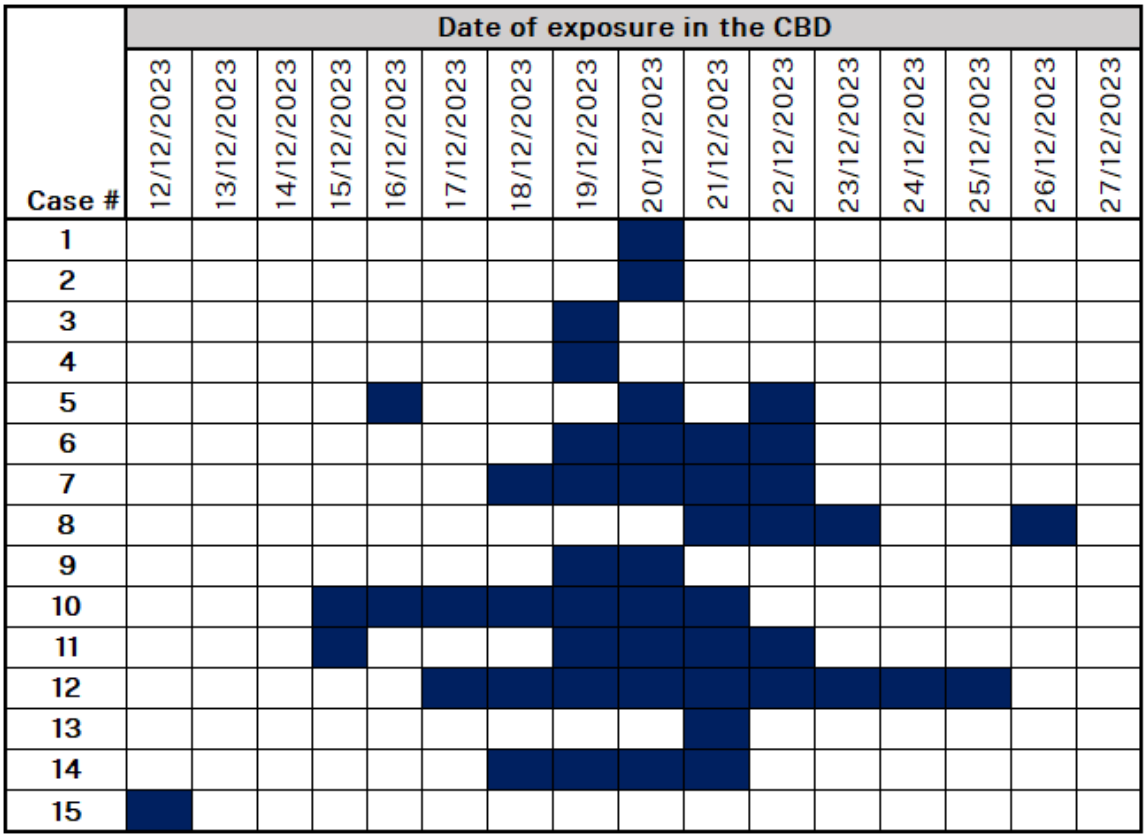


Figure 2.2 *Legionella pneumophila* patients and the date/s they visited the central business district (CBD) during their exposure period, December 2023. (n= 15)



Environmental health investigation

From 3-12 January 2024, 166 CWS were sampled across 118 sites, along with three water fountains. *Figure 2.3* shows the targeted environmental investigation areas where CWS were inspected and sampled across the five days of testing.

One (0.6%) CWS was positive for *Legionella pneumophilia* serogroup 1 at a level of 150 cfu/ml. Following initial decontamination of the CWS, the CWS continued to test positive at levels of >500 cfu/ml, requiring additional decontamination, investigation, and management strategies.

Genomic investigation

Five environmental and two clinical Lp1 isolates were available for whole genome sequencing. All five environmental isolated were from the same positive CWS and were sampled across several days and sites within the CWS. All seven genomes belong to the same sequence type (ST211) which is a common *L. pneumophila* sequence type found in Sydney. Isolates were 0 to 5 SNPs apart, suggesting a probable link between the environmental source and clinical cases (

Figure **2.4***)*. Of note, a clinical sample (24-001-0010) and an environmental sample (24-

001-0103) collected four days apart were genomically indistinguishable (i.e. showed 0 SNP difference). All cases were between 11 and 14 SNPs different to the reference genome.

Figure 2.3 Map of the locations visited and walking routes of *Legionella pneumophilia* case-patients and the areas of the focused environmental health investigations, Sydney CBD, December 2023 to January 2024. (n= 15)

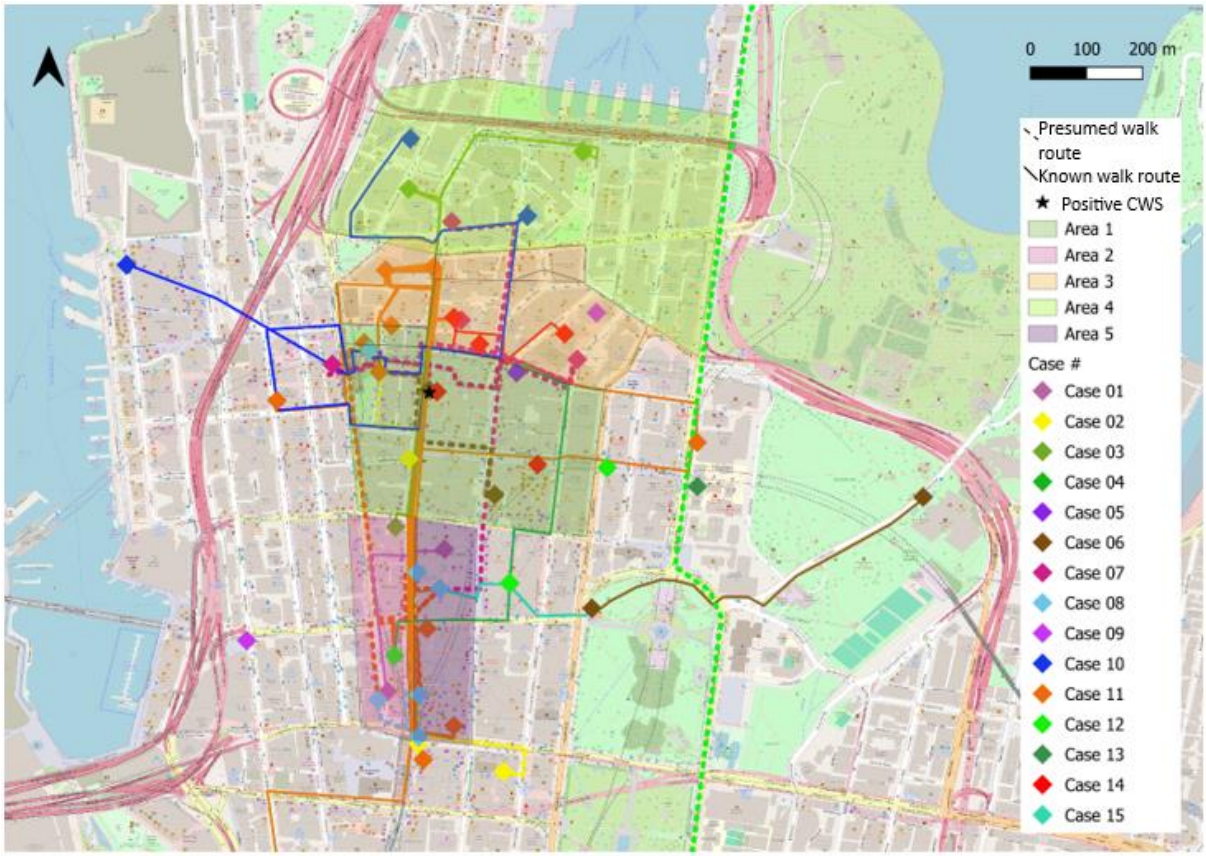
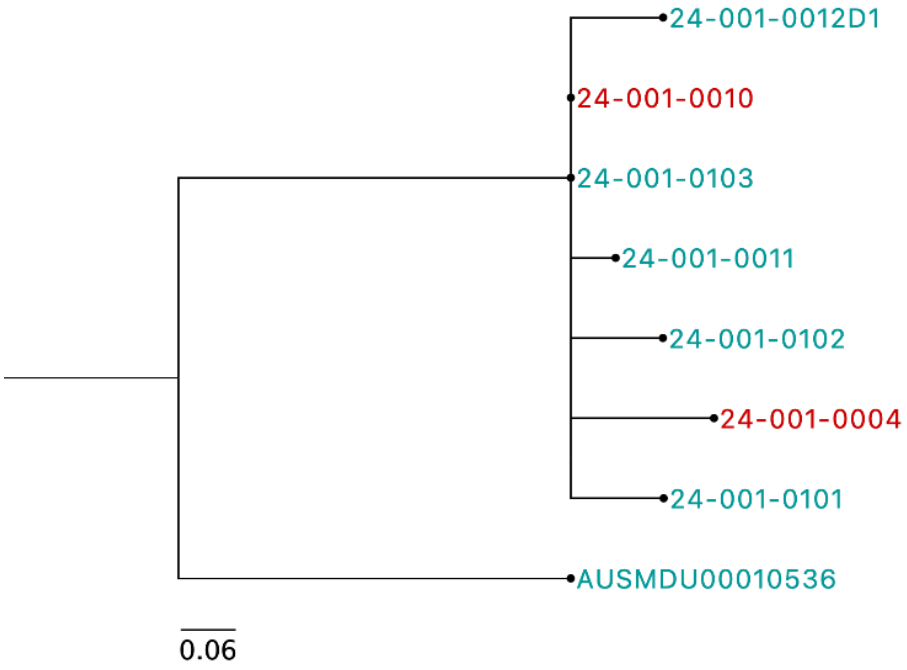


Figure 2.4 Phylogenetic tree of Lp1 genomes of in the Sydney CBD cluster, December 2023 to January 2024. Environmental isolates are coloured blue and clinical isolates are coloured red.



Discussion

Between late December 2023 and early January 2024, 15 people who had visited the Sydney CBD during their exposure period were identified with Legionnaires' disease (LD) due to Lp1. All were epidemiologically linked to the outbreak. A thorough investigation of possible sources related to case-patients' movements took place. Lp1 was isolated from one CWS, with genomic sequencing from five environmental and two clinical isolates showing a probable link between the environmental source and case-patients. Seven weeks after the outbreak one additional case-patient was epidemiologically linked to the outbreak, after the National Incident Room (NIR) was notified of a person who had visited the CBD during the key exposure period and subsequently developed LD due to Lp1 and required intensive care on return to their home country.

A key strength in this outbreak investigation was the ability to rapidly obtain exposure information from case-patients and liaise with the local government to establish an environmental investigation area. Despite staffing limitations over the Christmas holiday period, we were able to mobilise rapidly and conduct extensive field investigations. The collaboration between stakeholders ensured rapid communications to building managers within the CBD informing them of the outbreak and instructing them to begin disinfection of CWS to mitigate ongoing *Legionella* exposure to the community. As this communication occurred at initiation of the outbreak investigation, it is possible that some CWS were disinfected prior to sampling. For this reason, systems may no longer have contained *Legionella* at the time of testing, thus limiting our ability to detect all CWS contaminated with *Legionella*.

In addition to the communications to building managers, we also delivered rapid communications to clinicians and the public, which prompted testing amongst the community, facilitating active case finding. The delay between illness onset and prompt from public health for sputum collection, limited some case-patients' ability to produce a sputum sample that was suitable for culture and genomic sequencing. Whilst detection of Lp1 urinary antigen is a rapid way to diagnose people with legionellosis, a sputum culture is required for genomic sequencing, however this is not always obtainable.

This investigation was also subject to the limitation that due to the density of CWS in the CBD not all CWS in the investigation area were able to be prioritised for testing. Therefore, there could have been a CWS classified as low risk that may have contributed to this outbreak but was not tested. Finally, the positive tower may not have been the source for some or all cases, as there is the possibility that another CWS was positive

and effectively decontaminated prior to testing and the tower we present in this outbreak was secondarily contaminated.[2]

We suspect that dust from a nearby construction site contributed to the contamination of the CWS, and ongoing contamination even after initial disinfection. The United States (US) Centre's for Disease Control and Prevention (CDC) investigated the sources of *Legionella* outbreaks between 2000 and 2014, which found that of all outbreaks related to external sources, 43% were due to nearby construction.[19] A 2010 study also showed an association between construction and LD, in which they found widespread contamination of potable water within a hospital with *L. pneumophila* during a period of major construction.[20] The authors noted that construction nearby the hypothesised exposure site was completed within seven days of the first notification of *L. pneumophila* in a patient. Our inspectors noted high levels of construction dust in and around the cooling water system that had Lp1 contamination, from building demolition in the adjacent block. This highlights the need for those responsible for CWS maintenance to consider additional cleaning and monitoring when construction is occurring nearby.

There is also evidence to suggest that changes in weather conditions could also contribute to *Legionella* contamination.[21, 22] In Sydney, like other regions globally, legionellosis cases tend to peak during autumn or summer, particularly during periods of increased rainfall and humidity, with a lag of 1–2 weeks between weather conditions and case onset.[14] In the two weeks preceding the outbreak, Sydney experienced a heatwave with temperatures reaching 40 degrees Celsius and relatively humidity averaging 81% for the month of December 2023.[23, 24] There is evidence to support association between temperature and relatively humidity and the occurrence of legionellosis, as these conditions allow the bacteria to survive for longer in the environment and provide ideal conditions for bacteria growth.[21, 25] A 2023 study from Switzerland investigated the impacts of air pollution on LD in Switzerland which showed a strong association between elevated daily mean temperature 6-14 days before occurrence of LD.[25] Another study found that the risk of disease increased when temperature increased at high relative humidity, which indicated that airborne *L. pneumophila* could survive for longer in the environment, such as areas of pooled water following rain events.[21] A 2024 study, looking at associations between weather and LD in Sydney found that there were significant associations between LD cases and mean relative humidity and temperature at 9am and 3pm.[14] Periods of higher-than usual temperature should also be a prompt to enhance CWS maintenance.

Considerations should also be given to review the current threshold for notification of

Legionella detections in CWS. The contaminated CWS in this outbreak did not reach the reporting threshold of 1,000 cfu/ml, yet our findings suggest that this was the source of the outbreak. This has also been found in prior outbreaks, including a cluster in Western Sydney in 1998.[26] Notification of any detection of Lp1 on routine testing would facilitate prompt follow up by local government and allow earlier identification and mitigation of any issues.

Conclusions

Our investigation indicates a contaminated CWS may have been the source of this outbreak, potentially precipitated by nearby construction and preceding hot weather. This emphasises the importance of proactive CWS management, including building occupiers revising their RMP and having mitigation measures in place to address increased contamination from external sources. These findings support strengthening the current regulations to reduce the risk of Lp1 contamination of CWS, for example through lowering the *Legionella* notification threshold to identify and address increased *Legionella* levels as a proactive public health measure.

Following conclusion of this outbreak a debrief was held with all members of the outbreak management team, this resulted in recommendations and updates to standard operating procedures.

Acknowledgements

The authors thank pathology service providers in NSW for their contribution to legionellosis surveillance and to Eby Sim (University of Sydney) and Basel Suliman (NSW Health Pathology) for their expert assistance in the typing and genotyping of *Lp*1 isolates.

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Appendix I

Legionellosis case interview form

Case name: ..... DOB: ...../...../..... Notification ID: .....
First name Surname

Legionellosis Investigation Form

*Information required for NNDSS core data set. No enhanced surveillance data are collected at the national level.

☐ ***L. pneumophila**** ☐ ***L. longbeachae**** ☐ **Unspecified*** ☐ **Other-specify***.....

Public Health Unit ..... Outbreak ID*: .....

Completed by: .....

Telephone: ..... Fax: .....

NOTIFICATION:

Date PHU notified: ...../...../..... Date initial response: ...../...../.....

Notifier: ..... Organisation: .....

Telephone: ..... Fax: ..... Email: .....

Treating Dr: .....

Telephone: ..... Fax: ..... Email: .....

CASE DETAILS: **UR No:** .....

Name: .....
First name Surname

Date of birth*: ...../...../..... Age*: .....Years* .....Months* Sex*: ☐ Male ☐ Female .....

Name of parent/carer: .....

☐ Aboriginal* ☐ Torres Strait Islander* ☐ Aboriginal & Torres Strait Islander* ☐ Non-Indigenous* ☐ Unknown*

English preferred language: ☐ Yes ☐ No – *specify* ..... Ethnicity – *specify* .....

Permanent address: .....

..... Postcode*: .....

Home telephone: ..... Mobile: ..... Email: .....

Occupation: ..... Work telephone: .....

Temporary address *(if different from permanent address)*: .....

..... Postcode: .....

Telephone: ..... Mobile: ..... Email: .....

General Practitioner: Dr .....

Address: ..... Postcode: .....

Telephone: ..... Fax: ..... Email: .....

SoNG Legionellosis Investigation Form - Legionellosis *21 March 2017* 1 of 5

Case name: ..... DOB: ...../...../..... Notification ID: .....
First name *Surname*

CLINICAL DETAILS:

Date of onset*: ...../...../..... Date of first consultation: ...../...../.....

Fever ☐ Yes ☐ No ☐ Unknown

Cough ☐ Yes ☐ No ☐ Unknown

Pneumonia ☐ Yes ☐ No ☐ Unknown *If yes, radiologically confirmed?* ☐ Yes ☐ No ☐ Unknown

Other clinical symptoms *(please tick)*:

☐ Headache ☐ Anorexia ☐ Malaise ☐ Nausea ☐ Vomiting ☐ Confusion ☐ Myalgia ☐ Diarrhoea

☐ Other – *specify* .....

Hospitalised: ☐ Yes ☐ No ☐ Unknown Hospital: ..... Date: ...../...../..... to ...../...../.....

Admitted to ICU: ☐ Yes ☐ No ☐ Unknown Hospital: ..... Date: ...../...../..... to ...../...../.....

Complications: ☐ Yes – *specify* ..... ☐ No ☐ Unknown

Outcome: ☐ Survived ☐ Died of condition* Date of death: ...../...../..... ☐ Unknown

---

LABORATORY*:

Public Health Units should encourage sputum (or, where available, bronchial washing, induced sputum or lung biopsy) culture to be sent to the state reference laboratory for typing and to enable matching of any isolates with any available environmental samples.

Laboratory: ..... First collection date: ...../...../.....

Isolation of Legionella: ☐ Yes -*specify site* ..... ☐ No ☐ Not done

Legionella urinary antigen: ☐ Detected ☐ Not detected ☐ Not done

Legionella PCR/NAT: ☐ Detected -*specify site* ..... ☐ Not detected ☐ Not done

☐ Fourfold rise in titre: 1st ..... Date: ...../...../..... 2nd ..... Date: ...../...../.....

☐ Single high titre (≥512): ..... Date: ...../...../.....

RISK FACTORS:

Age ≥ 50 years: ☐ Yes ☐ No ☐ Unknown

Smoker: ☐ Yes ☐ No ☐ Unknown

☐ Current smoker

☐ Ex-smoker Year quit ..... No. of years a smoker .....

Chronic disease: ☐ Yes ☐ No ☐ Unknown *If yes, specify below (please tick)*:

☐ Respiratory ☐ Chronic renal disease ☐ Cardiac ☐ Diabetes

☐ Other .....

Immunocompromised: ☐ Yes ☐ No ☐ Unknown *If yes, specify below (please tick)*:

☐ Immunosuppressive medications (e.g. Corticosteroids) – *specify* .....

☐ Oncology treatment ☐ Transplant recipient

Other risk factors: ☐ Yes – *specify* ..... ☐ No

Case name: ..... DOB: ...../...../..... Notification ID: .....
First name *Surname*

EXPOSURE PERIOD:

Date: ...../...../..... to **Date:** ...../...../.....
(Onset of symptoms – 10 days) (Onset of symptoms – 2 days)

EXPOSURES FOR *L. pneumophila*

ENVIRONMENTAL EXPOSURES: (include all exposures within the exposure period)

Potential exposure sources	**Exposure history**	**If Yes to any exposure source, please provide details below**
		Name of place or device, address/location and dates visited or used
Hospitalised (cooling water systems, warm water systems, respiratory devices, NG tubes)	☐ Yes ☐ No ☐ Unknown	Hospital: ..... Ward:..... Admission date: ...../...../..... Discharge date: ...../...../.....
Resided in a residential care facility (including temporary or respite care)	☐ Yes ☐ No ☐ Unknown	Facility: .....
Shops and shopping complexes (cooling water systems)	☐ Yes ☐ No ☐ Unknown	
Clubs, cinemas, hospitals (as a visitor), hotels, conference facilities (cooling water systems)	☐ Yes ☐ No ☐ Unknown	
Pools/aquatic centres, spas (including home spas), water parks	☐ Yes ☐ No ☐ Unknown	
Water fountains or sprinklers (including overhead misting sprinkler systems)	☐ Yes ☐ No ☐ Unknown	
Car/truck wash	☐ Yes ☐ No ☐ Unknown	
Dental treatment	☐ Yes ☐ No ☐ Unknown	
Humidifier, nebulisers or other respiratory devices	☐ Yes ☐ No ☐ Unknown	
Other – consider CBD, industrial/building sites, sporting venues , aquariums, water misters	☐ Yes ☐ No ☐ Unknown	

Case name: ..... DOB: ...../...../..... Notification ID: .....
First name *Surname*

TRAVEL DETAILS: (include any travel within exposure period)

Travel history		**If Yes to any travel, please provide details below**		
		Dates travelled	**Country/State visited**	**Places visited (e.g. hotels stayed)**
Domestic (within Australia)	☐ Yes ☐ No ☐ Unknown			
Overseas	☐ Yes ☐ No ☐ Unknown			

EXPOSURES FOR *L. longbeachae*

GARDENING EXPOSURES: (include all exposures within the exposure period)

Exposure source	**Exposure history**	**If Yes, please provide details below**
		Name of place or brand, address/location and relevant dates
General gardening activities	☐ Yes ☐ No ☐ Unknown	
Washed hands routinely after gardening activities	☐ Yes ☐ No ☐ Unknown	
Use potting mix or landscaping materials	☐ Yes ☐ No ☐ Unknown	
Prior knowledge of risks from potting mix or landscaping materials	☐ Yes ☐ No ☐ Unknown	
Wore gloves	☐ Yes ☐ No ☐ Unknown	
Wore mask	☐ Yes ☐ No ☐ Unknown	
Watered hanging baskets	☐ Yes ☐ No ☐ Unknown	
Visited a plant nursery/gardening centre/landscaping centre	☐ Yes ☐ No ☐ Unknown	

Case name: ..... DOB: ...../...../..... Notification ID: .....
First name *Surname*

PLACE ACQUIRED:

☐ Within the state
☐ Other Australian state/territory – *specify* .....
☐ Other country – *specify* .....
☐ Unknown

ENVIRONMENTAL ASSESSMENT:

Was an environmental assessment undertaken? ☐ Yes ☐ No ☐ Unknown If Yes, Date commenced: ...../...../.....

Details:

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ADDITIONAL COMMENTS:

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SoNG Legionellosis Investigation Form - Legionellosis *21 March 2017* 5 of 5

Appendix II

Legionellosis outbreak media release

NSW HEALTH
Media Release

NSW GOVERNMENT

3 January 2024

LEGIONNAIRES' DISEASE ALERT FOR SYDNEY CBD

NSW Health is advising people who have been in the Sydney CBD area in the past 10 days to be on alert for symptoms of Legionnaires' disease after seven people who have developed the disease spent time in the area in the last three weeks.

The three women and four men, ranging in age from their 20s to 70s, independently visited locations in the CBD between Bathurst Street, Sussex Street, Elizabeth Street and Circular Quay in the 10 days prior to their symptoms. All have been admitted to hospital for treatment of pneumonia.

All seven people have been identified with the Legionella bacteria that causes Legionnaires' disease, which is often associated with contaminated cooling towers of large buildings.

People can be exposed to the bacteria if contaminated water particles from a cooling system are emitted into the air and breathed in. Legionnaires' disease cannot be spread from person to person.

Symptoms of Legionnaires' disease can develop up to 10 days from the time of exposure to contaminated water particles in the air and include fever, chills, a cough and shortness of breath and may lead to severe chest infections such as pneumonia.

People who develop this disease are diagnosed by a urine or sputum test and chest X-ray and usually require antibiotic treatment in hospital. Those most at risk are people with underlying lung or other serious health conditions and people who smoke.

NSW Health environmental health officers are working closely with the City of Sydney Council to inspect cooling towers. Review of maintenance records of cooling towers in the CBD area will also help determine further towers to be inspected and sampled.

Managers of buildings with cooling towers are being contacted and informed of the cluster. Building owners should ensure that their cooling towers are operated and maintained in compliance with the NSW Public Health Regulation 2022.

Public health units in local health districts across NSW follow up cases of Legionnaires' disease and work closely with local councils in the management of cooling towers.

NSW HEALTH Media
Tel. 02 9391 9121 A/Hours. 02 9962 9890 Web. www.health.nsw.gov.au
healthdirect AUSTRALIA – providing expert health advice 24 hours a day to NSW residents – Tel. 1800 022 222

Chapter III

Establish or evaluate a surveillance system

Analysis of a public health dataset

Section 1 Evaluation of the South Eastern Sydney Local Health District (SESLHD) acute respiratory infections (ARI) report

Section 2 Annual report of acute respiratory infections (ARI) in South Eastern Sydney Local Health District (SESLHD), 2023

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Abbreviations

ABS	Australian Bureau of Statistics
ARI	Acute respiratory infections
ED	Emergency department
LGA	Local government area
NCIMS	Notifiable Conditions Information System
NSW	New South Wales
PHREDSS	Public Health Rapid Emergency, Disease and Syndromic Surveillance
PHU	Public Health Unit
PISA	Pandemic Influenza Severity Assessment
RSV	Respiratory Syncytial Virus
SESLHD	South Eastern Sydney Local Health District
WHO	World Health Organization

Prologue

Introduction

This project was an evaluation of the weekly South Eastern Sydney Local Health District (SESLHD) Acute Respiratory Infections (ARI) report as well as an analysis of the annual acute respiratory infections impact in SESLHD. The final product, the annual report, incorporated findings from the evaluation to produce an annual report for 2023 to meet the needs of stakeholders. Since the implementation of the weekly ARI reports in 2021, there had been no formal evaluation to determine its effectiveness, readability, and whether it fully utilised the range of surveillance data available at the District level. This evaluation aimed to assess the impact of the report, ensure it met stakeholder needs, and redefine the report's post-pandemic surveillance objectives. Following the evaluation, a comprehensive data analysis of yearly respiratory virus activity in the District was conducted to identify trends and patterns. By combining insights from the evaluation and data analysis, the goal was to develop an updated ARI report that is more useful, informative, and aligned with the evolving needs of healthcare professionals.

Given the large body of work in this chapter, it has been presented in two sections. Section 1 will detail the evaluation of the original ARI report, and Section 2, will detail the analysis and new annual report structure using 2023 data.

My Role

I was responsible for survey design, collating responses, analysis and documentation of evaluation results. I also sourced data from external sources, ensuring direct access for the raw data (not in pdf reports or extracted from emails) where possible, and ensuring formats were appropriate for use in R. I created the framework for the new report design and built the entire program in R for both a weekly report and an annual report. Both are set up so the reports can be run automatically with no editing of dates or calculated fields. I was responsible for all design and development for both reports and distribution of the initial pilot reports to the District. I also developed work place instructions and designed all local processes for the local epidemiology team. I hosted information sessions for the epidemiology team and staff specialists providing insights to the function and design of the report. I collated one-page quick reference guides for each of the annual and weekly reports and I also have held individual sessions with the epidemiology team demonstrating how to produce the report and troubleshooting where required. I continue to support production of the reports.

Lessons Learnt

This project was the first time I had ever used R Markdown, and I was equal parts nervous and excited to use this tool. R code can be incredibly fickle, so having patience is key to being able to find the solution rapidly. I also realised by the end of this project that I now know how to ask a question to get the answer I am looking for. This came from having to seek answers from the community of R users on a frequent basis. Initially I found myself knowing what I wanted to do, but unable to ask for it accurately. But by the time we hit the third figure to build I was on a roll! I think this also came from having more familiarity with R programming language and understanding more of the basic functions. This project has greatly enhanced my confidence in my R skills and following completion of this project and the development of these reports, I now feel confident in my R skills and answering questions about R from my colleagues.

I also further indulged in teaching, which I thoroughly enjoyed! I really loved being able to help the team transition to using this report and watching them also develop new skills, it was a very rewarding process.

Public Health Impact

The redevelopment of the ARI report at SESLHD has enabled provision of data on transmission, severity, and impact of COVID-19, influenza, and RSV, helping to inform district-level planning, resource allocation, and outbreak management. By identifying trends in vulnerable populations, such as the elderly and young children, the report supports targeted interventions, improves preparedness for future respiratory outbreaks, and enhances the capacity to protect high-risk groups.

Acknowledgements

I would like to acknowledge the PHREDSS, NSW Health Pathology, SESLHD Workforce and the FluTracking Australia teams for generously providing the data for this report. I would also like to thank the survey respondents, for their time to complete the evaluation survey.

I would also like to sincerely thank the NSW Health R Club people for their generosity when it comes to knowledge sharing and their endless patience and encouragement for people new to the R landscape.

Chapter III – Section 1

Evaluation of the South Eastern Sydney Local Health District (SESLHD) acute respiratory infections (ARI) report

Abstract

Introduction

In 2021, the South Eastern Sydney Local Health District (SESLHD) Public Health Unit (PHU) transitioned from separate influenza and COVID-19 reports to a combined weekly Acute Respiratory Infections (ARI) report to provide a comprehensive overview of respiratory illness. We conducted an evaluation of the ARI report to assess its usefulness, ensure it met stakeholder needs, and refine the surveillance objectives, as well as developing a more informative report aligned to the needs of healthcare professionals.

Methods

A survey was conducted among key ARI stakeholders from clinical and non-clinical areas to gather feedback on the report's acceptability, usefulness, and timeliness.

Results

Of the 120 stakeholders surveyed, 22 (18%) responded, 95% of respondents (21/22) reported reading the original ARI report and found it useful for monitoring infection rates and facility impacts. Feedback highlighted the need for improvements such as better readability, additional data on other respiratory viruses, and more interpretation of data. Insights from the survey and data review led to redesigning the report template using the WHO PISA tool, focusing on transmission, severity, and impact. The redesigned report integrated these findings, focusing on enhanced data sources, automation, and improved efficiencies.

Conclusion

The evaluation of the weekly report revealed its usefulness for monitoring disease trends but highlighted the need for broader data coverage and improved readability post-pandemic. Using the PISA framework and evaluation findings the report was redesigned to address these issues.

Introduction

The public health unit (PHU) within South Eastern Sydney Local Health District (SESLHD) has long produced regular infectious disease surveillance reports to keep both health professionals and the public informed about various circulating infectious diseases in the District. Historically, the PHU generated dedicated influenza reports throughout the influenza season. During the COVID-19 pandemic, the focus shifted to producing weekly COVID-19 surveillance reports due to the decrease in reported influenza cases. These reports provided a comprehensive overview of COVID-19 case numbers, geographic distribution, and demographics. The reports summarised outbreaks of high-priority groups such as aged and disability care services, serving as a critical resource for healthcare planning and preparedness across the District.

As the public health response transitioned back to routine operations in 2021, a need for broader infectious disease reporting evolved. To address this need, the PHU integrated its influenza and COVID-19 reporting into a combined weekly acute respiratory infections (ARI) report. This report was distributed internally to key stakeholders before being made publicly available on the LHD website.

Since the implementation of the weekly ARI report in 2021, there has been no formal evaluation to determine its usefulness, readability and whether it fully utilises the range of surveillance data available at the district level. This evaluation aimed to assess the report's current acceptability, ensure it meets stakeholder needs, and redefine its surveillance objectives post-pandemic. In addition to the evaluation, a comprehensive data analysis of yearly respiratory virus activity in the District was conducted to identify trends and patterns. By combining insights from the evaluation and data analysis, the goal was to develop an updated ARI report that is more useful, informative, and aligned with the evolving needs of healthcare professionals.

Methods

Describe the structure of the report

The current weekly ARI report was reviewed to identify areas that were no longer required post pandemic. Data sources used for the report were also identified, along with local workplace instructions to identify areas for improved efficiency.

Attributes of the report

We assessed several surveillance attributes of the report using an evaluation survey. The survey was created in Microsoft Forms[1] and emailed to all recipients on the existing distribution list for the weekly respiratory virus report. The email distribution list comprised of key staff from both clinical and non-clinical areas, including emergency departments (ED), infection control, intensive care services, hospital and District executives. The evaluation survey questions are shown in *Appendix II*.

The survey comprised both multiple choice and open-ended questions. A digital link was created for the survey and was included in the routine email that accompanies the report and remained open for two weeks. While respondents had the option to remain anonymous, facility and speciality information was collected. A maximum of two targeted reminders were sent to key stakeholders who had not yet completed the survey.

Acceptability

Stakeholders were asked about reading the report to determine if they read the email that provided a summary of key findings, read the PDF version of the full report, read both the email summary and the report, or did not read the email summary or report at all. If respondents indicated that they did not read the report at all they were provided the opportunity to provide any additional feedback and then the survey ended.

Additionally, data from the LHD's website was accessed to review web page traffic and usage patterns for the webpage where the weekly report was publicly available.

Usefulness and timeliness

We asked the respondents to report on the usefulness of the report on a scale of 1-10 - with a score of one indicating not useful at all and a score of ten indicating to be very useful - and how it informs their work. We also asked respondents about the timeliness of the report, if they thought the data in the report and frequency was suitable for informing of respiratory virus trends in the District. We also reviewed the process for compiling the weekly report, including data cleaning and analysis.

Stability

Data sources were identified and reviewed for how they were accessed and managed. The preparation, saving, and distribution methods of the report were reviewed, and the steps taken by staff to produce and distribute it. The workplace instruction was also reviewed to determine if it appropriately detailed how to produce the report.

Report design

The new report design template used feedback from the evaluation survey. The WHO PISA[2] tool was incorporated in the template to focus the report on three key assessment areas: transmission, severity, and impact.

Existing data sources identified during the evaluation were reviewed to improve accessibility and integration into the new report design. Additional data sources were identified to enhance the three key assessment areas. Once the data sources were established, a new report script was developed using R version 4.3.2[3] statistical software and R Markdown, [4] enabling automation into a word document based on the District's existing reporting template.

Dates and text elements were automated using calculations embedded within the script. The final output was generated in a Word document formatted according to the pre-approved reporting template.

To support this process, a detailed workplace instruction was created, multiple information sessions were conducted, and a step-by-step walkthrough of the report generation and script execution was provided. Additionally, a one-page quick reference guide was developed as a supplementary support tool. Ad-hoc support on an ongoing basis was also provided to the local epidemiology team.

Results

Structure of the report

The weekly report was approximately four pages long and comprised five key areas: key summary messages for local services, data summary, demographic data, residential facility outbreaks, and emergency department presentations and admissions. Data was presented on case numbers of COVID-19 and influenza by local government area (LGA) followed by epidemiological curves for both diseases. Test positivity was then presented as a line graph for COVID-19, influenza and respiratory syncytial virus (RSV) followed by pyramid graphs for COVID-19 and influenza case numbers by age and sex. Residential aged care facility exposures and outbreaks for COVID-19 and influenza were shown on a line graph. The final section of the report showed line graphs of current and previous years' presentations to ED and admissions from ED for respiratory, fever and unspecified infection, influenza like illness, COVID-19/coronaviruses and bronchiolitis.

