EPIDEMIOLOGY IN THE TIME OF COVID-19

A thesis submitted for the degree of Master of Philosophy
(Applied Epidemiology)

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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, except where due acknowledgement is made in the thesis.

I have clearly stated the contribution of others to my thesis as a whole, including statistical assistance, survey design, data analysis, significant technical procedures, professional editorial advice and any other original research work used or reported in my thesis. The content of my thesis is the result of work I have carried out since the commencement of my research higher degree candidature and does not include a substantial part of work that has been submitted to qualify for the award of any other degree or diploma in any university or other tertiary institution.

Freya Gray Hogarth

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Abbreviations

ACT	Australian Capital Territory
AHPPC	Australian Health Protection Principal Committee
ANU	Australian National University
CDC	Northern Territory Centre for Disease Control
CDESS	Communicable Disease Epidemiology Surveillance Section
CDNA	Communicable Diseases Network Australia
COVID-19	Coronavirus 2019
CIDTs	Culture-independent diagnostic test
Ct	Cycle threshold
DoH	Department of Health
HEMB	Health Emergency Management Branch
HSQF	Howard Springs Quarantine Facility
HREC	Human Research Ethics Committee
LLF	Lesson from the Field
MAE	Master of Philosophy (Applied Epidemiology)
MDU PHL	Microbiological Diagnostic Unit Public Health Laboratory
MJOI	Multi-jurisdictional outbreak investigation
MJO	Multi-jurisdictional outbreak
NIC	National Incident Centre
NNDSS	National Notifiable Disease System
NSW	New South Wales
OHPR	Office of Health Protection and Response
NSC	National Surveillance Committee
NT	Northern Territory
PHU	Public Health Unit
Qld	Queensland

REDCap	Research Electronic Data Capture
RT-PCR	Reverse transcription quantitative polymerase chain reaction
SARS-CoV-2	Severe acute respiratory syndrome coronavirus
SA	South Australia
Tas	Tasmania
Vic	Victoria
VARC	Victorian Aged Care Response Centre
WA	Western Australia
WGS	Whole genome sequencing
WHO	World Health Organization

Abstract

From March 2020 to November 2021, I undertook a field placement within the Office of Health Protection and Response (OHPR) at the Australian Government Department of Health. During this time, I also had the opportunity to work at the Northern Territory Centre for Disease Control (CDC). The placements and experiences allowed me to apply the skills of the epidemiology of infectious diseases I acquired through the program. This thesis details projects undertaken at the field placements to fulfill the core requirements of the Master of Philosophy (Applied Epidemiology) program. The projects comprise a multi-jurisdictional outbreak investigation into COVID-19 among returned attendees of a wedding in Bali, Indonesia, an analysis of the effect of the COVID-19 pandemic on salmonellosis in Australia during 2020, the establishment of a surveillance network for COVID-19 outbreaks, and an epidemiological study into in-flight transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) on Australian repatriation flights from India into Darwin. In this thesis, I also describe other public health experiences I gained during the MAE program, including my role in teaching, and responsibilities as part of the epidemiology and surveillance team assisting the national COVID-19 response, and analysis of current trend arboviral diseases with a focus on Bamah Forest Virus infection.

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Chapter 1.

Introduction to field placement and summary of experience

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Field placement overview

My field placement for the MAE program was in the Office of Health Protection and Response (OHPR) at the Australian Government Department of Health (DoH) during 2020-2021. Initially I was placed with the Communicable Disease Epidemiology and Surveillance Section (CDESS) within the Communicable Diseases Branch. Six days after starting my field placement, the World Health Organization declared the rapidly circulating severe acute respiratory syndrome coronavirus 2 (SARS-CoV2) a global pandemic of the associated disease coronavirus 2019 (COVID-19), and as a result I moved to the Health Emergency Management Branch (HEMB) for the remainder of 2020. During my second year, I also had the opportunity to spend three months at the Northern Territory Centre for Disease Control (CDC).

Situated in the OHPR, I was provided the opportunity to learn how public health works in Australia, and the coordination role and responsibilities of government at the federal and state levels. My MAE experience was heavily influenced by COVID-19, and there was a lot to learn. I was constantly reminded how lucky I was to be learning epidemiology during a "*once in a lifetime pandemic*". The experience was at times intense due to the volume and pace of learning that was required while responding to a rapidly changing pathogen and evolving situation globally. However, most days I did feel lucky, even when sliding backwards on the slippery slope of a steep learning curve.

In this chapter I provide a few highlights of my field placements and summarise my projects to demonstrate the range of competencies in applied epidemiology I met throughout my MAE.

Health Emergency Management Branch (HEMB)

HEMB has responsibility for prevention, preparedness and response activities related to national and international health emergencies, and functions as the National Focal Point NFP for Australia under the International Health Regulations. I was involved in daily activities of the National Incident Room (recently re-named the National Incident Centre, or 'NIC') as part of the COVID-19 Epidemiology and Surveillance Team. I was directly involved in establishing surveillance for COVID-19 outbreaks through COVID-Net (Chapter 2) and participated in two multi-jurisdictional outbreak investigations (MJOIs) (Chapter 3). These experiences provided valuable insights into the coordination and operational role of government in response to a health emergency. Another aspect of my placement in the NIC was investigating instances of in-flight transmission of SARS-CoV-2 as part of an airline study group that involved a wide variety of stakeholders from state and territory departments, the Ministry of Health in New Zealand, and the

Australian and New Zealand airline industry. I led one arm of the study that assessed SARS-CoV-2 infection among air crew (Chapter 2). I was also involved in contact tracing for the NIC COVID-19 Contact Tracing Task Force, as well as contract tracing on behalf of Victoria and South Australia (SA) during the second wave of the epidemic in mid-2020. It was unique for the NIC to participate in operational support for jurisdictions. Because I had gained experience building REDCap databases in my surveillance project (Chapter 2), I was responsible for rapidly building a contact tracing database for the NIC Task Force. I was responsible for assisting in the technical leadership of the task force during the SA outbreak, and was required to organise and train contact tracers, liaise with surveillance leads in SA, and report data twice daily back to SA. I also contributed to revising the contact script with senior epidemiologists and public health physicians. During my time in the NIC, I was also involved in the Victorian Aged Care Response Centre (VARC), where I worked with epidemiologists in the Strategic Intelligence & Planning Unit to develop epidemiology reports, streamline data sources, and strengthen communications between VARC and the Ageing and Aged Care Group. This involved attending regular meetings and collaborating with members from both groups to establish operating procedures for the reporting of aged care data.

Communicable Diseases Brach

The main responsibilities of CDESS include:

- development and maintenance of policies and national systems for communicable disease surveillance;
- ongoing review of the National Notifiable Disease List;
- coordination and response to national or multi-jurisdictional outbreaks of foodborne disease through OzFoodNet;
- describing the epidemiology of rare diseases that occur infrequently at state and territory levels; and;
- surveillance of notifiable human diseases.

During my time in CDESS, I participated in an MJOI of *Salmonella* Saintpaul coordinated by OzFoodNet. As part of the response, I conducted case interviews on behalf of the Victorian Department of Health and Human Services. I also undertook a quarterly report of arboviral diseases for the National Arbovirus and Malaria Advisory Committee (NAMAC). In addition, I presented a highlight on trends of arboviral diseases, with a focus on Barmah Forest Virus infection, to the Communicable Diseases Network of Australia (CDNA) and NAMAC.

Northern Territory Centre for Disease Control

The CDC is a Territory-wide public health unit with a primary role to control and prevent communicable and non-communicable diseases in the NT. I was seconded to the surveillance program to temporarily backfill their epidemiologist. The surveillance program takes responsibility for coordinating the activity of disease surveillance throughout the territory including planning, implementation, and evaluation of necessary public health responses, and the management of outbreaks.

During my time at CDC, the surveillance team were busy with COVID-19 planning and preparedness, including case and contact management of passengers from international repatriation flights arriving into the Howard Springs Quarantine Facility. During my placement, the NT experienced its first cases of COVID-19 community transmission associated with a mine site in the Tanami Desert. More than 900 people had left the mine site and travelled to multiple jurisdictions and over 700 people were required to isolate at the mine site. There were exposure sites in Darwin city, as well as in Alice Springs, Darwin, and Brisbane airports. The scale and complexity of the outbreak was very challenging from a surveillance point of view, and I gained many valuable learning experiences, particularly the importance of the command and response structure in emergency and incident management. While at CDC, my responsibilities included: contact tracing for foodborne disease and COVID-19; developing standard operating procedures for COVID-19 contact tracing; strengthening contact data systems by modifying the REDCap database; and epidemiology and surveillance reporting.

Summary of degree requirements

Design and conduct an epidemiological study

In April 2021, two repatriation flights carrying passengers from two regions of India experiencing major outbreaks of COVID-19 landed in Darwin. During the quarantine period a high proportion of passengers from the two respective flights were diagnosed with COVID-19. All passengers tested negative for SARS-CoV-2 by RT-qPCR in the 72 hours prior to flying. I performed a genomic epidemiological investigation of SARS-CoV-2 infection among the passengers, combining viral genome sequencing analyses with epidemiological analyses. Our study provides supporting evidence that 5 cases transmitted SARS-CoV-2 to at least 11 other passengers in-flight. These findings were supported by flight seating maps and the rigorous isolation and testing regimen of all passengers after arrival to Australia. These findings reinforce the need for strict infection control practices on board aeroplanes in addition to mandatory mask use, pre-departure testing, and robust quarantine processes.

Establish a public health surveillance system

I contributed to establishing COVID-Net, a national surveillance network for COVID-19 outbreaks. I participated in weekly network meetings, developed core data fields and data dictionaries, and built the online database to house the outbreak data. Following the implementation of COVID-Net, I conducted weekly analysis of the data and prepared weekly surveillance reports that summarised outbreaks across Australia. I also conducted a process evaluation of the network with key participants in state and territories. COVID-Net used nationally to contribute to our understanding of the epidemiology of COVID-19 outbreaks and in the future could provide evidence base for policy decisions. This project, in addition to the development of the NIC Task Force contact tracing database, the arboviral disease quarterly report, and the Barmah Forest Virus report, demonstrate my mastery of the Surveillance competency.

Investigate an acute public health event

I co-led an MJOI of COVID-19 among returned attendees of a wedding in Bali, Indonesia. As part of this investigation, I conducted a hypothesis generating telephone interview and designed a questionnaire that was used to conduct a retrospective cohort study among attendees. I also was responsible for writing the data analysis plan , cleaning, and analysing the data. We found that attendees participated in high-risk transmission behaviours across multiple events, such as kissing, dancing, sharing drinks and sharing shisha, and engaged in close physical contact, which may have contributed to the high attack rate. This outbreak highlights the significant role social gatherings can play in transmission of COVID-19 and underscores why it is important to limit gatherings and close physical contact to control the spread of COVID-19. I also contributed to contact tracing and nationally coordinated OzFoodNet meetings for a multi-jurisdictional outbreak of *Salmonella* Saintpaul, in addition to the investigation and response to the COVID-19 Tanami desert outbreak in the NT.

Analyse a public health data set

In Australia, *Salmonella* infections are one of the most common causes of foodborne gastroenteritis, and one of the leading causes of hospitalisation and deaths due to foodborne disease. I performed a descriptive analysis of salmonellosis cases in Australia during 2020 and compared the incidence to the historical 5-years (2015-2019). I found that observed changes in salmonellosis incidence in the context of the COVID-19 pandemic suggest reduced exposure to *Salmonella* due to restrictions to social gatherings and international travel, closure of dine-in restaurants and the hospitality sector, and changes in health-seeking behaviours that impacted diagnostic testing for salmonellosis. From Q2, states and territories with the application of longer COVID-19 public health measures reported greater reductions in salmonellosis incidence, while demographic and environmental factors in the Northern Territory and Western Australia may have had more of an impact on high salmonellosis rates in these jurisdictions.

Prepare a scientific manuscript for a peer-reviewed journal

I prepared the following manuscripts as first author:

- Genomic epidemiological investigation of in-flight transmission of SARS-CoV-2 on repatriation flights from India to Australia, April 2021 (Chapter 2), under peer review in Emerging Infectious Diseases; and
- COVID-19 outbreaks in Australia during a period of high epidemic control, 2020 (Chapter 3), under peer review in PLOS ONE.

I assisted with the following manuscripts as second author:

- Outbreak of COVID-19 at a wedding event in Bali, March 2020 (Chapter 4), published in *Communicable Disease Intelligence*; and
- Potential in-flight transmission of SARS-CoV-2 on Australian and international flights, 1 January-1 May 2020, in final draft.

Communication to a lay audience

I wrote a one-page summary to communicate findings of the outbreak investigation to study participants (Chapter 4).

Conference presentations

I gave the following oral presentations to national and international audiences:

- Establishing a surveillance network for COVID-19 outbreaks in Australia, 2020. South Asia Field Epidemiology and Technology Network, Inc. (SAFETYNET) videoconference, 7–8 September 2021.

- Arboviral disease trends in Australia: focus on Barmah Forest Virus infection. CDNA videoconference, 21 August 2021, and NAMAC videoconference, 12 October 2021.
- Genomic epidemiological investigation of in-flight transmission of SARS-CoV-2 on repatriation flights from India to Australia, April 202, CDNA videoconference, 1 December 2021.

Lessons from the field

I prepared a teaching exercise titled “The art of contact tracing” (Chapter 6). I also attended Lessons from the field exercises prepared by my fellow MAE colleagues.

Teaching

I planned, developed, and delivered the teaching session “Introduction to REDCap for data collection” to the first-year MAE scholars with colleagues from my cohort (Chapter 6).

Summary of core competencies

Table. Summary of MAE projects and the fulfilment of core competencies and course requirements

MAE competency	**Chapter 2:** Epidemiological study into SARS-CoV-2 transmission in-flight	**Chapter 3:** National Surveillance network for outbreaks of COVID-19	**Chapter 4:** Outbreak of COVID-19 at a wedding event in Bali	**Chapter 5:** Effect of COVID-19 public health measures on salmonellosis in Australia	**Chapter 6:** Teaching
Investigate an acute public health problem			✓		
Analyse a public health dataset		✓		✓	
Establish a surveillance system		✓			
Design and conduct an epidemiological study	✓				
Literature review	✓			✓	
Communication for lay-audience			✓		
Manuscript for peer review	✓	✓			
Conference presentation		✓			
Lessons from the field					✓
Teaching 1st years					✓

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Chapter 2. Epidemiological study

Genomic epidemiological investigation of in-flight transmission of SARS-CoV-2 on repatriation flights

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Prologue

Study rationale

From 2020–2021, mandatory supervised quarantine for returning travellers and other international arrivals was the cornerstone of Australia's border control and ability to control the importation risk of COVID-19. From 25 October 2020, Howard Springs Quarantine Facility (HSQF) in Darwin received passengers from government-assisted repatriation flights. In April 2021, a high incidence of COVID-19 was observed among passengers from two repatriation flights from India into Darwin. In the subsequent 7 days, over 40 passengers from the flights tested positive to SARS-CoV-2 infection. This study aimed to describe the genomic epidemiology of the cases and probable instances of in-flight transmission.

My role

I led this piece of work in collaboration with public health staff at the Northern Territory (NT) Centre for Disease Control Darwin Public Health Unit (CDC), Royal Darwin Hospital (RDH), and the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) in Victoria. I undertook case interviews and participated in contact tracing passengers of these flights. I retrospectively reviewed case interview forms, flight manifests, and pathology results of cases, and extracted key information to create a case line list. Data fields included case demographics, a 'yes/no' variable for symptoms, symptom onset date, serial test positive and negative dates, and flight seat numbers. Using a combination of the booking reference number on the flight manifests and information in the case interview forms, I mapped the seat location of cases on the flights, linked cases to family and travel groups, and assigned a group reference number to the cases. This was an important step for the analysis since cases were found to be heavily clustered within family groups.

Genomic sequencing of all confirmed cases of COVID-19 diagnosed in the NT were conducted by the MDU PHL. Sequencing and clustering analysis were done prospectively by laboratory staff at MDU PHL and RDH. I reviewed results and interpreted them alongside epidemiological findings to determine the most likely source of infection for cases. I provided a report of my analysis to MDU PHL to assist with the identification of transmission networks between flight cases and cases in other jurisdictions once sequences were uploaded to the national sequence sharing platform AusTrakka.

I conducted a literature review for this project, drafted the manuscript, and worked collaboratively with the co-authors to refine the content. We submitted the manuscript to the Emerging Infectious Diseases, where it is currently under peer review.

Lessons learnt

Since the start of the COVID-19 pandemic, the use of genomic sequencing has expanded from determining transmission chains for cases with multiple epidemiological links, to identifying highly transmissible variants within quarantine facilities to inform public health responses. While I was familiar with the use of genomics for the investigation of foodborne disease, this was my first experience applying genomic analyses in combination with traditional epidemiological methods for investigating transmission events.

I learnt about the potential challenges associated with the increasing growth of the SARS-CoV-2 genomic data set and relatively low levels of genetic diversity of the virus, which in practice may lead to sequences being incorrectly assigned if there is missing data. Initially, I was concerned with the varying levels of ambiguity in the genomic analyses and its use to support epidemiological links. For example, the accuracy of assignment depends on the number of sequences in that lineage and the quality of those sequences and how unique the single nucleotide polymorphisms (SNPs) are for that lineage.

I was also unsure how closely related case sequences must be to strongly suggest the existence of transmission networks between cases. My field supervisor on this project, Dr Ella Meumann, was excellent, and she stepped me through my anxieties. I learnt about Pangolin lineage designation, and how to read aligned sequences on a phylogenetic tree and comparing individual sequences. This was a valuable and practical learning experience. This study allowed me to gain an understanding of the pivotal role AusTrakka, Australia’s national sequencing platform, has played in underpinning Australia’s SARS-CoV-2 sequencing efforts. AusTrakka has allowed real-time inter-jurisdictional sharing of genomic data that has significantly impacted response times.

At the time cases were interviewed we had not anticipated a study of this kind, and a standard COVID-19 questionnaire was used for the purpose of collecting information that would inform the public health response. Without re-interviewing cases, it was difficult to exclude the possibility of other sources of infection for cases before or after their travel journey. In addition, lack of detailed information on passenger movement while on the flight limited the availability of data to characterise risk of transmission in-flight. These factors limited the analyses I could undertake, and I was challenged to conceptualise the use of the data available. In the end, I used descriptive statistics to describe the transmission event by person, place, and time.

Public health implications

Reports of suspected in-flight transmission events are relatively few, and the airline industry suggests the risk of contracting SARS-CoV-2 in-flight is low. Aerosol dispersion studies have demonstrated that mask wearing, in addition to aircraft cabin ventilation and filtration systems, provides a layer of protection that significantly reduces the risk of SARS-CoV-2 transmission during long duration flights. In addition to mask wearing, the Australian aviation industry has made considerable efforts to reduce the risk of flight associated transmission by enforcing passengers to undertake online check-in testing for SARS-CoV-2 in the 72 hours prior to flying. Our study adds evidence in addition to other reports that challenge the efficacy of face masks in limiting transmission between passengers not physically distanced. In addition, it is one of few reports that has identified genomic clusters where pre-departure testing has been implemented and reinforces the need for robust pre-departure testing and quarantine processes.

The integration of epidemiology and genomics has become a vital component of public health responses to COVID-19 by providing an early detection of possible quarantine breaches. Despite the large number of COVID-19 cases arising from the two flights, there was no evidence of further transmission within the quarantine facility, providing support for current infection prevention and control practices at HSQF.

MAE course requirements

The following MAE core course requirement were completed with is project:

- Design and conduct an epidemiological study.

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- AUSMAT for management of cases and contacts at HSQF;
- Dr Ben Polkinghorne for MAE supervision; and
- Dr Ella Meumann, for concept design, genomics expertise, and supervision on this project.

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Title: Genomic epidemiological investigation of in-flight transmission of SARS-CoV-2 on repatriation flights from India to Australia, April 2021

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Key words: SARS-CoV-2, Quarantine, COVID-19, Genome Viral, In-flight transmission, Genomics, Epidemiology, Airplane, India, Australia

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Abstract

To investigate severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection among passengers from two Australian repatriation flights from India in April 2021, we performed epidemiological analyses and viral genome sequencing. All passengers tested negative for SARS-CoV-2 by RT-qPCR in the 48 hours prior to flying, and on arrival, entered mandatory supervised quarantine where they undertook isolation and routine testing. SARS-CoV-2 was detected in 14% (47/345) of passengers. Of these, 45% (21/47) tested positive on day 0 of the quarantine period and 55% (26/47) tested positive ≥ 1 day after arriving in quarantine. Genome sequencing linked 51% (24/47) of these cases to six genomic clusters. Seating proximity and test positive dates of cases provided supporting evidence that five cases transmitted SARS-CoV-2 to at least 11 other passengers, indicating instances of probable flight-associated transmission. Our findings reinforce the use of masks in-flight in addition to robust pre-departure testing to prevent in-flight transmission.

Introduction

In Australia, the first epidemic wave of coronavirus disease (COVID-19) occurred during March 2020 and was characterised by returned international travellers and residents who had acquired their infection overseas. From March 25, 2020, Australia closed its borders to all but Australian citizens and permanent residents, and since March 28, 2020, international arrivals have been required to undergo mandatory supervised quarantine at designated facilities for at least 14 days. This initial response, combined with the implementation of targeted public health measures, contributed to the end of the first wave. While Australia has since experienced larger epidemic waves characterised by local transmission, the adoption of a suppression strategy has resulted in periods of COVID-19 control throughout the country.[1,2]

Mandatory supervised quarantine has been the foundation of Australia's border controls to reduce the risk of importation of COVID-19. Since October 23, 2020, a supervised outdoor quarantine facility implemented by the Australian Medical Assistance Team (AUSMAT) in Darwin, Northern Territory (NT), Australia, has received arrivals via government-assisted international repatriation flights. Arrivals undergo diagnostic testing for SARS-CoV-2 infection by reverse transcription quantitative polymerase chain reaction (RT-qPCR) on combined oral/deep nasal swabs once between days 0–2, on day 7, and again between days 10–14 of quarantine.[3] To reduce the incidence of COVID-19 in international arrivals, as of January 8, 2021, the airline implemented pre-departure SARS-CoV-2 RT-qPCR testing in the 48 hours prior to flying and all passengers were required to wear masks except for infants and children.[4]

In April 2021, two repatriation flights (flight 1 and flight 2) carrying passengers from two regions of India experiencing major outbreaks of COVID-19 landed in Darwin. Prior to this between October 2020 and April 2021, 225/9,651 (2%) repatriated passengers received at the facility had tested positive for SARS-CoV-2 during the quarantine period. The proportion of passengers positive from the two respective flights was substantially greater, at 15% and 13% respectively. Here we describe the genomic epidemiology of these cases including instances of probable in-flight transmission.

Methods

Management of the flight

On arrival to Darwin, passengers from flight 1 and flight 2 arrived at a separate air terminal then travelled by bus by seating cohorts to the Howard Springs International Quarantine Facility

(HSIQF), operated by AUSMAT and the National Critical Care and Trauma Response Centre (NCCTRC). Passengers were seated at least 1.5 meters apart and masks were mandatory for persons ≥ 12 years old unless there was a medical contraindication.[5] At the HSIQF passengers were physically separated into family groups in self-contained units that were well-ventilated with separate, non-communal bathroom facilities. Passengers were tested for SARS-CoV-2 by RT-qPCR on days 0 (at the air terminal), 7, and 12 of quarantine in addition to immediate testing if symptomatic. Individuals with a positive result were moved to a separate zone within the facility for COVID-19 management. Close contacts of COVID-19 cases were moved to a second separate zone and required to quarantine for at least 14 days from their last exposure to the case and were monitored daily for fever and respiratory symptoms.[3] On April 16, 2021, following confirmation of high number of cases on flight 1, to further mitigate transmission to and between staff and/or passengers AUSMAT/NCCTRC enhanced safety measures including the requirement for staff working with cases or close contacts to be fully vaccinated, wear full personal protective equipment, and undergo daily testing for SARS-CoV-2 by bilateral nasal swab rapid antigen testing in addition to daily saliva PCR confirmation.

Public health investigation

Australian state and territory health departments are required by law to report, investigate, and manage confirmed COVID-19 cases and close contacts according to national guidance.[3] The NT Centre for Disease Control (CDC) public health staff interviewed all confirmed cases and performed passenger contact tracing for the flights. Flight manifests were reviewed, and seat numbers were confirmed on interview with the cases. Aircraft close contacts included passengers in the same row or in the two rows ahead or behind a confirmed case (termed “2x2 area”) within the case’s infectious period. Close contact information was entered into a Research Electronic Data Capture (REDCap) database managed by the CDC.[6] Airline medical personnel performed contact tracing of aircrew operating on the flights in the course of the standard operations of an airline. This involved reviewing flight manifest and crew rosters, medical assistance reports, and risk assessment of contact with affected passengers.

The vaccination status of a passengers aged ≥12 years were collected by the airline for repatriation and quarantine purposes. Passengers were classified as fully vaccinated if they had received two doses of the same COVID-19 vaccine at least 14 days apart, and partially vaccinated if they had only received one dose.

SARS-CoV-2 testing, genomic sequencing, and bioinformatics analysis

Testing for SARS-CoV-2 was performed on swabs collected from the oropharynx and bilateral deep nasal passages, using the RT-qPCR assay from AusDiagnostics (Australia) with primers for the ORF1a and ORF8 genes. RT-qPCR cycle threshold (Ct) values reported in this manuscript are for the ORF8 target.

Genomic sequencing and consensus sequence generation were undertaken at the Microbiological Diagnostic Unit Public Health Laboratory at the Doherty Institute, Melbourne as described by Lane et al.[7] In brief, tiled amplicons were generated using the ARTIC version 3 primers (https://github.com/artic-network/artic-ncov2019/tree/master/primer_schemes/nCoV-2019), libraries were prepared using NexteraXT, and sequencing was undertaken on the NextSeq500/550 or iSeq100 (Illumina) using 150bp paired-end reads. Reads were aligned to the Wuhan-Hu-1 reference (Genbank MN908947.3) to generate consensus sequences, which were uploaded to GISAID (https://www.gisaid.org; Supplementary Table S1). SARS-CoV-2 lineages were assigned using Pangolin v3.1.5.[8, 9] Genomes belonging to lineages B.1.617.2 (Delta variant) and B.1.617.1 (Kappa variant) were included in a phylogenetic analysis with 300 publicly available SARS-CoV-2 genomes for context. To select context genomes, all 3,162 B.1.617 sequences from India between April 1, 2021, and April 15, 2021 with ≤5% missing or ambiguous base calls were downloaded from GISAID (https://www.gisaid.org/) on September 13, 2021, and 300 of these were randomly selected for inclusion (Supplementary Table S2). Genomes were aligned to the Wuhan-Hu-1 reference genome using MAFFT v7.464.11[10], and problematic sites (https://github.com/W-L/ProblematicSites_SARS-CoV2#human-friendly-version-of-the-vcf-file; last updated July 28, 2021) were masked from the alignment. Phylogenetic analysis was undertaken using IQ-TREE v1.6.12[11] using a generalised time reversible model with 4 gamma categories and 1,000 ultrafast bootstrap replicates. The phylogenetic tree was annotated using the ggtree package in R v4.0.2. Genomic clusters from the flights were identified by visualisation of the phylogenetic tree.

Case definitions

We determined the likely source of infection for each case by combining epidemiology with genomic sequencing data. Unless a negative RT-qPCR result indicated otherwise, we assumed the pre-symptomatic infectious period to be 1–3 days[3, 12, 13], and the incubation period to range from 1–14 days.[13, 14-18.] Currently there is limited evidence to determine the pre-symptomatic infectious and incubation periods for emerging SARS-CoV-2 variants[19-21], and these definitions are based on previous circulating lineages of SARS-CoV-2.

We defined arrival cases as passengers on flight 1 and flight 2 landing in Darwin on April 15 and 17 2021 respectively who tested positive to SARS-CoV-2 by RT-qPCR on day 0 of their quarantine period. Quarantine cases were defined as passengers who tested positive to SARS-CoV-2 by RT-qPCR ≥ 1 day after arriving in quarantine. Their infection was determined to result from probable flight-associated transmission if they were seated inside the 2x2 area of an arrival case; they were not a travel cxompanion of an arrival case; they returned a SARS-CoV-2 virus genome sequence separated by ≤2 single nucleotide polymorphisms to that of an arrival case in the 2x2 area; and their SARS-CoV-2 genome was located on the same clade as the arrival case in the 2x2 area.

Ethics

Surveillance activities were conducted for and on behalf of the Northern Territory Government under the auspices of public health legislation.[22] The study was approved by the Human Research Ethics Committee of the Northern Territory Department of Health and Menzies School of Health Research [approval number 2020-3737].

Results

A total of 345 passengers travelled from India to Darwin on flight 1 and flight 2, of whom 47 passengers subsequently tested positive for SARS-CoV-2; 21 on arrival and a further 26 within the first seven days of quarantine. No flight crew cases were identified. Of 345 passengers, 24 (6%) passengers had received at least one dose of COVID-19 vaccine; 14 passengers were fully vaccinated, and 10 passengers were partially vaccinated. We summarise flights and associated genomic clusters below.

Flight 1 Chennai to Darwin

Flight 1 arrived in Darwin on April 15, 2021, directly from Chennai, India, after a flight time of 11 hours and 55 minutes (Figure 1). On and after arrival in Darwin, 24/164 (15%) flight 1 passengers tested positive for SARS-CoV-2 by RT-qPCR; 8 passengers tested positive on arrival, and 16 passengers tested positive in the subsequent 7 days. The median age for cases was 31 years (range 0–73 years), 13 were male, and 11 were female. The Ct value was available for 7/8 (88%) arrival cases, with the median value 15.6 cycles (range 12.4–34.1 cycles). One arrival case developed symptoms on day 1 of quarantine; the remaining arrival cases were asymptomatic. Of the 8 arrival cases, one case was fully vaccinated for COVID-19, and a second arrival case was partially vaccinated. Of subsequent quarantine cases, symptoms developed in 50% (8/16); the median time of symptom onset was 5 days (range 0-7 days) after arrival, and the median number of days from arrival to a positive test was 5 days (range 1-7 days). Of the 16 quarantine cases, one case waxs fully vaccinated for COVID-19, and a second case was partially vaccinated.

SARS-CoV-2 genome sequences were successfully generated for 22/24 (92%) cases from flight 1; 16/22 (72%) belonged to the B.1.617.2 sublineage (Delta variant), and 6/22 (27%) belonged to the B.1.617.1 sublineage (Kappa variant). Of 22 cases, 18 (82%) belonged to one of four distinct genomic clusters (Figure 2).

Cluster 1

Cluster 1 included 9 cases with B.1.617.2 (Delta variant) infection (Table 1; Figure 1; Figure 2; Figure 3). Two arrival cases (arrival cases A and B) belonging to this cluster were asymptomatic and had Ct values of 14.3 and 15.6 cycles. No plausible epidemiologic link prior to the flight was identified between the two arrival cases. Arrival case B, seated in row 43, was within the same 2x2 area as 7 individuals who were subsequently diagnosed with COVID-19 while in quarantine; these included 3 of their own family members (quarantine cases C, D, and E; family group I) and 4 members of a separate family (quarantine cases F, G, H, and I; family group II), all of whom were seated in row 43 and tested positive for SARS-CoV-2 on day 5 of quarantine. Members of family group I may have been infected before, during, or after the flight, while family group II who were travelling in the same row were attributed to probable flight-associated transmission.

Cluster 2

Cluster 2 included 5 cases with B.617.1 (Kappa variant) infection (Table 1; Figure 1; Figure 2; Figure 3). One case (arrival case J) had a Ct value of 12.4 cycles and developed COVID-19 symptoms on day 1. This case was seated in row 42. Three members of a different family group (quarantine cases L, M, and N; all belonging to family group III) seated in row 43 subsequently tested positive to SARS-CoV-2 on the routine day 7 test. The infections of these three cases were determined to result from probable flight-associated transmission. A further quarantine case (quarantine case K) diagnosed on day 5 of quarantine was seated separately in row 51 and had no known epidemiologic links to the other cases in the cluster.

Cluster 3

Cluster 3 included 3 cases belonging to B.1.617.2 (Delta variant) (Table 1; Figure 1; Figure 2; Figure 3). One case (arrival case O) seated in row 3 was asymptomatic and had a Ct value of 14.9 cycles. Their partner (quarantine case P; family group IV) had a negative arrival test but tested positive for SARS-CoV-2 on day 1 of quarantine. A third case (quarantine case Q) seated in row 4, not travelling with the other two cases, tested positive for SARS-CoV-2 on day 2. The infection of this case was determined to result from probable flight-associated transmission.

Cluster 4

Cluster 4 included 2 cases belonging to B.1.617.2 (Delta variant) (Table 1; Figure 1; Figure 2; Figure 3). The two cases (quarantine case R and S) seated in row 55 belonged to the same family group (family group V) and both tested positive to SARS-CoV-2 on the routine day 7 test.

Flight 2 New Delhi to Darwin

Flight 2 arrived in Darwin on April 17, 2021, directly from New Delhi, India, after a flight time of 13 hours and 15 minutes (Figure 1). On and after arrival in Darwin, 23/181 (13%) flight 2 passengers tested positive for SARS-CoV-2 by RT-qPCR; 13 passengers tested positive on arrival, and 10 passengers tested positive in the subsequent 7 days. The median age for cases was 34 years (range 2–46 years), 13 were male, and 10 were female. The Ct value was available for 11/13 (85%) arrival cases, with the median value 14.9 cycles (range 8.4–20.2 cycles). Two arrival cases developed symptoms on days 0 and 1 in quarantine respectively. All subsequent quarantine cases were asymptomatic; the median number of days from arrival to a positive test was 3.5 days (range 3-7 days). Of 13 arrival cases, one case was partially vaccinated for COVID-19, while no quarantine case was either partially or fully vaccinated.

SARS-CoV-2 sequences were successfully generated for 19/23 (83%) cases from flight 2; 11/19 (58%) belonged to the B.1.617.2 sublineage (Delta variant), 4/19 (21%) belonged to the B.1.617.1 sublineage (Kappa variant), 3/19 (16%) belonged to the B.1.1.7 sublineage (Alpha variant), and 1/19 (5%) belonged to the A.23.1 sublineage. Of 19 cases, 6 (32%) belonged to one of two distinct genomic clusters (Figure 2).

Cluster 5

Cluster 5 included four cases belonging to B.1.617.2 (Delta variant) (Table 1; Figure 1; Figure 2; Figure 4). One case (arrival case T) seated in row 48 had a Ct value of 12.8 cycles and developed symptoms on day 1. Three further cases (quarantine cases U, V, and W) in row 48 belonging to two different travelling groups (including family group VI) tested positive for SARS-CoV-2 on routine day 7 testing. The infections of these three cases were determined to result from probable flight-associated transmission.

Cluster 6

Cluster 6 included two cases belonging to B.1.1.7 (Alpha variant) (Table 1; Figure 1; Figure 4). One case (arrival case X) developed symptoms on day 0 and had a Ct value of 11.7 cycles (Table 6; Figure 2). A member of their family (quarantine case Y; family group VII) subsequently tested positive for SARS-CoV-2 on day 4.

Discussion

Epidemiologic investigations and genome sequencing data suggest probable flight-associated transmission occurred on flight 1 and flight 2 from India to Australia. Our findings suggest 5/21 (24%) arrival cases on flight 1 and flight 2 transmitted SARS-CoV-2 to at least 11 other passengers, with secondary attack rates among passengers of 6% (8/143) and 2% (3/168), respectively. Transmission before, during, or after the flight was possible for five genomically-linked cases belonging to arrival case family groups; one case belonging to a genomic cluster was seated outside the usual 2x2 parameters used to identify close contacts of passengers; and two quarantine cases (cluster 4) were genomically-linked to each other but not to an arrival case. Five quarantine cases from flights did not belong to a genomic cluster, and genomic sequences were unavailable for a further two cases.

Despite the large number of COVID-19 cases arising from the two flights, there was no transmission outside family groups or in staff within the quarantine facility, which validates the stringent infection control procedures implemented at HSIQF. Our findings were supported by flight seating maps and the rigorous isolation and testing regimen of all passengers after arrival to Australia. From mid-March 2021, India experienced a second wave of COVID-19 driven by B.1.617.2 (Delta variant). At the time of the flight departures, daily confirmed case numbers exceeded 200,000[23-34], and modelled estimates mid-April suggested actual daily new infection numbers were several million.[25] Given the incidence and likely high prevalence of COVID-19 in India and the timing of symptom onset of quarantine cases, other potential sources of exposure for quarantine cases, such as the airport terminals are likely. However, both the in-flight spatial and genomic clustering of arrival cases to subsequent quarantine cases, and the time interval between the flight and positive COVID-19 test, suggest exposure during the journey in the instances described here.