Survey respondents

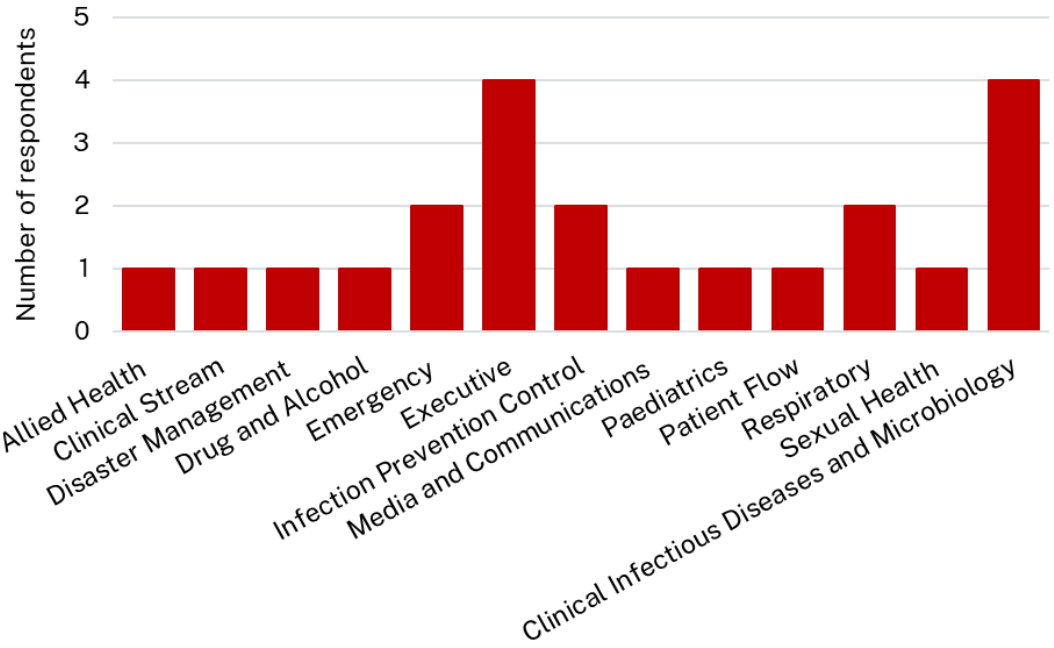
There were an estimated 120 stakeholders on the ARI report email distribution list of which 22 (18%) responded to the survey (*Table 1*). Additional efforts were made to increase the response ratee, through targeted reminder emails.

Table 1 Location of respondents who completed the evaluation survey on the weekly respiratory report (n =22)

Location	N	%
St George Hospital	6	27%
SESLHD	6	27%
Prince of Wales Hospital	3	14%
Sydney Eye Hospital	2	9%
Sydney Children's Hospital	2	9%
Population and Community Health	1	5%
St Vincent's Hospital	1	5%
Royal Hospital for Women	1	5%
Total	22	100%

Figure 1 shows the area in which the respondents currently work. Fifteen (68%) of the respondents were from hospitals in the District, with the remainder in executive/District-wide positions.

Figure 1 Area of work for respondents who completed the evaluation survey of the weekly respiratory report (n = 22)



Attributes of the report

Acceptability

Twenty-one (95%) respondents read the report, with 67% (n = 14/21) reporting reading both the report and the accompanying email summary. Twenty four percent (n = 5/21) only reported reading the email summary, and 10% (n = 2/21) reported reading only the full report and not the email summary.

Some of the feedback themes from accessing the report are summarised below.

- Helpful in monitoring rates of infections and impact on facilities
- Quick and easy to understand [email summary], if unable to review full report
- Graphs useful for comparisons

The one respondent who indicated they no longer read the report was prompted to provide a reason for this response. They indicated that the information in the report was no longer required.

If respondents indicated that they did not read the report (n=1/21) or read the email summary only (n=5/21), the survey ended. Respondents who answered reading the report or both the report and email summary (n=16/21) continued the survey and were then asked about specific aspects of the report.

The webpage data extracted for the period of 1 January to 2 August 2023 showed minimal interactions, with only four sessions recorded for accessing the page where the weekly report is published and no interaction with the link to the PDF version of the

report during this time. It is suspected that this interaction with the webpage is local PHU staff checking the report had been published appropriately.

Usefulness and timeliness

Feedback indicated that report was helpful for monitoring infection rates and facility impact, the email summary was appreciated for being quick and easy to understand, and the graphs were useful for comparisons.

Sixteen respondents rated the usefulness of the weekly report on a scale from 1 -10. The results indicated that 88% (14/16) of respondents rated the report as very useful (scores of 7 or higher), with six of the 16 (38%) respondents providing a rating of eight out of ten.

The report was considered useful for increasing awareness of trends, understanding the prevalence of specific viruses, and evaluating impacts on emergency departments and workforce planning. Respondents expressed that the report was also used to inform clinical teams and shared through regular newsletters. All (16/16) respondents agreed that the report was timely, with it being distributed on the Monday of each week, reporting on the previous week's data.

Themes of how the report informs the respondents' work are summarised below:

- Awareness of trends
- Prevalence of specific viruses
- Impacts on emergency departments and planning for surge in presentations/admissions
- Report is shared with teams or other clinicians to evaluate impact on the facility
- Published in a regular newsletter to nursing and medical teams
- Impacts on workforce

Respondents were asked to comment on each of the sections/figures within the report, these responses are summarised below

Key messages for local services

This section was found to be useful for all respondents as it gave a quick overview of the report without the need to read further. There was feedback to better consolidate this information, so it provides better clarity and readability. All 16 (100%) respondents found this section useful. However, despite all respondents indicating it was useful, some respondents did provide additional feedback on the section:

- *"Too wordy, very text heavy, dot points would increase the readability".*

- *"Information on number of new cases was more useful when testing was compulsory".*
- *"More information on paediatric populations"*
- *"Deaths and aged care outbreaks not useful"*

Case numbers and rates by local government area

Some respondents no longer found this section useful post-pandemic. Sixty-nine percent (11/16) of respondents found this helped inform their work, 31% (5/16) did not find this section helpful to inform their work. Those who indicated it was no longer useful, stated that breakdown by LGA is no longer relevant.

> "*LGA breakdown was previously useful during the pandemic to help inform pop up testing or vaccination clinics".*

Epidemiological curves and test positivity

Most respondents found the epidemiological curves useful to see disease trends, but responses collected on the graphs for test positivity indicated more interpretation in the report might be needed as respondents didn't understand how to interpret the figures. Feedback on the epidemiological curves and test positivity is summarised below.

- Epidemiological curves

  "Ability to see a full year of trends compared to previous years".

  "Yearly data can be overshadowed by large peaks from previous years".

  "Great way to see trends quickly".

  "Not useful to include historical data from pandemic".

- Test positivity

  "More useful, shows virus prevalence at time points".

  "Interesting and quick and easy to see trends".

  "Very helpful for labs and infection prevention and control"

  "Not as useful anymore, only reviewed and shared with colleagues when in a COVID wave".

Age and sex distribution

Feedback on the age and sex distribution figures is summarised below.

> *"Sex distribution not useful"*

"Age distribution useful"

"Not an area usually reviewed".

"Not that useful to inform work or impact on hospitals".

Aged care facility outbreaks

"Not relevant to department/area".

"Useful indicator for hospital impact".

"Interesting to see how elderly are affected".

Emergency department presentations and admissions

Fifteen of 16 (94%) respondents found the figures showing the ED presentation and admission trends useful.

One of 16 (6%) respondents did not find the figures on emergency department presentations and admissions useful as they said by this point in the report they were "*seeing too many graphs*".

Feedback from the emergency department data is summarised below:

"This section is comprehensive enough".

"Dependent on clear infection control instructions, an overview of the state or LHD in the report would be beneficial, or links to find them".

"Table is useful as a quick update on trends".

"Complements the rest of the report well".

Additional feedback

Respondents were asked about inclusion of RSV into the report and what data they would like to see incorporated. Eleven of the 16 (69%) respondents answered this question, which is summarised below:

- Numbers and trends
- Graphical view of incidence
- Test positivity.
- Rates or comparators of adult vs paediatrics.

We also asked about including data in the report that is not currently shown, All 16 respondents provided a response to this question. The key themes are summarised below:

- Addition of other respiratory virus testing
- Summary box indicating increase in other infections and a link to see further information.
- Infection control guidance or the most current guidelines
- Interactive intranet page document instead of the static pdf

Stability

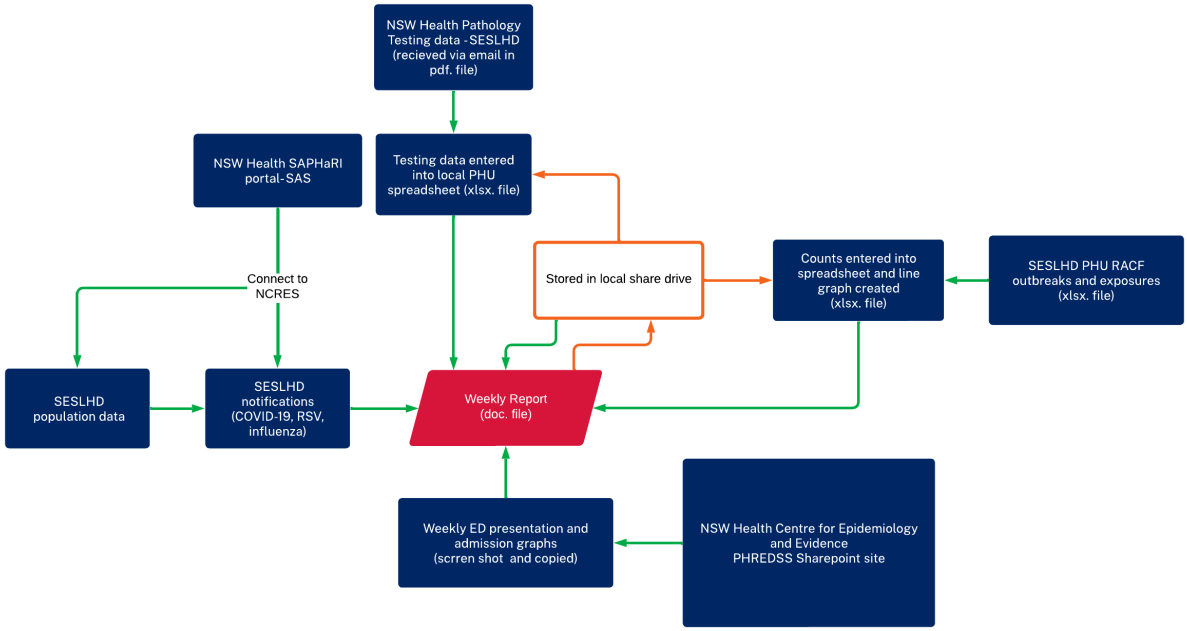
Case numbers and case demographics such as age, sex and local government area are compiled from the state Notifiable Conditions Information Management System. This is analysed in SAS software, to produce tables, epidemiological curves and pyramid graphs. Tables and figures are then copied into a word document, containing the report template. Data on test positivity is obtained from a weekly email produced by New South Wales Health Pathology Randwick. Data is extracted from an attached pdf report and entered in a local Excel spreadsheet, where test positivity is calculated and a line graph is produced showing test positivity for COVID-19, influenza and RSV.

Outbreaks and exposures of aged care facilities in the district are collated from a local public health unit line list used by the PHU to monitor outbreaks and exposures in the District. Each week the epidemiology team perform a manual count of exposures and outbreaks of COVID-19 and influenza and enter this into a separate spreadsheet to create the line graph produced in the report.

The graphs showing SESLHD emergency department presentations and admissions are copied from the Public Health Rapid Emergency, Disease and Syndromic Surveillance (PHREDSS) SharePoint site and copied into the report.

Figure 2 shows the data sources used to compile the weekly report.

Figure 2 Flow chart showing data sources used to create weekly respiratory report



New Report Design

From the feedback in the evaluation, data on COVID-19, influenza and RSV was included in the design of the new report, for the three key assessment areas of transmission, severity and impact.

Transmission

Transmissibility was assessed using weekly percentage positivity rates, age rates, and sewage surveillance data. Notification data for SESLHD was obtained via NCIMS, which contained all laboratory tests for all infections, using a connection written into R script. Laboratory testing data from NSW Health Pathology-Randwick (SESLHD) was maintained from the old report. Population data from the ABS and are the official estimates for 2022, were sourced from the NSW Health SAPHaRI portal to calculate disease rates by age group.[5] FluTracking for SESLHD was obtained from FluTracking Australia. However, this data was only available on an annual basis. Prior to the pandemic, FluTracking was only conducted during the expected influenza season, so comparative data prior to 2020 is only available from April to October. The raw data from the COVID-19 Sewage Surveillance Program was not available at the local level, and so the graphs used in the report were copied from the NSW Health Respiratory Surveillance Report.

Severity

Severity was assessed using the proportion of people presenting to EDs in the District to who are admitted. This was done using data obtained from PHREDSS for SESLHD, which

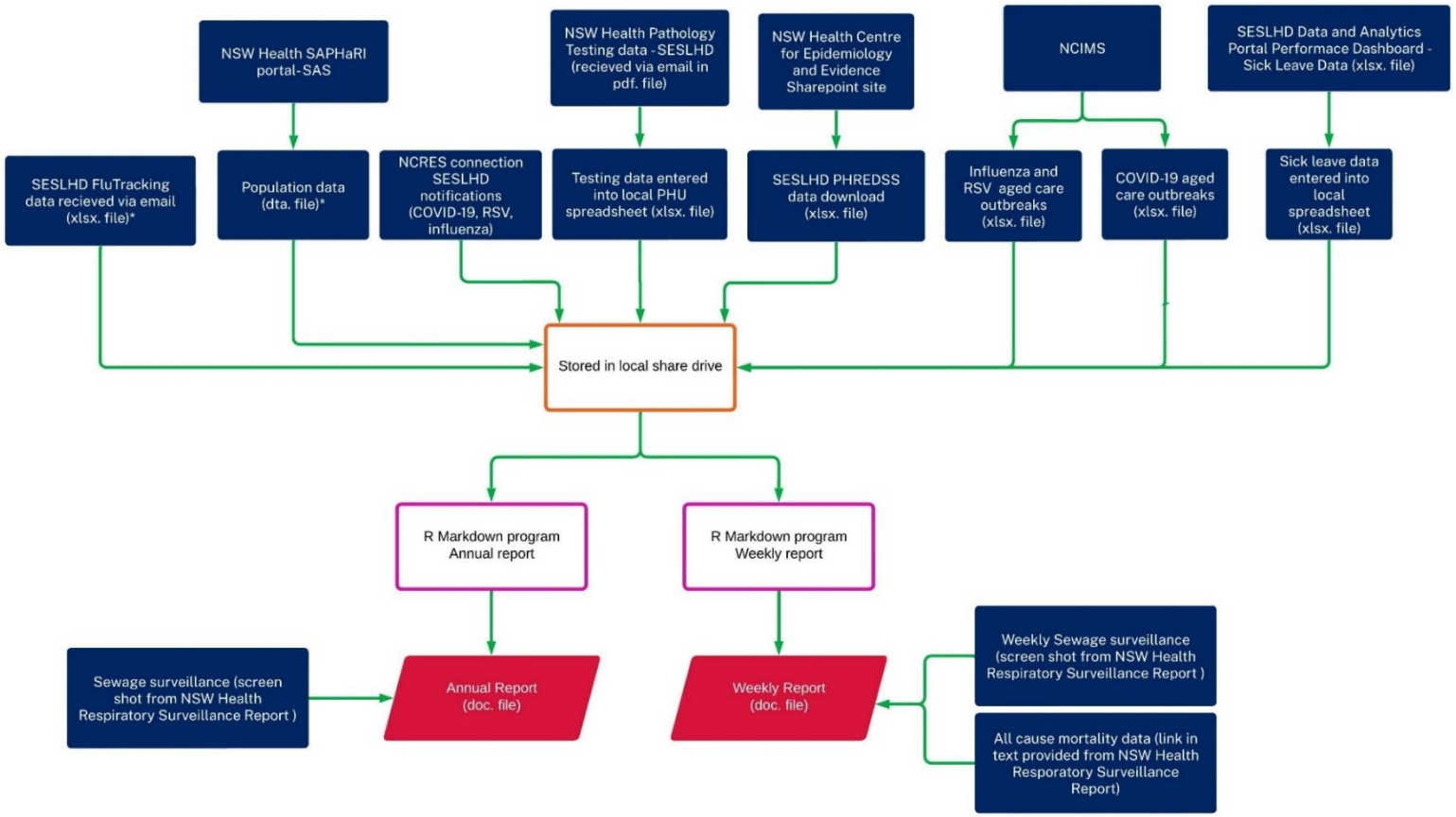
provides daily information about presentations to NSW public hospital EDs and subsequent admission to hospital categorised by symptom profile and age group.[6] The data was used to report on COVID-19, influenza-like illness and bronchiolitis (which is mainly caused by RSV). This data was not able to be made public and could only be used for internal reporting. Death data was unavailable at the local level.

Impact

Impact was assessed using weekly outbreaks in aged care facilities and ED presentation counts. PHREDSS data was also used in this section to show year on year comparisons. Whilst the raw data was unavailable, graphs from the PHREDSS online dashboard were used, as was done in the pre-evaluation report. Data on aged-care facility outbreaks from NCIMS was also obtained. A full overview of the data used to create the new report is shown in *Figure 3*.

An example weekly report is presented in *Appendix I*. A full report of the evaluation finding was collated and provided to the Directors of Public Health and Population Health.

Figure 3 Flow chart showing data sources and process for developing the new report format



Discussion

Overall, the feedback was positive for the weekly respiratory viruses' report with the respondents finding it useful to help inform their work. Most of the respondents were from clinical areas in the District and use the report to understand the impact increasing disease transmission will have on their services. Breakdowns of data by LGA and gender were no longer relevant in a regular reporting model but are useful in an epidemic or pandemic situation. There is a desire to continue breakdowns by age and include data on other respiratory viruses including RSV. Feedback indicated that some respondents might lack a clear understanding of the indicators in a respiratory surveillance report and could be misinterpreting the data.

The weekly respiratory virus report contained comprehensive and reliable data sources, but it was no longer suited to a post pandemic climate where individual case numbers were no longer useful indicators for measuring the impact or severity of respiratory diseases.[7] Despite the recognition that the report was no longer suitable for respiratory surveillance in the District, there were several key takeaways from the evaluation that benefitted the development of the new report. Firstly, whilst there were a small proportion of respondents to the survey, the people who did respond were from key clinical areas in the District. Secondly, these respondents indicated that the email summary provided with the weekly report, was easy to understand, enabling stakeholders to grasp key points without needing to read the full report. This feature was found to be useful for those with limited time. Thirdly, stakeholders felt that the report was timely in its distribution and data was up to date. Fourthly, graphs and visual data were valued for their ability to illustrate trends quickly and aid in comparisons, helping stakeholders understand and communicate data effectively. Finally, information in the report was used to inform clinical teams and prepare for surges on the healthcare system by guiding workplace planning, demonstrating its practical application in healthcare settings.

Despite these strengths of the existing report there is also several weaknesses identified in the report's format. Firstly, feedback indicated that some sections, such as the key messages, were seen as too wordy or text heavy. Suggestions were made to condense the bullet points for better readability and clarity. Secondly, the breakdown of cases by LGA was considered less useful post pandemic and that it was more relevant during outbreaks or epidemics to inform local interventions such as testing and vaccination clinics. Thirdly, whilst the graphs were useful, some of the feedback indicated that more

interpretation is needed, particularly for test positivity rates. Fourthly, there was limited engagement with the online version of the report on the LHD website, suggesting the public were unaware of its availability or no longer find it necessary. Stakeholders may also find this format not as accessible or unnecessary, limiting the reports reach. Lastly, stakeholders expressed a desire to include data on other respiratory viruses and comparisons between adult and paediatric populations. The incorporation of these findings and feedback could enhance the new report's comprehensiveness and utility.

The design of the new report using the PISA framework aimed to address these issues and ensure the report was adequate in its surveillance of respiratory disease in a post pandemic environment. Recognising the need for standardisation and consistency in measuring influenza and other respiratory disease activity, the World Health Organization (WHO) developed the Pandemic Influenza Severity Assessment (PISA) tool.[2] This tool, established after the 2009 influenza pandemic, defines severity using three indicators: transmissibility, severity, and impact.[2] It aims to standardise reporting and enable real-time global assessments.[2, 8] The PISA tool recommends that transmissibility and impact indicators are measured using weekly rates, and that disease seriousness is measured using a cumulative value.[8] We applied the PISA framework to redevelop the ARI report to align it with best practices and support accurate and meaningful interpretation.

However, despite the new design there was unavailability of important data, such as local mortality figures and weekly FluTracking updates. These gaps will restrict the ability to monitor disease transmission and impact fully. Additionally, some data, such as sewage surveillance, had to be adapted from state-level reports, which somewhat reduced the efficiency the new format aimed to achieve.

Given the limited interaction with the online report, it may be worthwhile reconsidering the value of publishing it in its current format. Instead, respiratory virus trends could be communicated through more engaging platforms, such as social media. The low public engagement with the online version of the report also suggests a need to rethink accessibility and dissemination strategies. The internal stakeholders who receive the report via email, are the primary users, and there was little evidence to suggest that anyone outside of the PHU staff accessed the report online.

Despite the unavailability of some of the data, the new report format and data sources addresses the PISA framework comprehensively. The inclusion of RSV and data categorised by age groups has allowed for standardised disease severity assessment. This is a great addition to the report as standardised disease severity assessments

enable cross cohort comparisons of disease burden between different viral pathogens, aiding healthcare facility preparedness and planning.[7]

Conclusion

The evaluation of the weekly respiratory report highlighted the positive reception of the weekly respiratory viruses report among stakeholders, particularly in clinical areas, who found it useful for monitoring disease trends and planning responses. Despite the report's strengths – such as timely distribution, clear summaries, and effective data visualisation – the report had limitations in a post-pandemic context. Individual case numbers and detailed local breakdowns are less relevant outside of epidemic situations, and there is a need for greater data interpretation to enhance stakeholder understanding. Feedback suggested expanding the report to include other respiratory viruses such as RSV and improving readability by condensing key information. The design of the new report, using the PISA framework, aims to address these issues, but challenges do remain due to data availability constraints. Despite this, additions like age-specific data and standardising severity assessments will strengthen the report's ability to effectively monitor respiratory virus transmission, severity and impact on the healthcare system.

It is recommended that following implementation of the new reporting format, it is again evaluated in the same manner to ensure the new report is achieving its aims.

Chapter III – Section 2

Annual report of acute respiratory infections (ARI) in South Eastern Sydney Local Health District (SESLHD), 2023

Abstract

Introduction

Acute respiratory infections (ARI) are common. They are typically mild and short-lived, however can result in severe outcomes. This report presents an overview of respiratory infections in SESLHD in 2023, including COVID-19, influenza and RSV, drawing information from several different data sources.

Methods

Notification data was obtained from the Notifiable Conditions Information Management System (NCIMS), pathology testing data was obtained from New South Wales (NSW) Health Pathology Randwick. Data on hospital presentations and admissions was collected from the Public Health Rapid Emergency, Disease and Syndromic Surveillance (PHREDSS). Data were cleaned and analysed in R statistical software. Transmission was assessed using test positivity rates, FluTracking surveys, and COVID-19 sewage surveillance. Severity was assessed by calculating proportions of people admitted to hospital, while impact was assessed using hospital presentations and aged care facility outbreaks.

Results

COVID-19 test positivity peaked twice during 2023, with the highest rates in those aged 65 years or older, likely due to ongoing testing and transmission in aged care. Influenza peaked in winter, while respiratory syncytial virus (RSV) mainly affected children under five. COVID-19 and bronchiolitis saw spikes in emergency department (ED) presentations and COVID-19 was the leading cause of ARI outbreaks in aged care facilities, peaking at 33 outbreaks in April. Data limitations, such as the lack of local mortality figures and weekly FluTracking updates impacted the completeness of the analysis.

Conclusion

The 2023 annual report provided valuable insights into COVID-19, influenza, and RSV transmission, impact and severity.

Introduction

Acute respiratory infections (ARI) are common. They are typically mild and short-lived, however can result in severe outcomes.[7] This report presents an overview of respiratory infections in South Eastern Sydney Local Health District (SESLHD) in 2023, including COVID-19, influenza and respiratory syncytial virus (RSV), drawing information from several different data sources. These data assist in understanding the distribution of acute viral respiratory illness activity in the community, the severity of the disease, which populations might be at risk of severe disease, and impact of acute viral respiratory illness on the community and health system in SESLHD.

Methods

An annual report for 2023 was prepared using the newly integrated data sources and script along with incorporating feedback from the stakeholder survey as presented in section one. Notification data was obtained from the Notifiable Conditions Information Management System (NCIMS), pathology testing data was obtained from New South Wales (NSW) Health Pathology Randwick. Data on hospital presentations and admissions was collected from the Public Health Rapid Emergency, Disease and Syndromic Surveillance (PHREDSS). Data were cleaned and analysed in R statistical software. Transmission was assessed using test positivity rates, FluTracking surveys, and COVID-19 sewage surveillance. Severity was assessed by calculating proportions of people admitted to hospital, while impact was assessed using hospital presentations and aged care facility outbreaks.

Transmission

Data on COVID-19, influenza and RSV were included in the report. Disease positivity rates were calculated using local laboratory testing data and routine notification data for SESLHD residents from the state Notifiable Conditions Information System (NCIMS) for each of the pathogens. Rates of notifications by age-groups were calculated per 100,000 population.

FluTracking data was used to calculate proportions of SESLHD residents reporting influenza-like illness in the online weekly survey conducted by the FluTracking team.[9] COVID-19 sewage surveillance data from the local sewage outlet (Bondi) was extracted from the NSW Health COVID-19 Sewage Surveillance Program website.

Severity

Public Health Rapid Emergency, Disease and Syndromic Surveillance (PHREDSS) data

was used to show the number of presentations and admissions to hospitals in SESLHD.[6] Proportions of people admitted were calculated amongst those presenting with COVID-19, influenza-like illness or bronchiolitis.

Impact

PHREDSS data were used to report numbers of COVID-19, influenza-like illness (ILI), and bronchiolitis presentations to hospitals in SESLHD compared to the previous 5 years. Outbreaks in residential aged care facilities located in SESLHD were counted for COVID-19, influenza and RSV for each month.

Results

The annual report details ARIs, with a focus on COVID-19, influenza and RSV, in SESLHD from 1 January to 31 December 2023.

Transmission

COVID-19 test positivity increased between March and June, with a second test positivity peak in December at 12%, despite notifications remaining low (*Figure 4)*, indicating a lower proportion of cases in the last quarter of the year were detected after mandatory RAT notification ceased and access to community PCR testing was restricted. The highest rates of COVID-19 were seen in those aged 65 years or older (*Figure 5*). This could be a result of continued testing and transmission in aged care facilities leading to an over representation of notifications in this population within the District.

Figure 4 Weekly COVID-19 notifications and test positivity, 2023, SESLHD

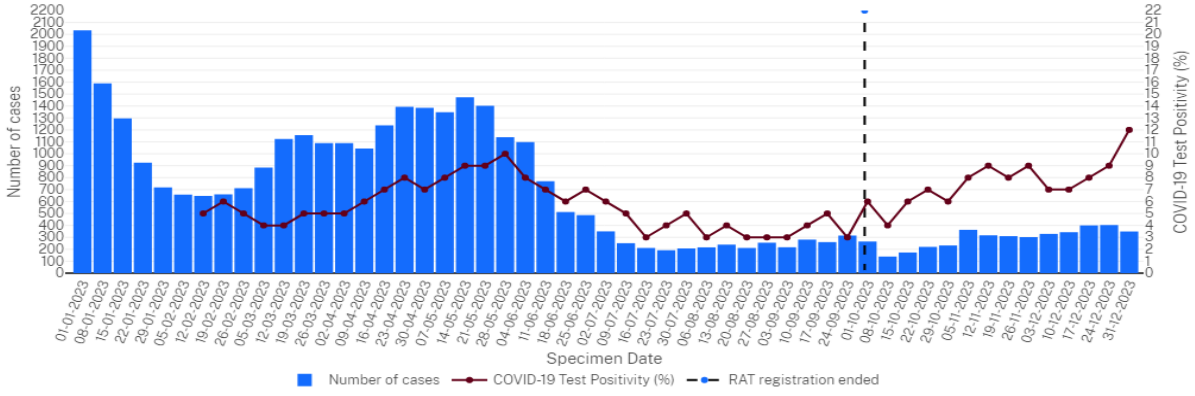
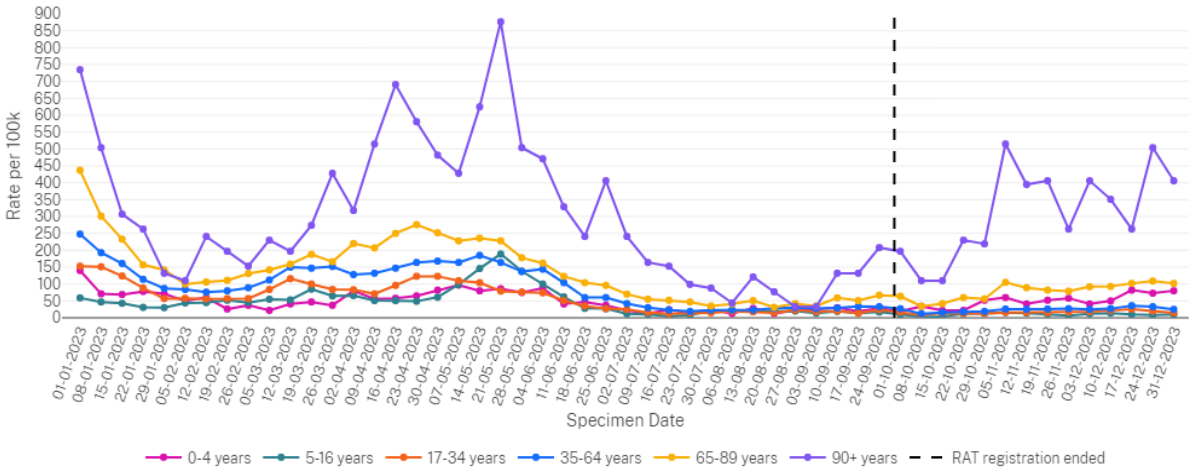


Figure 5 Rate of COVID-19 notifications by age group per 100,000 population, 2023, SESLHD



Influenza followed a usual seasonal trend with a peak over the winter months of May – September. Influenza B was the predominant strain during this time and test positivity peaked at 9% (*Figure 6*). Influenza A was detected for the entire 12 months and reported at higher levels than is usually seen during spring and summer. Influenza notifications were highest amongst children under 16 years and followed an upward trend during May through to July. The rate of influenza notifications among children 5-16 years peaked at 232 per 100,000 people in late June, followed by those aged 3-4 years with a rate of 211 per 100,000 people in early July (*Figure 7*).

Figure 6 Weekly influenza notifications by serogroup and influenza test positivity, 2023, SESLHD

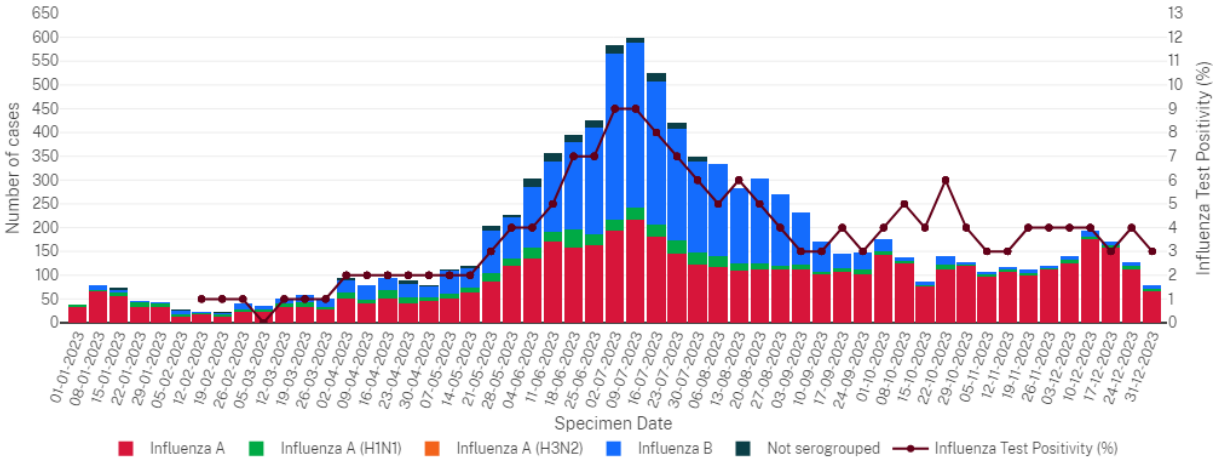
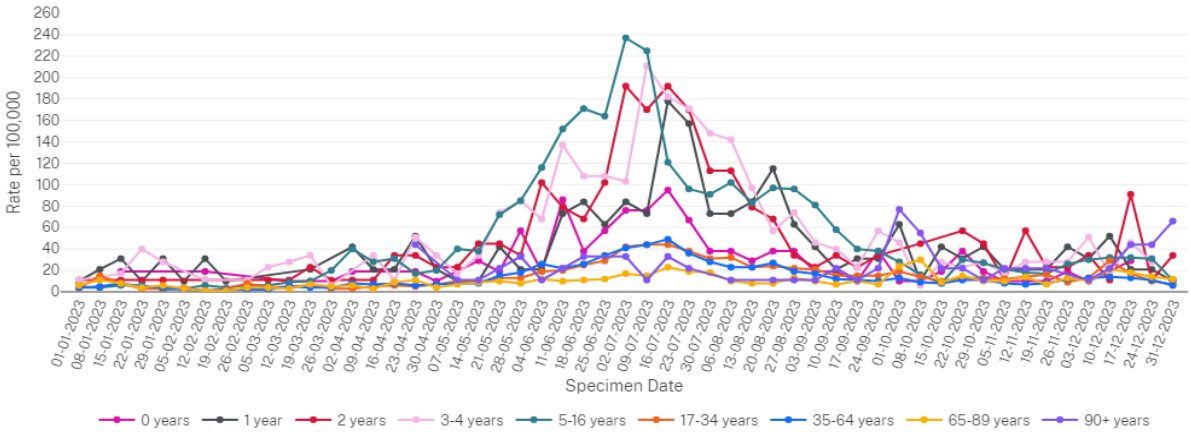


Figure 7 Rate of influenza notifications by age group per 100,000 population, 2023, SESLHD



RSV notifications increased four-fold from February to April, then persisted throughout the year with test positivity reaching a peak of 6% in April (*Figure 8*). Rates of RSV notifications were highest in children aged less than 5 years. The rate of RSV notifications among children aged 1 year peaked at 596 per 100,000 people in April (*Figure 9*). The age group with the next highest rate was in children aged 0 years with a rate of 410 per 100,000 people in early April.