While the aviation industry has adopted risk reduction approach to continue international travel (for example, online check-in, pre-flight testing, symptom screening, and mandatory use of masks in-flight)[26-28], the number of secondary cases we deemed infected in-flight has several implications for international repatriation processes. In response to these flights, the Australian Government suspended all repatriation flights from India and the airline modified the testing protocols to reduce the likelihood of passengers testing positive on arrival. When repatriation flights resumed on May 15, 2021, the airline instituted mandatory 72-hour pre-flight quarantine of passengers within India, and augmented the testing of passengers to include a SARS-CoV-2 rapid antigen test on entry to the pre-quarantine, followed by a RT-qPCR required at 48 hours prior to the flight and a further rapid antigen test on the day of departure (*28*). From May 15 to October 14, 2021, 13/4,543 (0.29%) passengers on repatriation flights from India to Darwin, ans

30/10,679 (0.28%) passengers on repatriation flights overall, tested positive to SARS-CoV-2 during the quarantine period. These findings suggest that controls introduced by the airlines, in addition to decreasing incidence in countries of origin and increasing vaccination rates, likely contributed to low incidence of COVID-19 on flights during this period. Furthermore, other than on the two flights reported here, among repatriated passengers between October 2020 and October 2021 there were only two other instances where genomics supported transmission links between cases not travelling together; these were between a passenger and a flight attendant, and between a passenger and two other passengers (a couple) seated in a different section of the aircraft.

Other published reports have used genomic data to identify in-flight transmission events (*29, 30*), however there are few reports of genomic clusters where pre-departure testing has been implemented.[31] Our investigation demonstrates the value of integrating genomic data with epidemiologic investigations for confirming and refuting SARS-CoV-2 transmission. In addition to the genomic clusters presented here, genomics disproved epidemiological links between cases that were thought to have been associated with the flights. For example, case L was seated in the same row as a genomically unrelated arrival case, and instead was linked to arrival case J (cluster 2) (Figure 2). Quarantine cases R and S (cluster 4) were not genomically linked to two arrival cases seated the rows behind (Figure 2). Additionally, on flight 2 three quarantine cases seated in rows 55 and 57 were genomically unrelated to an arrival case in row 56 (Figure 3).

Our findings add evidence in addition to other reports[31, 32] that challenge the efficacy of face masks in limiting the spread of SARS-CoV-2 between passengers not seated at 1.5 metre distance. The airline industry suggests the risk of contracting SARS-CoV-2 in-flight is low[26, 33, 34], and studies have demonstrated that mask wearing, in addition to aircraft cabin ventilation and filtration systems (that is high rates of air exchange, high efficiency particulate air filters, and downward flow of air) provides a layer of protection that significantly reduces the risk of SARS-CoV-2 transmission during travel.[26, 33, 35] While transmissibility of the SARS-CoV-2 Delta variant (B.1.617.2) is understood to be 40–60% higher than the Alpha variant (B.1.1.7) and almost twice as transmissible than previous circulating SARS-CoV-2 lineages[21,36-38], there is insufficient evidence to determine the effectiveness of these measures against the transmission of the Delta variant in-flight. Our investigation identified 3/9 (33%) arrival cases (B, O and T) with Delta infection transmitted SARS-CoV-2 to eight quarantine cases (F, G, H, I, Q, U, V, and W), compared to 1/7 (14%) of cases with other SARS-CoV-2 sublineages. Since April 2021, the Delta variant has spread rapidly and presents challenges to control of the virus globally.[39-42] Considering international borders around the world have begun to reopen to travel and tourism, more comprehensive studies into the transmission dynamics of SARS-CoV-2 variants on aircraft are needed.

This study has some limitations. Our case definition determines infection of a quarantine case to result from probable flight-associated transmission if a quarantine case was seated within the 2x2 area of an arrival case, and assumes validity of the current public health guidance for contact tracing of airplane passengers exposed to SARS-CoV-2. While other in-flight transmission studies[29, 32,2 4] report flight-associated cases spanned further than 3 rows, and up to 9 rows from an infectious case, they lack available data on passengers' individual use of masks. Since we did not re-interview cases for our investigation, we were unable to ascertain mask compliance and physical movement which may have been associated with transmission, including whether quarantine case K (cluster 2) was infected during the journey. However, from initial case interviews we can confirm that no cases had prior exposure to COVID-19, and we are confident that we ascertained all quarantine cases and therefore minimised selection bias.

In conclusion, this report describes transmission of SARS-CoV-2 on repatriation flights from India to Australia at a time of extreme incidence and consequent COVID-19 impact in India in the context of low vaccination coverage among passengers, and supports the value of genomic sequencing for transmission clusters. Our findings reinforce the need for strict infection control practices on board aircraft in addition to mandatory mask use, pre-departure testing, and robust quarantine processes.

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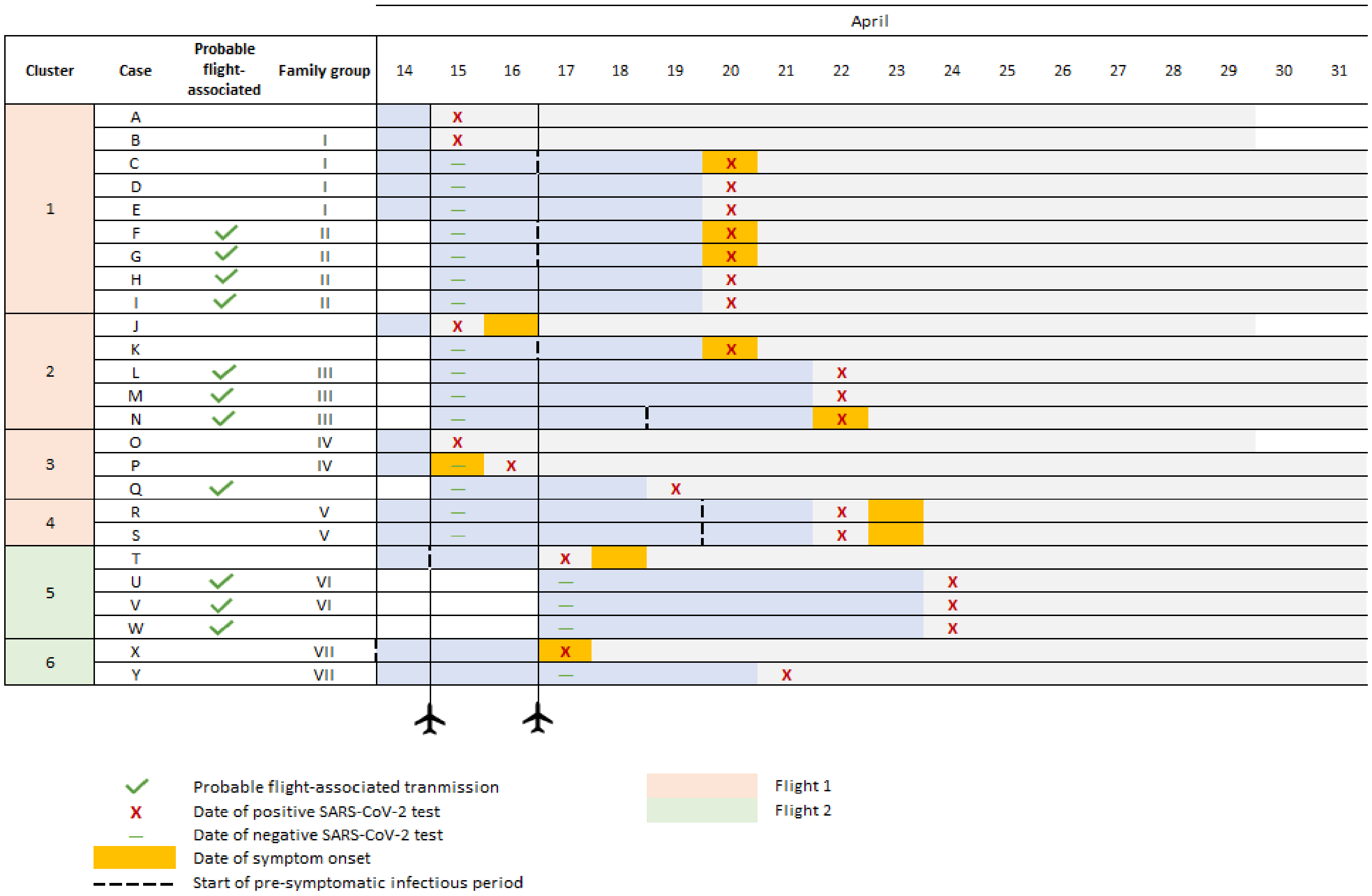

Cluster	Case	Probable flight-associated	Family group	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
1	A				X																
	B		I		X																
	C		I		—					🟨 X											
	D		I		—					X											
	E		I		—					X											
	F	✓	II		—					🟨 X											
	G	✓	II		—					🟨 X											
	H	✓	II		—					X											
	I	✓	II		—					X											
2	J				X	🟨															
	K				—					🟨 X											
	L	✓	III		—							X									
	M	✓	III		—							X									
	N	✓	III		—							🟨 X									
3	O		IV		X																
	P		IV		🟨 —	X															
	Q	✓			—				X												
4	R		V		—							X	🟨								
	S		V		—							X	🟨								
5	T						X	🟨													
	U	✓	VI				—							X							
	V	✓	VI				—							X							
	W	✓					—							X							
6	X		VII				🟨 X														
	Y		VII				—				X										

✓ Probable flight-associated tranmission
X Date of positive SARS-CoV-2 test
— Date of negative SARS-CoV-2 test
🟨 Date of symptom onset
- - - - - Start of pre-symptomatic infectious period

Flight 1
Flight 2

Figure 1. Clinical timeline SARS-CoV-2 genomic clusters in passengers from flight 1 from Chennai to Darwin, April 15, 2021, and flight 2 from New Delhi, to Darwin, April 17, 2021

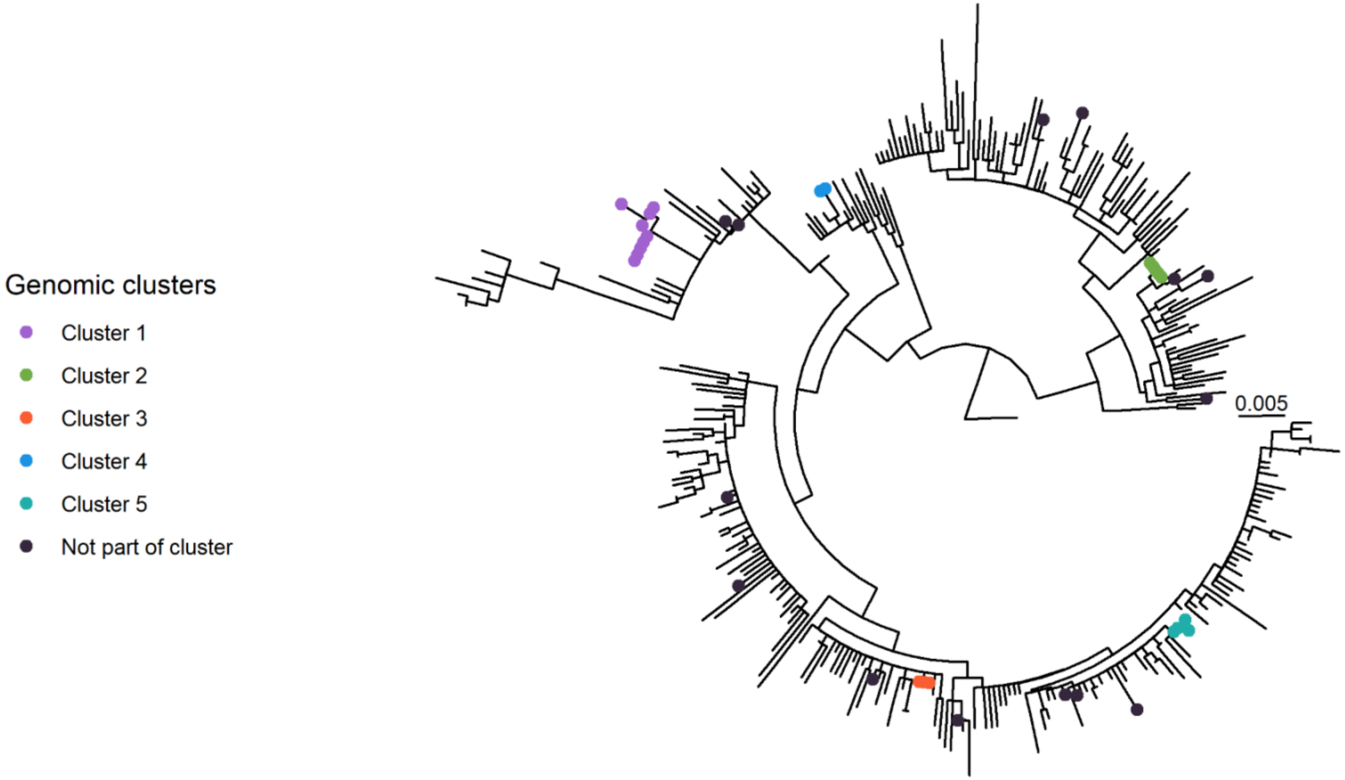

Figure 2. SARS-CoV-2 B.1.617 maximum likelihood phylogenetic tree including genomes from passengers with COVID-19 from flight 1 from Chennai to Darwin, April 15, 2021, and from flight 2 from New Delhi, to Darwin, April 17, 2021. The tree was rooted with the MN908947.3 reference genome, and the scale bar indicates substitutions/site

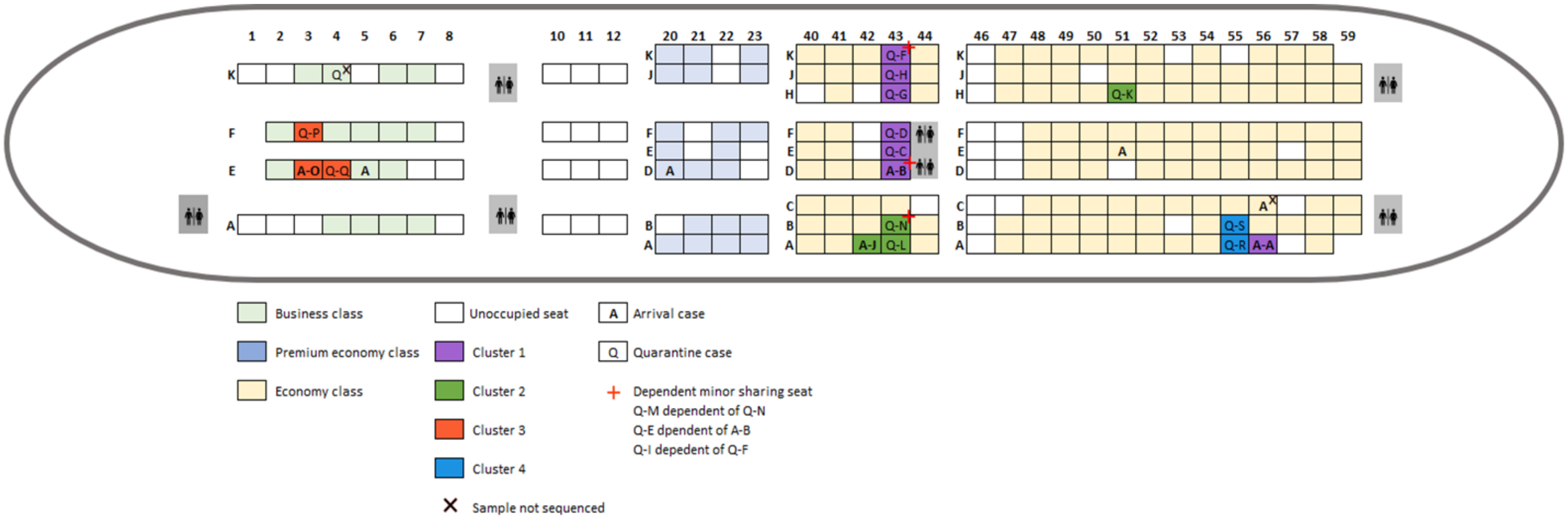

Figure 3. Seating plan and spatial distribution of arrival and quarantine cases of SARS-CoV-2 aboard flight 1 from Chennai, India, to Darwin, Australia, on April 15, 2021. Passengers are identified by cluster as determined by viral genome sequencing, and not associated with a cluster. Note that quarantine cases E and I and (cluster 1) and quarantine cases N (cluster 2) were minors sharing a seat with an adult.

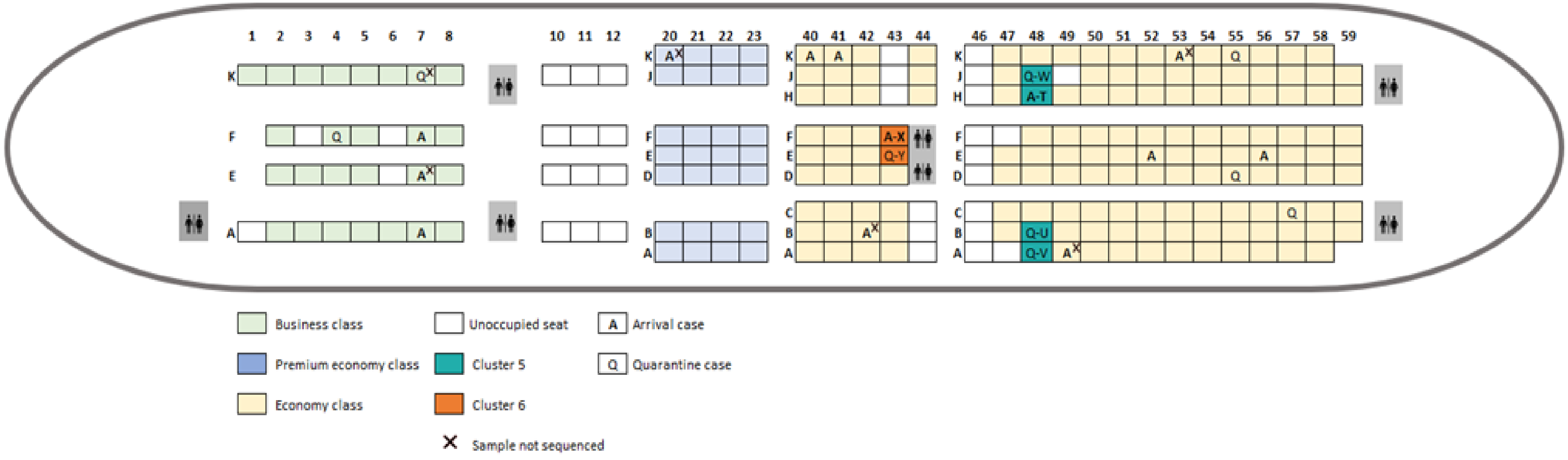

Figure 4. Seating plan and spatial distribution of arrival and quarantine cases of SARS-CoV-2 aboard flight 2 from New Delhi, India, to Darwin, Australia, on April 17, 2021. Passengers are identified by cluster as determined by viral genome sequencing, and not associated with a cluster.