Figure 8 Weekly RSV notifications and RSV test positivity, 2023, SESLHD

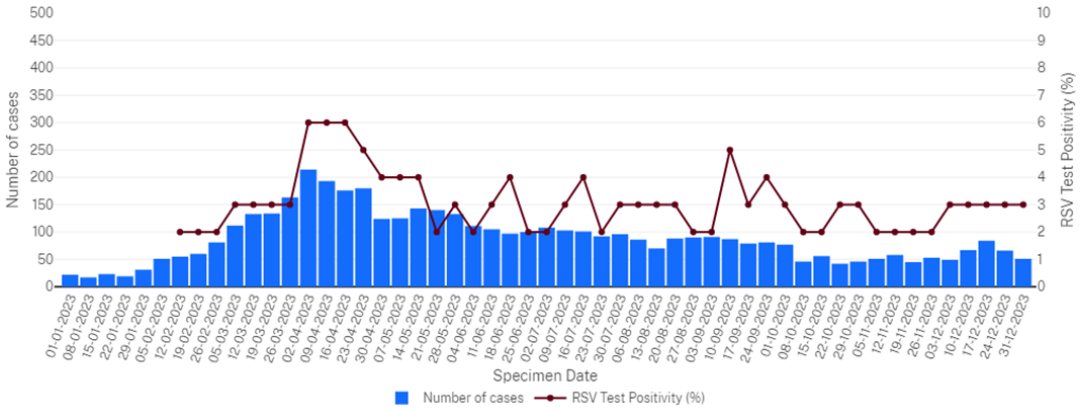
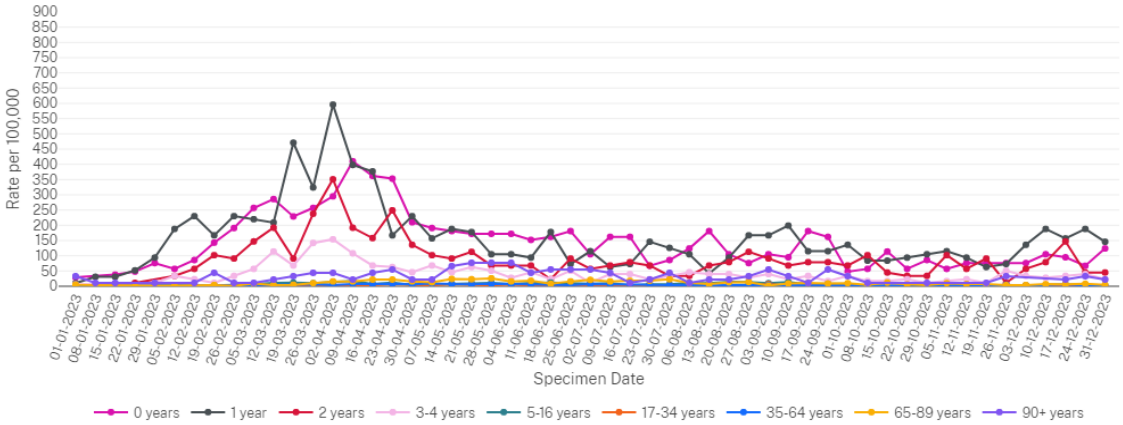
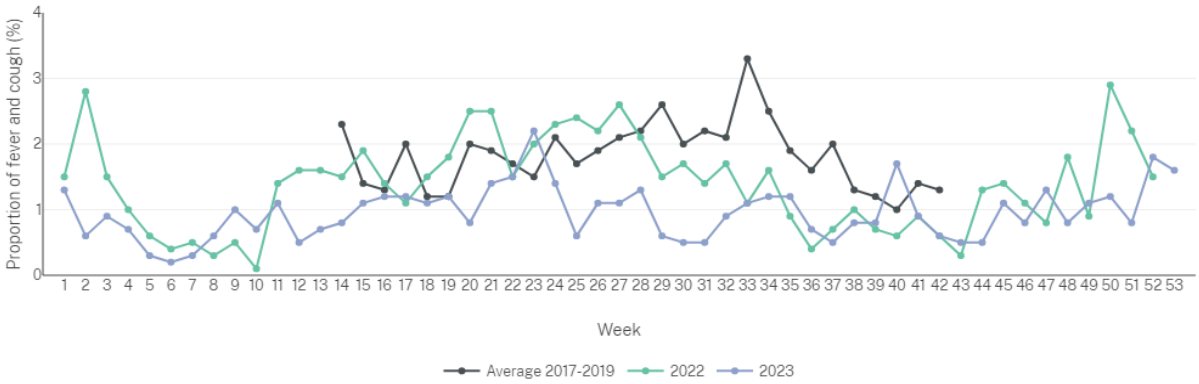


Figure 9 Rate of RSV notifications by age group per 100,000 population, 2023, SESLHD



FluTracking data showed that people reporting fever and cough was overall less in 2023 compared to 2022 (*Figure 10*). Proportions increased during the winter months before decreasing towards the end of spring and then increasing in December, aligning with COVID-19 trends

Figure 10 Proportion of SESLHD FluTracking participants who reported fever and cough, by weekend ending, 1 January to 31 December 2023, SESLHD



Severity

Presentations to EDs for COVID-19 were high in January, then increased during April to June and again in December. Hospital admissions increased during the same time periods. The proportion of people requiring admission remained stable throughout the year ranging between 35-45% of people presenting to ED requiring admission to hospital.

ILI presentations and admissions peaked during June and July. The proportion of people requiring admission was highest during February and November, however the absolute number of presentations during those months was small.

Bronchiolitis data was presented for children aged 0-4 years. There was a steep increase

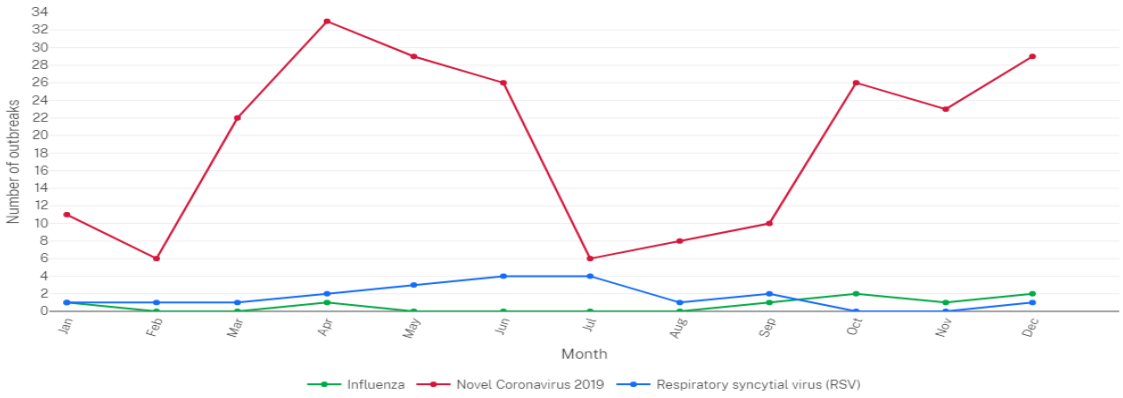
in the first three months, with the peak seen in April. Admissions followed a similar trend. Proportions of children requiring admission ranged from 35-55%.

Impact

Presentations for COVID-19 were high at the beginning of the year, then declined by March, before increasing towards the end of the year. Influenza-like illness presentations remained low throughout 2023, with a slight peak in mid-year. Bronchiolitis presentations fluctuated throughout the year, with increases during March to August.

COVID-19 was the main cause of ARI outbreaks in residential aged care facilities during 2023. The number of outbreaks of COVID-19 reported in a month reached a peak of 33 in April. Outbreaks of influenza and RSV remained low throughout the year (*Figure 11*).

Figure 11 Acute respiratory infection outbreaks in SESLHD residential aged care facilities



Discussion

The 2023 annual report provided a detailed analysis of COVID-19, influenza and RSV activity in SESLHD, highlighting key trends and age-specific impacts. COVID-19 test positivity peaked in March and December, while influenza and RSV followed typical seasonal patterns, with influenza B predominating in winter and RSV impacting children under five.

The annual report successfully integrated multiple data sources, offering a structured design that facilitates clear comparisons across age groups and time periods. This approach made it a valuable tool for understanding local epidemiological trends and informing future seasonal planning and response. The use of the WHO PISA indicators helped standardise severity assessments, aligning the report with recommended reporting practices.

The report highlighted trends in respiratory virus transmission. COVID-19 test positivity peaked twice in 2023, primarily among older adults, likely due to continued testing in aged care settings experiencing outbreaks. Influenza followed expected seasonal patterns but saw increased notifications for influenza A during spring and summer. RSV had the greatest impact on children, with the notification rate peaking in April. These findings highlight the importance of ongoing monitoring of age specific trends, particularly in vulnerable groups.

Additionally, the report showed how fluctuations in respiratory illness affected ED presentations and hospital admissions. Both COVID-19 and bronchiolitis saw peaks in ED presentations and admissions, particularly in the children under five for bronchiolitis. COVID-19 remained the predominant cause of ARI outbreaks in aged care settings, underscoring the need for continued robust outbreak management strategies in aged care settings.

Conclusion

The 2023 annual report highlighted key trends in COVID-19, influenza, and RSV activity in SESLHD, providing insights into age-specific impacts and seasonal patterns. The integration of several data sources and the use of WHO PISA indicators enabled standardised severity assessments, enhancing the report's utility for local planning and preparedness. COVID-19 remained the main cause of ARI outbreaks in aged care settings, highlighting the need for ongoing targeted monitoring and robust outbreak management strategies.

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6. NSW Health. Rapid Surveillance Using PHREDSS 2023 [Available from: https://www.health.nsw.gov.au/epidemiology/Pages/rapid-surveillance-using-PHREDSS.aspx.

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Appendix I

Example weekly report

South Eastern Sydney Local Health District

Weekly Acute Respiratory Infections Report

Issued 27 May 2024

Key messages for local services

This report details acute respiratory infection (ARI) surveillance data, with a focus on COVID-19, influenza, and respiratory syncytial virus (RSV), in South Eastern Sydney Local Health District (SESLHD) for the week ending 26 May.

	Transmission	Severity	Impact
COVID-19	MODERATE ⬆	BASELINE ➡	MODERATE ⬆
Influenza	MODERATE ⬆	BASELINE ➡	LOW ➡
RSV	MODERATE ⬇	BASELINE ➡	MODERATE ⬇

- COVID-19 transmission and impact are increasing and are now at moderate levels. The positivity rate of PCR tests increased by 1% to 8% this week. Notifications were predominately from older adults aged 90+ years.
- Influenza transmission is increasing, indicating the start of the Winter influenza season. Impact on aged-care facilities and hospitals remains low. Notifications were predominately from children under 5 years.
- Respiratory syncytial virus (RSV) transmission and impact remain moderate, but there are indications that both are declining. Notifications were predominately from children under 3 years.

Data sources and methods

This report adopts new approaches to monitoring respiratory virus activity to align with NSW Health respiratory surveillance methods and World Health Organization surveillance guidelines. Changes to respiratory virus testing over time affect the number of cases notified, meaning case numbers are not a good measure of respiratory virus in the community and limit the validity of comparing trends between years. The data sources used for this report have been referenced throughout the document. All data used in this report is limited to SESLHD unless otherwise stated.

Public Health Unit Page | 1 SESLHD-PublicHealthEnquiry@health.nsw.gov.au

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Acknowledgements

The public health unit would like to acknowledge the Public Health Rapid Emergency, Disease and Syndromic Surveillance (PHREDSS), NSW Health Pathology - Randwick and St George, and the SESLHD Workforce teams for providing the data used for this report.

Report Details		
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Approved by:	Dr Anthea Katelaris	A/Director PHU
Distributed to:	SESLHD ARI e-list	
Next report to be issued:	03 June 2024	

Transmission

The following section uses data such as test positivity, rate of disease notifications, and sewage surveillance as indicators for community transmission and infection rates.

Notification and test positivity for COVID-19, influenza, and RSV

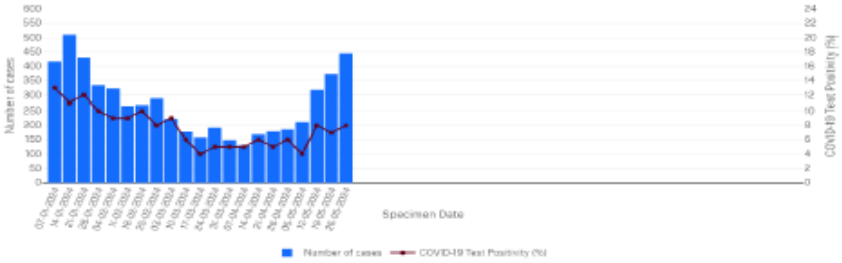
Notification data is obtained from laboratory tests for infections. Test positivity data is calculated using testing data from NSW Health Pathology-Randwick and St George. Test positivity is a better indicator than notifications about the level of virus circulating in the community as notification numbers depend on how many tests are performed. The positivity rate rises when there are high levels of virus transmission, irrespective of the number of tests that are performed.

COVID-19

Figure 1 shows the weekly number of COVID-19 notifications and test positivity. The positivity rate of PCR tests increased by 1% from 7% to 8% this week.

Interpretation: The proportion of positive results among PCR tests conducted at NSW Health Pathology-Randwick and St George increased at the beginning of May, suggesting that the level of COVID-19 infection in the community is increasing, at moderate levels.

Figure 1: Weekly COVID-19 cases and test positivity, 01 January to 26 May 2024, SESLHD

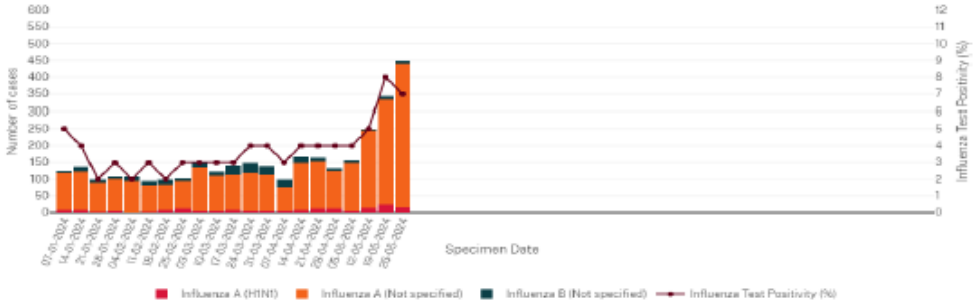


Influenza

Figure 2 shows weekly influenza notifications by serogroup, and test positivity. The most prevalent influenza strain currently circulating is Influenza A. Test positivity for influenza decreased by 1% from 8% to 7% for the week ending 26 May.

Interpretation: The proportion of positive results among PCR tests conducted at NSW Health Pathology-Randwick and St George increased since the beginning of May, suggesting that the level of influenza infection in the community is increasing, marking the beginning of the influenza season.

Figure 2: Weekly influenza cases, by serogroup and influenza test positivity, 01 January to 26 May 2024, SESLHD

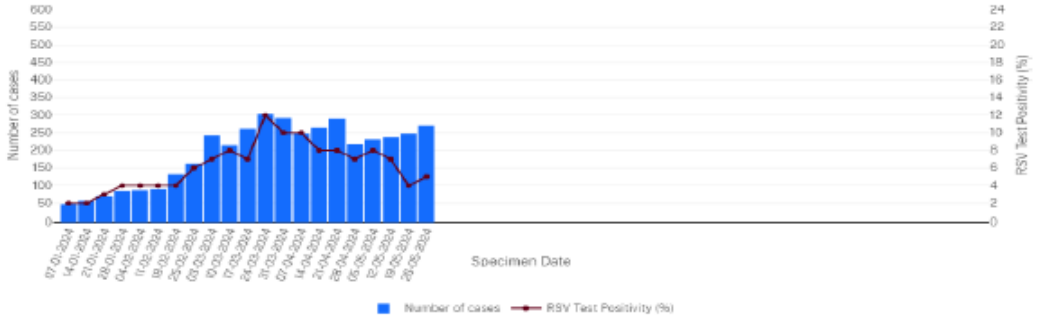


RSV

Figure 3 shows the weekly number of RSV notifications and test positivity. RSV test positivity increased by 1% from 4% to 5% for the week ending 26 May.

Interpretation: The proportion of positive results among PCR tests conducted at NSW Health Pathology-Randiwck and St George is showing a decline, suggesting that the level of infection in the community is decreasing compared to April.

Figure 3: Weekly RSV cases and RSV test positivity, 01 January to 26 May 2024, SESLHD



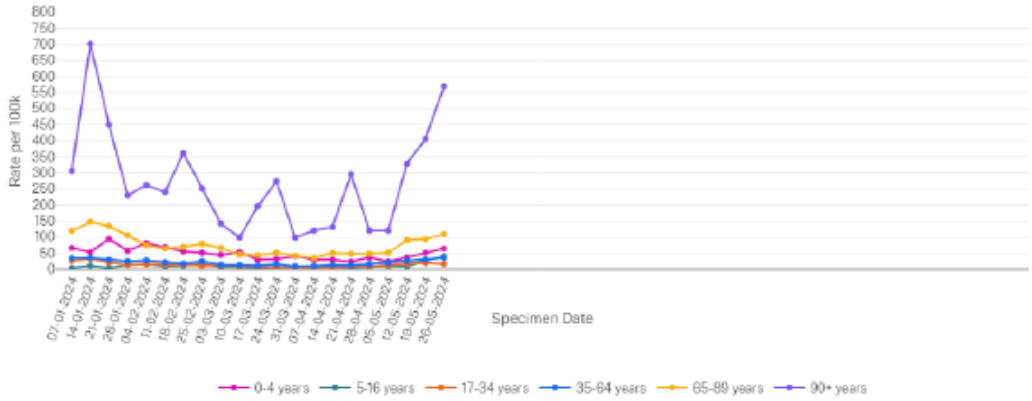
Rates of COVID-19, influenza, and RSV notifications by age

COVID-19

Overall, the highest rates of COVID-19 notifications are seen in those aged 90+ years. The 17-34 years age group had the lowest rate of notifications at 17 per 100,000 population for the week ending 26 May.

Interpretation: The age group with the highest rate of COVID-19 is 90 years and above, although this could be due to increased testing related to outbreaks in residential aged care facilities.

Figure 4: Rate of COVID-19 notifications by age group per 100,000 population, 01 January to 26 May 2024, SESLHD

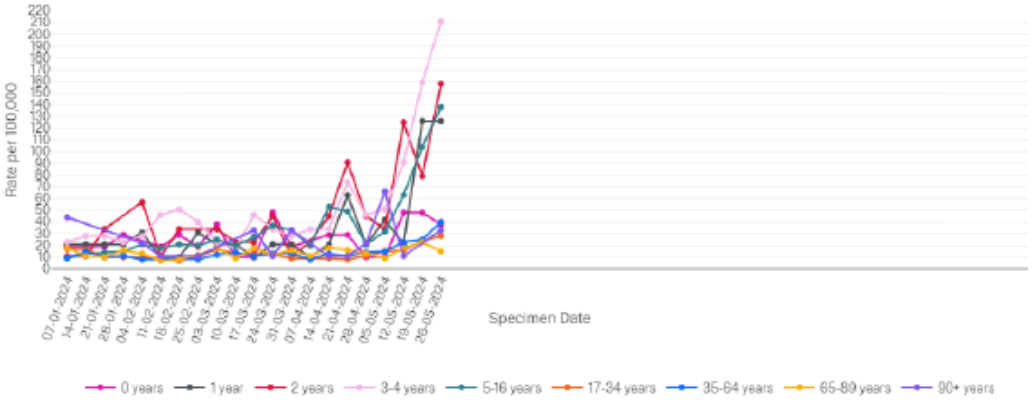


Influenza

The highest rates of influenza notifications are seen in those 3-4 years. The 65-89 years age group had the lowest rate of notifications for the week ending 26 May.Notification rates dropped in most age groups this week.

Interpretation: Children continue to have the highest rates of notification for influenza.

Figure 5: Rate of influenza notifications by age group per 100,000 population, 01 January to 26 May 2024, SESLHD

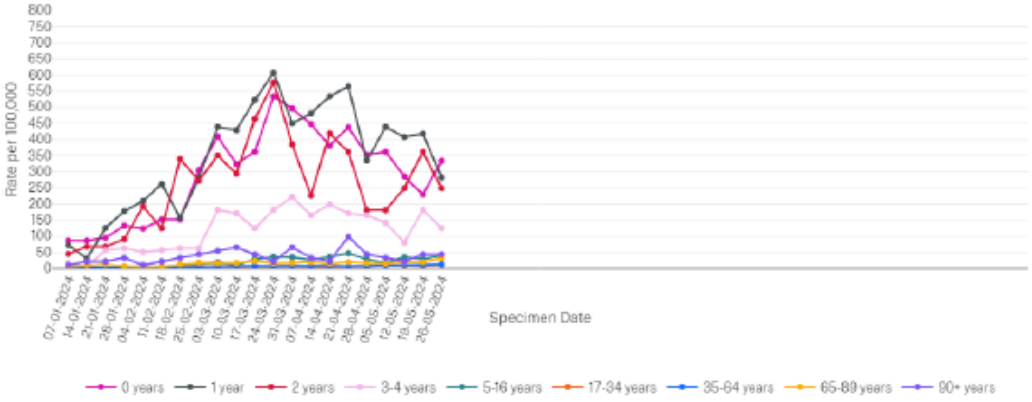


RSV

Rates of RSV notifications were highest in children aged less than 5 years. The highest rate was seen in children aged 0 years at a rate of 334 per 100,000. The lowest rates of notification were seen in the 17-34 years at a rate of 15 per 100,000.

Interpretation: RSV is mostly being detected in young children, and currently older adults have a low rates of notified RSV infection.

Figure 6: Rate of RSV notifications by age group per 100,000 population,01 January to 26 May 2024, SESLHD



Data source: Population data were sourced from the Australian Bureau of Statistics (ABS) and are the official estimates from the ABS for 2022.

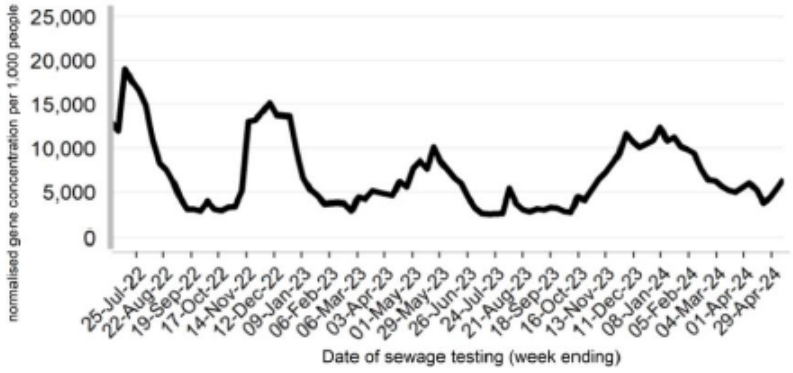
COVID-19 sewage surveillance program

Sewage surveillance gives an indication of levels of infection in the community. This can be used to estimate changes in the level of transmission, even if people do not get tested. For more information, please see the COVID-19 Sewage Surveillance Program website: https://www.health.nsw.gov.au/Infectious/covid-19/Pages/sewage-surveillance.aspx.

Figure 7 shows the level of SARS-CoV-2 (the virus that causes COVID-19) in the Bondi sewage catchment. There is some lag in the timing of when this data is available.

Interpretation: Gene concentrations of SARS-CoV-2 per 1,000 people have been at low-moderate levels in the Bondi catchment since February 2024. There is an indication that levels may be increasing, consistent with increased community transmission.

Figure 7: SARS-CoV-2 gene concentration, per 1,000 people in Bondi sewage catchment, 01 July 2022 to 18 May 2024



Severity

Public Health Rapid Emergency, Disease and Syndromic Surveillance

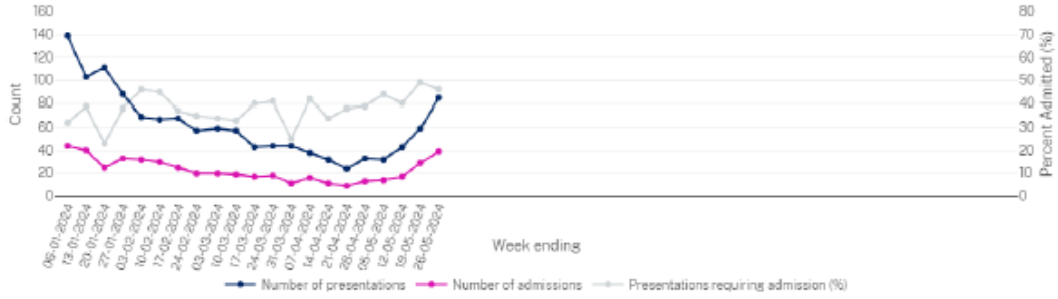
PHREDSS provides daily information about presentations to NSW public hospital emergency departments and subsequent admission to hospital categorised by symptom profile. Presentations and admissions categorised as COVID-19, influenza-like illness, and bronchiolitis (which is mainly caused by RSV) are reported below. The proportion of people admitted to hospital, is an indicator of the severity of illness and impact on the health system.

COVID-19

Presentation to EDs for COVID-19 continue to increase since the beginning of the month. The proportion of people being admitted following presentation is relatively stable – currently 46%.

Interpretation: Among people who present to ED for COVID-19, the proportion of individuals requiring admission is stable, though the number of people being admitted is increasing as case numbers increase.

Figure 8: 'COVID-19/coronaviruses' weekly counts of unplanned emergency department (ED) presentations and admission following presentation,01 January to 26 May 2024, persons of all ages, SESLHD

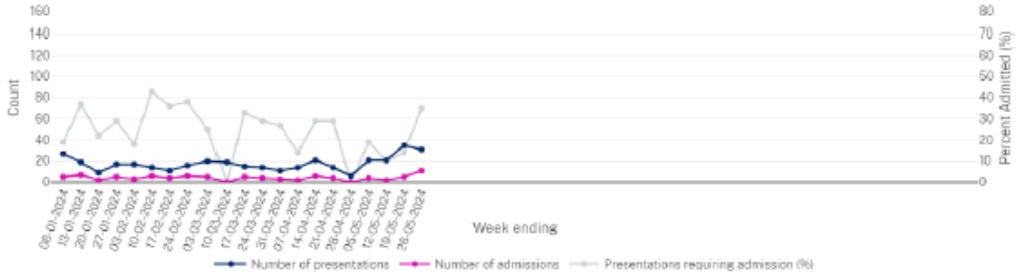


Influenza-like illness

ED presentations and admissions for influenza-like illness have dropped to low levels. The proportion of people requiring admission following presentation increased by 21% from 14% to 35% for the week ending 26 May, though numbers are low.

Interpretation: Impact of influenza is increasing in line with the start of the influenza season. However, presentation rates remain low and there are no increased severity signals from ED data.

Figure 9: Influenza-like illness' weekly counts of unplanned emergency department (ED) presentations and admission following presentation,01 January to 26 May 2024 persons of all ages, SESLHD

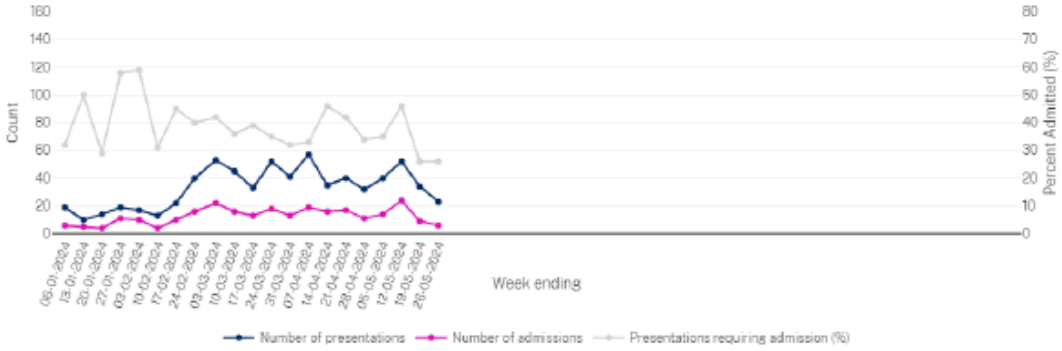


Bronchiolitis

Presentations and admissions for bronchiolitis have been high since late February, however the proportion admitted has been stable. The proportion of children aged 0-4 years requiring admission following presentation is currently 26%.

Interpretation: Presentations and admissions for bronchiolitis have been above the expected level since late February for children aged less than 5 years. The stabilisation of presentations over 3 weeks and decrease in number requiring admission last week could indicate a slight alleviation on impact on this age group. The severity of illness is stable.

Figure 10: Bronchiolitis weekly counts of unplanned emergency department (ED) presentations and admission following presentation,01 January to 26 May 2024, children aged 0-4 years, SESLHD



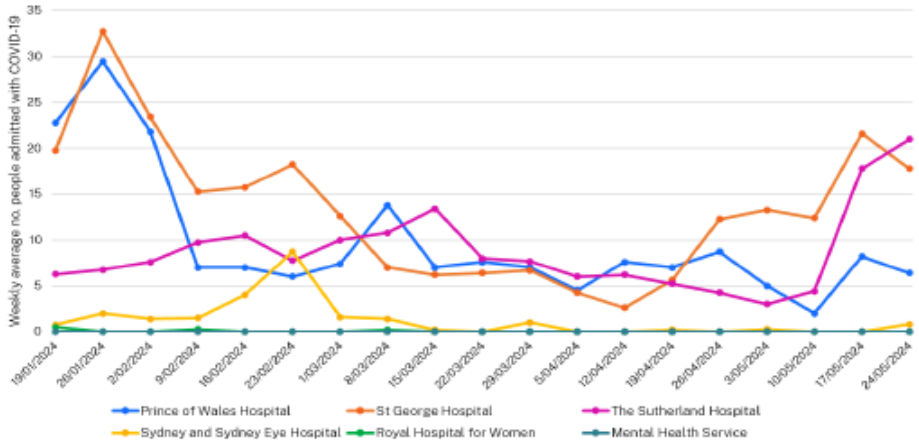
Impact

COVID-19 Hospital Admission Tracking

The COVID-19 admission tracking data is sourced from the Access and Patient Flow Portal for SESLHD facility. It reflects the current count of patients occupying beds, irrespective of their admission date, who have tested positive for COVID-19. In the past week, on average, 46 beds were occupied by people admitted with COVID-19.

Interpretation: The average number of people currently admitted with COIVD-19 has increased.

Figure 11: Average number of people admitted with COVID-19 in SESLHD hospitals, 16 January to 24 May 2024

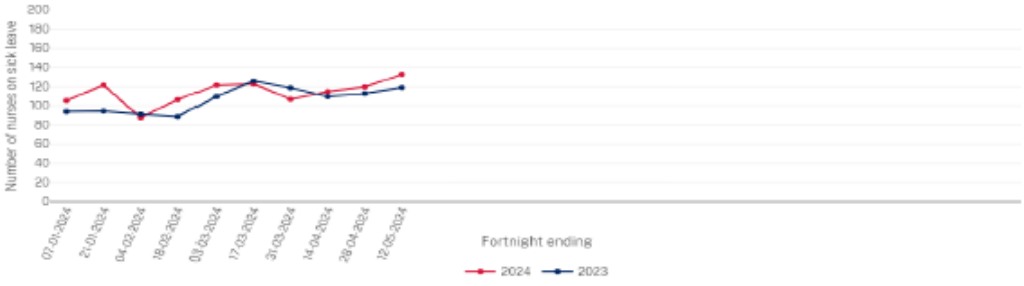


Healthcare Worker Furloughing

The inclusion of healthcare workers in sick leave statistics is helpful to assess the level of respiratory viruses circulating in the community during periods of decreased community testing and assess the impact of respiratory illnesses on the workforce, although the absence of recorded reasons for sick leave may overestimate the true burden.
Healthcare workers are included in these statistics if they are a full-time or equivalent nursing staff member in SESLHD who were paid sick leave.

Interpretation: Overall, sick leave across the district has remained stable and similar to 2023.

Figure 11: Number of FTE nursing staff in SESLHD on sick leave by fortnight ending, 01 January to 12 May 2024



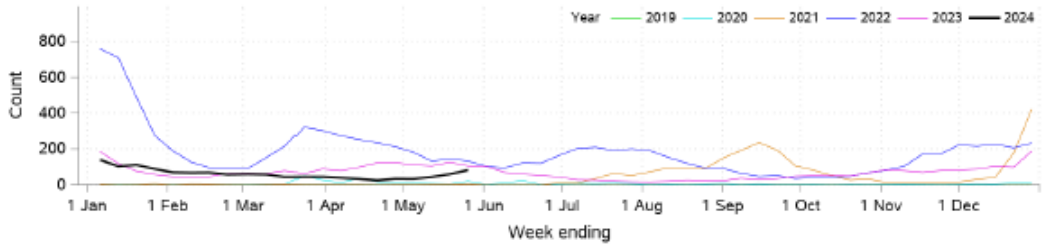
Emergency Department Presentations

PHREDSS provides daily information about presentations to NSW public hospital emergency departments and subsequent admission to hospital, categorised by symptom profile. COVID-19, influenza-like illness, and bronchiolitis (which is mainly caused by RSV) presentations in 2024 are reported below (black line) compared to previous years. It includes presentations to all public emergency departments in SESLHD, including Sydney Children's Hospital and St Vincent's Hospital. These PHREDSS indicators are useful for monitoring the impact on emergency departments.

COVID-19

Interpretation: There is a stable and relatively low number of COVID-19 ED presentations.

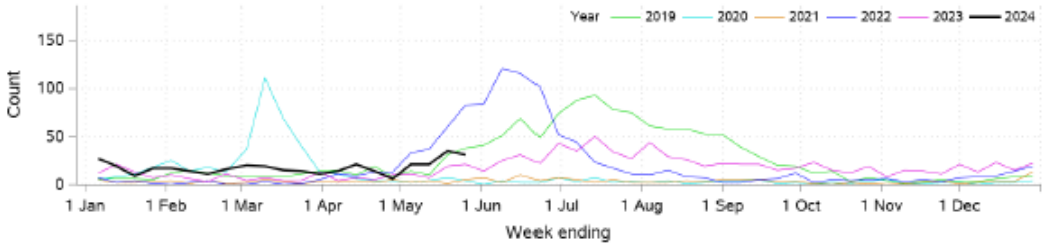
Figure 13: 'COVID-19/coronaviruses' monthly counts of unplanned emergency department (ED) presentations, 01 January to 26 May 2024, persons of all ages, SESLHD



Influenza-like illness

Interpretation: ILI presentations are in-line with previous years, and are generally increasing, indicating the start of the Winter influenza wave.