Table 1. Detailed information of cases belonging to SARS-CoV-2 genomic clusters detected after flight 1 from Chennai, India, to Darwin, on April 15, 2021, and flight 2 from New Delhi, to Darwin, April 17, 2021

Cluster	Case	Age group (years)	Sex	Family group	Pango lineage	Ct value	Symptom onset date	Date tested positive	Vaccinated (Y/N)	Seat no. on flight
1	A	30–39	M	–	B.1.617.2	14.3	Asymptomatic	Apr 15	N	56B
1	B	40–49	M	I	B.1.617.2	15.6	Asymptomatic	Apr 15	N	43D
1	C	20–29	F	I	B.1.617.2	11.6	Apr 20	Apr 20	N	43E
1	D	1–5	F	I	B.1.617.2	11.6	Asymptomatic	Apr 20	N	43F
1	E	<1	M	I	B.1.617.2	12.2	Asymptomatic	Apr 20	N	43D
1	F	30–39	M	II	B.1.617.2	22.6	Apr 20	Apr 20	N	43K
1	G	10–19	F	II	B.1.617.2	18	Apr 20	Apr 20	N	43H
1	H	1–5	M	II	B.1.617.2	26.5	Asymptomatic	Apr 20	N	43J
1	I	<1	F	II	B.1.617.2	19	Asymptomatic	Apr 20	N	43K
2	J	20–29	F	–	B.1.617.1	12.4	Apr 16	Apr 15	N	42A
2	K	50–59	M	–	B.1.617.1	16.6	Apr 17	Apr 20	N	51H
2	L	1–5	M	III	B.1.617.1	22	Asymptomatic	Apr 22	N	42B
2	M	1–5	M	III	B.1.617.1	18.1	Apr 22	Apr 22	N	43B
2	N	30–39	F	III	B.1.617.1	20	Asymptomatic	Apr 22	N	43B
3	O	50–59	F	IV	B.1.617.2	14.9	Asymptomatic	Apr 15	Y	3E
3	P	60–69	M	IV	B.1.617.2	14.9	Apr 15	Apr 16	Y	3F
3	Q	10–19	F	–	B.1.617.2	11.4	Asymptomatic	Apr 17	N	4E

Cluster	Case	Age group (years)	Sex	Family group	Pango lineage	Ct value	Symptom onset date	Date tested positive	Vaccinated (Y/N)	Seat no. on flight
4	R	50–59	M	V	B.1.617.2	14.9	Asymptomatic	Apr 22	N	55A
4	S	60–69	F	V	B.1.617.2	14.9	Apr 22	Apr 23	N	55B
5	T	10–19	M		B.1.617.2	11.7	Apr 17	Arp 18	N	48C
5	U	30–39	M	VI	B.1.617.2	16.1	Asymptomatic	Apr 24	N	48B
5	V	30–39	F	VI	B.1.617.2	12.8	Not available	Apr 24	N	48A
5	W	1–5	M		B.1.617.2	24.5	Asymptomatic	Apr 24	N	48J
6	X	30–39	M	VII	B.1.1.7	10.9	Asymptomatic	Apr 17	N	43F
6	Y	40–49	M	VII	B.1.1.7	13.1	Asymptomatic	Apr 17	N	43E

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Chapter 3. Establishment of a surveillance system

COVID-Net: A national surveillance network for COVID-19 outbreaks in Australia, 2020

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Prologue

Organisation of this chapter

This chapter details my involvement in the establishment of COVID-Net from the initial planning phase from late March to 27 December 2020. The methods and results are divided into two parts and outline:

1. The establishment of the network against its aims.
2. A process evaluation conducted in October 2020 to ensure the network aims were being achieved efficiently and effectively.

The results include a manuscript approved for peer review publication that summarises all outbreak data collected by COVID-Net from 1 January to 27 December 2020.

Rationale

In March 2020, Australia detected a rapid increase in COVID-19 outbreaks among returning passengers from international cruise ships. At the national level, there was no standardised mechanism to collate and record information on the number and epidemiology of these outbreaks, which was required for national surveillance to inform national policy and response. To meet this need, the Australian Government Department of Health (DoH) established COVID-Net, a national surveillance network for COVID-19 outbreaks.

My role

I was involved in the establishment of COVID-Net from the development stage until the end of 2020. I worked with the data team at the DoH to build and pilot an external facing Research Electronic Capture (REDCap) online outbreak register to house outbreak data collected by COVID-Net. In the initial development phase, I contributed to establishing core data fields and outbreak definitions by conducting literature reviews and collaborating with key stakeholders in states and territories. I then created a data entry guide and a data dictionary for the register. Over the course of 2020, I collaborated with COVID-Net epidemiologists and national surveillance bodies to develop additional outbreak summary fields and enhanced data fields on outbreaks in health care settings. I attempted to align these fields with those already collected by states and territories in their outbreak investigations. I subsequently updated the data dictionary and maintained the register by routinely checking for data completeness and quality, highlighting inconsistencies and data quality issues. I also contributed to weekly network meetings and developed agenda items and presentation topics relevant to the epidemiology of COVID-19 outbreaks and investigations.

I conducted weekly analyses of COVID-Net data and prepared weekly COVID-Net surveillance reports. The reports prepared by myself and the COVID-Net team at the DoH were used to inform internal whole of government situational reports, public facing COVID-19 epidemiology and surveillance reports, responses to senate estimate questions, responses to queries from other departments and from the general public, and talking points for ministerial briefs.

I presented the outcome of this work in an oral conference presentation at the 2021 South Asia Field Epidemiology and Technology Network, Inc. (SAFTEYNET) videoconference on 8 September 2021.

Lessons learnt

This was my first experience collaborating with state and territories at the national level, for which I learnt a number of lessons. This project was the most challenging for me to complete due to the complexity associated with building a surveillance system in a very short period and adapting it as the situation changed during the peak of a pandemic. I gained an understanding of the role of the DoH in national surveillance, and I learnt about the importance of data sharing agreements required to underpin the development of any national surveillance system. While national legislation provides authorisation for the disclosure or use of notifiable disease data, it does not necessarily compel the disclosure of information from jurisdictions. While government relies on the use of such data to guide national response efforts, there are many sensitives to sharing data between state and territories and the DoH. These sensitivities include how shared data is collected, stored and used while maintaining strong security and privacy protections. They also include concerns about the publication of shared data that could be seen to be, or be misinterpreted as, ‘comparing’ performance of the state and territories. While engaging with state and territories it was extremely important to build trust in data sharing through transparency of how data collected by COVID-Net would be used to benefit the COVID-19 national response. This highlighted the importance of stakeholder engagement at all stages of system development.

Although I did not formally evaluate COVID-Net, I performed a process evaluation with key jurisdictional stakeholders in October 2020. Through this evaluation, I examined the various attributes of a surveillance system, for which I had learnt a lot about during the development of COVID-Net. The evaluation highlighted to me the need to balance system objectives with stakeholder priorities, a key lesson I will take forward in my epidemiology career.

Lastly, through the process of creating the COVID-Net database and subsequently analysing the data, I developed skills in establishing a REDCap database and online data entry mechanisms, data management (collecting, cleaning, storing, monitoring, and reviewing data) and R programming. I also learnt to interpret data in a way that could be easily communicated to a wide audience. I was then able use my skills in REDCap to support others in the department and to rapidly build a contact tracing database for the DoH contact tracing task force. At the beginning of the MAE I had no experience in database development, data management, or use of statistical software, so this was a major personal achievement.

Public health implications

Globally, the COVID-19 pandemic has required a rapid repurposing of established surveillance systems for COVID-19.[1] At the time of writing, I am unaware of any other countries that have designed and implemented a national surveillance network for COVID-19 outbreaks and clusters of this kind. Surveillance of outbreaks is necessary to monitor transmission of SARS-CoV-2 within the Australian context, to identify settings at greatest risk of transmission, and to monitor the effectiveness of public health interventions aimed at controlling transmission in those settings. At the time of writing, COVID-Net data is being used nationally to contribute to our understanding of the epidemiology of COVID-19 outbreaks, contributing to the evidence base for current and future public health policy. My manuscript documenting these outbreaks is currently under peer review by the international journal PLoS ONE as sharing knowledge is a key public health responsibility.

Communications

This project resulted in the following communications of finding:

- Recorded presentation South Asia Field Epidemiology and Technology Network, Inc. (SAFTEYNET) videoconference, 7–8 September 2021

MAE course requirements

This project meets the following core MAE activity requirements:

- Establish or evaluate a disease surveillance system or health information system
- Presentation at a national scientific conference
- Peer-reviewed publication

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I gratefully acknowledge the following people:

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Abstract

Introduction

In April 2020, in response to the novel coronavirus disease 2019 pandemic, the Australian Government Department of Health (DoH) established COVID-Net, a national surveillance network for novel coronavirus outbreaks. The aim of the network was to support jurisdictional capacity to capture surveillance data on outbreaks, facilitate national investigations into cross-border outbreaks, and conduct investigations into transmission of SARS-CoV-2 to inform policy and public health response.

Methods

COVID-Net was structured as a network of epidemiologists positioned in state and territory health departments, coordinated by a lead epidemiologist in the DoH National Incident Centre (NIC). Establishment of the network involved the development of a series of core and enhanced data fields for reporting, creation of a secure online electronic database to capture COVID-19 data nationally, and weekly information sharing meetings. In October 2020, I undertook a process evaluation of COVID-Net to ensure the network aims were being achieved efficiently and effectively. The evaluation consisted of a series of semi-structured interviews with jurisdictional Communicable Diseases Network of Australia (CDNA) and National Surveillance Committee (NSC) representatives.

Results

As at 27 December 2020, the COVID-Net outbreak register held data on 853 outbreaks linked to 13,957 confirmed cases, including information about the outbreak setting, duration, number of hospitalisations, and deaths. The network met weekly via videoconference to share information and approaches to COVID-19 outbreak investigation. COVID-Net epidemiologists also worked to improve understanding of the epidemiology of COVID-19 through contributions to applied research.

Conclusion

Establishing a national surveillance network during the early stages of a pandemic posed many challenges, including the recruitment of COVID-Net epidemiologists at a time of limited specialised human resource availability. In addition, the network lacked support from key jurisdictional stakeholders due to the perceived limited impact the network's findings would have on the immediate public health response. Despite this, the network achieved a number of its

primary objectives, including the capture of surveillance data on outbreaks of COVID-19 across Australia.

Introduction

COVID-19

On 31 December 2019, a cluster of pneumonia of unknown aetiology reported to be associated with a seafood market in Wuhan City, Hubei Province, China was notified to the World Health Organization (WHO) by the Wuhan Municipal Health Commission (WHO).[2] The causative agent was identified on 9 January 2020 as a novel coronavirus, subsequently known as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2).[2, 3] The virus spread rapidly across the country and cases were identified outside mainland China in Japan, South Korea, Thailand, and the United States of America by 20 January 2020. The coronavirus 2019 (COVID-19) outbreak was declared a Public Health Emergency of International Concern by the WHO on 30 January 2020 [4]. At this point, China had reported 7,711 confirmed and 12,162 suspected cases, and there were 83 cases in 18 other countries.[4] On 11 March 2020, due to the alarming levels of inaction globally, the WHO characterised the outbreak a pandemic.[4, 5] As of 27 December 2020, 191 countries had reported COVID-19 cases, with the number of cases globally exceeding 79 million, with more than 1.7 million deaths.[6] At this time Australia had reported 28,289 confirmed COVID-19 cases and 908 deaths.[7]

Clinical features

COVID-19 has an incubation period of around 5–6 days (range 1–14 days).[8] The predominant symptoms reported in cases are cough, sore throat, fatigue, and fever.[9, 10] While studies have reported that 18%–38% of people infected with SARS-CoV-2 do not develop symptoms, asymptomatic testing is generally not recommended and the true rate of asymptomatic infection is unknown.[11, 12] The majority of COVID-19 cases recover without clinical intervention; however, approximately 20% of global cases have required hospitalisation for more severe outcomes such as shortness of breath and pneumonia.[10, 13] In Australia the overall case-fatality rate (CFR) for COVID-19 is 3.3%.[14] The elderly and those with comorbid conditions are more likely to experience severe disease, and the CFR increases with age.[8, 14, 15]

Laboratory testing and diagnosis

Nucleic acid testing (NAT) using real time polymerase chain reaction (RT-PCR) is the primary diagnostic method for SARS-CoV-2.[8] Upper respiratory swabs of the deep nasal and oropharynx are recommended.[8] Serology can be helpful for the diagnosis of past infection, and is used to investigate suspected cases who were NAT negative or did not undergo NAT testing during the acute stage of illness.[8]

Transmission

Basic reproductive number (R_0) estimates for SARS-CoV-2 range from 2–4, and are similar to, or higher, than for severe acute respiratory syndrome and pandemic influenza virus.[8, 16] The predominant mode of human-to-human transmission of SARS-CoV-2 is via droplets and fomites from an infected person.[17] Airborne transmission of SARS-CoV-2 can occur when associated with aerosol-generating behaviours (i.e. sneezing, coughing, shouting) and high-risk aerosol-generating medical procedures.[8] Indoor and enclosed spaces where persons are in close proximity to each other and there is low airflow increases the risk of aerosol concentrations [18, 19]. These specific environments can create potential for superspreader events, where one infectious individual infects a large number of secondary cases.[20] Superspreader events may lead to rapid growth in case numbers and challenge efforts to control outbreaks.[18, 20, 21]

The infectious period of COVID-19 is still being determined; in Australia, for the purposes of contact tracing, cases are considered to be infectious from 48 hours prior to onset of symptoms.[8] However, the risk of transmission from symptomatic or pre-symptomatic cases is considered to be higher than from asymptomatic cases, as viral RNA shedding is higher at symptom onset.[8]

Preventative measures

Public health measures to lower the risk of SARS-CoV-2 infection to the individual include good hand and respiratory hygiene, in addition to physical distancing.[8, 22] The WHO recommends thorough hand washing with soap and water or using an alcohol-based sanitiser.[22] Good respiratory hygiene includes covering your mouth and nose when coughing or sneezing, and where possible, sneezing into the elbow or a disposable tissue, rather than into the hands. Maintaining at least a 1.5 metre distance between yourself and others reduces the risk of exposure to droplets.[23] Public gatherings and social gatherings are known to significantly increase the risk of the virus spreading.[23, 24]

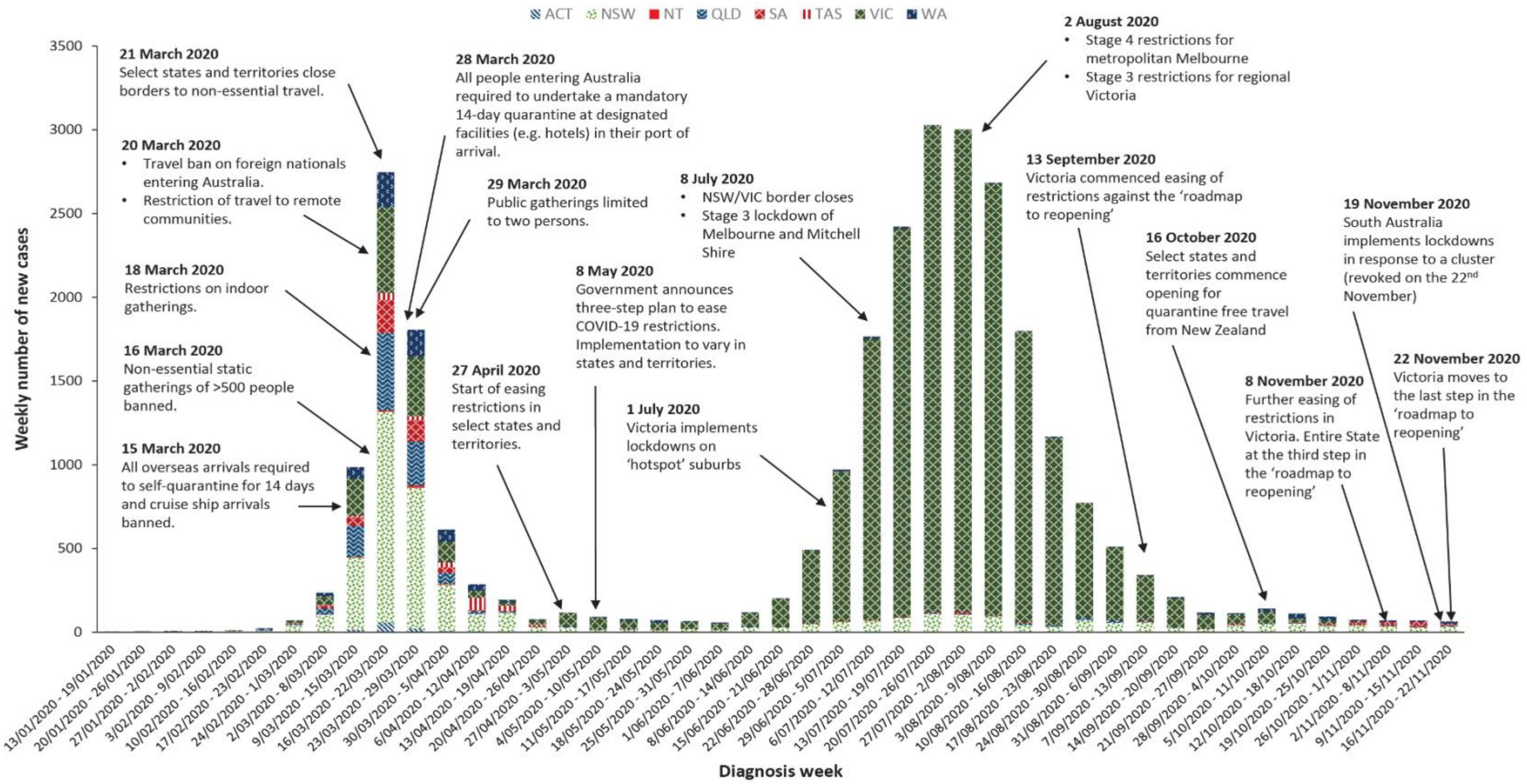
COVID-19 response in Australia

In Australia, the first case of COVID-19 was identified on the 25th of January 2020 in a man who had recently arrived from Wuhan province. [25]. The first epidemic wave of COVID-19 in Australia was characterised by cases arriving on international cruise ships and by air. This was followed by local transmission in settings where people congregate. In response, the Australian Government restricted international travel, and Australian state and territory governments instituted extensive non-pharmaceutical interventions, including lockdowns, case isolation, and tracing and quarantine of contacts. These measures are summarised in Figure 1.

From July to August 2020, the state of Victoria experienced a second wave characterised by an increase in locally acquired cases and community transmission that originated from a genomic cluster associated with a hotel used to quarantine individuals returning from overseas. From genomic and epidemiological data released by the Department of Health and Human Services in Victoria (Vic DHHS), we know that to 14 August 2020, 67% (3,594/5,395) of COVID-19 samples in Victoria tested were associated with the cluster.[26]

Public health importance

In Australia, COVID-19 is of significant public health importance. A variety of control measures were implemented early in the response and contributed to the very low numbers and CRF of cases in Australia when compared internationally.[6] On 10 February 2020, COVID-19 was made a nationally notifiable disease listed under the *National Health Security Act 2007*, which allows state and territory health departments to report cases to the National Notifiable Disease Surveillance System (NNDSS).[27] Since 15 March 2020, all federal, state, and territory governments enacted laws or made regulations designed to control the spread of SARS- CoV-2. As a human listed disease under the *Biosecurity Act 2015,* individuals must complete a mandatory quarantine in designated facilities for 14-days after returning to Australia from overseas.[8] In addition, biosecurity enforcement officers have authority to issue human biosecurity control orders that require people to provide their contact information and health details, restrict behaviour, and accept isolation from the community for specific period.



21 March 2020
Select states and territories close borders to non-essential travel.

20 March 2020
- Travel ban on foreign nationals entering Australia.
- Restriction of travel to remote communities.

18 March 2020
Restrictions on indoor gatherings.

16 March 2020
Non-essential static gatherings of >500 people banned.

15 March 2020
All overseas arrivals required to self-quarantine for 14 days and cruise ship arrivals banned.

28 March 2020
All people entering Australia required to undertake a mandatory 14-day quarantine at designated facilities (e.g. hotels) in their port of arrival.

29 March 2020
Public gatherings limited to two persons.

27 April 2020
Start of easing restrictions in select states and territories.

8 May 2020
Government announces three-step plan to ease COVID-19 restrictions. Implementation to vary in states and territories.

8 July 2020
- NSW/VIC border closes
- Stage 3 lockdown of Melbourne and Mitchell Shire

1 July 2020
Victoria implements lockdowns on 'hotspot' suburbs

2 August 2020
- Stage 4 restrictions for metropolitan Melbourne
- Stage 3 restrictions for regional Victoria

13 September 2020
Victoria commenced easing of restrictions against the 'roadmap to reopening'

16 October 2020
Select states and territories commence opening for quarantine free travel from New Zealand

19 November 2020
South Australia implements lockdowns in response to a cluster (revoked on the 22nd November)

8 November 2020
Further easing of restrictions in Victoria. Entire State at the third step in the 'roadmap to reopening'

22 November 2020
Victoria moves to the last step in the 'roadmap to reopening'

Figure 1. COVID-19 notifications in Australia by week of diagnosis and jurisdiction to 22 November 2020, with timing of key public health measures

Adapted [reprinted] from "COVID-19 Australia: Epidemiology Report 30" by COVID-19 National Incident Room Surveillance Team, 2020, Comm Dis Intell, 44, https://doi.org/10.33321/cdi.2020.44.91. Copyright 2020 by Commonwealth of Australia

Aim and objectives

This project describes the establishment of COVID-Net, a national surveillance network for COVID-19 outbreaks. COVID-Net's primary aims were to:

- Support jurisdictional capacity to collect national surveillance data on COVID-19 outbreaks.

The secondary objectives were to:

- Coordinate national investigations into multi-jurisdictional outbreaks (MJOs) of COVID-19.
- Conduct investigations into transmission of SARS-CoV-2 to inform policy and public health response.

Methods

Scoping and design

The absence of a pre-existing surveillance system for COVID-19 outbreaks necessitated the development of a network able to operate within the capacity and legislative framework of Australia's de-centralised public health system. At the start of the pandemic, the Communicable Diseases Network of Australia (CDNA) — which provides national public health co-ordination and leadership for the prevention and control of communicable diseases — and the DoH NIC were aware of the need to estimate the frequency of outbreaks due to the rapid number of cases associated with international arrivals occurring across the country.

The design of OzFoodNet, Australia's highly successful surveillance network for foodborne disease, was considered a model that could be implemented rapidly within state and territory health departments. In addition, jurisdictions were already familiar with the OzFoodNet model, that consisted of a network of epidemiologists embedded in each state and territory health department, coordinated by an epidemiologist based in the DoH. The COVID-Net epidemiologists would be directly funded by the DoH to provide additional support to jurisdictions for COVID-19 outbreak investigation and reporting, while meeting COVID-Net's aims and objectives.

The development of the network involved engagement with relevant stakeholders, developing and applying case definitions, and developing outbreak data fields and a database to store the data.

Stakeholders

During the development and implementation of COVID-Net, it was necessary to consult all relevant stakeholders (Table 1).

Table 1. COVID-Net Stakeholders and their roles and responsibilities

Stakeholder	Role	Responsibility
DoH (National Incident Centre)	COVID-Net coordination and managing the funding arrangements of the network	• COVID-Net coordinator and administrator • CDNA and National Surveillance Committee liaison • Data and report dissemination • Data custodian • Recruitment of epidemiologists
CDNA COVID-19 Jurisdictional Expert Group (JEG)	Oversight of the COVID-Net and coordinate between the DoH and departments of health	• COVID-Net oversight • Control over relevant jurisdictional data • Review network surveillance data • Network recommendations to AHPPC
State and territory Departments of Health	Coordination of state-based response to outbreaks	• Sate-wide surveillance • Outbreak investigation • Data collection and owners • Reporting to COVID-Net
National Surveillance Committee (NSC)	Sub-committee of CDNA, provides oversight of national surveillance priorities	• COVID-Net oversight and recommendations • Control over relevant jurisdictional data • Review network surveillance data

Legislation for surveillance

COVID-Net was established under provision of surveillance legislation for a notifiable infectious disease. The *National Health Security Act 2007* supports the sharing of information about significant public health events and authorises the disclosure of personal information when required to support a national or international response effort.[27] The Act enables State and Territory health authorities to exchange public health surveillance data with the DoH.[27]

COVID-Net definitions

Case definition

COVID-19 surveillance case definitions are defined in the COVID-19 Series of National Guidelines (SoNG) and are under continuous revision with improved understanding of the virus.[8] The current version of the SoNG is available from the Department of Health website at: https://www1.health.gov.au/internet/main/publishing.nsf/Content/cdna-song-novel-coronavirus.htm.[8] As of 27 December 2020, cases of COVID-19 were classified as "suspected", "probable", and "confirmed" based on symptoms, epidemiology, and testing results. A "close-contact" of a confirmed case is known to be at increased risk of exposure to SARS-CoV-2 due to the mode in which the virus transmits.

Outbreak definition

Globally, the definition of a COVID-19 outbreak is relative to local context. In Australia, the definition also varied between jurisdictions throughout 2020. For COVID-Net, we adopted a sensitive definition, similar to that used in identifying gastrointestinal outbreaks. An outbreak was defined as:

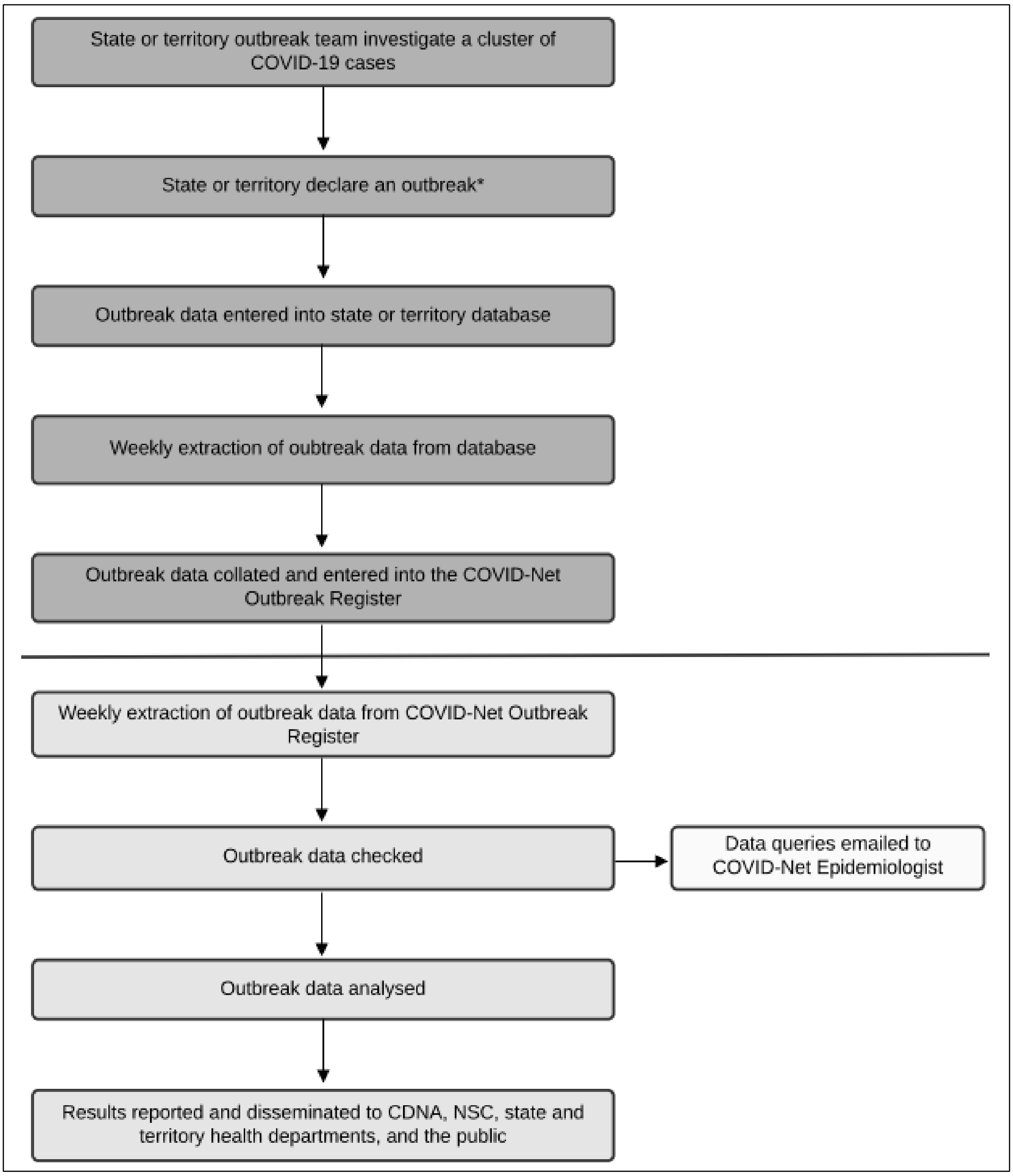
- Two or more confirmed cases (who did not reside in the same household) among a specific group of people within 14 days and/or over a specific place where illness was associated with a common source.

Outbreak register

The development of an outbreak register proceeded in two distinct phases (Table 2). A summary of the reporting framework is outlined in Figure 2.

Table 2. Development of the COVID-Net outbreak register, 2020

Phase	Aim	Details
Phase 1: April – June 2020	To facilitate rapid uptake and collection of data (optimising timeliness and acceptability)	1. De-identified outbreak information was entered into a Microsoft Excel spreadsheet template by COVID-Net epidemiologists and emailed to the "COVID-Net inbox". 2. Outbreak reports were merged in Excel and stored on a secure drive at DoH.
Phase 2: July – September 2020	To optimise stability, security, and data quality, and reduce data manipulation load (without sacrificing acceptability).	3. Creation of a secure web-based REDCap (Research Electronic Data Capture) register. 4. COVID-Net Epidemiologists made external users of the register and entered and managed data directly.



**Some state and territories would also enter cluster data before an outbreak was declared*

Figure 2. COVID-Net flow of data and reporting from the jurisdiction to the NIR, and on to stakeholders

Data collection

Data were reported weekly to the COVID-Net outbreak register across three REDCap electronic data collection instruments. In the register, data contained in the three instruments were compiled into a single outbreak record. The data dictionary is provided in Appendix A. A unique outbreak reference number was assigned to each record by the reporting state and territory. This number correlated to the case identification number in the existing state-based notifiable disease data management system. For confirmed cases linked to an outbreak, the same outbreak reference number was transmitted in the 'outbreak reference number' field to the National Notifiable Disease Surveillance System (NNDSS), although this field was not consistently completed by all jurisdictions.

Instrument 1: Weekly report

The weekly report instrument consisted of 16 core data fields that were revised over the course of 2020. Appendix A summarises the fields as at 27 December 2020. COVID-Net epidemiologists were consulted to identify a minimum data set that was consistent across state and territories. Outbreaks were reported as *open* — defined as those where a new epidemiologically linked case was identified in the previous 14 days —or *closed*.

Fields were intended to be dynamic and flexible to adapt to national surveillance needs. In November 2020, we revised and expanded the 12 outbreak settings to 13 settings, with 56 sub-settings, to better define where outbreaks were occurring. These settings were applied to existing outbreaks retrospectively.

Instrument 2: Outbreak summary

The outbreak summary instrument consisted of 24 enhanced fields (Appendix A) that were added to the register in late August 2020. The fields were intended to be provide jurisdictions with a standardised data set that when considered with Instrument 1, provided a complete summary of the outbreak. The fields were made optional because they were outside the scope of what was required for national surveillance purposes. The instrument was intended to be completed retrospectively once an outbreak was closed and data could be reconciled.

Instrument 3: Enhanced surveillance of outbreaks in health care settings

A supplementary instrument for outbreaks in health care settings consisted of 13 enhanced fields (Appendix A) that were added to the database in early November 2020. At the time, outbreaks in health care settings were common, even when community transmission was relatively low. Over half of COVID-19 cases in health care workers were estimated to have been acquired in a health care setting, and the Chief Medical Officer of Australia advocated for COVID-Net to collect these enhanced fields for the purpose of understanding the risks of SARS-CoV-2 infection for different types of health care workers.[28, 29]

COVID-Net Process Evaluation and surveillance system attributes

A formal evaluation of COVID-Net was not undertaken as this was not possible within the timeframe of my MAE. In October 2020, I was a major contributor in a process evaluation of COVID-Net to ensure the network aims were being achieved efficiently and effectively. The evaluation consisted of a series of semi-structured interviews with CDNA and NSC representatives, and surveillance managers in all states and territories. The evaluation was intended to be formative and provide in-depth information on the acceptability and usefulness of the network. The information generated from the process evaluations were used to guide the DoH in how to adapt and improve COVID-Net in 2021.

I used the Centre for Disease Control's necessary attributes for a surveillance system[30] to guide the evaluation. The attributes I discussed were usefulness – the ability of the system to contribute "to the prevention and control of adverse health related events, including an improved understanding of the public health implications of that event"[30], simplicity – refers to "both its structure and ease of operation"[30], sensitivity – refers to the ability for the system to detect outbreaks, representativeness – refers to the ability for the system to "describe the occurrence of the health related and its distribution over time and its distribution in the population by place and person"[30], acceptability – reflects "the willingness of persons, and organisations to participate in the system"[30], data quality – refers to the completeness and validity of the data recorded in the system, and stability – refers to "the reliability (i.e. the ability to collect, manage, and provide data properly without failure) and availability (the ability to be operational when it is needed)" of the system.[30]

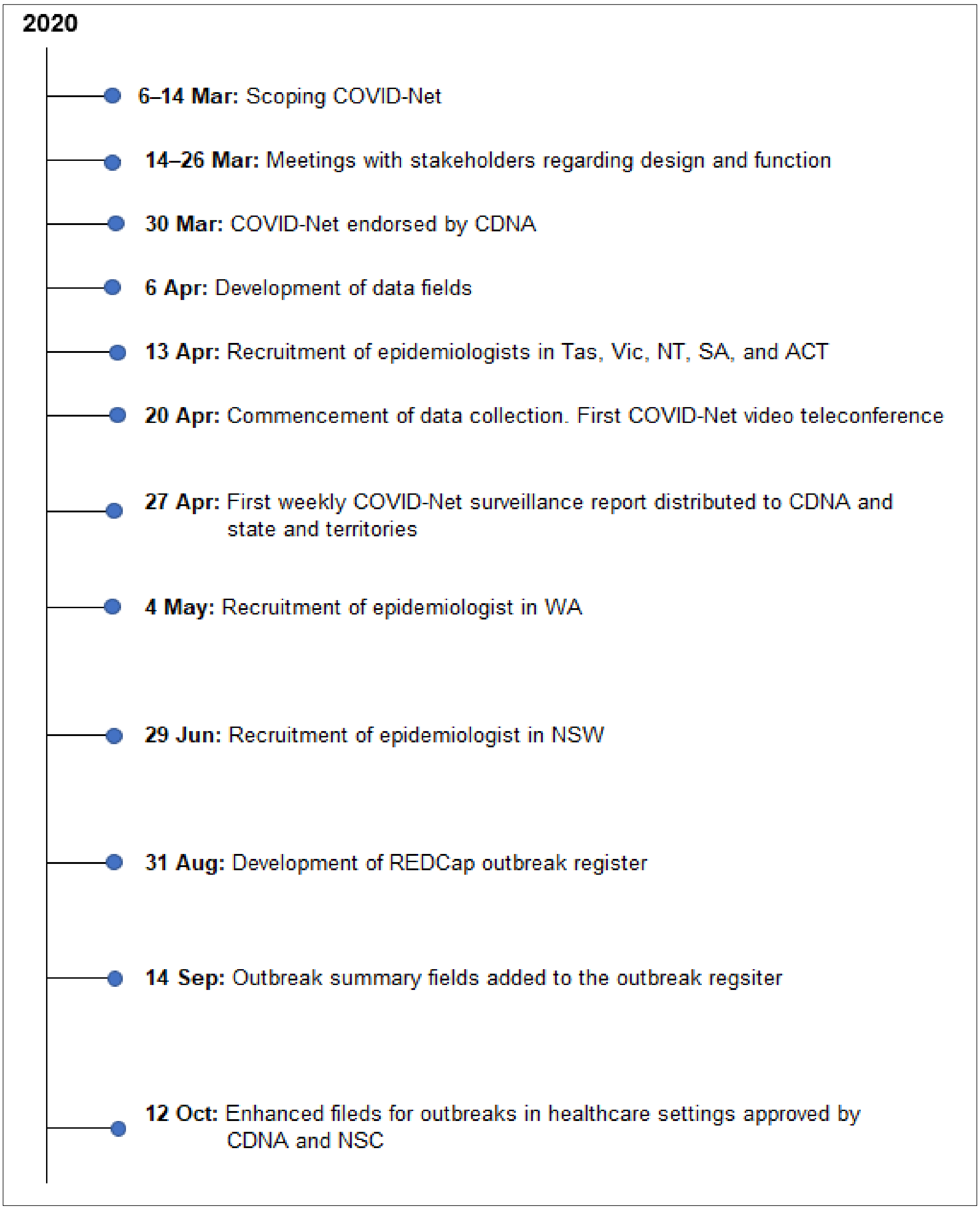
Ethical considerations

COVID-Net was conducted under the *National Health Security Act 2007* in response to a public health emergency. The Australian National University Human Research Ethics Committee under protocol 2017/909 provides a waiver of consent for Master of Applied Epidemiology students for surveillance projects.

Results

Timeline

COVID-Net was proposed by the DoH in late March 2020. The timeline for the establishment of surveillance activities is shown below in Figure 3.