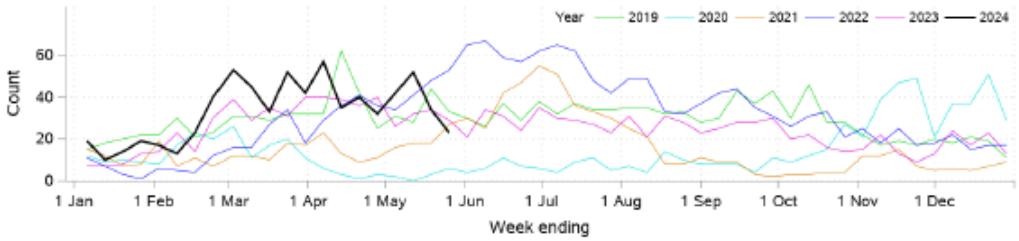
Figure 14: 'Influenza-like illness' monthly counts of unplanned emergency department (ED) presentations, 01 January to 26 May 2024, persons of all ages, SESLHD



Bronchiolitis

Interpretation: There is a slight decline in bronchiolitis presentations, compared to the elevated levels seen in March.

Figure 15: 'Bronchiolitis' monthly counts of unplanned emergency department (ED) presentations, 01 January to 26 May 2024, persons of all ages, SESLHD

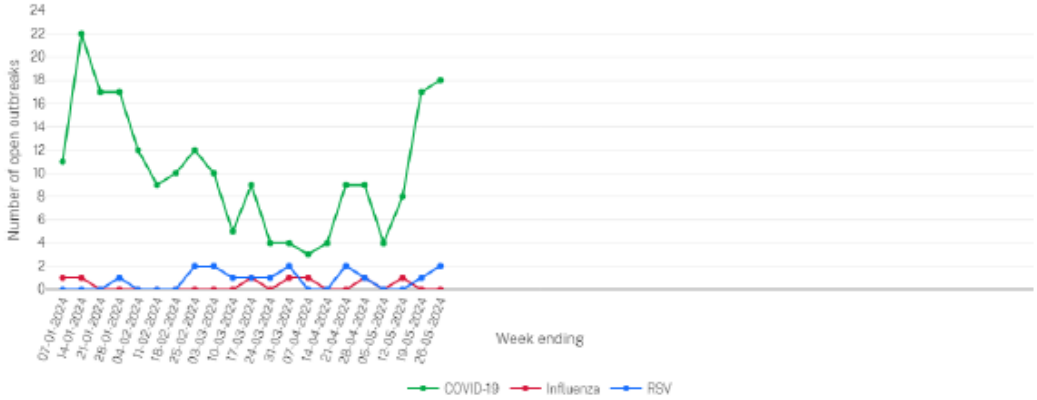


Outbreaks in residential aged care facilities

Figure 16 shows weekly residential aged care facility (RACF) outbreaks caused by acute respiratory infections (ARI) that are active each week. There were 20 ARI outbreaks active for the week ending 26 May, 18 due to COVID-19 and 2 due to RSV.

Interpretation: COVID-19 continues to be the main cause of respiratory outbreaks in aged care, and the number of outbreaks has increased through May. Influenza and RSV outbreaks are minimal and steady.

Figure 16: Open weekly acute respiratory infection outbreaks in SESLHD residential aged care facilities, 01 January to 26 May 2024



Excess All-cause Mortality

NSW Health receives daily reports of deaths reported to NSW Registry of Births, Deaths and Marriages (BDM). Deaths from all-causes are tracked against previous death rates at the same time of year to detect when respiratory outbreaks may be more severe. Increased excess mortality (population-wide impact) may be due to increased transmission or increased virulence of the virus.

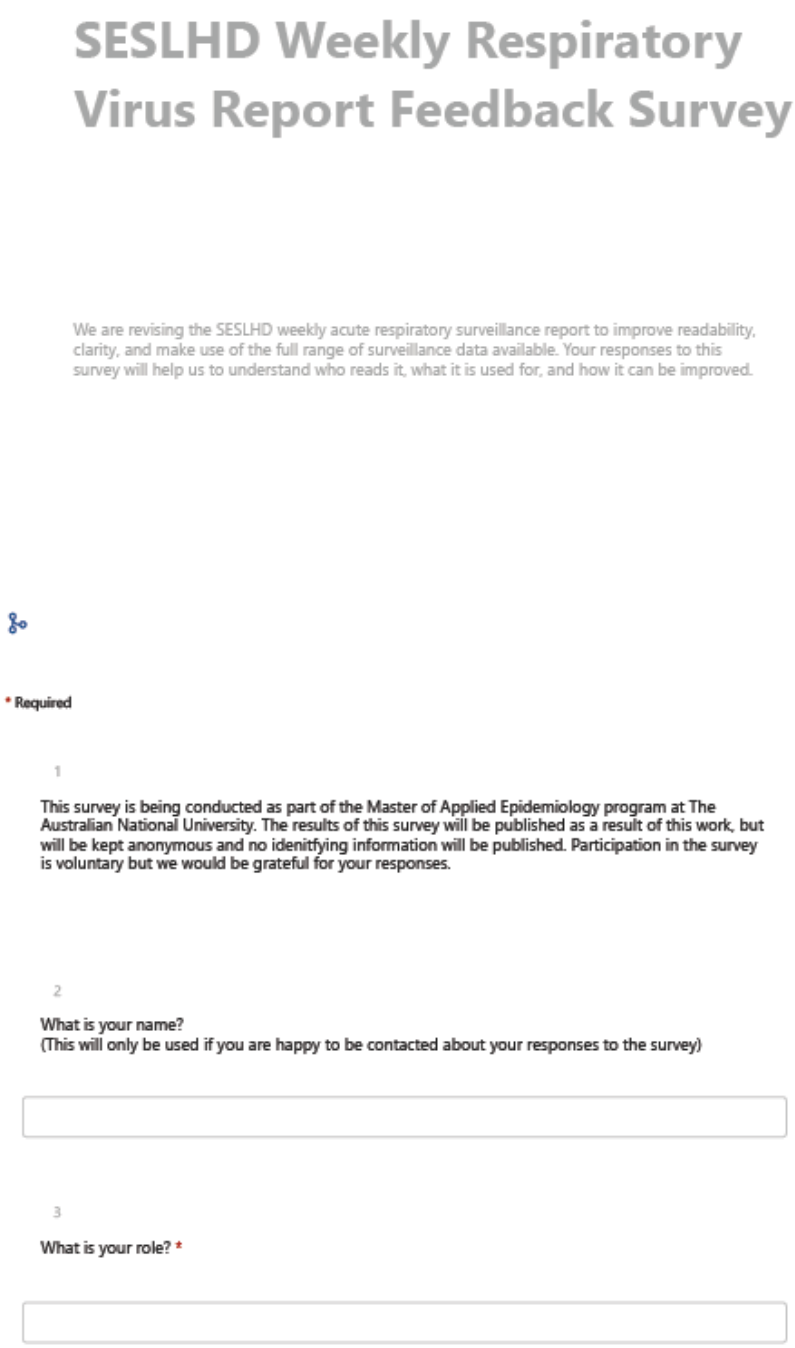
Data is reported with a 4-week lag to allow for delays in reporting to BDM. The data is available at a state-level only.

All-cause mortality in the week-ending 31 March was below the seasonal baseline.

Please visit the NSW Respiratory Surveillance Report to view the data (Figure 4).
https://www.health.nsw.gov.au/Infectious/covid-19/Pages/reports.aspx

Appendix II

Evaluation survey



SESLHD Weekly Respiratory Virus Report Feedback Survey

We are revising the SESLHD weekly acute respiratory surveillance report to improve readability, clarity, and make use of the full range of surveillance data available. Your responses to this survey will help us to understand who reads it, what it is used for, and how it can be improved.

* Required

1

This survey is being conducted as part of the Master of Applied Epidemiology program at The Australian National University. The results of this survey will be published as a result of this work, but will be kept anonymous and no idenitfying information will be published. Participation in the survey is voluntary but we would be grateful for your responses.

2

What is your name?
(This will only be used if you are happy to be contacted about your responses to the survey)

3

What is your role? *

4

Where do you currently work? (facility and area)
e.g POWH, Infection Control *

5

Do you currently read SESLHD Weekly Respiratory Virus Report? *

- ◯ Yes
- ◯ No

6

Please indicate what information you currently read from the SESLHD Weekly Respiratory Virus Report? *

- ◯ Email summary only
- ◯ Weekly Respiratory Virus Report document
- ◯ Email summary AND read the attachment

7

Would you like to provide any feedback on the email summary, or the report if you have previously read it?

8

Why do you not read the Weekly Respiratory Virus Report? *

9

How useful do you find the Weekly Respiratory Virus Report? *

0	1	2	3	4	5	6	7	8	9	10

Not useful at all — Very useful

10

How does the Weekly Respiratory Virus Report inform your work? *

11

Do you think the Weekly Respiratory Virus Report is timely? *

- ◯ Yes
- ◯ No

12

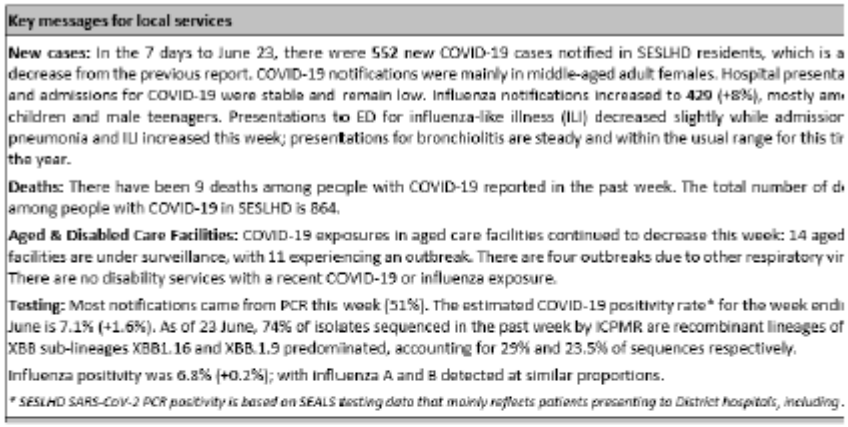
Why is the Weekly Respiratory Virus Report not timely? *

13

Are there any specific sections in the report you read or lookout for? *

14

Thinking about the 'Key messages for local services' at the beginning of the Weekly Respiratory Virus Report, do you find this useful? *



Key messages for local services

New cases: In the 7 days to June 23, there were **552** new COVID-19 cases notified in SESLHD residents, which is a decrease from the previous report. COVID-19 notifications were mainly in middle-aged adult females. Hospital presenta and admissions for COVID-19 were stable and remain low. Influenza notifications increased to **429** (+8%), mostly am children and male teenagers. Presentations to ED for influenza-like illness (ILI) decreased slightly while admissior pneumonia and ILI increased this week; presentations for bronchiolitis are steady and within the usual range for this tir the year.

Deaths: There have been 9 deaths among people with COVID-19 reported in the past week. The total number of d among people with COVID-19 in SESLHD is 864.

Aged & Disabled Care Facilities: COVID-19 exposures in aged care facilities continued to decrease this week: 14 aged facilities are under surveillance, with 11 experiencing an outbreak. There are four outbreaks due to other respiratory vir There are no disability services with a recent COVID-19 or influenza exposure.

Testing: Most notifications came from PCR this week (51%). The estimated COVID-19 positivity rate* for the week endi June is 7.1% (+1.6%). As of 23 June, 74% of isolates sequenced in the past week by ICPMR are recombinant lineages of XBB sub-lineages XBB1.16 and XBB.1.9 predominated, accounting for 29% and 23.5% of sequences respectively.

Influenza positivity was 6.8% (+0.2%); with Influenza A and B detected at similar proportions.

** SESLHD SARS-CoV-2 PCR positivity is based on SEALS testing data that mainly reflects patients presenting to District hospitals, including .*

◯ Yes

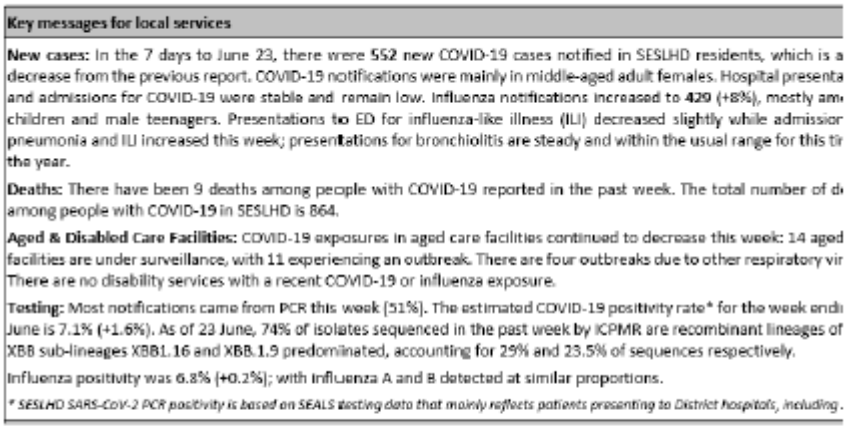
◯ No

15

Why do you not find the 'Key messages for local services' section useful?

16

Do you have any additional comments about this section?



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Influenza positivity was 6.8% (+0.2%); with Influenza A and B detected at similar proportions.

** SESLHD SARS-CoV-2 PCR positivity is based on SEALS testing data that mainly reflects patients presenting to District hospitals, including .*

17

Do you find the case numbers and rates by Local Government Area for COVID & influenza helpful to inform your work? *

Data summary

1. Case numbers

Table 1: SESLHD COVID PCR and RAT positive cases by LGA of residence and notification week

LGA	7 days	14 days	28 days	Total (Since 03/2020)	7-day crude rate per 100,000*	Total crude rate per 100,000*
Bayside	33	66	158	80,317	16.6	40,372
Georges River	27	50	163	75,193	16.7	46,553
Randwick	31	67	186	77,924	20.1	50,609
Sutherland Shire	75	128	300	121,362	31.4	50,732
Sydney	13	24	80	36,589	16.5	46,337
Waverley	18	38	67	34,990	24.6	47,733
Woollahra	12	22	53	25,342	20.9	44,179
SESLHD	**209**	**395**	**1,007**	**451,717**	**21.5**	**46,551**

Table 2: SESLHD influenza positive cases by LGA of residence and notification week

LGA	7 days	14 days	28 days	Total for 2023 YTD	7 day crude rate per 100,000*	2023 total crude rate per 100,000*
Bayside	69	164	382	1,091	34.7	548
Georges River	49	101	270	886	30.3	549
Randwick	64	133	271	879	41.6	571
Sutherland Shire	89	225	604	1,501	37.2	628
Sydney	24	52	120	318	30.4	403
Waverley	29	48	126	520	39.6	709
Woollahra	28	52	115	434	48.8	757
SESLHD	**352**	**775**	**1,888**	**5,629**	**36.3**	**580**

*based on DPIE LGA projection data 2021.

- ◯ Yes
- ◯ No

18

Do you have any additional feedback about this section?

19

Do you have any feedback about the epidemiological curves of COVID-19 and influenza case numbers?

Figure 1: SESLHD COVID-19 cases by test type, week of notification and year

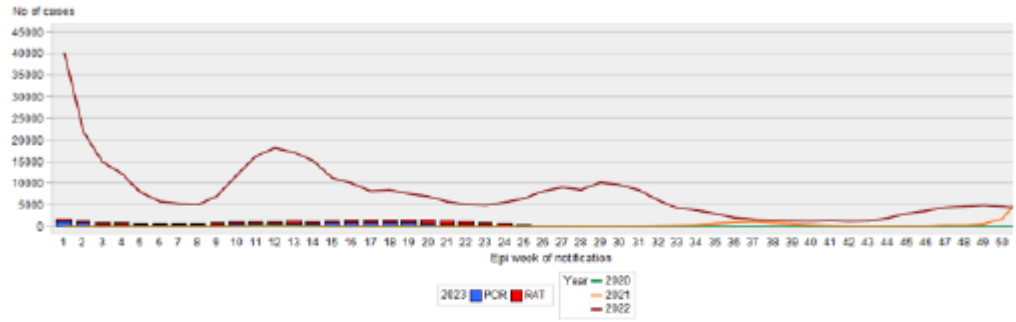
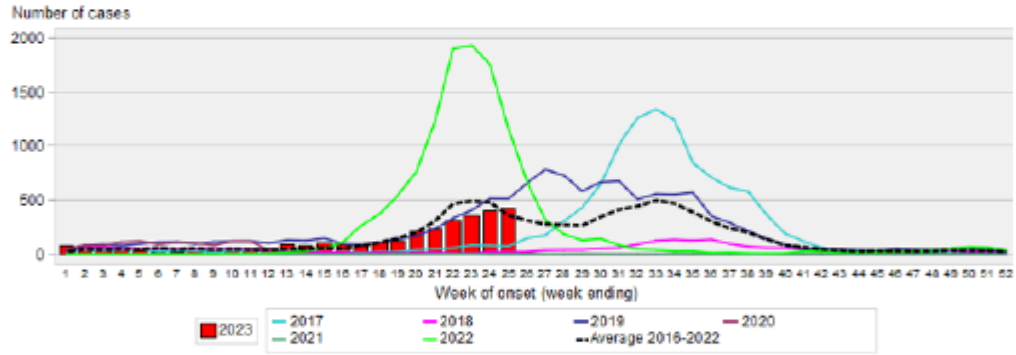


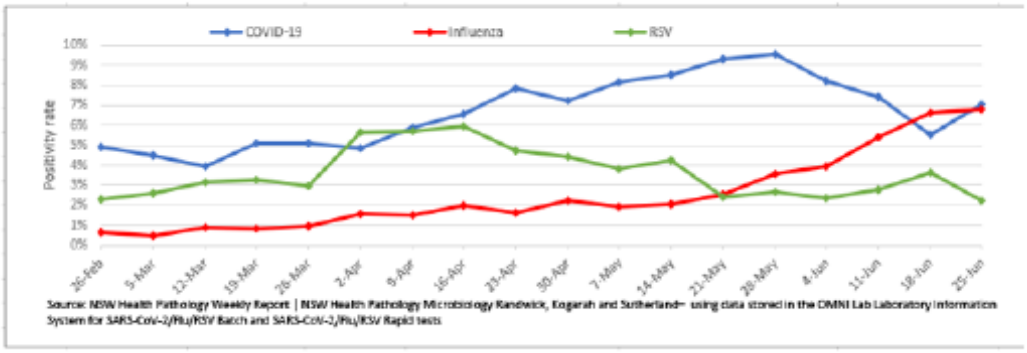
Figure 2: SESLHD influenza cases by week of notification and year



20

Do you have any feedback about the test positivity figure?

Figure 3: SEALS respiratory test positivity rate by week, week ending 25 June 2023

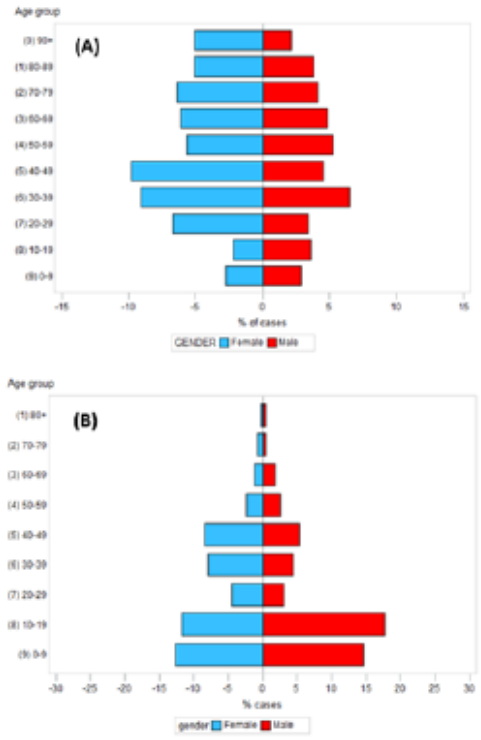


21

Do you have any feedback on the graphs of age and gender distribution of cases in the last 7 days?

2. Demographic Data

Figure 4: Percentage of (A) COVID and (B) Influenza cases in the last 7 days by age group and gender

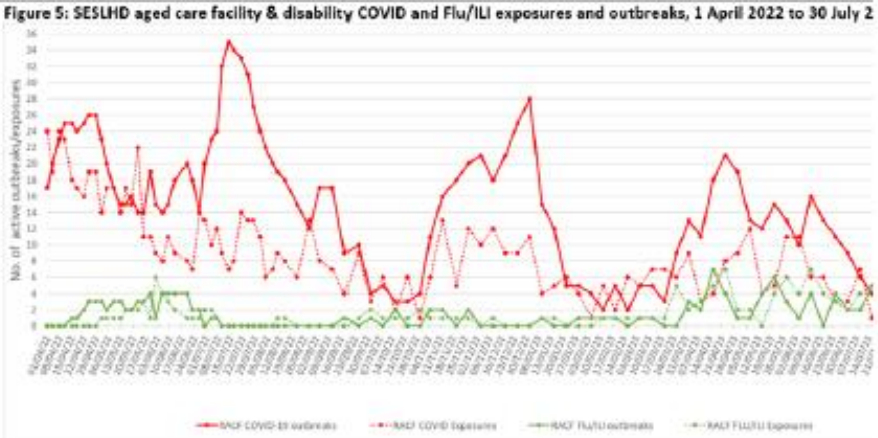


22

Do you have any feedback on the residential facility outbreaks graph?

3. Residential facility outbreaks reported to the Public Health Unit

Figure 5: SESLHD aged care facility & disability COVID and Flu/ILI exposures and outbreaks, 1 April 2022 to 30 July 2



NB. 'Flu/ILI' outbreaks include outbreaks caused by RSV and other respiratory viruses

23

Do you find the table on Emergency Department presentation and admission trends useful? *

4. Emergency department presentations and admissions

Table 3: Emergency Department presentations within SESLHD week ending 30 July 2023

Diagnosis / Category	Trend since last week	Compared to average for time of year (2018-2022)	Comment
Respiratory, fever and unspecified infection presentations	Steady	Similar	
Influenza like illness (ILI) presentations	Increased	Higher	1.2x higher than last week 1.9x higher than usual
Coronaviruses/SARS presentations	Steady	N/A	
Bronchiolitis presentations	Steady	Similar	

Data is from NSW Public Health Rapid Emergency Department Surveillance System. Increase or decrease indicates change >20% compared to the previous week

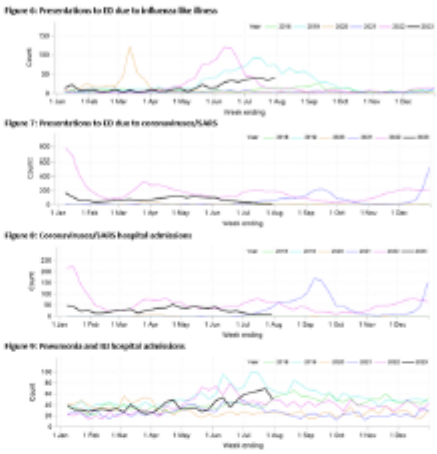
- ◯ Yes
- ◯ No

24

Why do you not find the table on Emergency Department presentation and admission trends useful?

25

Do you find the figures on Emergency Department presentations and admissions trends useful? *



- ◯ Yes
- ◯ No

26

Why do you not find the figures on Emergency Department presentations and admissions trends useful?

27

Is there anything else you would like to comment regarding the Emergency Department data?

28

What reporting of Respiratory Syncytial Virus (RSV) activity would you like to see in the report?

29

Is there anything additional you would like to see included in the weekly Public Health ARI report that is not currently included? *

30

Do you have any further comments or feedback about the weekly ARI report?

Chapter: IV

Design and conduct an epidemiological study

Factors associated with delayed diagnosis of hepatitis B in South Eastern Sydney Local Health District.

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Abbreviations

APDC	Admitted Patient Data Collection
AUD	Alcohol use disorder
CHB	Chronic hepatitis B
CheReL	NSW Centre for Health Record Linkage
DC	Decompensated cirrhosis
DNA	deoxyribonucleic acid
ESLD	End-stage liver disease
GHSS	Global Health Sector Strategy
HBV	Hepatitis B virus
HCC	Hepatocellular carcinoma
HCV	Hepatitis C virus
HIV	Human immunodeficiency virus
LGA	Local government area
LHD	Local health district
NCIMS	Notifiable Conditions Information Management System
NHR	National HIV Registry
NSW	New South Wales
RBDM	Registry of Births, Deaths and Marriages
SESLHD	South Eastern Sydney Local Health District
VHCRP	Viral Hepatitis Clinical Research Program
WHO	World Health Organization

Prologue

Rationale

This chapter summarises my epidemiological project; a population-based cohort study exploring factors associated with delayed diagnosis of hepatitis B in South Eastern Sydney Local Health District (SESLHD). This study addresses the public health challenges of hepatitis B virus (HBV), where late diagnosis can lead to severe outcomes such as decompensated cirrhosis (DC) and hepatocellular carcinoma (HCC).[1, 2] Despite global efforts to eliminate HBV by 2030, Australia's diagnosis rates remain below target, with delayed diagnosis contributing to poor survival rates due to liver complications.[3] The higher chronic hepatitis B prevalence among people born overseas, along with health access disparities in culturally and linguistically diverse communities, reinforces the requirement for targeted interventions.[4] In SESLHD, where 30% of the population is from non-English speaking backgrounds, tailored strategies for timely HBV diagnosis are crucial.[5] This research aimed to provide local data to guide more effective prevention and screening efforts.

My Role

Under the guidance of Professor Gregory Dore and the Viral Hepatitis Clinical Research Program (VHCRP) at the Kirby Institute, I was able to use a large, linked dataset to conduct a population-based cohort study, for which I filtered the data to investigate factors associated with HBV late diagnosis for SESLHD residents. I performed data cleaning and preparation, descriptive and analytical analysis, and collated all results and findings of the study.

Lessons Learnt

Always check your code, more than once and never undervalue the importance of local context when conducting population analyses! This was my first experience with a large dataset, and I was nervous about making a mistake and potentially losing data during the analysis. I also faced the challenge of translating STATA code into R. One of my biggest hurdles was ensuring the data was correctly coded, especially as the wider research team was analysing the data for all of New South Wales (NSW), while I was just focused on a subset of this data for SESLHD.

To ensure accuracy, I double checked my code against previous work from the team to verify correct filtering of the data. This was also a learning experience as this was the first time I had built my code from start to finish. This meant I often had to re-order coding operations to achieve the desired datasets and outputs for analysis. Due to the

smaller sample for my local analysis, I ended up with small numbers for some local government areas (LGAs). Toward the end of the analysis, it became apparent that one of the local government areas (LGAs) was missing from the descriptive data. As I was still developing my knowledge of HBV in the district, I had thought, given the small numbers, that this was an acceptable finding. However, my supervisor pointed out that this was an anomaly and the LGA should be included.

This led to two days of backtracking through my code to identify the issue. Through this process, I gained a much deeper understanding of the data, and discovered the LGA coding across the linked datasets was disparate. I proposed a solution for this issue and after consultation with my supervisors, a consensus was reached on how to best code the variable appropriately for analysis.

Public Health Impact

This research aimed to provide local evidence to guide more effective and targeted HBV prevention and screening in SESLHD.

Acknowledgements

I would like to sincerely thank the team from the Viral Hepatitis Clinical Research Team at The Kirby Institute for provision of the data as well as their guidance and support throughout this project. Specifically, Professor Gregory Dore, Dr Heather Valerio, Shane Tillakaeratne and Dr Marion Barault, for your guidance, support and welcoming nature into your team. It has been a true pleasure to collaborate with you.

Abstract

Objective

Hepatitis B virus (HBV) remains a public health challenge, with chronic HBV infection leading to advanced liver disease complications including decompensated cirrhosis (DC) and hepatocellular carcinoma (HCC). Prevention of HBV related DC and HCC relies on effective interventions, particularly antiviral therapy, with late diagnosis a missed opportunity for their earlier introduction. This study investigated factors associated with late HBV diagnosis in a large metropolitan area of Sydney, Australia (South Eastern Sydney Local Health District [SESLHD]).

Methods

A population-based cohort study used a linked dataset, consisting of notification data for HBV, human immunodeficiency virus (HIV) and hepatitis C virus (HCV), and hospital admission data. Late diagnosis was defined as HBV notification at or within two years of a decompensated cirrhosis (DC) or HCC diagnoses. Cross-tabulation and unadjusted and adjusted logistic regression analyses were performed exploring the association of late diagnosis with demographic, temporal, geographic, and clinical factors.

Results

Between 2002 and 2022, 10,910 individuals in SESLHD were notified with HBV, with 296 (3%) diagnosed with DC or HCC. Late diagnosis occurred in 102 (34%) of these individuals and was more common in females (43%) versus males (31%), individuals born between 1945 and 1964 (55%), and those born in West/South Asia (43%). Female sex was the only factor independently associated with late HBV diagnosis (adjusted odds ratio [aOR] 1.92, 95%CI 1.08-3.42). There were trends towards associations with late HBV diagnosis for birth cohort (≥1965) (aOR 2.02, 95% CI 0.85-4.82), overseas birth (aOR 1.92, 95% CI 0.96–4.01), history of alcohol use disorder (aOR 2.72, 95% CI 0.86–8.96), and year of DC or HCC diagnosis being (aOR 0.57, 95% CI 0.28–1.16 2016-2021 vs 2001-2008).

Conclusion

A third of people with HBV related advanced liver disease complications are diagnosed late, reducing opportunities for effective interventions. Strategies to enhance earlier HBV diagnosis, particularly for women, are required to reduce HBV disease burden and advance HBV elimination efforts. These findings underscore the importance of localised data-and benefits of data linkage.

Introduction

Hepatitis B is an infection of the liver caused by hepatitis B virus (HBV).[1] The infection can be acute (short and self-resolving) or chronic (long term).[1] Chronic infection can put people at risk of death from the sequelae of cirrhosis and liver cancer, with approximately 1.1 million deaths attributable globally to decompensated cirrhosis (DC) and hepatocellular carcinoma (HCC) in 2022.[1, 2] The World Health Organization (WHO) estimated that around 254 million people were living with HBV infection globally, with only 13.4% diagnosed.[6]

In 2016, the World Health Assembly embraced the Global Health Sector Strategy (GHSS) focusing on viral hepatitis and aimed for the elimination of HBV as a public health threat, intending to achieve a 65% reduction in mortality (now revised to ≤4 per 100,000 population per year) and diagnosis target of 90% by 2030.[7] CHB is a significant public health burden and is now the most prevalent blood-borne viral infection in Australia.[8] In 2021 there were an estimated 200,385 people living with CHB in Australia, representing 0.8% of the population, with an estimated 73% of those people diagnosed, below the 2022 National Strategy target of 80%.[3]

Without effective interventions such as antiviral therapy, around one quarter of people who have CHB will develop HCC or DC, despite being generally asymptomatic.[9] Prognosis for individuals with DC is poor, with a 5-year survival rate ranging from 14% to 35% and poorer for HCC with 5 year survival of 18-20%.[10,11] Prior to these complications, CHB often has an extended asymptomatic phase which probably contributes to delayed diagnosis.[12] This highlights the need for improvements across the cascade of care, including screening, early diagnosis, linkage to care, and initiation of treatment.[13]

Australia's Fourth National Hepatitis B Strategy 2023-2030, outlines key drivers of adverse HBV outcomes including stigma, racism, discrimination, legal issues and other social and structural determinants of health.[14] In Australia three-quarters of people with CHB are either born overseas or identify as Aboriginal or Torres Strait Islander.[3] Country of birth is a key predictor of CHB risk.[4] With an estimated 70% of all people living with CHB in Australia in 2021 born overseas.[14] Migration patterns to Australia will continue to influence the future population of individuals living with CHB, and potentially influence numbers of people diagnosed and national goals of elimination.[3, 14] The national strategy has highlighted the requirement to comprehensively understand the needs of diverse priority populations impacted by hepatitis B across cultural, ethnic, linguistic, social, and geographical dimensions.[14] The higher prevalence of CHB among those born overseas,

combined with evidence that culturally and linguistically diverse communities in Australia face broader health care access disparities, highlights the importance of targeted health interventions.[4]

South Eastern Sydney Local Health District (SESLHD) is one of the most populous local health districts in metropolitan Sydney, and home to a diverse population, of which 30% of people are from a non-English speaking background.[5] With this in mind, local measures for CHB case finding and diagnosis need to be tailored to specific populations within the district. We used an existing population-based linked dataset comprising all HBV notifications made in New South Wales (NSW), to analyse the factors associated with late diagnosis of HBV for SESLHD residents through a population-based cohort study. The aim of the study was to generate local data to inform targeted initiatives to improve the HBV cascade of care in SESLHD, thereby contributing to the monitoring of HBV to guide the development of improved prevention strategies.[15]

Methods

Study setting, data sources and record linkages.

The study used an existing linked data set provided by the Viral Hepatitis Research Centre at the Kirby Institute. Data linkage had been undertaken by the NSW Centre for Health Record Linkage (CheReL). The data spine comprised all HBV and HCV notifications made in NSW as recorded by the NSW Notifiable Conditions Information Management System (NCIMS) from 1993. Under the Public Health Act 1991, mandatory notification for all individuals with positive HBV serology (HBV surface antigen) and tests is required in NSW or HBV deoxyribonucleic acid (DNA) is required in NSW.[16] HBV notifications were linked using deterministic and probabilistic linkage algorithms, using demographic details (including full name, gender, date of birth, and address). between notifications and hospitalisations (as recorded by the Admitted Patient Data Collection database (APDC) which holds all hospital admission from July 2001). [15] Duplicate HBV notifications were excluded from all analyses.

The APDC includes data from all inpatient admissions in public and private hospitals since July 2001. Each record contains demographic, administrative, and diagnostic information coded at discharge according to the ICD-10. People living with HIV coinfection were identified through the National HIV Registry (NHR), which holds HIV notifications since 1985.

Ethics approval was previously obtained from New South Wales Population and Health

Services Research Ethics Committee (PHSREC) (HREC/2019/ETH0177). This project also received mutual recognition from the Australian National University Human Research Ethics Committee (H/2024/0786).

Study period

Linked data was extracted for the following periods: NCIMS (1993-31 March 2022), APDC (01 July 2001-2022), NHR (1994-2022). The study period was from 2002 to 2022.

Study population

The study population included people with an HBV notification and first hospitalisation with DC or HCC from 2002 to 2022 who resided in SESLHD at time of ESLD. The study was bound by the geographical area of SESLHD as defined by the 2011 NSW local health district (LHD) boundaries, determined by the LHD of residence at time of hospital admission (all hospitals regardless of LHD of facility in NSW) and were that was missing LHD of residents at time of notification was used. The ICD-10 diagnosis codes used to identify hospitalisations occurring as DC and HCC are presented in *Appendix II.*

Study outcome

The primary study outcome of interest was late diagnosis (no, yes) of HBV, as defined by a HBV notification after, at the time of, or within 2 years before DC or HCC diagnosis.

Exposure variables

The primary variable of interest was late HBV diagnosis among people with DC or HCC hospitalisation, during the study period (2002-2022). Other variables of interest were age at HBV notification (categorised into birth cohorts, ≤1944, 1945-1964, ≥1965), sex (male, female, missing/unknown), local government area (LGA) of residence (Bayside, Georges River, Randwick, Sutherland Shire, Sydney, Waverley, Woollahra), country of birth and history of alcohol use disorder (AUD). History of AUD (no, yes) was defined as any AUD-related hospitalisation occurring before HBV notification. AUD is a standard term used to define continued drinking despite adverse mental and physical consequences. AUD was defined according to hospitalisation with any of the ICD-10 codes as shown in *Appendix II*.