2020

- **6–14 Mar:** Scoping COVID-Net
- **14–26 Mar:** Meetings with stakeholders regarding design and function
- **30 Mar:** COVID-Net endorsed by CDNA
- **6 Apr:** Development of data fields
- **13 Apr:** Recruitment of epidemiologists in Tas, Vic, NT, SA, and ACT
- **20 Apr:** Commencement of data collection. First COVID-Net video teleconference
- **27 Apr:** First weekly COVID-Net surveillance report distributed to CDNA and state and territories
- **4 May:** Recruitment of epidemiologist in WA
- **29 Jun:** Recruitment of epidemiologist in NSW
- **31 Aug:** Development of REDCap outbreak register
- **14 Sep:** Outbreak summary fields added to the outbreak regsiter
- **12 Oct:** Enhanced fileds for outbreaks in healthcare settings approved by CDNA and NSC

Figure 3. Timeline of the development of COVID-Net surveillance activities, 6 March – 12 October 2020

Recruitment and jurisdictional participation

All state and territories agreed to participate in COVID-Net in March 2020. However, initial recruitment of epidemiologists was significantly impacted by the first wave in COVID-19 cases in late March 2020 (Figure 3). State and territories were required to increase capacity of their public health workforces to manage the large volume of contact tracing required to be undertaken by public health units. New South Wales (NSW) lacked the time and capacity to recruit to the position until June 2020 and were unable to refill the position when the epidemiologist left in early September. Smaller states such as Tasmania (Tas) had difficulty recruiting skilled staff who were not already working on the COVID-19 response. Instead, the Tasmanian Department of Health and Human Services (DHHS Tas) supported the COVID-Net role through other epidemiologists within the department.

Three jurisdictions — Western Australia (WA), Northern Territory (NT), and Queensland (Qld) – were the only states able to retain COVID-Net epidemiologists throughout 2020. Given funding for COVID-Net was not guaranteed past 2020, long-term contracts for epidemiologists could not be offered. Consequently, the network had difficulty retaining positions which affected the representativeness of the network by all states and territories. During the second wave (from June – December 2020), South Australia Health (SA Health) and DHHS Vic were unable to replace epidemiologists who left the positions in July and October respectively. These departments allocated designated persons to be the COVID-Net focal point and continued to report mandatory data.

Weekly videoconference

The first COVID-Net meeting was held on 21 April 2020. The network continued to meet weekly via videoconference to share resources and information, including operational site and situational updates, outbreak investigation protocols, lessons learnt, and updates of applied research projects being undertaken.

Data collection

REDCap provided a software platform that supported flexible data collection through an online web browser. The interface was intuitive to use, and data fields could be easily added or altered to adapt to changing information needs. By exporting data before changes were made, the data could be re-entered using the import feature. The logging function meant there was not the risk inherent in using Excel of losing historical data that was overwritten. I was responsible for designing and developing both the outbreak register and data specifications. REDCap was only accessible by created users, and the design of the register enabled each epidemiologist to enter, access, and view their own data through a secure data access group. Tas and the Australian Capital Territory (ACT) were already using REDCap for COVID-19 case contact tracing. In the development stage I consulted with epidemiologists in ACT and Tas to pilot the database with dummy data. Compared to Microsoft Excel, they found REDCap to be a stable platform that increased both simplicity and efficiency of reporting.

During 2020, state and territories made considerable efforts to improve the timeliness of contact tracing and case-based notification systems. NSW and Vic experienced challenges in entering data into REDCap due to the lack of capacity to learn an additional system in the absence of a dedicated COVID-Net human resource. This resulted in both states reporting data in a comma-separated values (CSV) file extracted from their existing data management system. I then recoded the data to the raw values automated by the REDCap codebook and imported back into the register. Data import is a useful tool in REDCap that eliminates errors associated with manual data entry.

While I worked closely with COVID-Net epidemiologists to develop a standard dataset with clear definitions, there were inconsistencies in the data reported by jurisdictions due to the different ways in which outbreaks were investigated and cases defined. For example, Vic linked all cases to the exposure site of the index case and were unable to separate the *primary* versus *associated* cases of an outbreak. Although we attempted to standardise definitions, local interpretations were made in the context of each jurisdiction’s COVID-19 response and a single definition was not appropriate. Therefore, for this example, there was no one correct method for defining when one outbreak was over and the other began (i.e. when a secondary case in one outbreak becomes the index case in a separate outbreak).

Data Completeness

I did not formally evaluate the outbreak register for data quality against the CDC guidelines (29), however through managing the data I routinely inspected it for quality and completeness. The instruments were designed to maximise completeness through use of the “mandatory fields” option to force a response. In addition, responses were formatted to a field type (such as a drop-down box or tick box) that required a single response to improve data quality. Data quality rules were also applied to free text fields to force appropriate responses (i.e. numeric, date, maximum length etc.).

While the mandatory data fields were generally consistently completed by all state and territories, there were instances when jurisdictions were unable to provide specific data. For example, NSW were unable to provide hospitalisation data for outbreak cases. While the optional fields were poorly completed, this was acceptable since they were unable to be easily completed by jurisdictions who had different files captured in their state-based data systems.

At the time of writing, no enhanced fields for outbreaks in health care settings were completed. During the second peak of COVID-19 cases, surveillance of health care workers was highly sensitive. While the national guidance at the time recommended testing of all staff with any fever or symptoms of acute respiratory illness, it was not mandated by jurisdictions, and some hospitals had failed to set up enhanced surveillance of health care workers. In May 2020, an occupation field was added to the NNDSS COVID-19 dataset and included the option of a 'Healthcare worker', as defined as an individual who works within a hospital or other health care setting (including primary and community care) and has direct or indirect contact with patients or infectious materials (such as a doctor, nurse, orderly, paramedic, laboratory technician, pharmacist, administrative staff, or cleaner). There were jurisdictional variations in the definition of a health care worker, and overall, there were poor levels of completeness of these fields in the NNDSS. In addition, NSW and Vic had already published reports containing data on infections in health care workers intended to increase understanding of the virus and how it can spread within healthcare settings. Due to the sensitivity of the data and the perception of reporting duplication from those jurisdictions reporting this data there was an overall unwillingness to report these enhanced fields to COVID-Net.

Analysis and Dissemination

From 27 April 2020, COVID-Net outbreak and surveillance reports were submitted to the CDNA on a weekly basis for noting (Appendix B). As of 15 November, the weekly surveillance reports were extended to fortnightly reports due to decreased incidence of COVID-19 outbreaks across states and territories.

COVID-Net data were analysed on a weekly basis using standardised R scripts I had developed with the COVID-Net team. The representativeness of outbreak data to reflect all jurisdictions was dependant on timely reporting. This was not always possible during the first and second waves and often the picture of where outbreaks were occurring nationally was incomplete. A COVID-Net surveillance report was generated and disseminated back to jurisdictions for internal departmental distribution, to CDNA, and to NSC. Together with the COVID-Net team at the DoH, we improved timeliness of reporting by automating surveillance reports in R Markdown.[31]

R Markdown is a formatting syntax that allows a document to be generated that includes both text content as well as the output from embedded R code chunks within the document.

COVID-Net data were used to support other national surveillance activities through contributions to: Whole of Government COVID-19 Situational Reports; NIC COVID-19 Epidemiology Reports; the Pandemic Health Intelligence Plan used to support the Australian Health Protection Principal Committee (AHPPC) decision-making about COVID-19;, and ad-hoc requests for outbreak data from policy groups and the DoH executive and Minister’s office. Data collected by COVID-Net were also able to be publicly requested through the Department of Health’s Data Access and Release policy [32].

A manuscript awaiting peer review publication summarises all outbreak data collected by COVID-Net between 1 January and 27 December 2020 (Appendix C).

COVID-Net Process Evaluation

The evaluation sought the perspectives of participants on the aims and objectives of COVID-Net and whether the system had met these.

Overall, 7/8 jurisdictions were strongly supportive of COVID-Net’s aims and objectives. Participants cited benefits such as: cross-jurisdictional sharing of information and processes; cross-jurisdictional support for outbreak response; and strengthening of connectedness with the DoH. Although COVID-Net was not required nor had the opportunity to coordinate national multi-jurisdictional outbreak (MJO) investigations of COVID-19, participants considered this a valuable role for the network going forward. While coordinated investigations into foodborne disease outbreaks were recognised within the scope of OzFoodNet, this network was built on a high level of trust over a long period of time, and clear guidelines had been established to assign roles and functions during an investigation. The failure of COVID-Net to meet this aim was therefore not unexpected given the short time frame in its development.

In 6/8 jurisdictions the COVID-Net epidemiologists integrated well into existing COVID-19 epidemiology and surveillance teams. Larger jurisdictions such as NSW, Vic, and Qld reported an overlap in the role and responsibilities of the COVID-Net epidemiologist and other epidemiologists working on COVID-19 outbreaks. The overlap in roles was unavoidable since most epidemiological work in state and territories were focused on outbreaks. This was largely a reflection of the timing of the response, since it was not practical nor desirable for there to be a single epidemiologist working on outbreaks and learning the skills required of the position. A separation of the COVID-Net epidemiologist role was experienced in smaller jurisdictions— such as the NT— where the position was highly valuable since it doubled capacity of the epidemiology team. Although integration of the position worked best if the epidemiologist was known to the jurisdiction previously, this circumstance gave potential for the position to support multiple roles in the surveillance team because of prior knowledge of local operating procedures and processes. The extent and nature of epidemiological support to the local site varied and became problematic in instances when the epidemiologist was diverted from their COVID-Net responsibilities to support other work.

One of the weaknesses of the COVID-Net establishment process was a lack of initial engagement with CDNA and NSC in setting clear and specific surveillance objectives. Key NSC stakeholders challenged COVID-Net's role within national surveillance and were very concerned that collected data would be used for research objectives rather than for public health action. Furthermore, in some jurisdictions, undertaking epidemiological investigations into SARS-CoV-2 transmission was not desirable or feasible because it detracted from immediate response efforts. Others were of the opinion the role should focus on improving data quality of COVID-19 enhanced data fields in the NNDSS and using these to infer the required data. However, the relevant fields (e.g. Outbreak Reference ID) also had poor levels of completeness and they were unable to identify risk factors that contributed to spread of an outbreak.

The process evaluation was used as an opportunity to develop the future working agreements for COVID-Net epidemiologists operating under secondment arrangements from the DoH. At the time, this operational model for employment had several limitations. First, short-term contract arrangements meant it was difficult to recruit and retain qualified epidemiologists. Second, there was less flexibility to easily share information due to legalities of access to, and reporting from, jurisdictional data systems. Instead, participants indicated they were supportive of a National Partnership Agreement model, which would provide jurisdictions with the funding to hire someone themselves and overcome these limitations. Formalising epidemiologists' roles and responsibilities was also identified to be useful as it would allow jurisdictions to define how performance indicators for epidemiologist would be met.

Discussion

COVID-Net reported outbreaks across Australia, including information about the outbreak setting, duration, and severity of cases. The network met weekly via videoconference to share information and approaches to COVID-19 outbreak investigation, and COVID-Net epidemiologists worked to improve understanding of the epidemiology of COVID-19 through contributions to applied research. As at 27 December 2020, COVID-Net met two of its aims;

supporting jurisdictional capacity to collect national surveillance data on COVID-19 outbreaks and conducting investigations into transmission of SARS-CoV-2.

Usefulness

COVID-Net was useful because it provided operational information that was not previously available to the Australian Government. Surveillance of outbreaks informed understanding of transmission dynamics in Australia relative to national and jurisdictional interventions. The frequency, setting, size, duration, and severity of outbreaks nationally are now summarised in weekly surveillance activities. These data provide insight into where outbreaks were occurring nationally and the highly affected settings. Given a large proportion of outbreaks occurred in four settings, this data may be used by workplaces and industry, and the government, in the development of risk mitigation policies. Now COVID-19 vaccination has begun, the network should plan for future surveillance activities to prepare for monitoring transmission dynamics within the Australian population. Robust outbreak investigations may indicate groups with lower vaccine coverage and will assist with estimating vaccine effectiveness.

Multi-jurisdictional outbreaks (MJOs) of COVID-19 occurred in 2020, and investigations require a rapid and coordinated response. The usefulness of COVID-Net would be increased if it strengthened capabilities to coordinate MJOIs. For this objective to be met, COVID-Net should develop clear operational guidelines that clearly state roles and responsibilities of the NIC and jurisdictions in the event of an MJO. In addition, the MJOs would require the endorsement and guidance of CDNA to proceed. Regular and effective communication between COVID-Net epidemiologists, CDNA, and relevant stakeholders involved in the response would be essential to facilitate timely and appropriate contact tracing procedures, transfer of information between jurisdictions, and for reporting.

Simplicity

The dynamic nature of COVID-19 meant that outbreak classifications and types of information collected by the network were continually reviewed. This was a complex process because it involved review of current literature, consultation from epidemiologists and public health experts, and clearance from CDNA before changes could be implemented. On some occasions, this required multiple reviews before changes could be agreed upon, and these processes created an administrative burden on the network.

In the initial phase, reporting outbreak data via Excel was the simplest way to provide data to COVID-Net. While the online outbreak register optimised data collection because it reduced time spent on editing and transferring data, it did require familiarisation with REDCap. While this was not difficult, it did take time that exceeded capacity in some jurisdictions without a dedicated

COVID-Net resource. For the COVID-Net team in the NIC, the register allowed data to be easily and securely stored, and managed. The R Markdown script developed for weekly surveillance reporting was technically difficult without familiarity with R programming language, however, once set up the benefits of this function were the accuracy in its output and efficiency in reporting by following a few simple steps.

Flexibility

REDCap as a software platform for the outbreak register allowed flexibility in adapting to changing information needs. While the components of the register themselves were flexible to change, new fields were required to be cleared through several different bodies. While not a function of the system itself, this reduced the reduced flexibility for making changes as it contributed additional time, personnel, and allocated funds. Like any national system, these processes were designed to maintain uniformity to support best practice for surveillance of communicable diseases. Therefore, improving flexibility of this process was not feasible or appropriate.

Data quality and representativeness

The COVID-Net model as a surveillance network was designed to maximum representativeness of outbreak data nationally. Data quality varied by jurisdiction and was dependent on COVID-Net epidemiologists to facilitate data collation and reporting. The network was also reliant on the quality of information collected during the outbreak investigation and available for extraction in the existing state data management system at the time of reporting. Therefore, data reported to COVID-Net was not always representative of the current situation in jurisdictions if their own data was not complete. In addition, these data collections were not often retrospectively updated, so data was representative of a certain point in time

As discussed previously, there was potential for variations in the classification of outbreaks, however where possible, COVID-Net definitions ensured data was consistent and comparable. While data validation rules improved data quality of free text fields, the network would benefit from a formal evaluation of ‘blank’ or ‘unknown’ responses to items. To reduce the reporting burden, both mandatory and optional fields should be reviewed and for their utility.

Acceptability

A key failure by COVID-Net was the lack of development of operational and governance frameworks early in the response. Limited engagement with stakeholders to establish such frameworks and set surveillance priorities were identified as key contributing factors limiting the acceptability of the network in selected jurisdictions. This limitation affected other attributes of the system such as representativeness, stability, and data quality — reflecting the unwillingness of some jurisdictions to participate in COVID-Net, while others became increasingly disengaged. A formal evaluation of COVID-Net should focus on the acceptability of the network with key stakeholders, and future priorities of the network must be set in collaboration with surveillance bodies such as CDNA and NSC.

Since each jurisdiction managed its pandemic response its own way, meeting national reporting requirements were often not necessarily in the interest of state and territory's COVID-19 response. While COVID-Net epidemiologists participated in applied research projects, such as coordinating investigations into transmission of SARS-CoV-2 in health care settings and on airplanes, it was unfeasible for some sites to participate on top of existing workloads. In addition, some stakeholders considered these activities to be largely research based rather than informing the immediate public health response, limiting the acceptability of the network in these jurisdictions. The enhanced field for outbreaks in health care settings struggled to gain endorsement at NSC due to this reason.

Sensitivity

Care must be taken when interpreting the sensitivity of COVID-Net since this attribute has not remained constant over time. As understanding of SARS-CoV-2 has increased, there were changes to public health guidance around diagnostic testing and contact management, which likely improved case ascertainment and increased the sensitivity of state-based systems to detect outbreaks. Due to the infectiousness of SARS-CoV-2 and asymptomatic spread, Vic and Qld moved to the presence of a single case in a high risk setting as an outbreak definition. Higher rates of screening of staff and residents in certain high-risk settings such as in hotel quarantine and aged care inevitably improved outbreak detection in these settings, resulting in a bias towards detecting more cases and outbreaks. A review of the COVID-Net outbreak definition is therefore recommended.

In addition, COVID-Net as a surveillance network relied on the ability of public health departments to investigate epidemiological links between the cases. The more widespread use of genomics over the pandemic period has no doubt improved jurisdictional capacity to link cases to outbreaks, including the ability to monitor changes in transmission chains.

Timeliness

COVID-Net surveillance reports were disseminated to stakeholders in a timely fashion, to allow for the network to adapt to the needs of its stakeholders and respond to comments or suggestions to make the reports more useful. While stakeholders agreed they were useful for monitoring outbreak trends and effectiveness of control measures, the weekly reports had limited impact on the immediate response. Furthermore, while the adaptability of COVID-Net to changing information needs, the process for change were often slow as they required consultation with all jurisdictions and surveillance committees.

Stability

The COVID-Net register as a data system was stable, secure, and accessible from anywhere with Internet access. In the NIC, R scripts were saved within the COVID-Net R project to maintain accessibility for the team. The system of data entry and transfer was immediate and stable but relied on a COVID-Net epidemiologist entering data. The stability of the network was impacted by late recruitment of epidemiologists during the first wave followed by poor retainment during the last half of 2020, while poor acceptability in some jurisdictions meant it was not stable at all. The network was not stable in certain jurisdictions that did not support it. A comprehensive assessment of the network's stability should be reviewed alongside its impact in 2020 and should involve a specific assessment of working arrangements for epidemiologists that ensure longevity of the position.

Conclusion

COVID-Net was developed in response to a surveillance need identified during the 2020 COVID-19 pandemic response. Although the COVID-Net model allowed for rapid and flexible information sharing and data collection, the network struggled to establish strong relationships that fostered collaboration between key stakeholders and jurisdictions. If the network were to continue, concentrated efforts should be made by the DoH to collaborate closely with CDNA and NSC to clearly define and formalise the aims and objectives of COVID-Net and establish agreed operational and governance frameworks, and act on suggested recommendations to strengthen key attributes of the network. If maintained and strengthened, COVID-Net would be ready to support the response to any future pandemics.