Country of birth was grouped by regions (Africa, Americas/Europe/New Zealand, Australia, Oceania/East Asia, West/South Asia, Unknown), to support local public health policy planning, but was collapsed to be Australia/Overseas analysis in the regression. People with unknown country of birth were removed from the regression, following consultation with a statistician.

The study period was sub-divided based on key stages of HBV treatment and prevention,

2001-2008 (prior to broad access to highly effective antiviral therapy), 2009-2015 (highly effective antiviral therapy), and 2016-2022 (elimination era).

Statistical analysis

Descriptive statistics including means and standard deviations (SD) were calculated for continuous variables that were normally distributed. Medians and interquartile ranges (IQR) were calculated where a continuous variable was not normally distributed. Frequencies with percentages were calculated for categorial variables.

Logistic regression was used to assess factors associated with late diagnosis, adjusting for potential confounding from all other variables, reported as adjusted odds ratios (aOR) with 95% confidence intervals (95%CI). Univariate analysis was conducted and used to calculate unadjusted OR, assess for statistical significance (p <0.05), examine SD's and 95% CI's for individual variables. A backward elimination approach was employed, where all exposure variables were included in the initial regression model and removed one-by-one, model fit assessed using the likelihood ratio test (LRT). Variables with clinical significance were retained in the final model even if they did not meet statistical significance in the univariate analysis. A statistician was consulted throughout the process and provided guidance in finalising the model to ensure both statistical rigor and clinical relevance.

The linked dataset was cleaned in the STATA v18.0 software (College Station, TX, USA). R statistical software, version 3.4.2, were used for all other analyses.[17]

Results

HBV notified population in SESLHD and study participants

Between 2002 and 2022, there were 10,910 individuals with an HBV notification in SESLHD. The median age for all notifications was 35 years (interquartile range 28-47). Overall, 54% of individuals were male, 14% were born in Australia, 36% were born in West/South Asia and 24% resided in Georges River LGA. Additionally, 86 people (1%) had a history of AUD (*Table 1*). We found no individuals in our cohort diagnosed with HIV or HCV coinfection.

Of individuals with an HBV notification, 296 (3%) had a diagnosis of ESLD, based on first hospitalisation for DC or HCC. The median age was 51 years (interquartile range 42-61 years), with most ESLD cases in individuals between 35 and 70 years (*Figure 1*). Males accounted for 74% of people diagnosed with ESLD, with a comparison of characteristics by sex in *Appendix I*. A higher proportion of individuals with ESLD were born in

West/South Asia (46% vs. 36%) and had a history of AUD (5% vs.1%) compared to all HBV notifications. Geographically, Georges River (23%) and Bayside (22%) LGAs contributed the largest proportions of people with ESLD (*Table 1)*

Late diagnosis among people with HBV-ESLD

Of the 296 people with ESLD in this study, 102 (34%) had a late HBV diagnosis. Among those with late HBV diagnosis the median age was 57 years (interquartile range 28-87 years). Although males constituted 68% of late diagnoses among those with ESLD, but females had a higher proportion with late diagnosis compared to males (43% *vs.* 31%) (*Figure 2)*. Individuals born between 1945 and 1964, represented 55% of late diagnoses, compared to people born before 1945 (23%) and after 1964 (23%). West/South Aisa was the country of birth region that contributed the largest proportion (43%) of people with a late HBV diagnosis. Among those with late HBV diagnosis more people had a history of AUD (9%) compared to all those with ESLD (9% vs. 5%) (*Table 1)*.

Factors associated with late diagnosis among people with HBV-ESLD

The only factor independently associated with late HBV diagnosis among people with HBV-ESLD was female sex (adjusted OR [aOR] 2.14, 95% CI 1.17–3.94). There were trends towards associations with late HBV diagnosis for birth cohort (≥1965) (aOR.2.02, 95% CI 0.85-4.82), overseas birth (aOR 1.92, 95% CI 0.96–4.01), history of AUD (aOR 2.72, 95% CI 0.86–8.96), and year of ESLD diagnosis being (aOR 0.57, 95% CI 0.28–1.16; 2016-2021 vs. 2001-2008)(*Table 2*)

Table 1 Demographic characteristics of people with a hepatitis B (HBV) notification in SESLHD (2002-2022), overall and among those with HCC/DC and a late HBV diagnosis (n =10, 910)*

Characteristics		All HBV notified	HCC/DC	HBV late diagnosis
		N (%)*	N (%)^	N (%)^
Total		**10,910**	**296 (3%)**	**102 (34%)**
Sex	Male	5,909 (54%)	220 (4%)	69 (31%)
	Female	4,950 (45%)	76 (2%)	33 (43%)
	Not Stated/Unknown	51 (0%)		
Age (yrs.)	Age at HBV notification, median (IQR)	35 (28-47)	51 (42-61)	57 (28-87)
Birth Cohort	≤1944	871 (8%)	79 (9%)	23 (29%)
	1945-1964	3,659 (34%)	166 (5%)	56 (34%)
	≥1965	6,379 (58%)	51 (0%)	23 (45%)
Local Government Area (LGA)	Bayside	2,111 (19%)	65 (3%)	21 (32%)
	Georges River	2,583 (24%)	69 (3%)	26 (38%)
	Randwick	1,533 (14%)	43 (3%)	14 (33%)
	Sutherland Shire	749 (7%)	26 (4%)	8 (31%)
	Sydney	2,121 (19%)	40 (2%)	20 (50%)
	Waverley	421 (4%)	10 (2%)	3 (30%)
	Woollahra	321 (3%)	4 (1%)	2 (50%)
	LGA outside of SESLHD	1,071 (10%)	39 (4%)	8 (21%)
Year of DC/HCC Diagnosis	2001-2008		91 (31%)	38 (42%)
	2009-2015		113 (38%)	38 (34%)
	2016-2021		92 (31%)	26 (28%)
Country of Birth	Africa	75 (1%)	6 (8%)	4 (67%)
	Americas, Europe, New Zealand	726 (7%)	58 (8%)	21 (36%)
	Australia	1,497 (14%)	65 (4%)	17 (26%)
	Oceania/East Asia	212 (2%)	20 9%)	12 (60%)
	West/South Asia	3,908 (36%)	135 (3%)	44 (33%)
	Unknown	4,492 (41%)	12 (0%)	4 (33%)
Alcohol Use Disorder (AUD)	No	10,824 (99%)	280 (3%)	93 (33%)
	Yes	86 (1%)	16 (19%)	9 (56%)

**Percentages are shown as column percentages*
^Percentages are shown as row percentages

Figure 1 Age (years) distribution among people with DC/HCC by late CHB diagnosis in SESLHD, 2002-2022 (n=296)

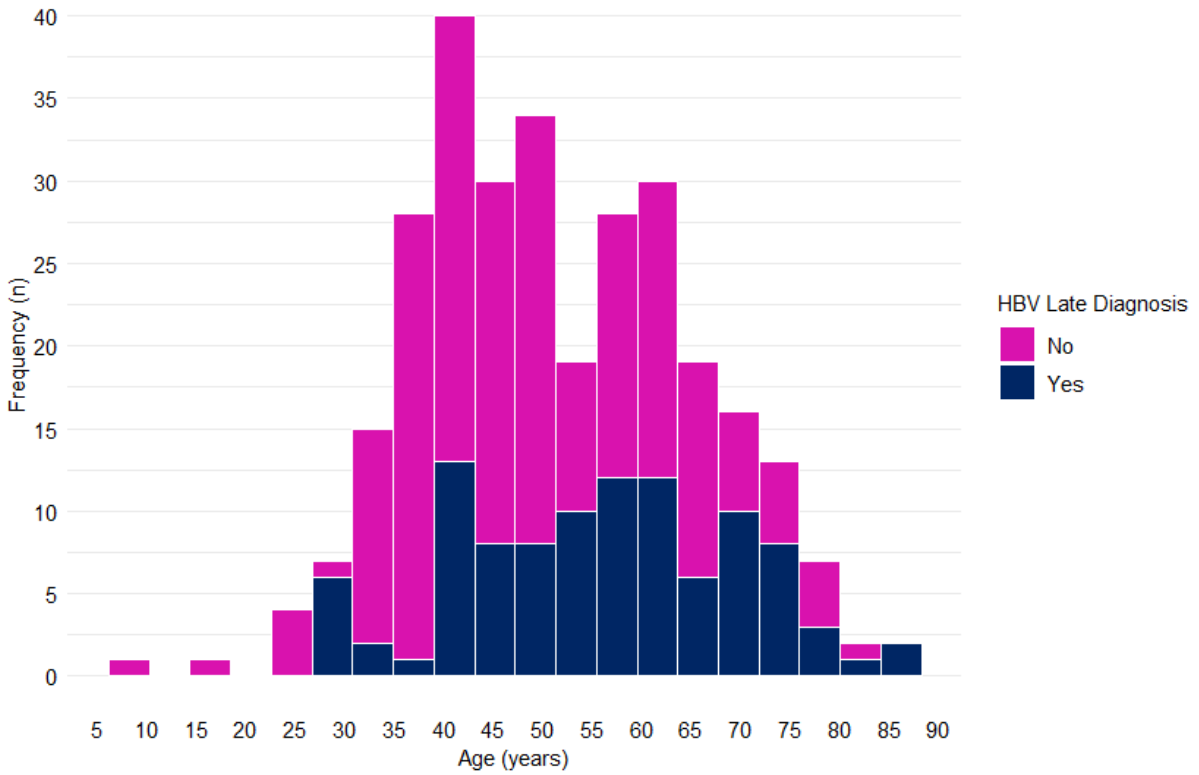

Figure 2 Distribution of late HBV diagnosis by sex of people with DC/HCC in SESLHD, 2002-2022 (n=296)

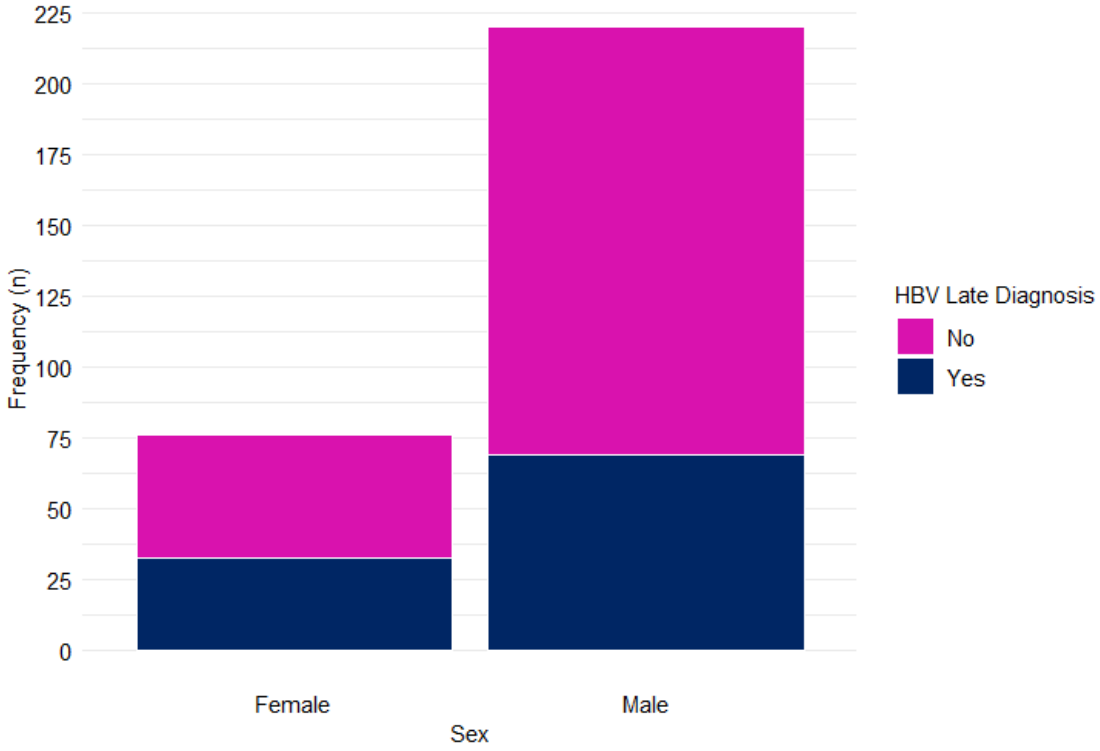

Table 2 Logistic regression (unadjusted and adjusted), evaluating factors associated with late HBV diagnosis among people with a diagnosis of decompensated cirrhosis (DC) or hepatocellular carcinoma (HCC) in SESLHD, 2002-2022 (n=296

		Late Diagnosis/ HCC-DC	Unadjusted		Adjusted	
Characteristics		n/N (%)	OR (95% CI)	p-value	OR (95% CI)	p-value
Sex	Male	69/220 (32%)	Reference		Reference	
	Female	33/76 (68%)	1.68 (0.98, 2.87)	0.06	2.14 (1.17, 3.94)	0.01
Birth Cohort	≤1944	23/79 (29%)	Reference		Reference	
	1945-1964	56/166 (34%)	1.24 (0.70, 2.24)	0.47	1.54 (0.81, 3.00)	0.19
	≥1965	23/51 (45%)	2.00 (0.96, 4.20)	0.06	2.02 (0.85, 4.82)	0.11
Local Government Area (LGA)	Sutherland Shire	8/26 (31%)	Reference		Reference	
	Georges River	26/69 (38%)	2.34 (0.97, 6.16)	0.06	1.34 (0.49, 3.86)	0.57
	Sydney-Waverley-Woollahra	25/54 (46%)	3.34 (1.34, 9.01)	0.01	1.66 (0.59, 4.93)	0.34
	Bayside	21/65 (32%)	1.85 (0.75, 4.94)	0.19	0.78 (0.28, 2.3)	0.64
	Randwick	14/43 (33%)	1.87 (0.70, 5.3)	0.22	0.99 (0.34, 3.05)	0.98
Year of diagnosis	2001-2008	38/91 (42%)	Reference		Reference	
	2009-2015	38/113 (34%)	0.71 (0.40, 1.25)	0.23	0.74 (0.38, 1.40)	0.35
	2016-2021	26/92 (28%)	0.55 (0.29, 1.01)	0.05	0.57 (0.28, 1.16)	0.12
Country of Birth	Australia	17/65 (26%)	Reference		Reference	
	Overseas	81/231 (35%)	1.6 (0.88, 3.03)	0.13	1.92 (0.96, 4.01)	0.07
Alcohol use disorder	No	93/280 (33%)	Reference		Reference	
	Yes	9/16 (56%)	2.58 (0.94, 7.44)	0.06	2.72 (0.86, 8.96)	0.08

Discussion

Our study identified important patterns in ESLD (DC and HCC), and late HBV diagnosis in SESLHD. Between 2002-2022 the overall number of ESLD cases declined and most cases were born between 1945 and 1964 and, predominantly male, and more likely to have a history of AUD. A third of people with first hospitalisation for ESLD had a late HBV diagnosis within two years of this clinical presentation. This late HBV diagnosis was associated with female sex, despite a majority of all cases being male. There were also trends towards associations with late HBV diagnosis, including for people born overseas. These findings will assist in informing local public health policy and practice.

Data linkage has enhanced our ability to assess disease severity and identify risk factors for late HBV diagnosis within the SESLHD. Through the linkage of administrative datasets including HBV notifications and hospitalisations, we have been able to gain valuable insights into the characteristics of individuals diagnosed later with HBV. This methodology demonstrates the power of linked data as a tool for health planning, enabling and considering a wide range of risk factors and improving the ability to capture hard-to-reach populations.[18] The use of linked data for this research has allowed for a focused analysis of SESLHD by combining patient characteristics from multiple sources, enriching the dataset and enabling a more nuanced investigation of population demographics for public health interventions.

Despite the strengths of using a linked data source, we acknowledge several study limitations. Firstly, HBV notifications in NSW are based on HBV serology and other markers (HBV DNA) that demonstrate active HBV infection rather than chronic HBV infection, although the vast majority would be expected to have chronic infection. Secondly, we relied on hospital coding data to diagnose DC and HCC, which may have led to either over-diagnosis or under-diagnosis, due to potential misclassification. Thirdly, administrative data used to define AUD has limited sensitivity, with reports indicting only 68% sensitivity and 97% for detecting heavy alcohol intake.[19] Fourth, discrepancies were found when coding LHD and LGA due to incomplete data, with the APDC showing a higher proportion of LGA misclassification compared to the notification data. This could have led to an over or under representation of certain LGAs. To address this, we used notification data for coding LGA because it was more complete, while APDC data was used for LHD coding as it was considered to retain more current patient information, thereby improving our analysis. Fifth, country of birth data was unavailable for a large proportion (41%) of individuals with an HBV notification. In the analysis people with an unknown country of birth were removed from the adjusted model (n=12). Lastly, we acknowledge that there were small numbers being analysed in the regression, therefore this may impact the statistical significance and perhaps a larger sample could show more factors that are associated with late HBV diagnosis that are statistically significant.

Our study revealed that although males made up most of the cohort and people with late diagnosis, a higher proportion of females with ESLD had late HBV diagnosis. While this may seem surprising, it aligns with existing research showing that outcomes often differ by sex in HBV.[20] In New South Wales all pregnant women must be offered screening for HBV, but our findings suggest that older women, particularly those born overseas, may fall outside this screening, resulting in missed diagnosis opportunities.[21] This situation

raises a question of equity in SESLHD. Research shows that women are often under-represented in HBV-related clinical care and translational studies, potentially contributing to gaps in timely diagnosis and care.[20] Addressing these disparities is crucial for more inclusive research and tailored interventions, which could improve screening, treatment, and resource allocation.

Although our study did not show an independent association between country of birth and late HBV diagnosis among those with ESLD, we believe this remains an important factor to consider in future screening and prevention strategies. Australia's hepatitis B population continues to grow, not only due to new domestic diagnoses but also because of individuals who acquired their infection in their country of birth before migrating.[9] Given the high rates of HBV among overseas-born populations, especially from regions with high endemicity, targeting these communities through culturally tailored screening programs could improve early diagnosis and reduce the burden of late-stage disease.[9, 22, 23]

Conclusion

Our study identified that a third of people with first hospitalisation for ESLD in SESLHD had a late HBV diagnosis, with female sex independently associate with late HBV diagnosis. Late HBV diagnosis proportion did vary geographically, with some specific LGAs being over-represented. Although we did not find a significant association between country of birth and late diagnosis, this remains a critical consideration for future public health interventions, given the large proportion of people born overseas in SESLHD. Targeting high-risk groups through culturally tailored screening and prevention programs could help to reduce the burden of late diagnosis of HBV. These findings underscore the importance of localised, data-informed strategies to improve early HBV diagnosis and prevention efforts contributing to the wider goal of HBV elimination.

Recommendations

1. **Enhance targeted screening programs:** Develop culturally tailored screening initiatives for high-risk groups, such as overseas born populations with high HBV endemicity. This can help improve early diagnosis and reduce the risk of ESLD.
2. **Increase awareness and access to screening for women:** Given the higher proportion of late CHB diagnoses among women, there is a need for targeted outreach to ensure these groups are adequately screened. Expanding efforts beyond standard antenatal screening to include older women could help address potential missed diagnoses.
3. **Localised public health strategies:** Using the associations with LGAs to inform local public health policies, resources and interventions to areas within the District with higher rates of CHB late diagnosis can be supported. This approach could improve the efficiency of prevention and treatment programs.
4. **Monitor and adapt strategies based on local epidemiology:** Regularly assess and updated local prevention and treatment strategies based on surveillance data. This will aid the adaptation of interventions to changing patterns in HBV diagnoses and ensure alignment with the goals towards HBV elimination.

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Appendix I

Additional tables and figures

Table 3 Frequency and percentage of individuals with DC/HCC by birth cohort and sex. (n =296)

Birth Cohort	Female n (%)	Male n (%)
≤1944	23 (30%)	56 (25%)
1945-1964	41 (54%)	125 (57%)
≥1965	12 (16%)	39 (18%)
Total	**76 (100%)**	**220 (100%)**

Table 4 Frequency and percentage of individuals with DC/HCC by local government area (LGA) and sex. (n =296)

Local Government Area (LGA)	Female n (%)	Male n (%)
Bayside	21 (28%)	44 (20%)
Georges River	20 (26%)	49 (22%)
Randwick	11 (14%)	32 (15%)
Sydney-Waverley-Woollahra	9 (12%)	45 (20%)
Sutherland Shire	7 (9%)	19 (9%)
LGA outside of SESLHD	8 (11%)	31 (14%)
Total	**76 (100%)**	**220 (100%)**

Table 5 Frequency and percentage of individuals with DC/HCC by country of birth and sex. (n =296)

Country of Birth	Female n (%)	Male n (%)
Australia	12 (16%)	53 (24%)
Americas, Europe, New Zealand	15 (20%)	43 (20%)
Africa	2 (3%)	4 (2%)
Oceania/East Asia	9 (12%)	11 (5%)
West/South Asia	33 (43%)	102 (46%)
Unknown	5 (7%)	7 (3%)
Total	**76 (100%)**	**220 (100%)**

Table 6 Frequency and percentage of individuals with DC/HCC by year of DC/HCC diagnosis and sex. (n =296)

Year of Diagnosis	Female n (%)	Male n (%)
2001-2008	23 (30%)	68 (31%)
2009-2015	25 (33%)	88 (40%)
2016-2021	28 (37%)	64 (29%)
Total	**76 (100%)**	**220 (100%)**

Table 7 Frequency and percentage of individuals with DC/HCC by alcohol use disorder (AUD) and sex. (n =296)

Alcohol Use Disorder (AUD)	Female n (%)	Male n (%)
Yes	2 (3%)	14 (6%)
No	74 (97%)	206 (94%)
Total	**76 (100%)**	**220 (100%)**

Appendix II

ICD-10 codes used for categorising alcohol use disorder

ICD-10 Code	Description
Z71.4	Alcohol abuse counselling and surveillance
I42.6	Alcoholic cardiomyopathy
E42.6	Alcohol-induced pseudo-Cushing's syndrome
G72.1	Alcoholic myopathy
G62.1	Alcoholic polyneuropathy
Z50.2	Alcohol rehabilitation
G31.2	Degeneration of nervous system due to alcohol
F10	Mental and behavioural disorders due to alcohol

Chapter: V

Evaluate a surveillance system

Enhancing Tuberculosis (TB) Contact Screening: An evaluation of TB surveillance systems and TB contact outcomes in South Eastern Sydney Local Health District.

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Abbreviations

eMR	Electronic Medical Record
IGRA	Interferon-γ gamma release assay
IQR	Interquartile range
LHD	Local Health District
LTBI	Latent tuberculosis infection
LTFU	Lost to follow-up
MoH	Ministry of Health
NCIMS	Notifiable Condition Information Management System
NSW	New South Wales
PHU	Public Health Unit
SD	Standard deviation
SESLHD	South Eastern Sydney Local Health District
TB	Tuberculosis

Prologue

Rationale

Evaluation of tuberculosis (TB) contact data has not previously been undertaken in South Eastern Sydney Local Health District (SESLHD). Understanding the relative performance of the multiple data systems, and the issues associated with each one, will enable current data to be better understood and may suggest more efficient ways to use existing systems. It will also inform the development of future surveillance systems for TB contact data. We evaluated the data collection process for TB contact data in SESLHD and assessed the data quality of contact data in the local TB clinical system and the state surveillance system, Notifiable Conditions Information Management System (NCIMS).

My Role

As this project had been proposed at the District level, I was responsible for all aspects, from the data collection to the analyses and the collation and distribution of results. I was responsible for the development of the project proposal. I coordinated meetings with the local TB clinic both remotely and in person. I was responsible for the development of data collection tools and templates and managing the data in an effective and appropriate way. Prior to data collection I created a data collection template which would provide for easier analysis of the data. I ensured all data was de-identified and stored in a secure manner. I conducted all the analyses and sought frequent feedback and guidance from my supervisors.

Lessons Learnt

TB contact data is complex! TB follow-up is complex! The data is quite diverse as there are so many pathways a contact can take in their follow-up journey, which makes it challenging to collate the data in a manner that is easily summarised for clear and useful interpretation. The respect I have for not only the disease but also the people who work in the field only continues to grow as I further develop my skills and knowledge in TB. I was grateful for having developed some experience in TB contact follow-up during my outbreak investigation prior to undertaking this project. This meant I had a foundational understanding of the mechanisms of contact follow-up and experience in collecting contact tracing data, which ensured I could create a robust data collection template that would make the analysis slightly easier. Although, I think my epidemiology skills also helped with this, as I ensured I collected the data in a way that would benefit the analysis, despite any incomplete data there might be.

Public Health Impact

The public health impact of this study stems from its identification of critical gaps and inconsistencies in TB contact data collection and reporting, which are essential for effective TB surveillance and control efforts. By highlighting discrepancies between local clinical systems and state epidemiological surveillance systems, as well as challenges faced by clinical staff in maintaining accurate data entry, the evaluation underscores the need for improvements in the accuracy, consistency and efficiency of TB contact tracing data. Enhanced data quality will allow for better monitoring of TB transmission, more effective follow-up with contacts and improved evaluation of prevention efforts. Ultimately, addressing these issues will support timely interventions, reduce the spread of TB, and contribute to stronger public health outcomes by ensuring that TB case and contact data are managed more effectively.

Acknowledgements

This piece of work would not have been possible without the support and collaboration of the local chest clinic at St George Hospital. I am eternally grateful to Danielle (Dani) Ferraro, Clinical Nurse Consultant (CNC) at St George Hospital Chest Clinic. Thank you for providing me the space within the clinic to undertake data collection and for your patience in responding to all the many questions and then follow-up questions I had throughout the process. Your passion for this field of work is undeniable and was clear in your enthusiasm and support for this project despite your unbelievably busy schedule. Thank you also to Kerrie Shaw, CNC at Prince of Wales Chest Clinic for taking the time in your busy day to explain your local processes and procedures within the clinic.

Abstract

Introduction

TB contact screening is essential for tuberculosis (TB) elimination in low-incidence countries like Australia. Contact tracing helps detect TB disease and TB infection, supporting treatment and follow-up. However, the District's TB data is collected through unconnected systems, creating the potential for inefficiencies and inaccuracies in surveillance and reporting. This evaluation aimed to assess the performance and data quality of these systems to improve TB contact data management and inform future surveillance enhancements.

Methods

Flowcharts were created to describe the data follow-up process. From the state Notifiable Conditions Information Management System (NCIMS), we extracted laboratory confirmed pulmonary TB case data for cases reported between 1 January 2022 and 30 June 2023. Contact follow-up data for these cases was extracted from the local chest clinic records and electronic medical records. Data were compiled, and cross-referenced, and NCIMS data was compared with clinic data. A descriptive analysis was performed, to assess data quality. Descriptive analyses assessed follow-up durations, screening rates, and contact pathways.

Results

The comparison between NCIMS and the local chest clinic identified errors in the accuracy of contact follow-up data. While NCIMS showed 100% data completeness for mandatory fields, local clinic records were often incomplete, due to primary use of electronic medical records (eMR) instead of contact line lists. Data entry errors in NCIMS included misclassifying TB cases as contacts and inaccuracies in tuberculin skin test (TST)/interferon-γ gamma release assay (IGRA) results. Follow-up data in NCIMS was not always updated when contact screening extended beyond the reporting period, leading to inconsistencies between the two systems in terms of accurate contact tracking and outcomes.

Discussion

The evaluation revealed discrepancies between NCIMS and local clinic TB contact data, including classification errors and incomplete documentation. Clinic staff reported difficulty in finding time away from clinical care to do manual surveillance data entry. Clearer guidelines and integrated systems are needed to ease reporting requirements for clinic staff, streamline data collection, and support accurate surveillance of TB.

Introduction

The screening of tuberculosis (TB) contacts is a priority action area as part of the World Health Organization's Action Framework Towards TB Elimination for Low-Incidence Countries.[1] TB contacts are people who have close contact with patients with infectious TB (TB disease) and are at high risk of infection.[2] Contact tracing of TB disease aims to identify cases of both TB disease and TB infection (also referred to as latent tuberculosis infection (LTBI)) and provide adequate treatment and follow up.[3] Contact tracing of TB supports the ongoing drive for TB elimination, specifically in low-incidence settings such as Australia.[3] In New South Wales (NSW), contact management, including tuberculin skin tests (TST) and preventative therapy for TB infection is guided by NSW Health policy directives.[4]

In NSW, TB contact investigations are undertaken by TB services (chest clinics) within each Local Health District (LHD) and supported by public health units (PHU) where requested by the chest clinics, or when significant public health risks occur.[5] The screening process for TB involves notifying identified contacts via phone, email, or letter, with all attempts documented in the contact's medical record.[5] Once contacted, contacts are informed of their exposure, and offered assessment and screening, which is of no cost to them if performed through the public hospital system.[5] If initial contact is unsuccessful, guidelines dictate that three attempts must be made, using methods such as phone calls, SMS and registered mail, with provisions for translation if required.[5] Contacts ideally undergo screening at two time periods: baseline testing within two weeks of their last exposure to the infectious case, and follow-up "break of contact" testing after 8 to 12 weeks. This allows assessment of conversions in this time period, suggesting recent exposure.[5] However, if the baseline testing is not able to be performed in the required timeframe, only a one-off screening in performed.

Screening assesses for TB disease through symptom evaluation, and TB infection using TST or interferon-γ gamma release assay (IGRA), depending on the contact's history.[5] Positive results lead to further evaluation with a chest X-Ray (CXR) and assessment by a TB clinician. People with evidence of TB infection may be recommended treatment or CXR surveillance.[5]

South Eastern Sydney Local Health District (SESLHD) is one of the largest health districts in metropolitan Sydney, covering a geographical area of 468 square kilometres, and containing four chest clinics.[6] In 2021 there were 90 cases of TB notified among SESLHD residents, making up 16% of the 558 cases notified in NSW and a rate of 9.3 per

100,000 people per year.[7]

Data on contacts of people with TB is important to inform service planning, policy development, and TB control efforts. Currently, data on TB contacts is collected across disparate systems in SESLHD: the local TB (chest) clinical systems – which varies between chest clinics in the District – and the state Notifiable Conditions Information Management System (NCIMS). They do not connect and have different purposes, including clinical management, medical record keeping, and public health surveillance. Anecdotally, this is known to create challenges in the efficiency, accuracy, and timeliness of TB contact surveillance data that is recorded in NCIMS and used for routine public health reporting. We also assessed the mandatory reporting fields in NCIMS for completeness.

Evaluation of the TB contact data system has not previously been undertaken in SESLHD. Understanding the relative performance of the multiple data systems, and the issues associated with each one, will enable current data to be better understood and may suggest more efficient ways to use existing systems. This evaluation was partially prompted by a report distributed to LHDs by the Ministry of Health (MoH), reporting on contact tracing completeness as per NCIMS data, and a desire to compare this to clinic records.

We assessed the data collection process for TB contact data in SESLHD, focusing on the quality of NCIMS surveillance data, compared with the local TB clinic records. The main objectives of this evaluation were to evaluate the data quality of NCIMS surveillance data by comparing it to the local TB clinic data, and to analyse the points at which contacts drop out of the TB screening pathway. Strengthening these data systems is essential to enhancing TB contact tracing and management, ultimately supporting more effective control and prevention of TB transmission across the District.

Methods

Site selection

All four TB services (chest clinics) within SESLHD have differing local systems. For this evaluation, we used the chest clinic with the greatest annual notifications of TB, the South clinic.

Describe the structure of the surveillance system

Meetings were conducted with clinic staff to introduce the evaluation and agree on the project scope. Site visits to the clinic were conducted to document the processes for

follow-up of TB cases and their contacts, as well as to clarify the roles and responsibilities of the PHU and local chest clinic in the evaluation.

During the site visit, the clinical nurse consultant (CNC), who manages the data entry into NCIMS, provided a detailed walkthrough of the processes followed when a TB case is notified to the clinic. This included how contacts are identified, how their information is managed, how contacts are followed up, and the procedures for data collection. The CNC further explained how data is entered into NCIMS, outlining each stage of the process. Additionally, areas that were identified as time consuming, challenging or inefficient were discussed, offering insights into potential areas for improvement.

Attributes of the surveillance system

Data quality

The NSW TB program was consulted to determine the mandatory reporting fields, and the method used to calculate contact screening outcomes, that are used for quarterly and yearly reporting. The mandatory reporting fields (*Table 2*) and proportions calculated for quarterly and annual reporting, enabled the comparison of the proportion of contacts recorded in the local clinic data for each TB case and the corresponding NCIMS record.

Local clinic data were compared to NCIMS, using the local chest clinic data as the 'gold standard' reference. All laboratory confirmed positive pulmonary TB case data within the local chest clinic jurisdiction was extracted from NCIMS between 1 January 2022 and 30 June 2023. A data extraction template was developed to retrieve cases and their associated contacts from local chest clinic databases. In instances where contact follow-up information was incomplete, electronic medical records (eMR) were consulted. For cases involving large-scale contact screening beyond the local clinic's jurisdiction, follow-up was conducted with other chest clinics across the state.

Data were compiled into two line lists: one for TB cases and their aggregate contact numbers (allowing for comparison to NCIMS contact summaries), and another for individual contacts of each case, which were cross referenced by the cases' unique NCIMS number. Data cleaning and analysis were performed using R statistical software (version 4.3.2).[8]

A flow chart was developed to illustrate the overall data sources used for TB contact follow-up. Descriptive analysis was performed on the TB cases using both NCIMS and local chest clinical systems data, to calculate median and means for continuous variables, and frequencies and percentages for categorial variables. Number of contacts and duration of contact follow-up for each case was calculated using the local chest

clinic data. Duration of follow-up (days) for each case was calculated from date of notification in NCIMS to the date the last contact of that case completed follow-up (if available) from the local chest clinic data. If NCIMS was missing any demographic information for the cases, then the local chest clinic data was used.

Outcome of individual contact screening

The individual contact line list from the local chest clinic was analysed to calculate the proportions of contacts identified, contacted and screened as well as the duration of follow-up based on prescribed screening pathways. A separate flow chart was created to depict the individual contact follow-up pathways. Descriptive analysis of contacts demographic features was performed, with means and standard deviations (SD) calculated for continuous variables where data is normally distributed and median and interquartile range (IQR) for non-normal distributions. Frequencies and percentages were calculated for categorical variables. Duration of follow-up for each contact was calculated from the date of first contact attempt made with each contact to the date of last follow-up with the clinic or upon completion of screening.

Results

Structure of the surveillance system

Local chest clinic data

Consultation with the local chest clinic showed that cases of TB are entered into NCIMS via automatic electronic laboratory record (ELR) notification. The clinic then creates a folder within their local shared drive and initiates a contact line-list for each case. The contact line list template was developed by the NSW TB program and is provided to all chest clinics in the state. Following interview/s with the case, contacts identified are entered into the contact line list, regardless of if personal information or contact details are available for the contact. The contacts are then contacted and if a name, date of birth and contact information is provided by the contact, the local chest clinic then creates an eMR record for the contact. Each contact attempt of an identified contact is recorded on the contact line list and in eMR (if one has been created). The follow-up of that contact is then recorded on the case's contact line list, including test date and results, outcomes of screening and if preventative treatment was commenced/completed, in addition to the contact's eMR. Where contact follow-up exceeded 12 weeks, it was found that the contact-line list was often not updated by the local chest clinic and only eMR was completed for the contact, with eMR becoming the main source of contact follow-up information.

NCIMS TB surveillance

The objectives identified for the collection of TB contact data in NCIMS were to monitor and evaluate the effectiveness of contact tracing, facilitate early diagnosis and management of contacts, assess treatment outcomes, support epidemiological surveillance and reporting, and ensure compliance with state and national guidelines. Each TB case is required to be entered into NCIMS, this is routinely done via ELR. However, on occasion this can also be done manually by chest clinic staff, the local PHU or the NSW TB program. TB contacts are not entered as individual records. For each case, a summary of the contact tracing is required to be entered. This summary data included the number of contacts identified, number of contacts screened, number of contacts with active TB (TB disease), number of contacts with a single positive TST/IGRA, number of contacts with a TST/IGRA conversion at the end of contact screen, number of contacts commenced on CXR surveillance, number of contacts commenced on preventative treatment, number of household contacts which are children under five years, number of household contacts screened that are children under five years, number of household contacts with a positive TST/IGRA that are children under five years, and number of household contacts commenced on preventative treatment that are children under five years.

To complete the summary data for contacts of a TB case, the local chest clinic uses the contact line list created for each case. The contact line list is preformatted on the first tab to display these summary figures for the clinic. The fields on the first tab are calculated based on data entered on the proceeding tab, the contact line list. The data entry for contacts into NCIMS must be completed quarterly, which is determined by the notification date of a case. In instances where the contact follow-up continues beyond the quarterly (~90 days) reporting time frame, for example, if a contact was placed on annual CXR surveillance or responded to the clinic months later, the contact summary data in NCIMS is not retrospectively updated by the local chest clinic.

Figure 1 illustrates this data flow process between each of the surveillance and data systems

Comparison of contact data from the two systems

Tuberculosis cases and contact summary

Twenty-nine cases of pulmonary TB occurred in the study period and were included in the analysis. Contact data for these cases was collated from NCIMS and the local chest clinic. From the 29 cases there were 167 contacts obtained from the local clinic data. Of 167 contacts from the clinic data, demographic characteristics and outcomes of 159 were

able to be included in the analysis of outcomes. Data for eight contacts followed up by another LHD clinic were not reported back to the chest clinic so were not able to be included in the individual contact follow-up outcomes, only aggregate data was reported, thus they are excluded from descriptive characteristics analysis for the 29 cases. Of the 29 cases 22 (76%) contacts were male and 7 (24%) were female. Twenty-eight (97%) of the cases were newly diagnosed and one (3%) was a recurrence (relapse or re-infection) following partial treatment overseas. The mean age for TB cases was 50 years (standard deviation [SD], 21 years). The median number of contacts for each TB case was 2 (interquartile range [IQR], 1-4). Most TB cases were born overseas, with the most common countries being Nepal (31%) and China (excludes SARs and Taiwan) (28%). The median duration for contact follow-up to be completed for each case was 204 days, with a range of 16-363 days and IQR of 98-253 days (*Table 1*).

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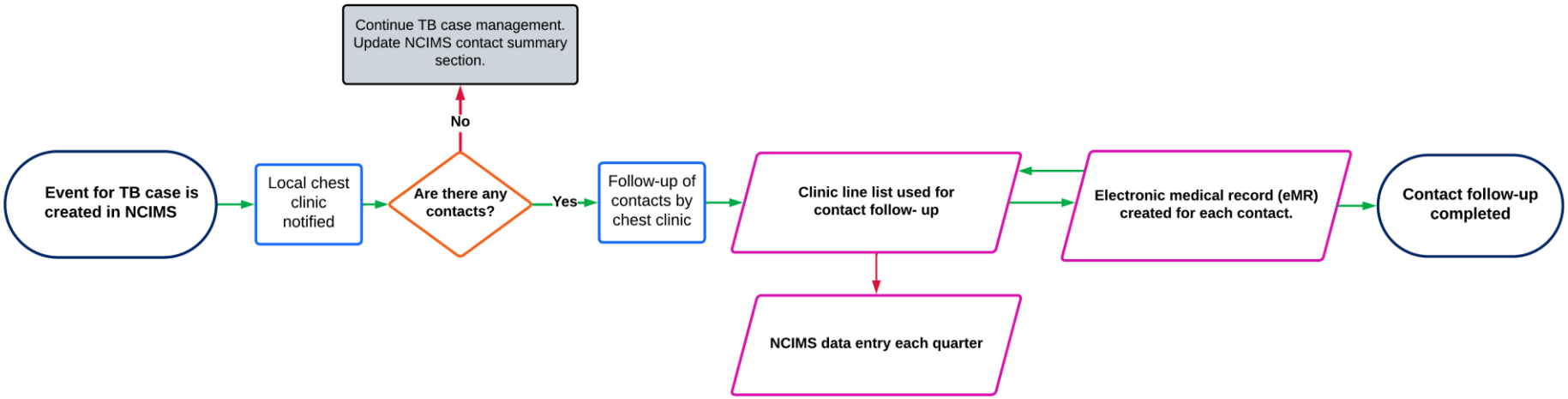
Figure 1 Flow chart of data flow process for a single TB case and their contacts and the associated surveillance and data systems and data entry points



Data quality

The comparison between NCIMS and the local clinic data showed discrepancies across all mandatory reportable fields (*Table 2*). Data completeness was 100% for all reportable mandatory fields in NCIMS. However, there were discrepancies in what is reported in NCIMS compared to the local clinic data. Data completeness was unable to be calculated for the local chest clinic data as they did not solely use the contact line list.

The discrepancies observed in the mandatory reportable fields in NCIMS and the local clinic data, as shown in *Table 2*, were reviewed in the local chest clinic line lists, which showed errors in the translation and entry of the data from the line lists into NCIMS. In two of the cases, there were five contacts who were identified as contacts, when they were diagnosed TB cases (recorded in contact line list as 'Positive on previous TB test'). Four of these TB cases were household members, and one was from the workplace. It is likely that the previously known TB case was the index case and therefore should not have been included in the contact screening numbers or follow-up. We also found that these TB cases were recorded in the contact counts as positive on initial TST/IGRA and commencing CXR surveillance in NCIMS.

Two of the 29 TB cases had contacts in NCIMS as positive on initial TST/IGRA, but in the clinic line list they were recorded as having a negative TST/IGRA on baseline and a positive break of contact (BOC) TST/IGRA. This should have been entered as a TSTS/IGRA conversion. There was one instance of a TST/IGRA conversion in NCIMS when it should have been recorded as a single positive TST/IGRA. Another data entry error was where a case had four contacts recorded in NCIMS as commencing CXR surveillance, but in the clinic line list it is shown two had a one off CXR as part of their screening and two declined an IGRA so were commenced on CXR surveillance. Of the remaining two contacts who proceeded with an IGRA, one was positive and the other negative, which was correctly recorded in NCIMS. The other example of this same data entry error was where a case had a contact recorded in NCIMS as commencing CXR surveillance, but in the clinic line list, the contact is recorded as having a one off CXR, not being placed on CXR surveillance, in addition to a positive IGRA. On review of the NSW TB Data Dictionary for NCIMS is it not clear if this field is for contacts who decline a TST/IGRA and were commenced on CXR surveillance or for contacts who had a positive TST/IGRA and declined preventative treatment and were placed on CXR surveillance.[9]

Table 1 Descriptive characteristics of TB cases obtained from NCIMS and local clinic data from a chest clinic in SESLHD, 1 January 2022 to 30 June 2023 (n = 29)

Descriptive characteristics	N (%)

Sex	Male	22 (76%)
	Female	7 (24%)
Age (yrs.)	Mean (SD)	50 (21)
	Range	22-97
Number of contacts	Median (IQR)	2 (1-4)
	Range	0-16
Contact follow-up duration (days)	Median (IQR)	204 (98-253)
	Range	16-363
Country of birth	Australia	1 (3%)
	Bosnia and Herzegovina	1 (3%)
	India	1 (3%)
	Indonesia	1 (3%)
	Korea, Republic of (South)	1 (3%)
	New Zealand	1 (3%)
	Malaysia	3 (10%)
	Philippines	3 (10%)
	China (excludes SARs and Taiwan)	8 (28%)
	Nepal	9 (31%)

SD = standard deviation, IQR = interquartile range

Table 2 Comparison of NCIMS mandatory reporting fields to local chest clinic data for 29 TB cases, SESLHD, 1 January 2022 to 30 June 2023

Reportable field	NCIMS N (%)	Local Chest Clinic* N (%)	Ratio NCIMS to clinic
Contacts found	168	167	1.01
Contacts screened	115 (68%)	110 (66%)	1.05
Contacts with active TB	0 (0%)	0 (0%)	-
Contacts with initial TST/IGRA positive	29 (25%)	26 (24%)	1.12
Contacts with IGRA/TST conversion	3 (3%)	5 (5%)	0.60
Contacts commenced CXR surveillance	9 (28%)	3 (10%)	3.00
Contacts commenced preventative treatment	9 (28%)	21 (68%)	0.43
Household contacts under 5yrs	7 (4%)	8 (5%)	0.88
Household contacts under 5 yrs. screened	7 (100%)	8 (100%)	0.88
Household contacts under 5 yrs. commenced preventative treatment	3 (43%)	3 (38%)	1.00
Household contacts under 5yrs positive TST/IGRA	0 (0%)	0 (0%)	-

TB = tuberculosis, TST = tuberculin skin test, IGRA = interferon-γ gamma release assay, CXR = chest X-ray surveillance
**Gold standard*

Tuberculosis contacts

Of the 159 contacts we had outcomes for, we excluded seven (4%) contacts from the descriptive analysis, as five were previously diagnosed TB cases and two were deemed not a contact.

From the remaining 152 contacts, 78 (57%) were male and the median age was 36 years (IQR 23-58 years). One hundred and three (68%) contacts had completed screening, 32 (21%) had not completed screening, 10 (7%) contacts were unknown if screening was completed and seven (5%) were still in the process of completing screening at time of data collection. *Figure 3* details screening completion by sex for the 152 contacts.

The largest proportion of contacts were in the 19-34 year age group (n = 41, 27%). *Figure 4,* shows the age distribution of contacts by screening completion. Forty-five (30%) contacts were born in Australia. The next most common regions of birth were South Asia (20%) and South East Asia (16%). Country of birth was not documented for 31 (20%) of contacts. The median duration of follow up for a contact was 73 days (IQR 19-134 days) (

Figure 5). One hundred and nine (72%) contacts were classified as high-risk contacts and the main setting for exposure was household (47%) and healthcare/workplace (38%) (*Figure 3). Figure 6* and *Figure 7* show screening outcomes by exposure setting and exposure risk

Figure 2 Age distribution by sex for 152 contacts using local chest clinic data systems from a local chest clinic in SESLHD

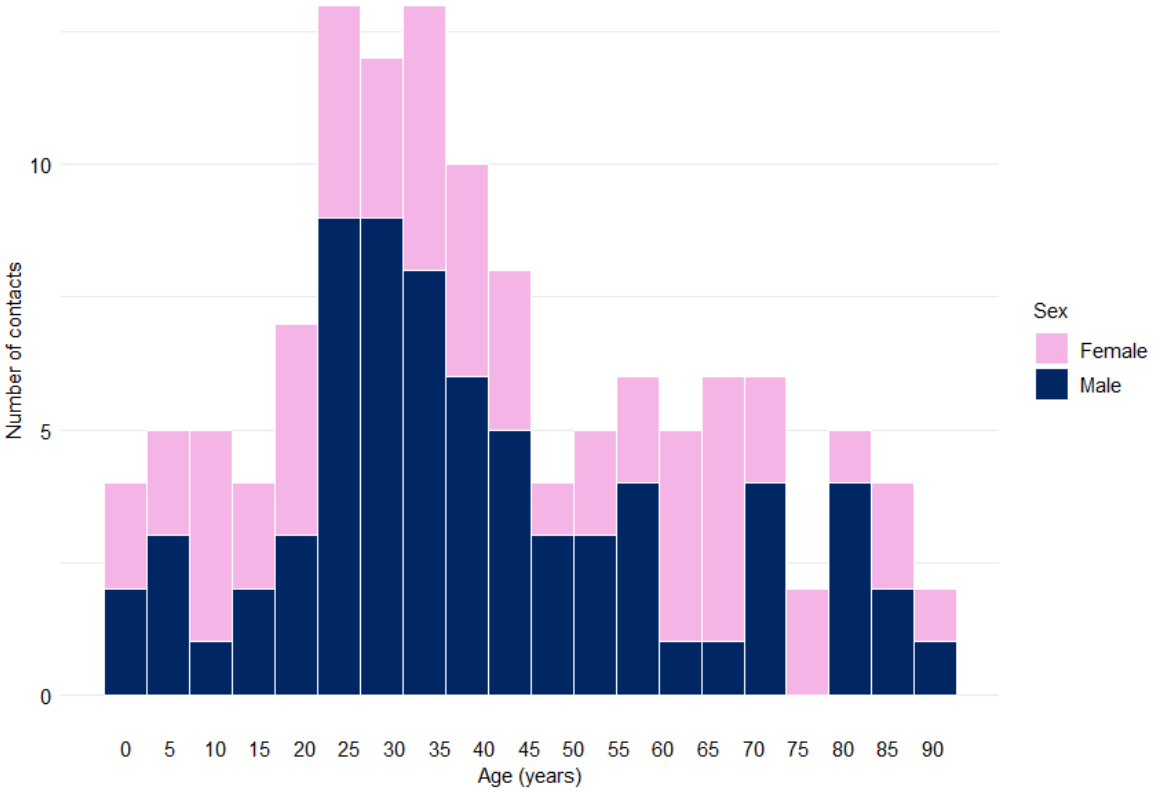


Figure 3 Screening completion for 152 contacts by sex using local chest clinic data systems from a local chest clinic in SESLHD

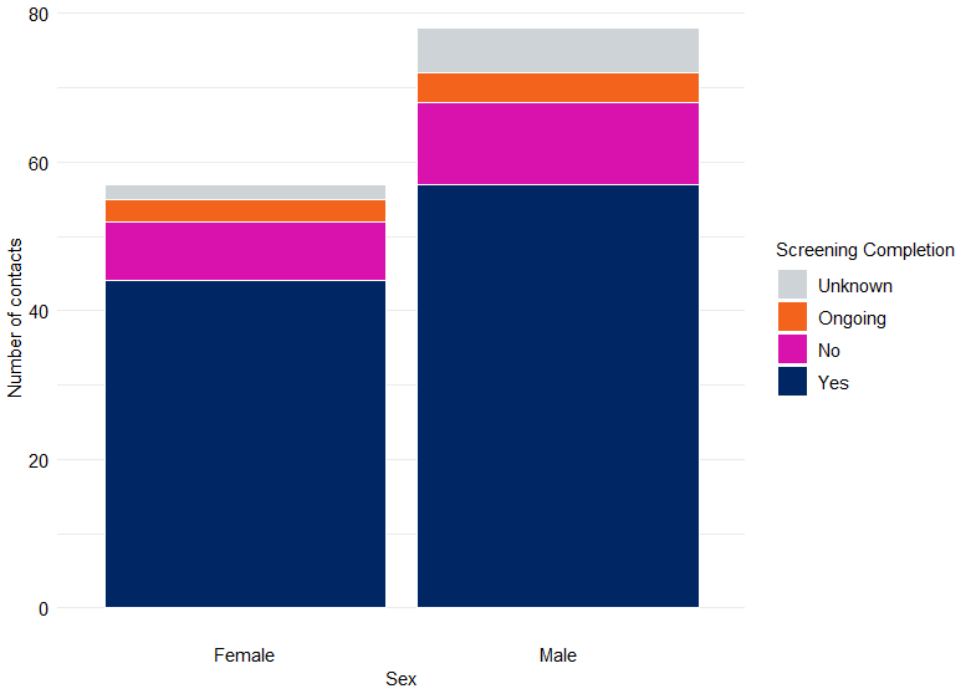


Figure 4 Outcome of screening by age for TB contacts using local chest clinic data systems from a chest clinic in SESLHD, (n = 152)

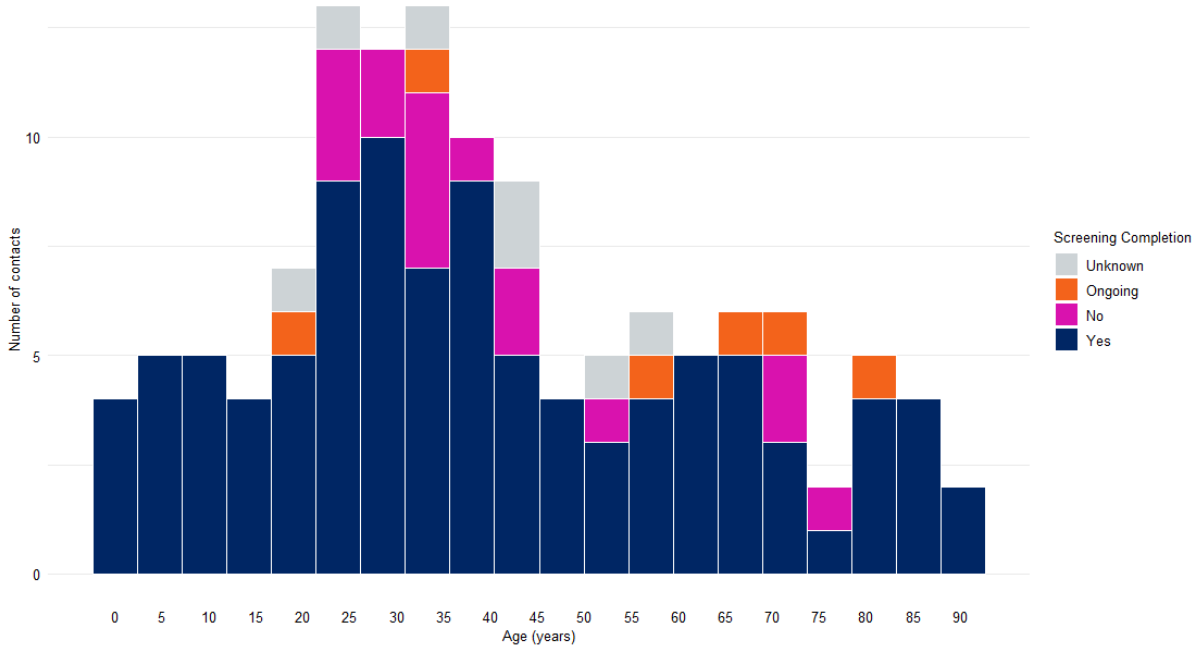
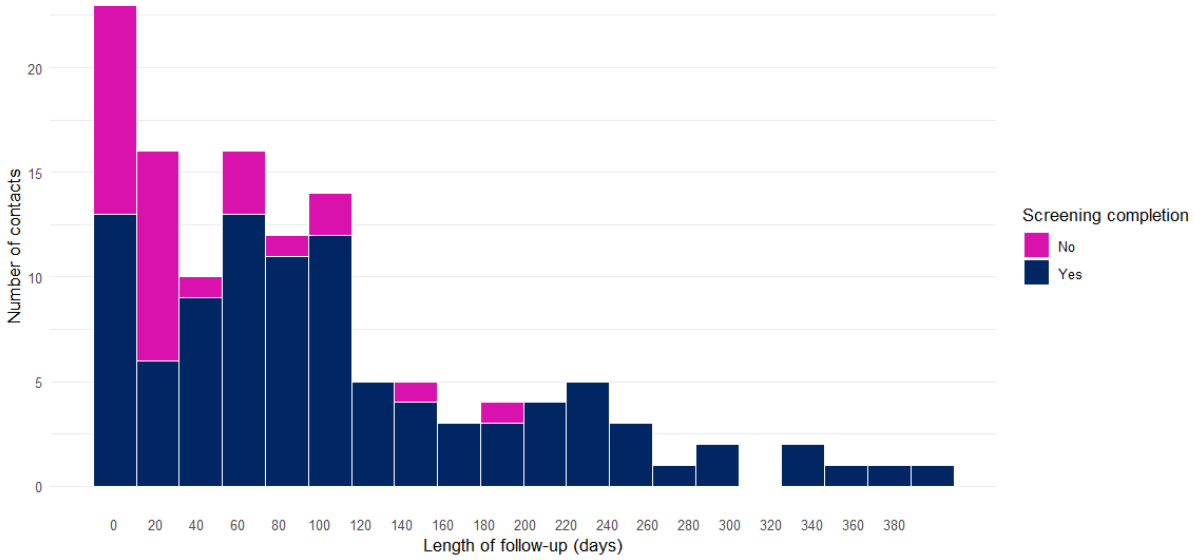


Figure 5 Duration of follow-up (days) by screening completion for 135 contacts from 29 TB cases using local chest clinic data systems from a local chest clinic in SESLHD*



N = 17 contacts removed from histogram due to ongoing screening or screening outcome unknown

Figure 6 Exposure setting of contacts by screening completion for 152 contacts from 29 TB cases using local chest clinic data systems from a local chest clinic in SESLHD

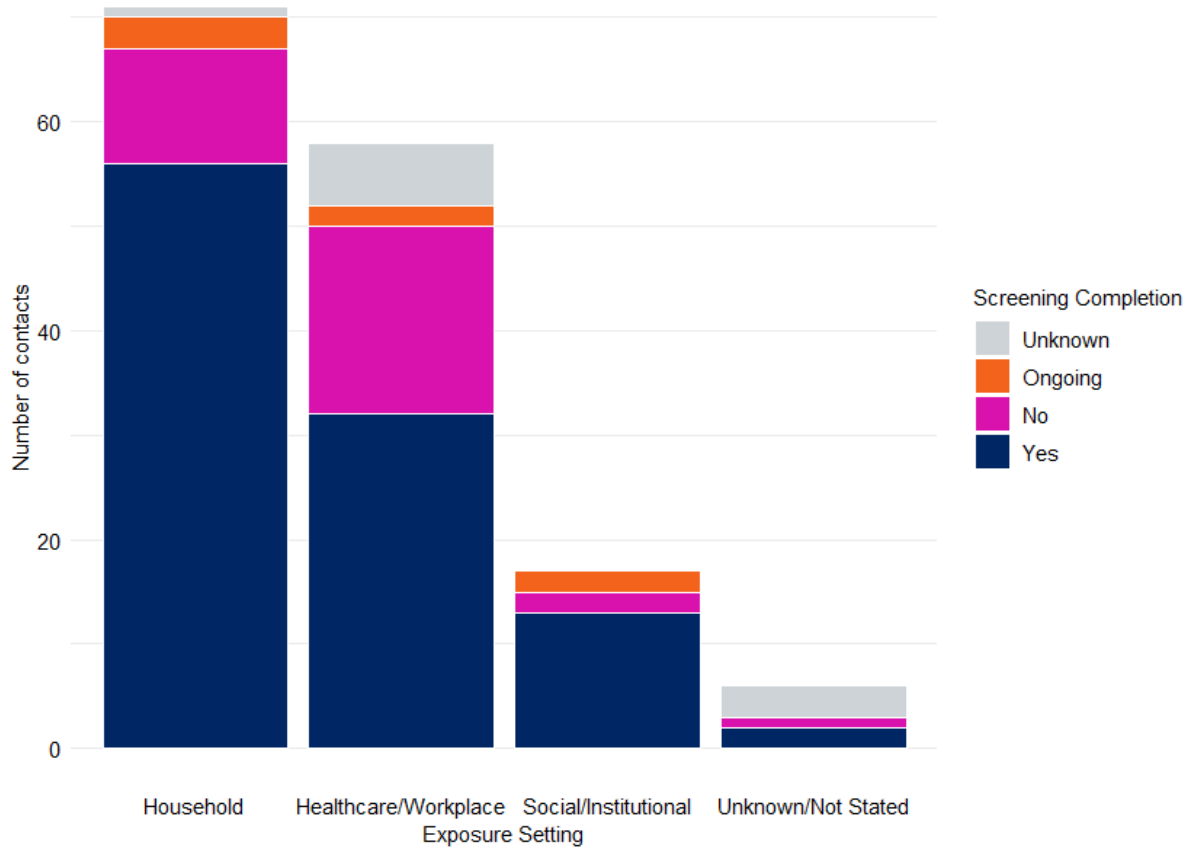


Figure 7 Risk category of 152 contacts from 29 TB cases using local chest clinic data systems from a local chest clinic in SESLHD

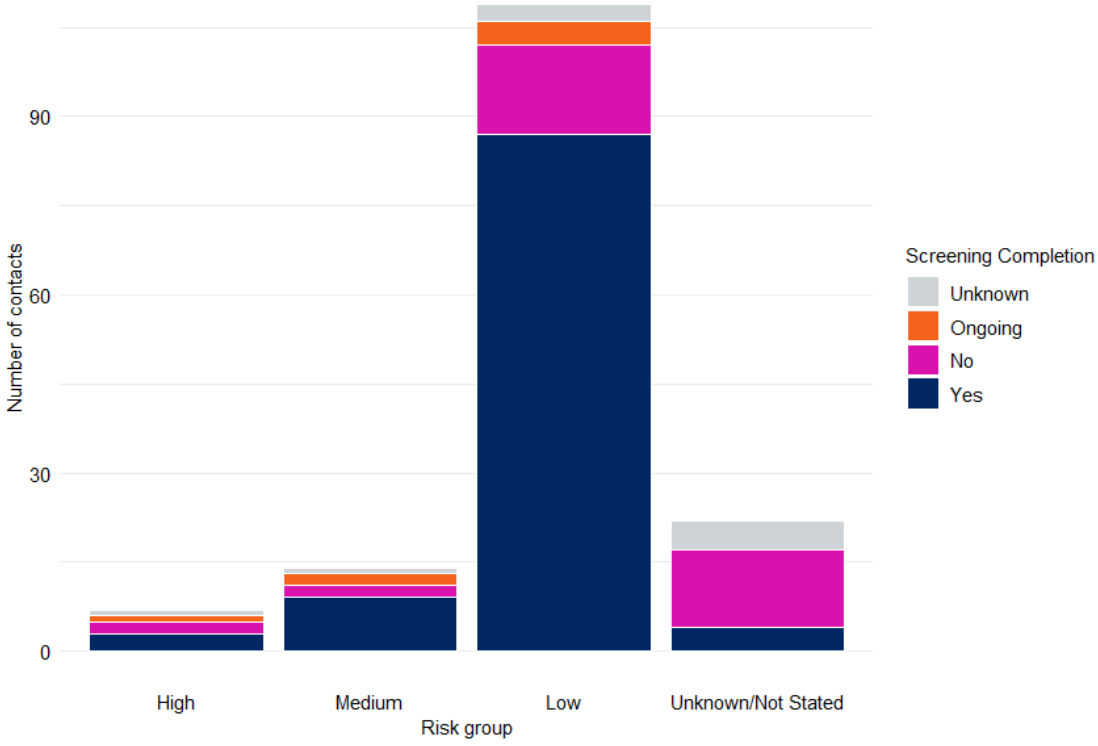
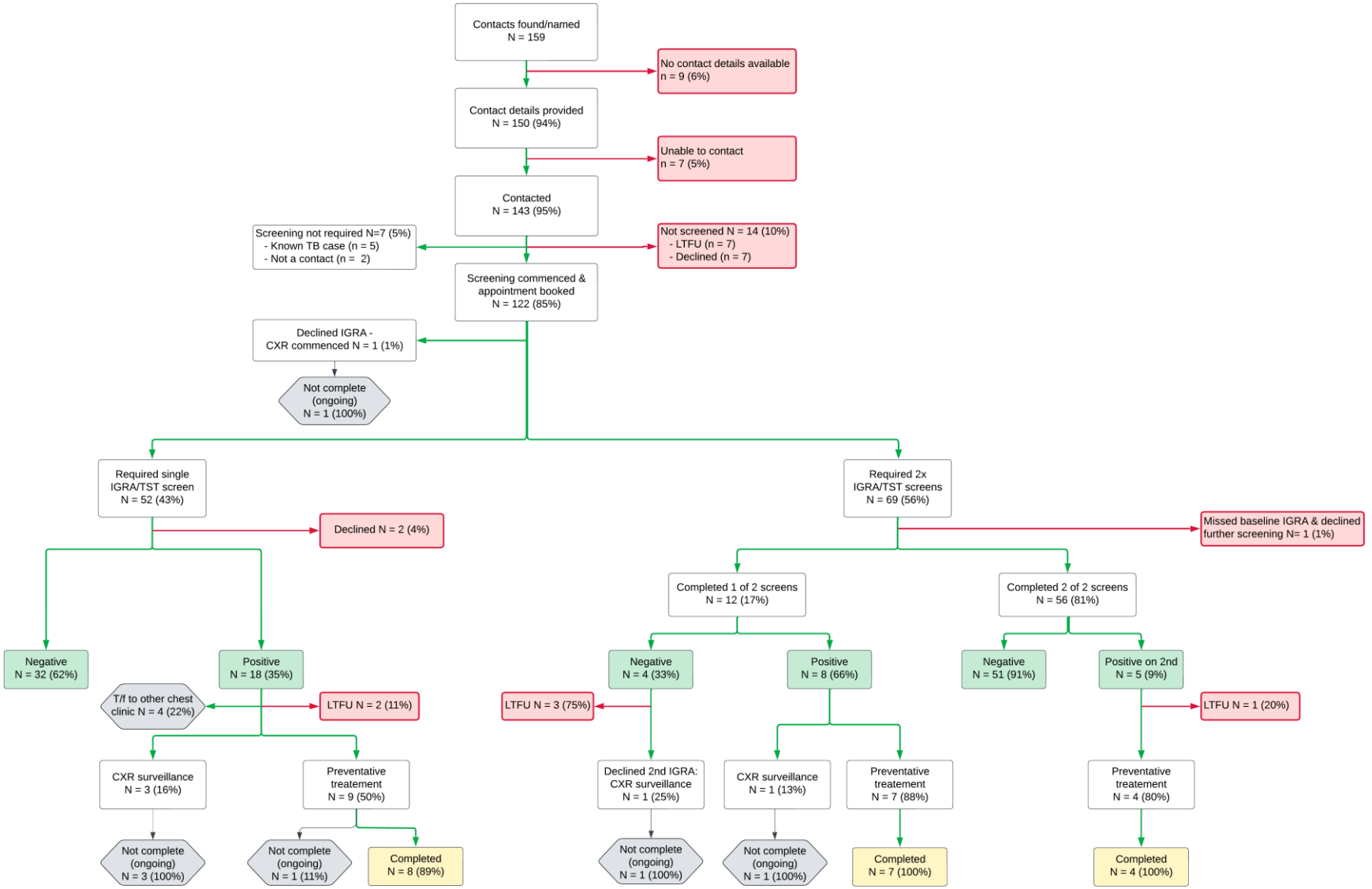


Table 3 Descriptive characteristics of TB contacts extracted from local chest clinic data systems from a local chest clinic in SESLHD, (n = 152)

Descriptive characteristics		N (%)
Sex	Female	57 (41%)
	Male	78 (57%)
	Unknown/Not Stated	17 (11%)
Age (yrs)	Median (IQR)	36 (23-58)
Age group	<5 years	7 (5%)
	5-19 years	13 (9%)
	19-34 years	41 (27%)
	35-49 years	25 (16%)
	50-64 years	18 (12%)
	≥65 years	23 (15%)
	Unknown	25 (16%)
Screening completion	No	32 (21%)
	Yes	103 (68%)
	Ongoing	7 (5%)
	Unknown	10 (7%)
Contact follow-up duration (days)	Median (IQR)	73 (19-134)
Contact follow-up duration group	<90 days	82 (54%)
	90-179 days	34 (22%)
	≥180 days	25 (16%)
	Unknown/Not Stated	11 (7%)
Exposure setting	Household	71 (47%)
	Workplace	55 (36%)
	Institutional	14 (9%)
	Unknown/Not Stated	6 (4%)
	Social	3 (2%)
	Healthcare	3 (2%)
Exposure risk	Low	7 (5%)
	Medium	14 (9%)
	High	109 (72%)
	Unknown/Not Stated	22 (14%)
Country of Birth (region)	Australia/New Zealand	45 (30%)
	Unknown/Not Stated	31 (20%)
	South Asia	30 (20%)
	South East Asia	24 (16%)
	North East Asia	13 (9%)
	Europe	6 (4%)
	South America	1 (1%)
	Africa	1 (1%)
	Middle East and Central Asia	1 (1%)

IQR = Interquartile range.

Figure 8 Overview of TB contact screening using chest clinic data systems from a local chest clinic in SESLHD, 1 January 2022 to 30 June 2023 (n=159)



Exploration of contact outcomes

Outcome of contact screening

Of the 159 contacts identified from the local clinic data systems, contact details (i.e a phone number, email address, or home or workplace address) were available for 94% (n=150); nine (6%) contacts lacked any contact details. One hundred and forty-three (95%) of the 150 contacts were contacted and made aware of their exposure to TB and 4% (n=7) were unable to be contacted. Of the individuals contacted, 85% (n=122) commenced screening. The remaining 15% (n=21) were not screened for various reasons: seven (33%) were lost to follow-up (LTFU) after several contact attempts, seven (33%) declined screening, five (24%) were already known TB cases and two (10%) were contacted and re-classified as having no exposure to TB (*Figure 8)*.

Among the 122 contacts who initiated screening, one person (1%) declined to have an IGRA or TST and was commenced on CXR surveillance that remains ongoing. Fifty-two (43%) individuals were recommended to have a one-off TST/IGRA test. Among these, 32 (62%) were negative and 18 (35%) were positive. Two contacts (4%) initially agreed to screening and scheduled an appointment, but later did not attend and, upon follow-up by the clinic, declined to proceed with the screening. Among the individuals who were positive on the one-off TST/IGRA, 33% (n=6) were not started on preventative therapy, four were transferred to another chest clinic and two were lost to follow-up. Nine (50%) were prescribed preventative therapy, of whom eight (89%) completed the treatment, one (11%) remains incomplete and is still ongoing. Three (16%) declined preventative treatment and were commenced on CXR surveillance, which is ongoing.

Sixty-nine (56%) of the 124 individuals were recommended to have two-stage TB screening, with an initial and a BOC TST/IGRA. Of these, one (1%) missed the baseline IGRA/TST and then declined to continue screening. Twelve (17%) completed the initial TST/IGRA, four (33%) were negative, three (75%) were LTFU, and one (25%) declined the second TST/IGRA and was placed on CXR surveillance that is still ongoing, and eight (65%) were positive. Of those that were positive on the initial TST/IGRA, one (13%) declined preventative therapy and was commenced on CXR surveillance that is still ongoing. Seven (88%) were commenced on preventative therapy and all (100%) successfully completed. Fifty-six (81%) completed both the initial and BOC TST/IGRA, 51 (91%) were negative and five (9%) were positive on BOC. From the five positive individuals, one (20%) was LTFU and four (80%) were commenced preventative treatment and all (100%) successfully completed.

Overall, the majority of contact drop out from the screening pathway occurred prior to

the initial appointment booking, from not having contact details, not making contact, or not agreeing to attend a screening appointment. One hundred and twenty-two of 152 (80%) eligible contacts had a screening appointment made. Of the 122 contacts who commenced screening, 115 (94%) completed screening (obtaining either a positive or negative result).