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Appendix A – COVID-Net Outbreak Register data fields

Instrument 1: Weekly report

Outbreak reference number
Jurisdiction

Multi-jurisdictional outbreak
Multi-jurisdictional outbreak reference number

Outbreak setting
Description of outbreak
Place of acquisition of the primary case

Specimen collection date of first case
Specimen collection date of the last positive case

People exposed
Primary cases (including probable)
Associated cases (including probable)

Hospitalisation
ICU
Died

Comments

Instrument 2: Outbreak Summary

Date investigation commenced
Investigation lead

Index case identification number

Case definition

Cases interviewed
Close contacts
Close contacts followed-up
Close contacts tested for COVID-19
Close contacts positive

Date of onset of first case
Date of onset of last case

Median age

Age range (min)
Age range (max)

Males
Females
Gender unspecified

Confirmed cases (primary & associated)
Probable cases (primary & associated)

Was viral genomics conducted?
Samples sequenced
Pangolin lineage
Representative sequence identification number

Provide a brief description of the outbreak

Instrument 3: Enhanced fields for outbreaks in health care settings

Type of facility

Total number of beds in the facility or ward (if confined)

Role type of the first primary outbreak case

Primary cases in HCW*/patient/visitor

Total cases in HCW (Medical Doctor/Nurse/Midwife/Other/Unknown)

HCW cases that worked in a high-risk setting (COVID-19 treatment facility/testing facility/Emergency Department/ICU)

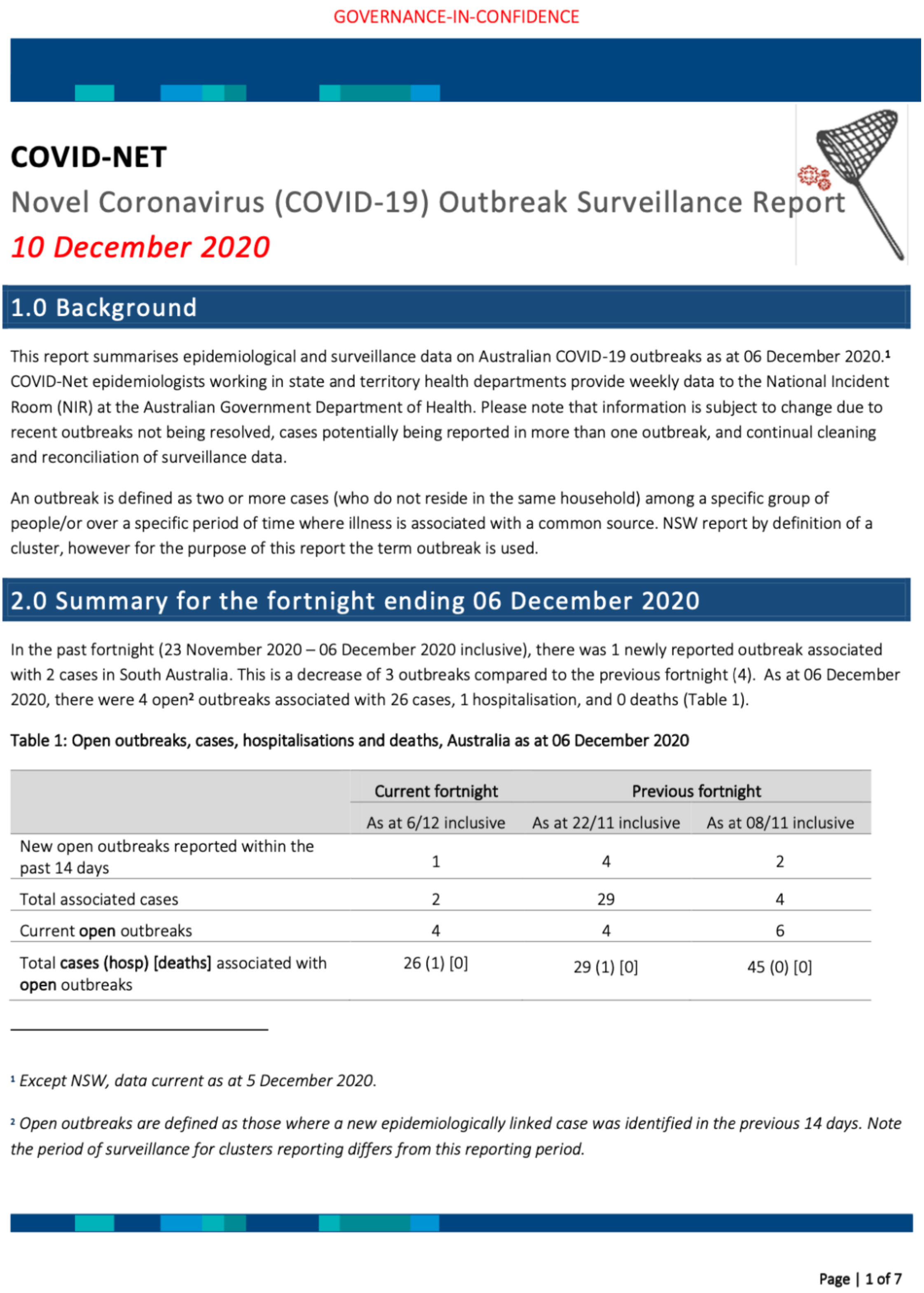
HCW hospitalised
Died (HCW/died)

HCW furloughed

List contributing risk factors

Health care worker

Appendix B – COVID-Net Outbreak Surveillance Report



GOVERNANCE-IN-CONFIDENCE

COVID-NET

Novel Coronavirus (COVID-19) Outbreak Surveillance Report

10 December 2020

1.0 Background

This report summarises epidemiological and surveillance data on Australian COVID-19 outbreaks as at 06 December 2020.[1] COVID-Net epidemiologists working in state and territory health departments provide weekly data to the National Incident Room (NIR) at the Australian Government Department of Health. Please note that information is subject to change due to recent outbreaks not being resolved, cases potentially being reported in more than one outbreak, and continual cleaning and reconciliation of surveillance data.

An outbreak is defined as two or more cases (who do not reside in the same household) among a specific group of people/or over a specific period of time where illness is associated with a common source. NSW report by definition of a cluster, however for the purpose of this report the term outbreak is used.

2.0 Summary for the fortnight ending 06 December 2020

In the past fortnight (23 November 2020 – 06 December 2020 inclusive), there was 1 newly reported outbreak associated with 2 cases in South Australia. This is a decrease of 3 outbreaks compared to the previous fortnight (4). As at 06 December 2020, there were 4 open[2] outbreaks associated with 26 cases, 1 hospitalisation, and 0 deaths (Table 1).

Table 1: Open outbreaks, cases, hospitalisations and deaths, Australia as at 06 December 2020

	Current fortnight	Previous fortnight	
	As at 6/12 inclusive	As at 22/11 inclusive	As at 08/11 inclusive
New open outbreaks reported within the past 14 days	1	4	2
Total associated cases	2	29	4
Current **open** outbreaks	4	4	6
Total **cases (hosp) [deaths]** associated with **open** outbreaks	26 (1) [0]	29 (1) [0]	45 (0) [0]

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[1] *Except NSW, data current as at 5 December 2020.*

[2] *Open outbreaks are defined as those where a new epidemiologically linked case was identified in the previous 14 days. Note the period of surveillance for clusters reporting differs from this reporting period.*

2.1 Open Outbreaks

Open outbreaks were reported across multiple settings^; Education - TAFE/University facility (1), Workplace/industry – fast-food restaurant (1), 'Other' - quarantine facility (1) and an extended family setting (1).

Table 2. Summary of open outbreaks by jurisdiction and setting, Australia, 6 December 2020

Jurisdiction	Cases (hosp) [deaths]	Description
Education		
SA	2 (0) [0]	There were 2 cases of COVID-19 associated with a newly reported outbreak at a TAFE/University facility.
Workplace/Industry		
SA	2 (0) [0]	There were 2 cases of COVID-19 associated with an outbreak in a fast food restaurant.
Other setting		
SA	22 (1) [0]	There were 22 cases of COVID-19 associated with 2 outbreaks in other settings; a quarantine facility (10) and an extended family setting (12).

^Definition of outbreak settings

Accommodation and Housing: *Includes high density housing, hostels and backpackers, hotels and serviced apartments, public housing, rough sleeping and temporary accommodation.*

Residential Aged Care (RAC): *Includes residential aged care facilities, commonwealth aged care facilities and home-care.*

Childcare: *Includes pre-school child care services and childcare services provided from home.*

Disability Services: *Includes disability services and private accommodation and support services*

Health care Facility/Other (HCF): *Includes primary care, disability, and allied health services.*

Hospital: *Includes inpatient acute and sub-acute hospital (including psychiatric units), day surgeries, and transitional care.*

Educational Facility: *Includes schools, universities, TAFE, kindergarten, after school care, other education and training facilities and higher educational facilities.*

Food Industry: *Includes abattoirs, factory based food production, meat and poultry processing facilities, food production (commercial fishing, grain, dairy) and fruit or vegetable farming.*

Hospitality and Entertainment: *Includes cinemas and theatres, bars and music venues and food premises (e.g. Restaurants, takeaway food, cafes)*

Travel & Transport: *Includes travel groups, cruise ships, cargo ships, mass transport (flights, trains, trams, buses), and other transport services (Uber and taxi).*

Justice and Emergency: *Includes emergency services, correctional facilities and prisons.*

Workplace/Industry: *Includes warehouses (not food), supermarkets, utilities, residential work sites, office spaces, manufacturing, logistics, food distribution centers, construction sites, retail and supermarkets.*

Other: *Includes other various settings not captured by the other exposure settings, e.g. extended family gatherings (where 2 or more separate households come together), religious services, and hostels, sports and recreation venues, cruise ships and other mass transport.*

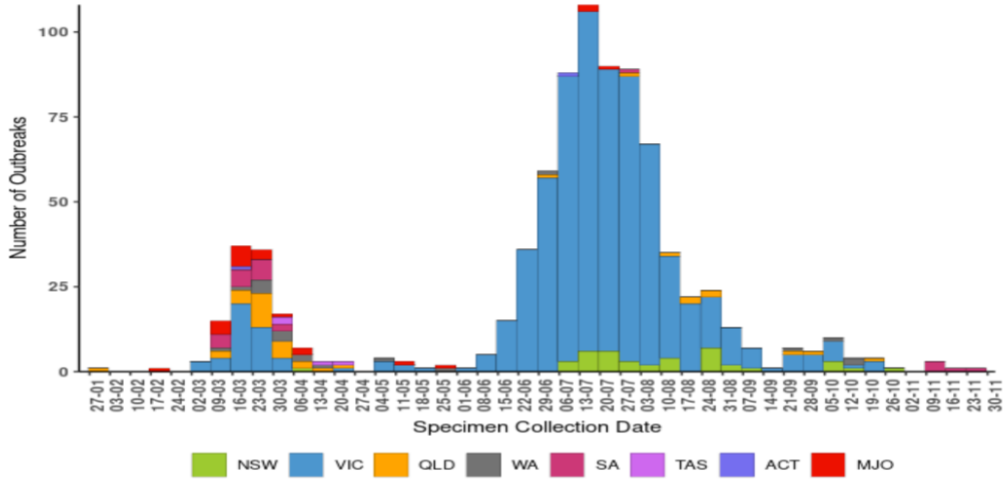
3.0 Overview of COVID-19 outbreaks in Australia

Since the beginning of the epidemic there has been 808 single jurisdictional outbreaks (outbreaks) associated with 12,367 cases in Australia [3](Table 1). The median number of cases associated with the outbreaks was 6 (range 2 - 260). In addition, there has been *22 multi-jurisdictional outbreaks* (MJO)[4] associated with 868 cases. The median number of cases associated with MJO was 15 range (2 - 331).

Table 3: Cumulative number of outbreaks and associated cases, hospitalisations and deaths, Australia* as at 6 December 2020

Outbreaks	MJO	Total cases	Total hospitalisations	Total deaths
808	22	13,235	2,007	799
Number from previous reporting period (change in past 14 days)[5]				
807 (+1)	22 (+0)	13,235 (+0)	2,007 (+0)	799 (+0)

Figure 2. Epidemic Curve of COVID-19 outbreaks, by jurisdiction, by week of specimen collection date in the first positive case, Australia, 6 December 2020



Interpretation: The first peak in outbreaks occurred mid-March. This was followed by a rapid increase in outbreaks which began in early July, corresponding with community transmission in Victoria (Figure 2.). The majority of outbreaks have been reported in Victoria (85%, 684 /830), NSW (5%, 40/830), and QLD (4%, 36/830).

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[3] *Totals do not include outbreaks reported by NSW prior to 5 July 2020 (excl. Newmarch House Aged Care Facility outbreak).*

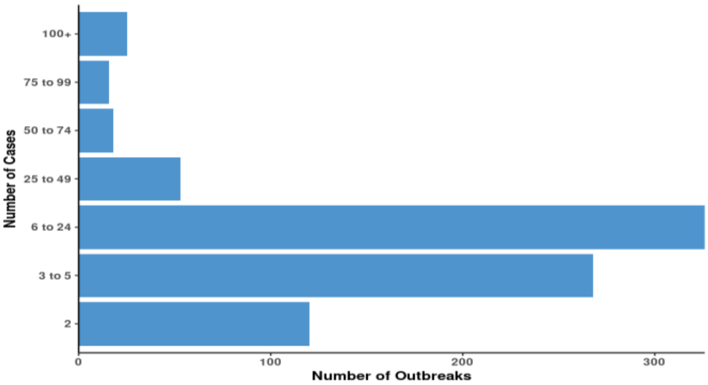
[4] *MJO are defined as involvement of multiple jurisdictions in the outbreak investigation & response irrespective of where the exposure has occurred.*

[5] *Changes in the past 14 days reflects new and reconciled numbers due to data cleaning*

Nationally, in (90%, 750/830) of outbreaks, the first known case of the outbreaks was found to have acquired infection in Australia, and 9% (73/830) acquired infection overseas. For 2 outbreaks, the acquisition of the first known case were unknown or could not be determined.

3.1 Size of outbreaks

Figure 3. Number of Outbreaks by size, by outbreak type, Australia, 6 December 2020



Interpretation: The majority (39%, 326/830) of outbreaks had 6 to 24 cases, and many (32%, 268/830) had only 3 to 5 cases. The largest single jurisdictional outbreak has occurred in residential aged care with associated with 260 cases (Figure 3).

Table 4: Outbreak size and median time interval between first and last specimen collected in the outbreak, Australia, 06 December 2020

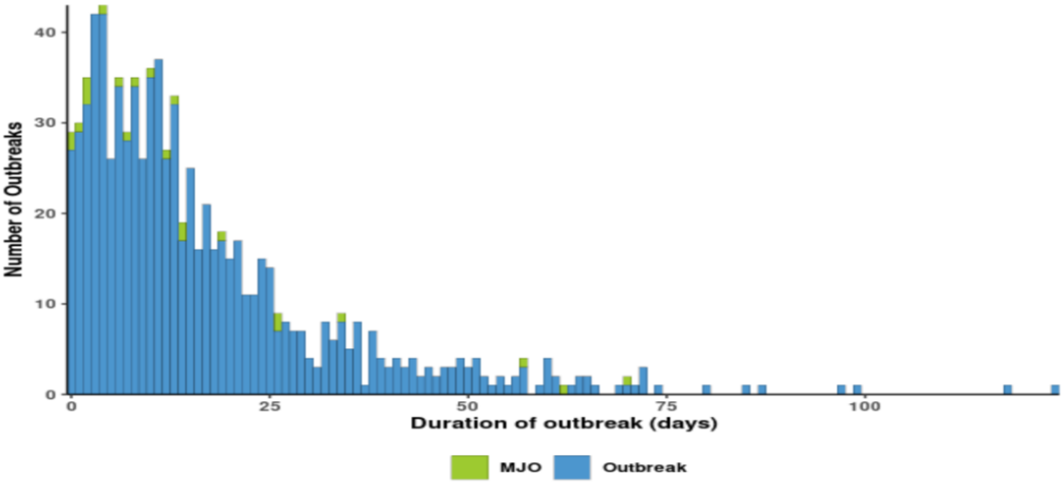
Size (number of cases)	Number of outbreaks n (%)	Median time interval (days)
2	121 (15%)	3
3 to 5	268 (32%)	8
6 to 24	326 (39%)	15
25 to 49	53 (6%)	25
50 to 74	18 (2%)	35
75 to 99	16 (2%)	37
100+	25 (3%)	50

. *Note: This table includes closed outbreaks in which date of the last specimen collected in the outbreak was provided (n = 827).*

The time interval (in days) between the first and last positive specimen collected in the outbreak was calculated as a proxy for outbreak duration. The median time interval increased proportionally to the number of cases associated with an outbreak. The median interval for smaller outbreaks of 3 to 5 cases was 8 days (range 0-99 days). There were 25 outbreaks with 100+ cases, with a median interval of 50 days (range 7- 124).

3.2 Duration of Outbreaks

Figure 5: Number of outbreaks by time interval between first and last positive specimen collected in the outbreak, Australia, 6 December 2020



Note: *This figure includes closed outbreaks and excludes open outbreaks.*

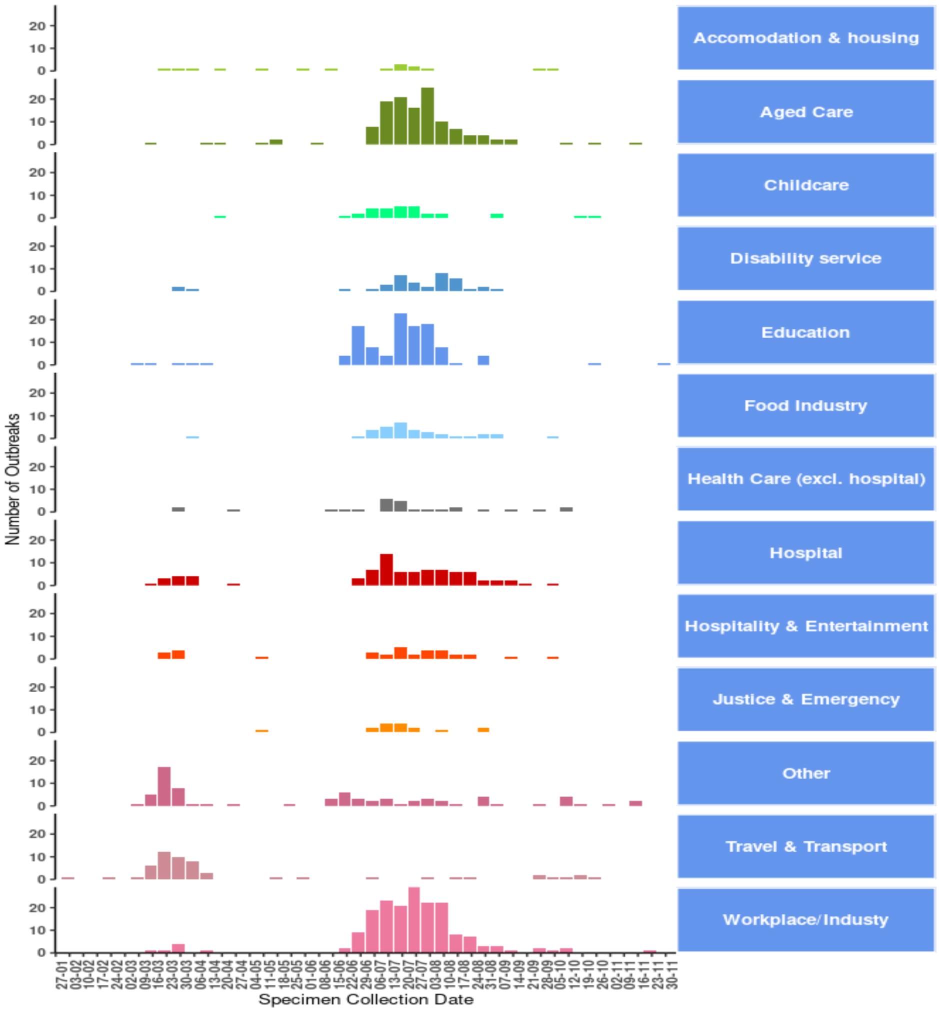
Interpretation: There were 29 outbreaks where all cases were detected on a single day (day "zero" as calculated by the interval in days between the first and last positive specimen date collected in the outbreak). In addition, there were 269 outbreaks where the interval was a week or less. There were 134 outbreaks where the interval exceeded 30 days, and for 28 outbreaks, the interval was over 60 days.