Discussion

This comparison of TB contact data between the state surveillance system (NCIMS) and the local chest clinic identified several deficiencies in the way TB contact data is recorded. Whilst data completion in NCIMS was 100% for mandatory reporting fields, there were issues with the data quality in how the information is transcribed from local clinic data systems into NCIMS. Errors were found in the classification of contacts, including instances where previously diagnosed TB cases were incorrectly included as contacts. Additionally, contact follow-up was often inconsistently documented, with the contact line list frequently not updated, or updated in NCIMS when contact follow-up extended beyond the reporting periods. Furthermore, differences were noted in the recording of screening results, particularly with TST/IGRA conversions, leading to misclassification of contacts. The findings underscore the need for improved consistency and accuracy in TB contact reporting across the surveillance systems.

As this evaluation is the first of its kind within SESLHD the findings of this study will provide valuable insights into how recording of TB contact data can be improved and streamlined. These findings also provide a foundation for further qualitative work to better understand the local chest clinic views and user experiences of the surveillance systems, along with exploring clinicians' views as to why TB contacts are unlikely to complete screening. Despite these strengths we do acknowledge several limitations of our work. Firstly, our sample is small, with only 29 TB cases and 159 contacts with screening outcomes reported, thus we were unable to perform any statistical analysis to explore factors associated with screening completion as we had initially intended. It was not feasible to review a larger cohort due to the poor quality of the data, saved in at least two locations, with data collection performed manually. The small number of contacts could also be a result of the public health measures, such as public mask wearing, social isolation and working from home, implemented during the pandemic.[10] Secondly, we were unable to evaluate all the local chest clinics in SESLHD as the other chest clinics used different local systems to our chest clinic sampled, making it not feasible to have a larger sample size and explore data collection and completion across all chest clinics in

SESLHD. Lastly, where a contact screen occurred outside of the SESLHD jurisdiction we were unable to obtain individual contact screening outcomes, leading to contacts missing from the individual analysis that were included in the aggregate analysis only. It was found that the contact line lists used in these large screens are expected to be returned upon completion to the local chest clinic managing the TB case, however we did not see this occur during our evaluation. We were also unable to obtain outcomes for four contacts who were referred to other chest clinics in NSW.

A key finding from this evaluation was the way in which contact data was entered into NCIMS and user understanding of the mandatory reporting fields. NSW Health TB Program has developed a user guide to TB data collection that is available on a local SharePoint site and is accessible to all chest clinics in NSW.[9] This tool also outlines the deadlines for data completion in NCIMS for the various reports generated using this data. This guide is predominantly for entering the case information and only features a small section on completing the contact tracing summary for the case. Notably there is no descriptor to explain that in the section for '*Contacts found*' this should not include previously diagnosed cases. This descriptor would be relevant in instances where the previously diagnosed case is a household member and likely the index case. Also, the definition provided for '*Number of contacts commenced on CXR surveillance'* doesn't specify if this is for people who were positive on screening and declined preventative treatment and were placed on CXR surveillance, or if this if for people who declined a TST/IGRA and were placed on CXR surveillance. This question appears after entering the number of contacts with a positive baseline or BOC TST/IGRA and the number of contacts commenced on preventative treatment, therefore it could be inferred that the numbers commenced on CXR surveillance are for those who were positive on screening and declined preventative therapy. It is clear from our findings that for data to be recorded accurately in NCIMS clearer definitions are needed to guide chest clinic staff, who are not epidemiologists, on how to complete the mandatory data fields in NCIMS.

We found from our evaluation that NCIMS is lacking key data fields that would be useful in showing the work undertaken by local chest clinic staff to follow-up TB contacts. Currently there is no way to record the number of overall contacts found whose names may not be known. From our findings we report that approximately 90% of contacts identified by TB cases were able to be contacted by Chest Clinic staff. This is an important finding, and higher than expected, and means that most contacts were able to be made aware of their exposure to TB regardless of if they proceed to or even complete the screening process. Whilst some may not go on to complete screening, it is beneficial

and still good public health practice to ensure an individual is aware of their exposure should they develop symptoms of TB or wish to seek treatment later. However, this proportion may be overestimated if many contacts are not even able to be identified or entered on the spreadsheet. This is a limitation of the surveillance system and needs to be acknowledged when interpreting contact data and completion rates, as well as capturing workloads of chest clinics.

A major challenge highlighted during this evaluation was the inconsistency in data collection not only between state and local systems but also within SELSHD, with chest clinics using differing operating systems for contact follow-up. Anecdotally, in speaking to clinic staff during this evaluation we found that chest clinic staff prioritise clinical management, and report being stretched for resources for this primary objective. Data collection and reporting is considered a lesser priority, and given the double data-handling, is a drain on their resources. Whilst clinic staff understand the importance of data collection, they report being too busy to complete this. As shown in *Figure 1* and explained above, clinic staff primarily use eMR for case and contact follow-up and having to enter data into several different data systems becomes cumbersome on already stretched clinic staff. If data quality is to improve when it comes to TB contact screening, we need to better understand the daily function and operation of local chest clinics and have better collaboration to develop tools that reduce the burden of data entry and collection for epidemiological reporting. There is also a clear need for NSW Health surveillance systems to internally link to one another to improve TB contact data and improve the useability of these systems from a clinical point of view. Currently, a "new NCIMS" is being designed, as well as a single statewide eMR system. These may provide an opportunity to streamline and improve surveillance data for TB cases and contacts

Conclusion

This evaluation has revealed discrepancies in TB contact data collection and reporting between NCIMS and the local chest clinic, as well as how data is captured and documented across different systems within the same health district. The findings underscore the need for clearer guidelines and definitions to support accurate data entry, particularly when it comes to contact classification and screening result reporting. Moreover, clinic staff, whose primary focus is providing essential clinical services under already stretched resourcing, face challenges in maintaining routine data entry. While they understand the importance of accurate data collection, their role as clinicians, rather than epidemiologists, can contribute to gaps in data entry.

To improve TB contact reporting, it is crucial to streamline data collection processes, foster better collaboration between local and state systems, and ensure that surveillance tools are both clinically practical and effective for epidemiological purposes. Recommendations include the review of the current NCIMS data entry guide to ensure clear definitions for completing mandatory reporting fields, training for staff to enhance data management skills, and integration of digital solutions that reduce manual data entry burden. These recommendations and findings will be presented to the NSW TB Program and the local chest clinic staff.

This report can also serve as a valuable input to the sub-working group currently being formed to configure a single digital patient record. Leveraging these findings in the planning and configuration process can help address existing data discrepancies and contribute to more accurate and integrated data management. Addressing these issues will enhance the accuracy and utility of TB contact data, ultimately improving public health outcomes and moving closer to achieving TB elimination.

Recommendations

1. **Clarify data entry guidelines:** Review and update NCIMS data entry guide to provide clearer definitions, particularly for contact classification and screening result reporting. This will help to reduce misclassification and improve the accuracy of contact data.
2. **Review opportunities to improve contact engagement and follow up in the early stage of the screening pathway**: This may include reviewing processes for contacting contacts and the scripts used in the initial conversation.
3. **Streamline data collection:** Develop integrated digital solutions that reduce the manual data entry burden on clinic staff, ensuring data is captured efficiently and accurately across systems. This includes better alignment between the state and local systems, leading to minimisation of double data handling. Additionally streamlining between local clinics is needed to help standardise data collection practices and improve overall data consistency.
4. **Leverage findings for system improvement:** Findings from this evaluation should be used to inform the design of the ‘new NCIMS’ and single digital patient record, to enhance integrated data management and improve outcomes to TB contact tracing.

References

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Chapter: VI

Teaching field epidemiology

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Abbreviations

LTBI	Latent tuberculosis infection
LFF	Lessons from the field
MAE	Master of Philosophy (Applied Epidemiology)
NSW	New South Wales
PHU	Public health unit
TST	Tuberculin skin test
TB	Tuberculosis

Teaching first year scholars- MAE Skills and Ask a Second Year

Introduction

The 2023 cohort of 22 scholars was divided into five groups to prepare short teaching sessions to deliver to the first year Master of Philosophy (Applied Epidemiology (MAE) Scholars. The scope of the teaching sessions could encompass technical or general skills that are not already covered in the MAE program. The session my group presented on 1 March 2024 was titled "MAE Skills and Ask a Second Year". Our teaching session provided an opportunity to share our learnings from a broad range of areas including time management, support networks, and useful methods for organising yourself in the program. The teaching session aimed to provide an interesting, helpful introduction to the 2024 cohort.

The learning objectives of the teaching session were to:

- Know how to manage multiple MAE projects effectively across the program period.
- Advocate for the MAE program within your field placement.
- Navigate the supervisor-scholar relationships.
- Identify key support networks to facilitate learning with the MAE program.

I worked within a group of three to develop a session on how to survive and thrive during the MAE program. The focus of our teaching was to provide relevant and useful information to the first year MAE scholars that we felt would have been beneficial to know in the first year of the program. As a group, we combined our shared learning experience thus far and consulted with our wider cohort to ensure we could share any insightful learning experiences they wished to also share with the first-year scholars. I assisted in writing the learning objectives and developed three slides that covered managing MAE projects and workload. I also contributed to the overall design and structure of the presentation (*Appendix I)*.

We employed a facilitator/guide teaching style[1] for our session, emphasising active engagement and interactive learning. We developed interactive Slido[2] activities, as shown in *Appendix I,* to help maintain engagement and understand the preconceptions of the 2024 cohort regarding key aspects of our session. This approach encouraged first-year students to ask questions and participate in discussions, fostering a collaborative

learning environment. The responses to these questions helped shape the information we presented, ensuring it was relevant and tailored to their needs. Overall, the feedback was positive, as shown in *Figure 1- Figure 5* below. The feedback indicated the first-year MAE cohort gained knowledge from the session, achieved the learning objectives, and rated our teaching performance highly.

The first-year scholars found us well prepared as presenters and thought the session was delivered in a clear and interesting manner. Technology was used effectively, and we were able to maintain their interest throughout the session. By adopting the facilitator/guide style, we ensured that the session was not only informative but also engaging and interactive, enhancing the learning experience for the first-year scholars.

Lessons Learnt

I learned that practising presentations is helpful to become comfortable and confident when delivering content to others. Familiarity with the content, drawn from our own experiences throughout the MAE program, boosted my confidence. This familiarity made it easier to share information effectively with the first-year cohort. Additionally, incorporating questions and prompts that encourage participation greatly enhanced engagement. This interactive approach benefited both the first-year students, as active participants, and our group, as presenters maximising the overall value of the session for everyone involved.

Feedback survey results from first-year scholars

Figure 1 How satisfied are you with the knowledge you gained from the session? (n=15)

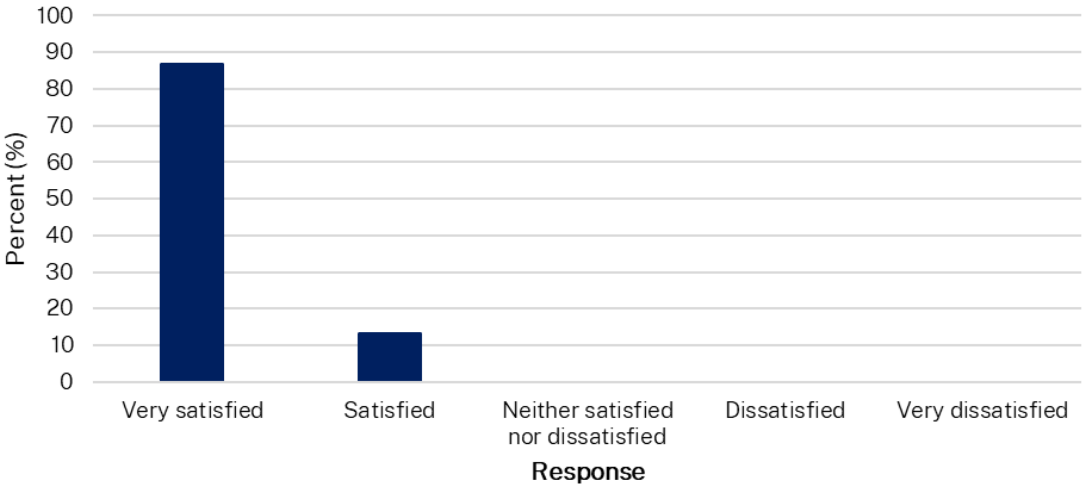


Figure 2 Do you feel you achieved the desired learning outcome? (n=15)

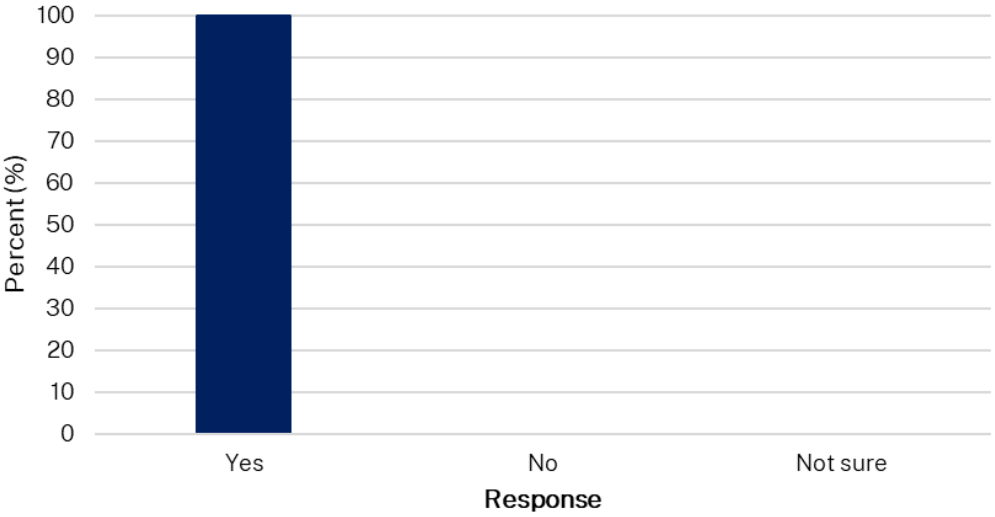
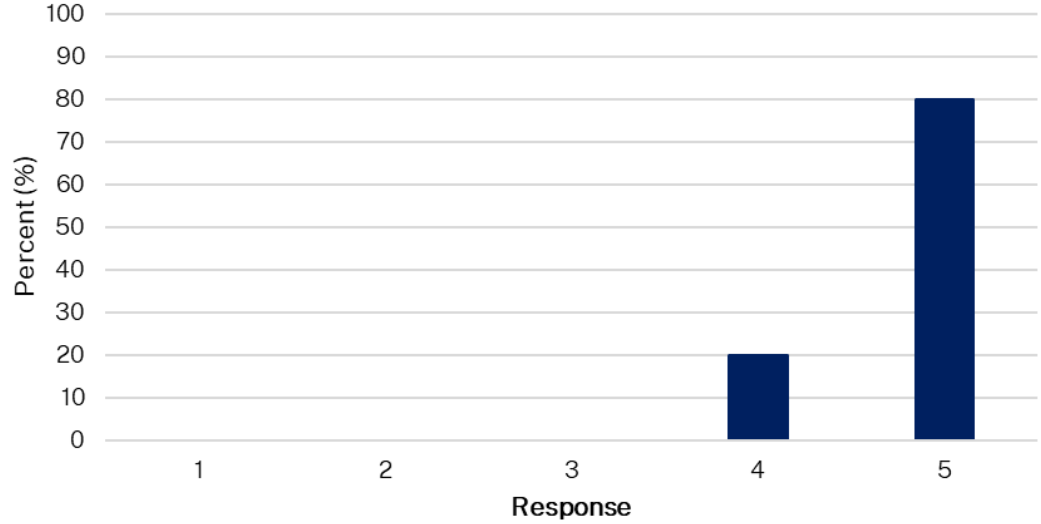


Figure 3 How would you rate the instructors' overall teaching performance? (n=15) *



**1= poor, 5=excellent*

Figure 4 How do you agree with the following statements? (n=15)

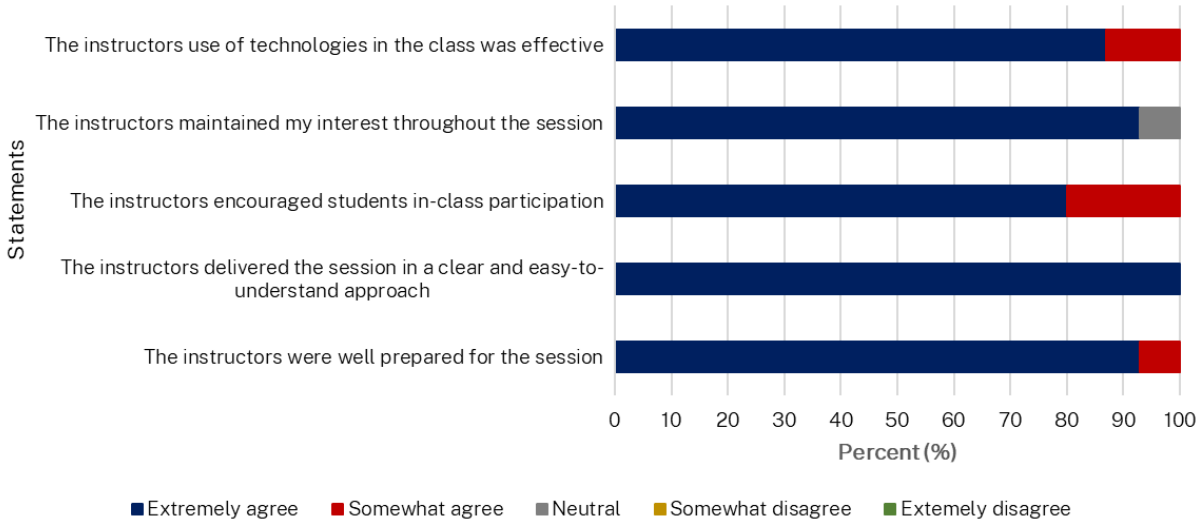
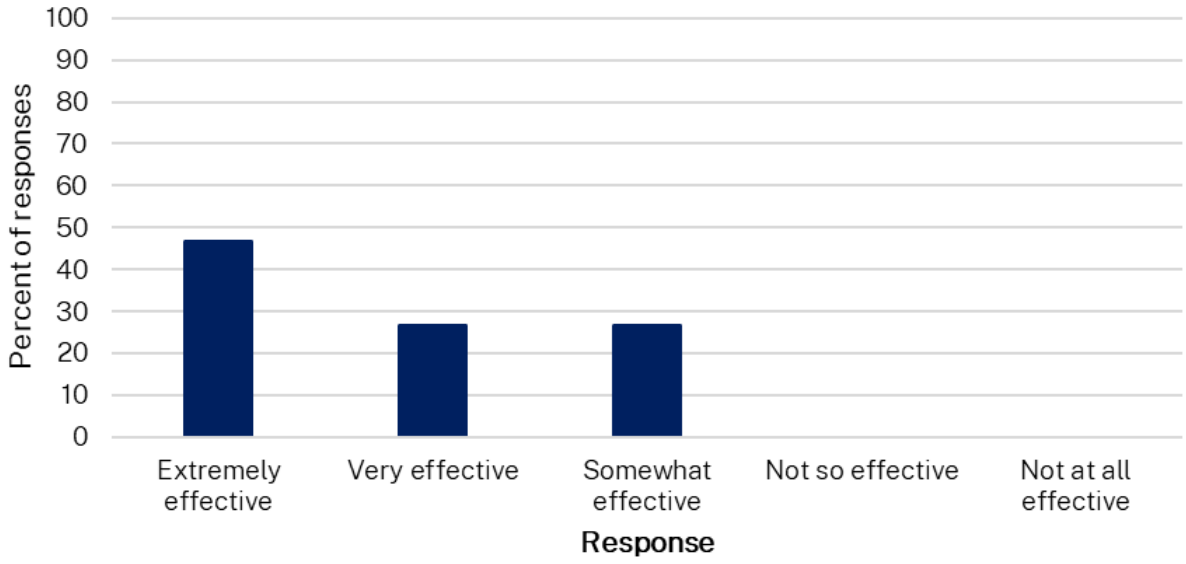


Figure 5 How effective were the learning activities used in this session? (n=15)



Lessons from the field - Tuberculosis (TB) contact tracing.

Introduction

Australia has one of the world's lowest incidence rates of tuberculosis (TB) and has maintained this status through excellent TB control over the last three decades, despite its proximity to some of the highest incidence countries in the world.[3] In 2018 Australia reported 1,438 TB notifications, representing a rate of 5.8 per 100,000 people, with 89% of those cases reported in people who were born overseas.[3] In the four years between 2015-2018 the most frequently reported countries of birth for TB cases diagnosed in Australia were India, Vietnam, the Philippines, China, and Nepal.[3]

The screening of TB contacts is a priority action area as part of the World Health Organization's Action Framework Towards TB Elimination for Low-Incidence Countries.[4] Contact tracing of active TB cases aims to identify both active TB cases and latent tuberculosis infection (LTBI) and then provide adequate treatment and follow up, which supports the ongoing drive for TB elimination, specifically in low-incidence settings such as Australia.[5] In New South Wales (NSW) contact management, including tuberculin skin tests (TST's) and preventative therapy is guided by the NSW Health policy directives.[6]

I developed this lesson based on my firsthand experience with a tuberculosis (TB) outbreak (*Chapter II – Section 1*) in a boarding house, where I conducted TB contact tracing for the first time. Prior to this, my field epidemiology experience was with COVID-19 contact tracing, making this TB investigation a particularly eye-opening and challenging endeavour. The outbreak occurred in a boarding house where we found that the architecture facilitated TB transmission, with numerous communal areas throughout the building.

I was aware that none of my colleagues in my lessons from the field (LFF) group had field placements in local public health units, so I communicated with my group and offered two lesson options: mapping using QGIS or TB contact tracing. The group indicated that they had limited to no experience with TB contact tracing in a low incidence setting, so I leveraged my experience to develop this lesson aiming to expand their knowledge and provide practical education that would be useful in their careers as field epidemiologists.

The teaching style I used for this activity was the facilitator/guide style.[1] This approach emphasised active engagement and interaction throughout the session, encouraging students to take an active role in their learning. By offering a choice for the lesson

content and incorporating practical, experience-based insights, I was able to foster a collaborative and participatory environment. This style was very useful for engagement of the group, facilitating discussion and ensuring the session was practical, informative, and interactive.

Lessons Learnt

I really enjoyed teaching this session and thoroughly appreciated the opportunity to share the aspects of TB and TB contact tracing that I initially found challenging to understand. Explaining these concepts to my peers in a way that I found useful not only reinforced my own understanding but also helped my peers grasp the complexities of TB transmission, exposure and risk assessments required to evaluate a case's infectiousness and identified contacts.

Overall, the feedback provided in the post session survey was very positive (*Table 1)*, with the session well-received. On reflection, it would have been beneficial to include different questions or scenarios beyond the pre-provided activities. This would have given students the opportunity to apply the knowledge gained from the pre-session activities. This was also noted in the feedback from one of the respondents, highlighting the potential of incorporating more interactive elements to the session.

Aim and objectives

Aim

To understand how to conduct TB contact tracing in a low incidence setting.

Learning objectives

By the end of this exercise, Scholars should be able to:

- Define what an infectious case of TB is.
- Describe how pulmonary TB is diagnosed.
- Describe how TB is transmitted between people.
- Classify the infectiousness of a case of TB.
- List the aims of TB contact investigation.
- Describe how the priorities for TB contact investigation are determined.

Feedback survey results

Table *1* Evaluation survey results of Lessons from the field - TB contact tracing (n=6)

Question		Average score	Range
How satisfied are you with the knowledge you gained from the session?		5	4-5
Do you feel you achieved the learning outcomes?		4.6	3-5
How satisfied are you with the following aspects of the session?			
	Facilitator/Trainer	5	5-5
	Materials provided	5	5-5
	Topic relevance	5	4-5
	Overall content	5	5-5
	Use of technology	5	3-5
	Time management	5	5-5
Did you have any experience with TB contact tracing prior to this session?			Yes 2(33%), No 4(67%)

Activities

I provided students with a list of prior readings to review that provided information on the general background of TB along with the New South Wales Health guidelines for TB contact investigations. I constructed questions that could be answered directly from the readings provided and asked students to review local policies and guidelines for TB contact tracing in their respective jurisdictions. This was also supported by a presentation as shown in *Appendix II.*

Documents provided

Lessons from the field: Tuberculosis (TB) contact tracing

Background

Australia has one of the world's lowest incidence rates of tuberculosis (TB) and has maintained this status through excellent TB control over the last three decades, despite its proximity to some of the highest incidence countries in the world. In 2018 Australia reported 1,438 TB notifications, representing a rate of 5.8 per 100,000 people, with 89% of those cases reported in people who were born overseas. In the four years between 2015-2018 the most frequently reported countries of birth for TB cases diagnosed in Australia were India, Vietnam, the Philippines, China, and Nepal.

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- List the aims of TB contact investigation.
- Describe how the priorities for TB contact investigation are determined.

Resources and readings

General background

- NSW TB Program Communicable Diseases Branch. Tuberculosis in NSW - Surveillance Report 2021. In: Branch NTPCD, editor. Sydney: Health Protection NSW; 2023. Available from: https://www.health.nsw.gov.au/Infectious/tuberculosis/Publications/2021-tb-report.pdf
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Contact investigation specific

- Health Protection NSW. NSW Health Tuberculosis Contact Investigations Guideline Sydney 2019. Available from: https://www1.health.nsw.gov.au/pds/ActivePDSDocuments/GL2019_003.pdf

Feedback survey

https://forms.office.com/r/fXLZVUa57B

Activities

1. How is TB transmitted?

Answers can be found in the NSW Health Control Guidelines

- TB is primarily transmitted by inhalation of infectious aerosols produced by persons with pulmonary or laryngeal TB during coughing, laughing, speaking, singing, or sneezing.
- Transmission can occur from potentially high-risk procedures including sputum induction, treatment using a nebuliser, bronchoscopy, drainage of an open abscess (especially if irrigation of a cavity), autopsy or any procedure in which an aerosol containing M. tuberculosis is generated.
- Invasion of M. tuberculosis may occur through mucous membranes (e.g. ingestion) or damaged skin.
- Extra-pulmonary TB, other than laryngeal, is generally not infectious, but can co-exist with infectious pulmonary TB.
  Laboratory acquisition via aerosolisation of specimen or culture material or by inoculation, may occur in the absence of adequate biocontainment practices.

2. Who is considered an infectious case of TB?

Answers can be found in the NSW Health Control Guidelines

A person is infectious when viable bacilli are aerosolised. In practice, the greatest risk of transmitting infection is in the period prior to diagnosis before effective treatment is initiated. Persons with pulmonary/laryngeal TB may be infectious up to three months prior to symptom onset. The risk of transmitting infection declines within days of commencing effective TB treatment.

3. Who is responsible for carrying out TB contact investigations in your jurisdiction?

Scholars are encouraged to look at available resources within their own jurisdiction to find their guidelines. The point of this exercise is so scholars are aware of the guidelines specific to their jurisdiction and how to locate them should they need to conduct TB contact follow up.

4. After becoming exposed to an infectious case of TB, when are people at increased risk of developing TB disease?

Answer available from NSW Health TB Contact Investigations Guideline

2 years

5. How do you determine the priorities for TB contact investigation?

Answer can be found in the NSW Health TB Contact Investigations Guideline

- The likely infectiousness of the index case.
- The risk of exposure of contacts to the index case, and
- The vulnerability of contacts to disease progression.

You are working in a local chest clinic; its July 2022 and you have just been notified of a TB case living in a boarding house in inner city Sydney.

The case is a 20-year-old female from France, who moved to Australia in September 2019. She presented to ED in early July 2022, with a four-month history of weakness, weight loss, fever, chills, and non-productive cough. She had a sputum collected which was 3+ positive on microscopy for acid fast bacilli (AFB) and was culture positive for *Mycobacterium tuberculosis*. Her chest x-ray showed several cavitations throughout her lungs. She has no known co-morbidities.

1. What is the case's infectious period?

The case has a 4-month history of symptoms prior to presentation to ED in July 2022. You could estimate the symptom onset to be March 2022, therefore she would be considered infectious from January 2022 (3 months prior to symptom onset).

2. What is the infectiousness of the case?

Answer can be found in the NSW Health TB Contact Investigations Guideline

High

- The case has symptoms consistent with active pulmonary TB, including a persistent cough. The also has detection of AFB in sputum (smear positive) and cavitations on her chest x-ray.

You interview the case again and find out she has been very breathless with a persistent cough that prohibited her from walking the few meters from her the bed to the door in her room at the boarding house. You note her room is on the third floor in the boarding house and the case tells you she can sometimes take up to 45mins to 1 hr to walk up the stairs to her room. She tells you that she often rests on the stairwell landings to catch her breath and wait for her cough to resolve prior to continuing up the stairs to her room.

The case also mentions that her brother returned home overseas in August 2021 and was diagnosed with TB and has significant cavitations on his chest x-ray. The brother had also been staying with his sister at the boarding house since January 2019. For the purposes of this exercise, you can assume he is the source for his sister's infection.

3. What are the aims of TB contact investigation?

Answer can be found in NSW Health TB Contact Investigations Guideline

- Identify and treat cases of TB disease among those in contact with the index case including identification of a possible case source case.
- Identify persons who have latent TB infection (LTBI) and offer treatment for LTBI or monitoring by chest radiography (CXR).
- Provide timely treatment, education and support for persons identified with evidence of disease or infection, and
- Provide education and support for all persons identified as having exposure risk.

4. What other information would you want to obtain from the case to conduct a contact investigation?

Answer can be found in the NSW Health TB Contact Investigations Guideline

You will want information on the following.

- If she has any friends in the boarding house or regularly speaks to anyone in the boarding house (case's home)
- Where does the case work or if she goes to university or is studying?
- If she has any friends, she regularly sees or if they visit her.

5. Are there any considerations for contact investigation in the ED?

Answer can be found in the NSW Health TB Contact Investigations Guideline

Yes, you should liaise with hospital Infection Control and/or staff Health to support the contact investigation process. Depending on the size and complexity of the investigation and the structure of local services, Infection Control and Staff Health units may be best placed to coordinate the process.

Additional teaching activities

Hepatitis D education session

During a morning handover meeting at the Public Health Unit (PHU), we were discussing hepatitis D. When I inquired further about the disease, it was suggested that I put together a short education session to present to the PHU team. The presentation *(Appendix II*) was to be no more than 10mins long and needed to inform the team on the foundations of hepatitis D, providing relevant epidemiological information that would benefit the infectious disease team when they receive a hepatitis D notification. Overall, the presentation was well received, and anecdotal feedback indicated that the team gained new knowledge during the presentation.

South Eastern Sydney Public Health Unit R Club

As part of my MAE journey, I have expanded my skills and knowledge in R statistical software. Concurrently, the PHU was transitioning from SAS to R for all epidemiological analysis. To facilitate this transition, I proposed establishing an R Club to the Epidemiology team at the PHU. In consultation with the team, I organised fortnightly catchups to learn new R skills and upskill the team, enabling them to confidently use the software. I developed example code and data for use during the sessions. My role was to lead these sessions, answer questions, and troubleshoot issues as they arose. I would ensure the team could run the code successfully and produce the same output, any errors or issues with a team member's code were then resolved prior to moving on in the session. Anecdotally, the team thoroughly enjoyed the sessions and appreciated the time taken to compile the resources. All resources have been saved in local share drives at the PHU, allowing the team to revisit any skills covered in the future if needed.

Ministry of Health R Club

The Ministry of Health hosts an R Club every fortnight for the Health Protection Network. Each session features different presenters showcasing unique skills or methods using R that are relevant to our day-to-day activities. Outside of the regular meetings, there is a chat group where members can post questions and receive support from the network. One of my MAE projects involved reproducing the local respiratory surveillance report using R, and I frequently utilised the chat group for troubleshooting and knowledge sharing. As an active member in the group, I was invited to present at an R Club meeting,

which I accepted.

I presented to colleagues from across New South Wales Health Protection on how to create a dual axis graph using a specific package in R. I created an example dataset and demonstrated the foundational steps for creating the graph. Then, I gradually expanded on the code, demonstrating further formatting and customisation to the graph step-by-step. Additionally, I compared the features of this package to another commonly used package for creating graphs and figures, highlighting the different commands that can achieve similar outcomes. Overall, the network was very grateful for the presentation as they expressed, they were unaware of some of the features of the package I demonstrated.

Tip of the Week

At the PHU the Infectious Diseases Team hold regular 'Tip of the Week' sessions, where team members share helpful tips or knowledge that benefit their work. I volunteered to present a session on useful tips and tricks for using Excel, as the team frequently use Excel spreadsheets in their daily follow up of infectious diseases. I focused on some of the simple features in Excel that the team had previously inquired about. The session was well received, and the team expressed gratitude, stating that they would be incorporating the new knowledge into their daily work.

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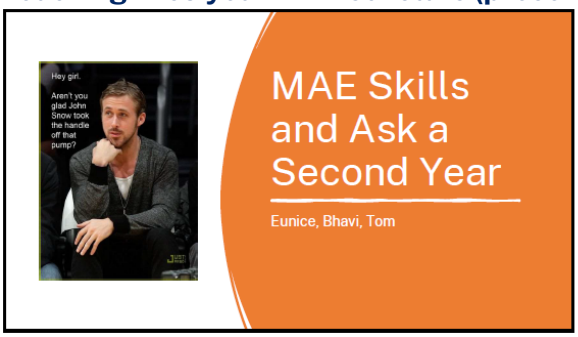
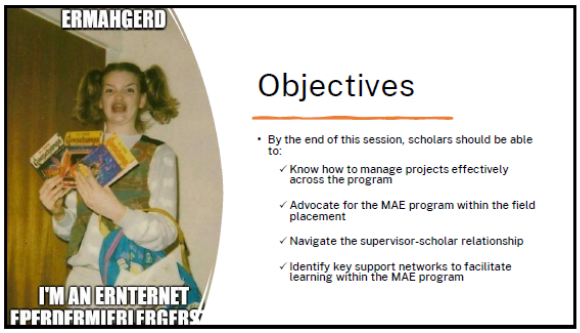
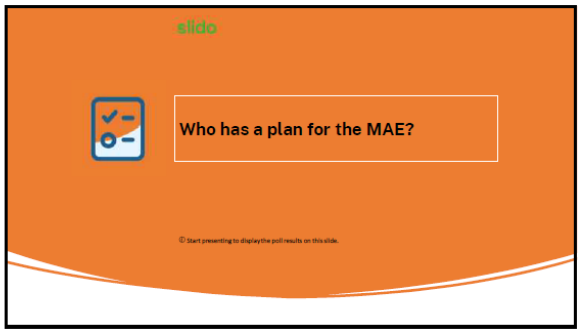
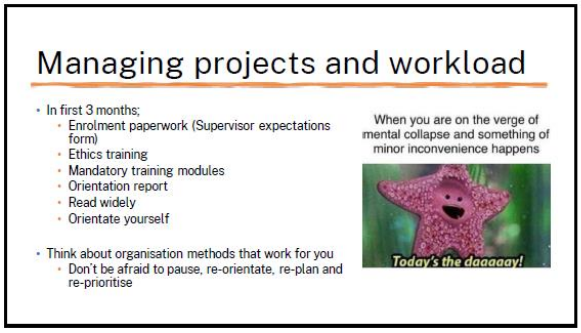
Appendix I

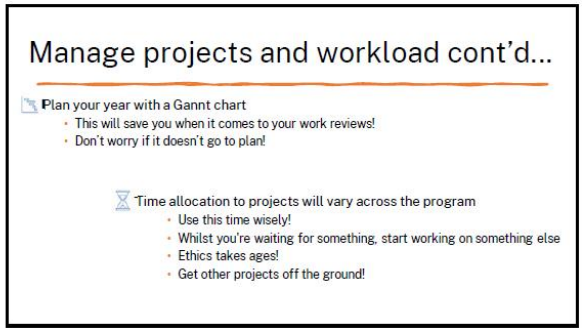
Teaching first-year MAE scholars (presentation slides)

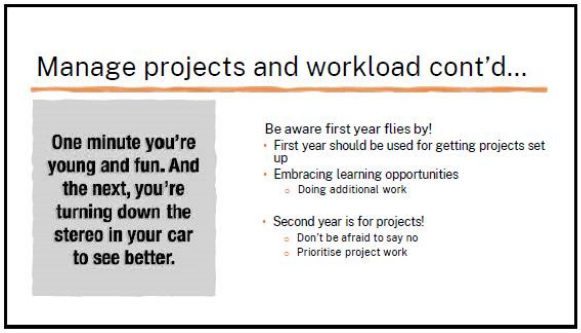


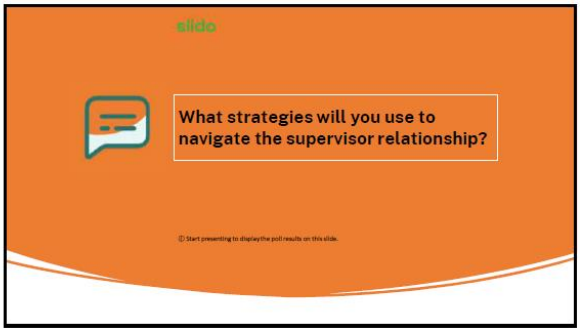












Scholar-supervisor relationship

- Unique aspect to the MAE is field and academic supervisor
- Identify goals and aims and set expectations early
- Open communication throughout the program to aim for no surprises
- Expect different things from different supervisors
- Managing busy supervisors

slido

Who do you think are your key support networks for the MAE?

© Start presenting to display the poll results on this slide.

Identify key support networks

- Fellow MAEs
- Current and past MAEs, within the organisation or state
- Find a public health mentor
- Friends and family
- ANU/Placement EAP

When ur friend gets upset and you get upset too because that's the kind of friend you are

Audience Q&A Session

slido

Audience Q&A Session

© Start presenting to display the audience questions on this slide.

Thank you and feedback

https://forms.office.com/r/xCP4Es2k8m

Appendix II

Lessons from the field- Tuberculosis (TB) contact tracing (presentation slides)

Lessons From the Field:
Session 1

Contact Tracing of Tuberculosis (TB)
in a low-incidence setting

Eunice Stiboy
MAE Scholar

13 March 2024

South Eastern Sydney Local Health District

Acknowledgement of Country

SESLHD acknowledges Aboriginal and Torres Strait Islander peoples of the Dharawal, Gadigal, Wangal, Gweagal and Bidjigal peoples as the Traditional Custodians of the lands we operate on. We pay our respects to Ancestors and Elders, past and present.

SESLHD is committed to honouring Aboriginal and Torres Strait Islander people's unique cultural and spiritual relationships to the land, waters and seas and their rich contribution to society.

South Eastern Sydney Local Health District

Aims and Objectives

Aim:
To understand how to conduct Tuberculosis (TB) contact tracing in a low-incidence setting.

Objectives:
By the end of this exercise, Scholars should be able to:

- Define what an infectious case of TB is.
- Describe how pulmonary T B is diagnosed.
- Describe how TB is transmitted between people.
- Classify the infectiousness of a case of TB.
- List the aims of TB contact investigation.
- Describe how the priorities for TB contact investigation are determined.

South Eastern Sydney Local Health District

Resources and readings

General background

- NSW TB Program Communicable Diseases Branch. Tuberculosis in NSW - Surveillance Report 2021. In: Branch NTPCD, editor. Sydney: Health Protection NSW; 2023. Available from: https://www.health.nsw.gov.au/Infectious/tuberculosis/Publications/2021-tb-report.pdf
- Implementing the WHO Stop TB Strategy: A Handbook for National Tuberculosis Control Programmes. Geneva: World Health Organization; 2008. 5, Contact investigation. Available from: https://www.ncbi.nlm.nih.gov/books/NBK310755/
- New South Wales Health. Tuberculosis Control Guideline Sydney 2022 Available from: https://www.health.nsw.gov.au/Infectious/controlguideline/Pages/tuberculosis.aspx#1.
- World Health Organisation. Towards tuberculosis elimination: an action framework for low-incidence countries (Section 4.2.4 pg 43). Geneva, Switzerland; 2014. Available from: https://iris.who.int/bitstream/handle/10665/132231/9789241507707_eng.pdf?sequence=1

Contact investigation specific

- Health Protection NSW. NSW Health Tuberculosis Contact Investigations Guideline Sydney 2019. Available from: https://www1.health.nsw.gov.au/pds/ActivePDSDocuments/GL2019_003.pdf

South Eastern Sydney Local Health District

Activities

1. How is TB transmitted?

South Eastern Sydney Local Health District

Activities

1. How is TB transmitted?

Answers can be found in the NSW Health Control Guidelines

- TB is primarily transmitted by inhalation of infectious aerosols produced by persons with pulmonary or laryngeal TB during coughing, laughing, speaking, singing, or sneezing.
- Transmission can occur from potentially high-risk procedures including sputum induction, treatment using a nebuliser, bronchoscopy, drainage of an open abscess (especially if irrigation of a cavity), autopsy or any procedure in which an aerosol containing M. tuberculosis is generated.
- Invasion of M. tuberculosis may occur through mucous membranes (e.g. ingestion) or damaged skin.
- Extra-pulmonary TB, other than laryngeal, is generally not infectious, but can co-exist with infectious pulmonary TB.
- Laboratory acquisition via aerosolisation of specimen or culture material or by inoculation, may occur in the absence of adequate biocontainment practices

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Activities

2. Who is considered an infectious case of TB?

South Eastern Sydney Local Health District

Activities

2. Who is considered an infectious case of TB?

Answers can be found in the NSW Health Control Guidelines

A person is infectious when viable bacilli are aerosolised. In practice, the greatest risk of transmitting infection is in the period prior to diagnosis before effective treatment is initiated. Persons with pulmonary/laryngeal TB may be infectious up to three months prior to symptom onset. The risk of transmitting infection declines within days of commencing effective TB treatment.

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Activities

3. Who is responsible for carrying out TB contact investigations in your jurisdiction?

South Eastern Sydney Local Health District

Activities

3. Who is responsible for carrying out TB contact investigations in your jurisdiction?

Scholars are encouraged to look at available resources within their own jurisdiction to find their guidelines.

The point of this exercise is so scholars are aware of the guidelines specific to their jurisdiction and how to locate them should they need to conduct TB contact follow up.

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Activities

4. After becoming exposed to an infectious case of TB, when are people at increased risk of developing TB disease?

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Activities

4. After becoming exposed to an infectious case of TB, when are people at increased risk of developing TB disease?

Answer available from NSW Health TB Contact Investigations Guideline

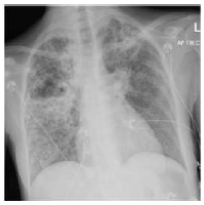
2 years

South Eastern Sydney Local Health District

Scenario

You are working in a local chest clinic; its July 2022 and you have just been notified of a TB case living in a boarding house in inner city Sydney.

The case is a 20-year-old female from France, who moved to Australia in September 2019. She presented to ED in early July 2022, with a four-month history of weakness, weight loss, fever, chills, and non-productive cough. She had a sputum collected which was 3+ positive on microscopy for acid fast bacilli (AFB) and was culture positive for *Mycobacterium tuberculosis*. Her chest x-ray showed several cavitations throughout her lungs. She has no known co-morbidities.



South Eastern Sydney Local Health District

Scenario

You are working in a local chest clinic; its July 2022 and you have just been notified of a TB case living in a boarding house in inner city Sydney.

The case is a 20-year-old female from France, who moved to Australia in September 2019. She presented to ED in early July 2022, with a four-month history of weakness, weight loss, fever, chills, and non-productive cough. She had a sputum collected which was 3+ positive on microscopy for acid fast bacilli (AFB) and was culture positive for *Mycobacterium tuberculosis*. Her chest x-ray showed several cavitations throughout her lungs. She has no known co-morbidities.

South Eastern Sydney Local Health District

Scenario

1. What is the case's infectious period?

South Eastern Sydney Local Health District

Scenario

1. What is the case's infectious period?

The case has a 4-month history of symptoms prior to presentation to ED in July 2022. You could estimate the symptom onset to be March 2022, therefore she would be considered infectious from January 2022 (3 months prior to symptom onset).

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Scenario

2. What is the infectiousness of the case?

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Scenario

2. What is the infectiousness of the case?

Answer can be found in the NSW Health TB Contact Investigations Guideline

High

- The case has symptoms consistent with active pulmonary TB, including a persistent cough. The also has detection of AFB in sputum (smear positive) and cavitations on her chest x-ray.

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Scenario continued

You interview the case again and find out she has been very breathless with a persistent cough that prohibited her from walking the few meters from her the bed to the door in her room at the boarding house. You note her room is on the third floor in the boarding house and the case tells you she can sometimes take up to 45mins to 1 hr to walk up the stairs to her room. She tells you that she often rests on the stairwell landings to catch her breath and wait for her cough to resolve prior to continuing up the stairs to her room.

The case also mentions that her brother returned home overseas in August 2021 and was diagnosed with TB and has significant cavitations on his chest x-ray. The brother had also been staying with his sister at the boarding house since January 2019. For the purposes of this exercise, you can assume he is the source for his sister's infection.

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Scenario

3. What are the aims of TB contact investigation?

South Eastern Sydney Local Health District

Scenario

3. What are the aims of TB contact investigation?

Answer can be found in NSW Health TB Contact Investigations Guideline

- Identify and treat cases of TB disease among those in contact with the index case including identification of a possible case source case.
- Identify persons who have latent TB infection (LTBI) and offer treatment for LTBI or monitoring by chest radiography (CXR).
- Provide timely treatment, education and support for persons identified with evidence of disease or infection, and
- Provide education and support for all persons identified as having exposure risk.

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Scenario

4. What other information would you want to obtain from the case to conduct a contact investigation?

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Scenario

4. What other information would you want to obtain from the case to conduct a contact investigation?

case

Answer can be found in the NSW Health TB Contact Investigations Guideline

You will want information on the following.

- If she has any friends in the boarding house or regularly speaks to anyone in the boarding house (case's home)
- Where does the case work or if she goes to university or is studying?
- If she has any friends, she regularly sees or if they visit her.

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Scenario

5. Are there any considerations for contact investigation in the ED?

South Eastern Sydney Local Health District

Activities

5. How do you determine the priorities for TB contact investigation?

South Eastern Sydney Local Health District

Activities

5. How do you determine the priorities for TB contact investigation?

Answer can be found in the NSW Health TB Contact Investigations Guideline

- The likely infectiousness of the index case.
- The risk of exposure of contacts to the index case, and
- The vulnerability of contacts to disease progression.

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Scenario

5. Are there any considerations for contact investigation in the ED?

Answer can be found in the NSW Health TB Contact Investigations Guideline

Yes, you should liaise with hospital Infection Control and/or staff Health to support the contact investigation process. Depending on the size and complexity of the investigation and the structure of local services, Infection Control and Staff Health units may be best placed to coordinate the process.

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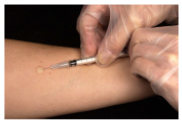
Examples

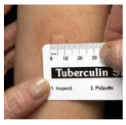
IGRA Blood Tubes

(can distinguish between vaccination)

Tuberculin Skin Test (TST)

also known as Mantoux test (cannot distinguish between vaccination)





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Any Questions???

Feedback Survey

https://forms.office.com/r/fXLZVUa57B

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Appendix III

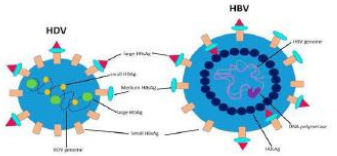
Other teaching activities: Hepatitis D (presentation slides)

What is Hepatitis D?

- Hepatitis D is caused by the Hepatitis D virus (HDV)
- Hepatitis is an illness that inflames and damages your liver
- Hepatitis affects the livers ability to make proteins and clear the blood of unwanted impurities "it's job"
- HDV can only infect people who are also infected with Hepatitis B virus (HBV)
- HDV-HBV co-infection is considered most severe form of chronic viral hepatitis
- HDV smallest virus known to infect humas

Why does HDV need HBV?

- HDV requires the HBV surface antigen (HBsAg) for its assembly in the body
- The outer coating of the virus consists of components taken from the HBV
- It does not need an active replication of HBV
- Can occur through co-infection or superinfection



Epidemiology

- Globally HDV affects nearly 5% of people who have a chronic infection with HBV
- Countries with the highest prevalence is Mongolia, Republic of Moldova and countries of Western and Middle Africa
- Numbers are decreasing, due to successful HBV vaccination programs
- HDV is rare in Australia and is a nationally notifiable disease
- Australia- around 20-30 cases diagnosed each
- Most cases from endemic areas

Signs & Symptoms and Incubation & Infectious periods

Signs and Symptoms
- Fever
- Loss of appetite
- Nausea and vomiting
- Abdominal pain
- Jaundice
- Dark urine and pale faeces
- Muscle and joint pain
- Rash

Incubation period
- 3-7 weeks

Infectious period
- All people with HDV infection

Transmission and exposure

Transmission
- Sexual contact
- Intravenous drug use (sharing needles or syringes)
- Broken skin (via injection)
- Contact with infected blood or blood products
- Sharing household items (razors, toothbrushes)

Who is at risk?
- Indigenous people
- People who inject drugs
- People with Hep C or HIV
- MSM
- Recipients of haemodialysis
- Commercial sex workers
- People not immune to HBV
- Infants born to mothers with HDV
- HH contacts of people with HDV

Public Health Follow-Up

- No specific follow up is required
- NSW Health Control Guidelines https://www.health.nsw.gov.au/Infectious/controlguideline/Pages/hepd.aspx

References

- https://www.health.gov.au/diseases/hepatitis-d
- https://www.cdc.gov/hepatitis/hdv/hdvfaq.htm#section1
- https://www.who.int/news-room/fact-sheets/detail/hepatitis-d
- https://www.sciencedirect.com/topics/medicine-and-dentistry/defective-virus#:~:text=Hepatitis%20Viruses&text=HDV%20is%20a%20defective%20virus,HDV%20uses%20for%20virion%20assembly.
- https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7438974/
- https://www.doherty.edu.au/news-events/news/how-prevalent-is-hepatitis-d-virus-infection-in-australia

Chapter: VII

Additional field placement activities

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Abbreviations

ARI	Acute respiratory infections
ANSTO	Australian Nuclear Science and Technology Organisation
ED	Emergency department
ICPMR	Institute for Clinical Pathology and Medical Research
NSW	New South Wales
OHB	One Health Branch
PHU	Public health units
RSV	Respiratory Syncytial Virus
SESLHD	South Eastern Sydney Local Health District

Seasonal arborvirus surveillance and control

The New South Wales (NSW) Health Arborvirus Surveillance and Monitoring Program aims to provide early recognition of mosquito-borne disease risk for the community.[1] It involves monitoring mosquito populations through trapping, identifying the dominant mosquito species, and testing them for the presence of virus.[1] There are two mosquito monitoring sites within South Eastern Sydney Local Health District (SESLHD) along Georges River at Alfords Point and Illawong.[1] During mosquito season, typically from November to April, environmental health officers from the Public Health Unit (PHU) set and collect mosquito traps weekly.[1] The collected mosquitoes are then sent to the Department of Entomology at the Institute for Clinical Pathology and Medical Research (ICPMR) at Westmead Hospital for analysis.[1]

Since 2023, the PHU has been conducting mosquito monitoring in Matraville near an international freight terminal to establish baseline data on mosquito species and their population in that area.[1] As part of this effort, mosquito control measures are being tested in the nearby Eastern Suburbs Memorial Park by placing s-methoprene pellets, a growth regulator for mosquito larvae, in water containers.[1]

During my Master of Applied Epidemiology, I was fortunate to participate in seasonal arborvirus control. I assisted the environmental health team in placing s-methoprene pellets in water containers at Eastern Suburbs Memorial Park (*Figure 1*). I also participated in the Environmental Health Workshop where I was able to learn about all the different types of mosquito traps used in the field and trapping in the District.

Figure *1* Participating in seasonal arborvirus control at Eastern Suburbs Memorial Park, 2023

Cruise ship vessel inspection

The PHU operates two public health programs for cruise ships visiting NSW ports: the Cruise Ship Health Surveillance Program and the Vessel Inspection Program. These programs involve responding to reports of infectious diseases, outbreaks and other public health concerns, as well as environmental health inspections of the vessels. In November 2023, I participated in the Vessel Inspection Program with the environmental health team to inspect a cruise ship at the international passenger terminal in Sydney. The inspection involved assessing hygiene and washing, childcare facilities, cleaning equipment and linen, medical and body holding facilities, legionella control and planning, drinking water, recreational (pools and spas) water, skin penetration, waste management and pest control. This experience provided valuable insights into assessing public health risks on commercial vessels, including emphasis on preventative measures, interdisciplinary collaboration, and biopreparedness in managing public health risks whilst at sea (*Figure 2)*.

Figure 2 Vessel inspection program Internation Passenger Terminal Sydney, NSW, November 2023

Residential aged care report

The public health unit (PHU) introduced a monthly residential aged care facility (RACF)

outbreak report in 2023, to inform the District aged care services on aged care outbreaks in the district. The report in its infancy provided a brief overview of COVID-19 outbreaks, by providing information on the number of outbreaks that occurred in the month, average attack, hospitalisation, death and vaccination rates. The report then expanded to a summary on the key themes that were discussed at a monthly meeting with the infectious disease team, about factors contributing to the outbreaks in each facility.

In mid-2022 I was made responsible for completing the monthly report and from this experience, I determined that the report required updating to improve readability and be more comprehensive for stakeholders. This update also included the inclusion of influenza and respiratory syncytial virus (RSV) reporting, which resulted in a monthly acute respiratory infections (ARI) outbreak report. In 2023 I transitioned the report from SAS and redeveloped the program in R Markdown to include automation and improve efficiency. In the program I developed automated calculations, preformatted text for data interpretations and direct rendering into a preformatted Word document that aligned with local health district branding and reporting guidelines. I was also responsible for the data collection template used in the monthly meetings, organisation and chairing of the meetings, data collection, cleaning and analysis, production and distribution of the report. An example of the report is shown in *Appendix I.*

Australian Nuclear Science and Technology Organisation (ANSTO)

The Australian Nuclear Science and Technology Organisation sits within SESLHD. I was fortunate to undertake a tour of the facility with the epidemiology team from the PHU. The purpose of the visit was to understand the various areas of the facility and gain an understanding of nuclear science and the public health risks. The site visit formed part of the PHUs biopreparedness activities.

Infectious disease network lunch and learn

Following the annual Communicable Disease and Immunisation Conference the public health network established a "*Lunch and Learn*" session for people across the network to provide people the opportunity to present the work accepted at the conference. This allowed for people who did not attend the conference to hear the presentations. I presented in both 2023 and 2024, for the tuberculosis and *Legionella* outbreaks respectively. There were several sessions run over the course of a few weeks during lunch, where each person presented their work, which was followed by a session for questions.

Multijurisdictional outbreak investigation of shigellosis

In July of 2023 an emergency department (ED) physician alerted the PHU to several cases of shigellosis (*Shigella flexneri 2a*) among passengers who had recently returned from overseas on the same flight. The travellers were not known to each other. The PHU commenced an investigation, reviewing recent shigellosis notifications to identify other cases with similar travel histories and matching flight details. As part of the investigation, I established a case linelist and conducted case interviews, to collect information such as food consumed during the flight, movements on the plane, and stopovers.

The PHU also notified the One Health Branch (OHB) at the Ministry of Health, prompting a statewide request for all PHUs to interview shigellosis cases about international travel, flight details and food consumed. Additional cases were identified across Australia, leading to the formation of a multijurisdictional outbreak investigation (MJOI) team. Since the investigation began in SESLHD, I had the opportunity to continue to attend these meetings, which provided valuable insights into the structure of such investigations and the role of multidisciplinary teams in outbreak response.

References

1. NSW Health - South Eastern Sydney Local Health District (SESLHD). Mosquito Control: Arbovirus surveillance and mosquito monitoring program 2024 [Available from: https://www.seslhd.health.nsw.gov.au/services-clinics/directory/public-health/mosquito-control.

Appendix I

SESLHD Acute Respiratory Outbreaks in Aged Care Facilities Report

South Eastern Sydney Local Health District

Acute Respiratory Outbreaks in Aged Care Facilities

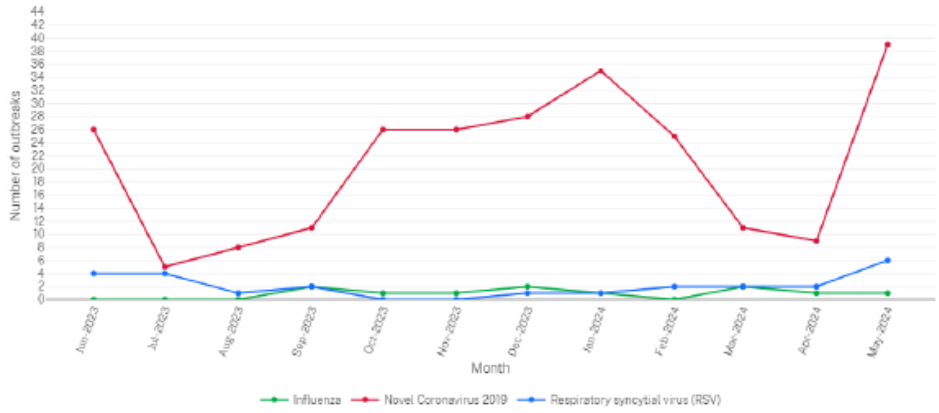
May 2024

Data Summary

In line with community virus transmission levels, the number of COVID-19 outbreaks in RACFs across SESLHD increased compared to April 2024. The number of influenza and RSV outbreaks remained low and steady. Contributors to the high impact of COVID-19 included:

- In some facilities low COVID-19 vaccination rates among residents
  - facilities reported that residents/families are refusing consent to vaccinate.
- Staff infections and poor infection prevention control.
- Residents refusing isolation/cohorting.
- Delayed detection of outbreaks; this could be a result of less severe infection in residents

Figure 1: Acute respiratory infection outbreaks in SESLHD residential aged care facilities, June 2023 to May 2024



Public Health Unit Page | 1 SESLHD-PublicHealthEnquiry@health.nsw.gov.au

Figure 2: COVID-19 rates across SESLHD residential aged care facilities, June 2023 to May 2024

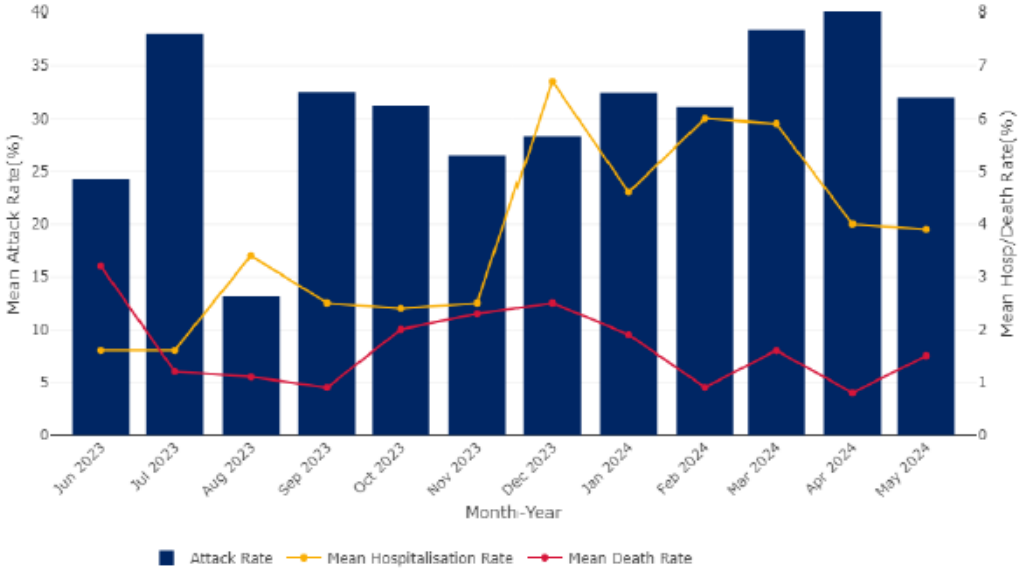


Figure 3: Influenza rates across SESLHD residential aged care facilities, June 2023 to May 2024

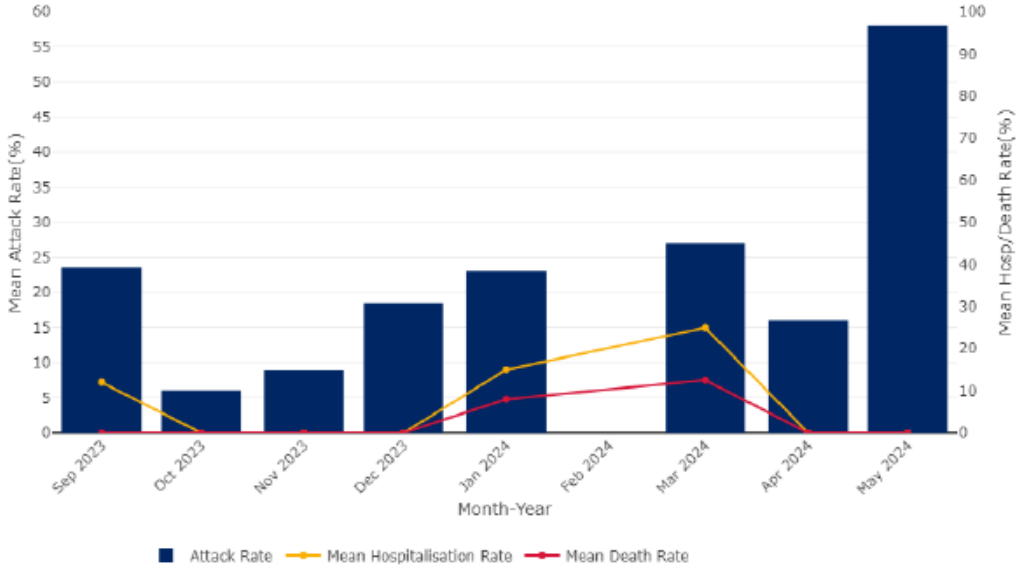


Figure 4: RSV rates across SESLHD residential aged care facilities, June 2023 to May 2024

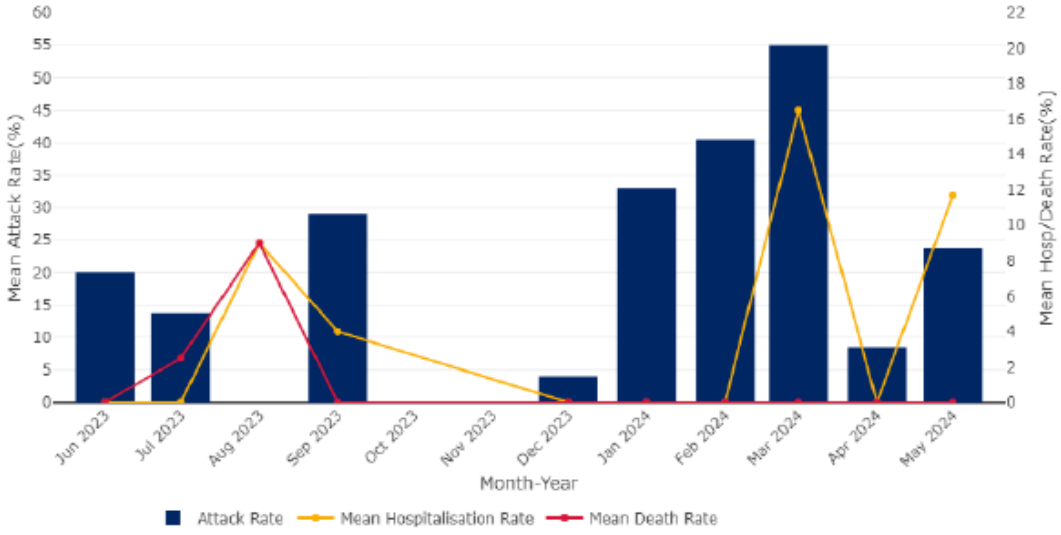


Table 1: COVID-19 outbreak summary statistics in SESLHD residential aged care facilities, January 2024 to May 2024

		Attack Rate (%)				Duration of Outbreak (days)				Vaccination Rate (%)			
Year	Month	Mean	Median	Q1	Q3	Mean	Median	Q1	Q3	Mean	Median	Q1	Q3
2024	Jan	32	28	16	44	14	13	10	19	46	41	16	77
	Feb	31	29	12	47	13	12	9	17	56	52	32	83
	Mar	38	23	15	61	19	17	11	20	45	50	30	56
	Apr	40	31	23	43	15	16	12	17	64	64	51	85
	May	32	30	20	40	15	14	11	20	52	57	24	78

Table 2: Influenza outbreak summary statistics in SESLHD residential aged care facilities, January 2024 to May 2024

		Attack Rate (%)				Duration of Outbreak (days)				Vaccination Rate (%)			
Year	Month*	Mean	Median	Q1	Q3	Mean	Median	Q1	Q3	Mean	Median	Q1	Q3
2024	Jan	23	23	23	23	11	11	11	11	46	46	46	46
	Mar	27	27	20	34	11	11	10	12	100	100	100	100
	Apr	16	16	16	16	7	7	7	7	1	1	1	1
	May	58	58	58	58	8	8	8	8	88	88	88	88

There where no Influenza outbreaks during Feb 2024

Table 3: RSV outbreak summary statistics in SESLHD residential aged care facilities, January 2024 to May 2024

		Attack Rate (%)				Duration of Outbreak (days)			
Year	Month	Mean	Median	Q1	Q3	Mean	Median	Q1	Q3
2024	Jan	33	33	33	33	11	11	11	11
	Feb	40	40	37	44	22	22	18	26
	Mar	55	55	32	78	10	10	8	12
	Apr	8	8	8	9	13	13	12	14
	May	24	14	9	38	11	14	7	15

Discussion Themes

Table 4 below shows a list of themes that were identified as part of the monthly outbreak review meeting at the PHU. Outbreaks are selected for discussion based on factors such as duration of outbreak, attack, hospitalisation, death, and vaccination rates. Themes are collected during the discussion and are summarised in the table below, not every facility that has an outbreak during the month is selected for discussion.

Table 4: Themes contributing to outbreak control challenges identified at RACF Monthly Meeting, May 2024

Theme	Monthly Count	%
Wandering	1	10
Community exposure	1	10
Dementia	1	10
Staff infections	1	10
Unclear source	1	10
High attack rate on baseline testing	1	10
Concurrent outbreaks	1	10
Late notification	1	10
Unable to cohort effectively	1	10
Delay in isolation	1	10
Group activities/ socialising	2	20
Shared rooms	2	20
Challenging resident population	2	20
Vaccine refusal	2	20
Ongoing transmission	4	40
Low vaccination	5	50
Total# facilities discussed	10	100

Table 5: Summary of RACF COIVD-19 outbreaks notified during May 2024 by SESLHD Residential Aged Care Facilities

NCIMS	Facility	Suburb	Outbreak Duration (days)	Resident Cases (n)	Attack Rate (%)	Hospitalisations (n)	Hospitalisation Rate (%)	Deaths (n)	Death Rate (%)	Vaccination (%)
[redacted]	[redacted]	Peakhurst	20	18	26	0	0	0	0	58
		Miranda	11	5	62	0	0	0	0	89
		Waverley	18	33	59	0	0	1	3	46
		Mortdale	7	3	15	1	33	1	33	21
		Peakhurst	13	6	33	0	0	0	0	72
		Elizabeth Bay	12	23	43	0	0	0	0	92
		Blakehurst	7	4	11	0	0	0	0	31
		Kogarah	19	16	37	0	0	0	0	12
		Hurstville	8	2	33	0	0	0	0	0
		Peakhurst	7	2	15	0	0	0	0	18
		Bexley	9	5	14	0	0	0	0	47
		Rushcutters Bay	30	23	20	0	0	0	0	16
		Randwick	16	8	44	0	0	0	0	77
		Mortdale	12	16	67	1	6	0	0	40
		Vaucluse	15	8	35	1	12	1	12	0
		Bexley	23	27	44	5	19	2	7	13
		Kirrawee	24	7	14	1	14	0	0	60
		Blakehurst	29	38	66	1	3	1	3	75
		Waterfall	9	7	28	1	14	0	0	0
		Surry Hills	15	25	37	0	0	0	0	54
		Maroubra	16	12	22	0	0	0	0	62
		Taren Point	16	24	20	2	8	0	0	65
		North Bexley	12	5	20	0	0	0	0	0
		Engadine	22	35	43	0	0	0	0	100
		Rose Bay	10	3	20	0	0	0	0	80
		Randwick	13	11	37	0	0	0	0	97
		Waverley	14	15	71	1	7	0	0	67
		Maroubra	11	7	28	1	14	0	0	92
		Sylvania	23	35	55	2	6	0	0	36
		Blakehurst	25	13	37	0	0	0	0	28
		Bronte	8	2	10	0	0	0	0	90
		Randwick	11	4	7	0	0	0	0	27
		Penshurst	17	5	31	0	0	0	0	75
		Jannali	13	9	33	1	11	0	0	85
		Heathcote	13	5	22	0	0	0	0	100
		San Souci	24	9	24	0	0	0	0	57
		Randwick	6	3	15	0	0	0	0	90
		Beverley Park	24	16	21	1	6	0	0	50
		Paddington	21	7	30	0	0	0	0	17

indicates facilities that were discussed at monthly outbreak discussion

Table 6: Summary of RACF Influenza outbreaks notified during May 2024 by SESLHD Residential Aged Care Facilities

NCIMS	Facility	Suburb	Outbreak Duration (days)	Resident Cases (n)	Attack Rate (%)	Hospitalisations (n)	Hospitalisation Rate (%)	Deaths (n)	Death Rate (%)	Vaccination (%)	Influenza Strain
[redacted]	[redacted]	Bronte	8	11	58	0	0	0	0	88	

Table 7: Summary of RACF RSV outbreaks notified during May 2024 by SESLHD Residential Aged Care Facilities

NCIMS	Facility	Suburb	Outbreak Duration (days)	Resident Cases (n)	Attack Rate (%)	Hospitalisations (n)	Hospitalisation Rate (%)	Deaths (n)	Death Rate (%)
[redacted]	[redacted]	Blakehurst	5	4	6	0	0	0	0
		Kirrawee	15	2	9	1	50	0	0
		Bexley	17	20	53	0	0	0	0
		Rose Bay	3	2	10	0	0	0	0
		Bangor	15	8	19	0	0	0	0
		Waverley	12	5	45	1	20	0	0

Report Details		
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Next report to be issued:	July 2024	