3.2 Setting of outbreaks

As at 6 December 2020, outbreaks have occurred across various settings; Workplace/Industry (22%, 182/830), RAC (15%, 128/830), education (13%, 111/830), hospitals (10%, 83/830), 'other' (9%, 75/830), travel and transport (7%, 55/830), disability services (5%, 39/830), food industry (4%, 34/830), hospitality and entertainment (4%, 34/830), childcare (4%, 30/830), HCF (3%, 27/830), accommodation and housing (2%, 16/830), justice and emergency (2%, 16/830).

Outbreaks in the RAC setting were associated with the largest number of outbreak cases (n=4,827) with a median of 8 cases (range 2-260), followed by workplace/industry (1,515 cases, median 5 (range 2-67)), and hospitals (1,326) with a median of 8 cases (range 2-182). There were 5 abattoir outbreaks associated with 408 outbreak cases, however these outbreaks were typically large, with a median of 88 cases (range 5-169). Outbreaks on cruise ships were also prominent in the first peak of outbreaks in mid-March. As at 31 May, there had been 14 outbreaks on a cruise ship associated with 752 cases with a median of 24 cases (range 2-331).

Figure 6. Number of COVID-19 outbreaks, by setting, by week of specimen collection date for the first positive case in each outbreak, Australia, 6 December 2020



Interpretation: The number of new outbreaks has declined across all settings following a peak in mid-July 2020. Prior to 1 June, the majority of outbreaks were associated with travel and transport (33%, 44/133), 'other' settings (26%, 35/133) and hospitals (10%, 13/133). From 1 June, most outbreaks have been in workplace/industry (25%, 177/697), RAC (18%, 122/697), education (15%, 105/697), and hospitals (10%, 70/697), driven by trends in the epidemic in Victoria (Figure 6).

Appendix C – Advanced draft of a paper for publication

Title: COVID-19 outbreaks in Australia during a period of high epidemic control, 2020

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Keywords: Australia, COVID-19, outbreak, SARS-CoV-2, policy making, epidemics, workplace, disease outbreaks, health policy, disease surveillance

Abstract

Objectives

To describe characteristics of COVID-19 outbreaks in Australia to guide policy development for mitigation of future outbreaks.

Design

A retrospective analysis of COVID-19 outbreaks affecting two or more people reported to COVID-Net—an Australian national surveillance network—from 28 January until 27 December 2020.

Setting and participants

The COVID-Net surveillance network covered all Australian states and territories, with an estimated population of 25,649,985 persons as at 31 June 2020.

Main outcomes

Epidemiology of COVID-19 outbreaks in Australia, including the setting in which they occurred, size, and duration.

Results

853 outbreaks of COVID-19 were reported; associated with 13,957 confirmed cases, of whom 2,047 were hospitalised, and 800 died. The pattern of outbreaks followed a similar trend to the epidemic in Australia, defined by two distinct peaks in mid-March and July. Victoria reported the greatest number of outbreaks across all settings aligned with the second wave of infections. Outbreaks most commonly occurred in the workplace/industry setting (22%, 190/853), followed by education (14%, 122/853), residential aged care (13%, 114/853) and hospitals (10%, 83/853). The majority (40%, 340/853) of outbreaks had 6 to 24 cases, and the median outbreak duration increased in proportion with the number of associated cases.

Conclusion

This report summarising COVID-19 outbreaks in Australia identifies settings of highest risk. Surveillance of outbreaks informs our understanding of transmission dynamics in Australia relative to national and jurisdictional interventions. For settings that are high risk for COVID-19, it is important to prioritise planning, surveillance, and implementation of control measures.

Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes coronavirus disease 2019 (COVID-19), has spread rapidly around the world since it was first identified in December 2019 (1). Basic reproductive number (R0) estimates for SARS-CoV-2 range from 2–4; similar to or higher, than for severe acute respiratory syndrome and influenza virus (2, 3). Because SARS-CoV-2 is highly infectious, COVID-19 outbreaks occur when people come into close contact with cases of COVID-19 (2, 4). Early reports indicated that SARS-CoV-2 predominantly spread via respiratory droplets and fomites, emerging literature suggests transmission via aerosols is important (2, 5).

Outbreak investigations provide insights into SARS-CoV-2 transmission dynamics, including the risk in different settings and as an indicator of community transmission. Indoor and enclosed spaces where persons are in close proximity and there is low airflow increase the risk of SARS-CoV-2 infection (6, 7). In these environments, behaviours such as sneezing, coughing, shouting, and singing result in greater volume of droplets suspended for longer periods (2, 8). These environments may result in superspreader events, where one infectious individual infects a large number of secondary cases (8, 9). Superspreader events are difficult to predict and result in epidemic growth that challenge control efforts (6, 10, 11).

In Australia during March 2020, the first epidemic wave of COVID-19 was characterised by cases arriving on international cruise ships and by air. This was followed by local transmission in settings where people congregate. Australian state and territory governments instituted extensive non-pharmaceutical interventions, along with case isolation, and tracing and quarantine of contacts. The Communicable Diseases Network Australia (CDNA) developed a national surveillance plan that included capturing data on outbreaks (12). The Australian Government established COVID-Net, a surveillance network to support jurisdictional investigation of COVID-19 outbreaks and collect national surveillance data. States and territories have reported outbreaks and clusters of COVID-19, with Victoria experiencing a second wave due to community transmission.

In this report, we characterise outbreaks using surveillance data during a setting of high epidemic control in Australia. We examine where outbreaks occurred and identify factors associated with transmission.

Methods

COVID-19 outbreak definition

We defined a case of COVID-19 as a person testing positive to a SARS-CoV-2 real-time reverse transcription-polymerase chain reaction (RT-PCR) assay, and a primary case as the first known case of the outbreak (2). If a case in one outbreak became the primary case in a secondary outbreak, the case may have been included in both outbreaks.

We defined a COVID-19 outbreak as two or more cases (who did not reside in the same household) among a specific group of people and/or over a specific period of time where illness was associated with a common source of infection. We defined a multi-jurisdictional outbreak as involvement of two or more jurisdictions in the outbreak, regardless of where exposure occurred.

Data sources

Our report includes outbreak data reported by all jurisdictions to COVID-Net, from 28 January until 27 December 2020 inclusive, while New South Wales (NSW) reported outbreaks from 5 July 2020 onwards. Local public health units investigated outbreaks and collected data that were reported by COVID-Net epidemiologists using a REDCap (Research Electronic Data Capture) database hosted at the Australian Government Department of Health (13).

Data collected for each outbreak included place of acquisition of the primary case, and number of cases, hospitalisations, and deaths. We categorised outbreaks as one of 13 settings and 56 sub-settings where the outbreak primarily occurred (Appendix 1). The outbreak duration was derived by the number of days between the first and last positive specimen collected in the outbreak, plus 14 days from the last specimen date.

We obtained the total number of COVID-19 cases notified up to 27 December 2020 from the National Notifiable Disease System (NNDSS).

Data analysis

We performed analyses in R 4.0.0 on a dataset extracted on 28 January 2021. We used population data from the Australian Bureau of Statistics Estimated Resident Population (as at 31 June 2020) to estimate rates of outbreaks by jurisdiction.

We analysed outbreak data by two distinct peaks relative to the 1 June 2020: from 28 January 2020 to 31 May 2020, and 1 June 2020 to 27 December 2020. We refer to these two periods as the first wave and second wave, respectively.

Ethics

Surveillance activities were conducted for and on behalf of the Australian Government Department of Health under the National Health Security Act 2007. The activities were approved by the Australian National University Human Ethics Committee [HREC/17/ANU/909].

Results

National overview

COVID-Net sites reported 853 outbreaks of COVID-19, associated with 13,957 confirmed cases, of whom 2,047 were hospitalised, and 800 died. The median number of cases associated with these outbreaks was 6 (range 2–331). As at 27 December, 49% (13,957/28,312) of all confirmed COVID-19 cases notified in Australia1 were associated with an outbreak affecting ≥2 persons.

The overall rate of COVID-19 outbreaks during the surveillance period was 3.3 outbreaks per 100,000 population. The highest rates were in Victoria (10.3 per 100,000 population; Table. 1). Victoria reported the largest proportion of outbreaks (81%, 691/853) and associated cases (83%, 11,610/13,957), followed by NSW (6%, 54/853 outbreaks, 5%, 642/13,957 cases). Overall, multi-jurisdictional outbreaks had the second highest proportion of cases (6%, 875/13,957), with a median number of cases of 15 (range 2 – 331; Table 1).

National trend

The pattern of outbreaks followed the wider epidemic in Australia, defined by two distinct waves relative to 1 June 2020 (Figure 1). Outbreaks in the first wave peaked in March 2020 and subsided by 31 May 2020, at which time COVID-Net sites reported 133 outbreaks. In the second wave, the source of infection for the primary case was locally acquired in 98% (705/720) of outbreaks compared to only 50% (67/133) in the first wave (odds ratio 47.7, 95% confidence interval 25.8–88.2), reflecting the impact of international travel restrictions progressively introduced from 15 March 2020.

Table 1. Outbreaks of COVID-19 by state and territory, Australia, 28 January – 27 December 2020

State or territory	Number of outbreaks	Median size (persons) per outbreak	Number hospitalised	Outbreak rate per 100,000 population
ACT	2	5	1	0.5
NSW [a]	54	9	N/A	0.7
NT	0	-	-	-
Qld	36	3	78	0.7
SA	23	4	26	1.3
Tas.	4	5	30	0.7
Vic.	691	6	1,660	10.3
WA	21	5	76	0.8
MJO	22	15	176	-
Total	853	-	2,047	-

[a] NSW commenced reporting COVID-19 outbreaks from 5 July 2020 onwards.

Abbreviations: COVID-19 = coronavirus disease 2019; ACT = Australian Capital Territory; NSW = New South Wales; NT = Northern Territory; Qld = Queensland; SA = South Australia; Tas. = Tasmania; Vic. = Victoria; WA = Western Australia, MJO = Multi-jurisdictional outbreak.

The number of outbreaks in the second wave was much larger, characterised by sustained community transmission in one state — Victoria. The number of outbreaks reported each week increased exponentially (Figure 1). The peak in the number of COVID-19 cases was observed nationally in August 2020 when outbreak numbers had started to decline.

Outbreak size and duration

The majority (40%, 340/853) of outbreaks had between 6 and 24 cases, and many (32%, 275/853) were smaller outbreaks of 3 to 5 cases. The median outbreak duration increased proportionally to the number of cases associated with an outbreak (Table 2).

The largest multi-jurisdictional outbreak occurred on a cruise ship among passengers and crew (n=854) (14). The number of secondary cases among Australian residents who were infected by passengers and crew on board the ship was difficult to ascertain for this outbreak. The largest single jurisdictional outbreak occurred in a residential aged care facility (RACF) (n=301) and lasted for 86 days.

Table 2. Outbreak size by duration, Australia, 28 January – 27 December 2020

Size (number of cases)	Number of outbreaks (%)	Median duration (days)	Duration range (min – max)
2	122 (14%)	18	14 – 86
3 to 5	275 (32%)	21	14 – 113
6 to 24	340 (40%)	29	15 – 132
25 to 49	56 (7%)	38	14 – 99
50 to 74	16(2%)	51	27 – 102
75 to 99	15 (2%)	54	33 – 111
100+	29 (3%)	64	21 – 138

Outbreak setting

During the two study periods, there were four settings where 60% (509/853) of COVID-19 outbreaks and 67% (9,350/13,957) of outbreak-associated cases occurred (Appendix 1; Appendix 2). Workplace/industry settings comprised 22% (190/853) of outbreaks and 11% (1,560/13,957) of cases (median=5, range 2–69). These outbreaks most frequently occurred in offices or call centres (n=31), unspecified workplaces (n=28), and non-food manufacturing (n=26). Educational settings comprised 14% (122/853) of outbreaks and 9% (1,189/13,957) of cases (median=6, range 2 – 209). Outbreaks in education settings occurred in secondary schools (n=52), primary schools (n=31), and combined primary-secondary schools (n=18). Outbreaks in RACF comprised 13% (114/853) of all outbreaks and 38% (5,275/13,957) of cases (median=11, range 2 – 301). Sixty-nine per cent (79/114) of these RACF outbreaks occurred between 1 June and 31 July 2020. Lastly, 10% (83/853) of outbreaks occurred in hospitals affecting 10% (1,326/13,957) of outbreak-associated cases. Among these, outbreaks most frequently occurred in acute care hospitals (n=69).

In the first wave, 33% (44/133) of COVID-19 outbreaks were reported in travel and transport settings, particularly among travel groups (n=21) and on cruise ships (n=14) (Figure 2). Locally acquired cases associated with these outbreaks occurred across the country. Of the 22 multi-jurisdictional outbreaks, 9 were associated with an outbreak on a cruise ship. Outbreaks among family and social gatherings (27 outbreaks; median=8, range 2–45) were prominent during the early stages of the epidemic when non-pharmaceutical interventions were not introduced. In the second wave, outbreaks and associated cases were predominantly reported from Victoria and were reported from a variety of settings (Figure 2). Notably, there was a substantial increase in the number of outbreaks in workplace/industry and educational settings compared to the first wave (Appendix 2)

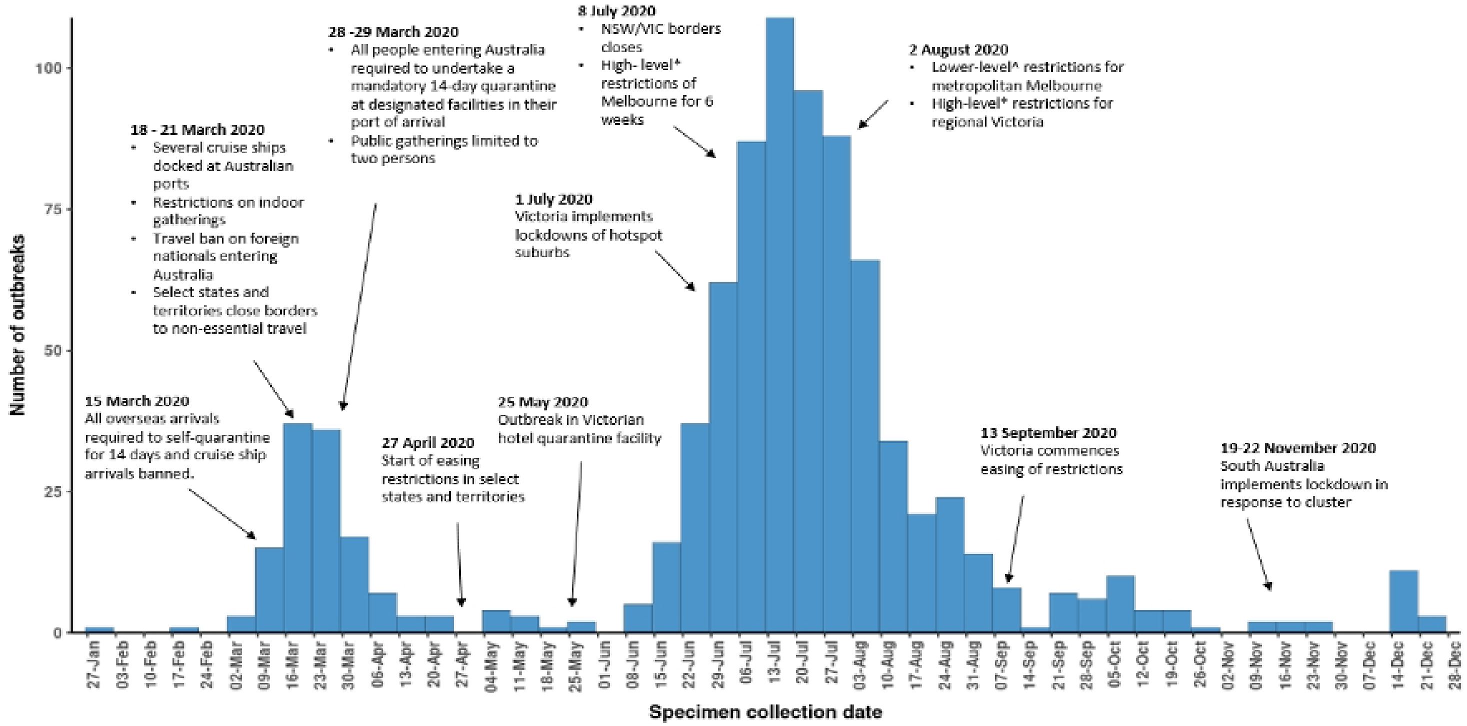

Figure 1. Number of outbreaks by specimen collection date of the primary case in the outbreak, Australia, 28 January – 27 December 2020, with timing of key public health measures

Adapted from "COVID-19 notifications in Australia: Epidemiology Report 30" by COVID-19 National Incident Room Surveillance Team, 2020, Comm Dis Intel, 44, https://doi.org/10.33321/cdi.2020.44.91. Copyright 2020 by Commonwealth of Australia. COVID-19 = coronavirus disease 2019; NSW = New South Wales; Vic. = Victoria. * High-level restrictions include compulsory mask-wearing in public; restrictions to travel within 5km from home; night-time curfew all non-essential retail and services closed; restaurants and cafes takeaway only; work from home unless essential worker; and online schooling. ^Lower-level restriction include: compulsory mask-wearing in public; exercise for two hours per day with one other person; restrictions to travel within 5km from home; some non-essential retail open; work from home unless essential worker; schools reopen for vulnerable children or whose parents cannot work from home.

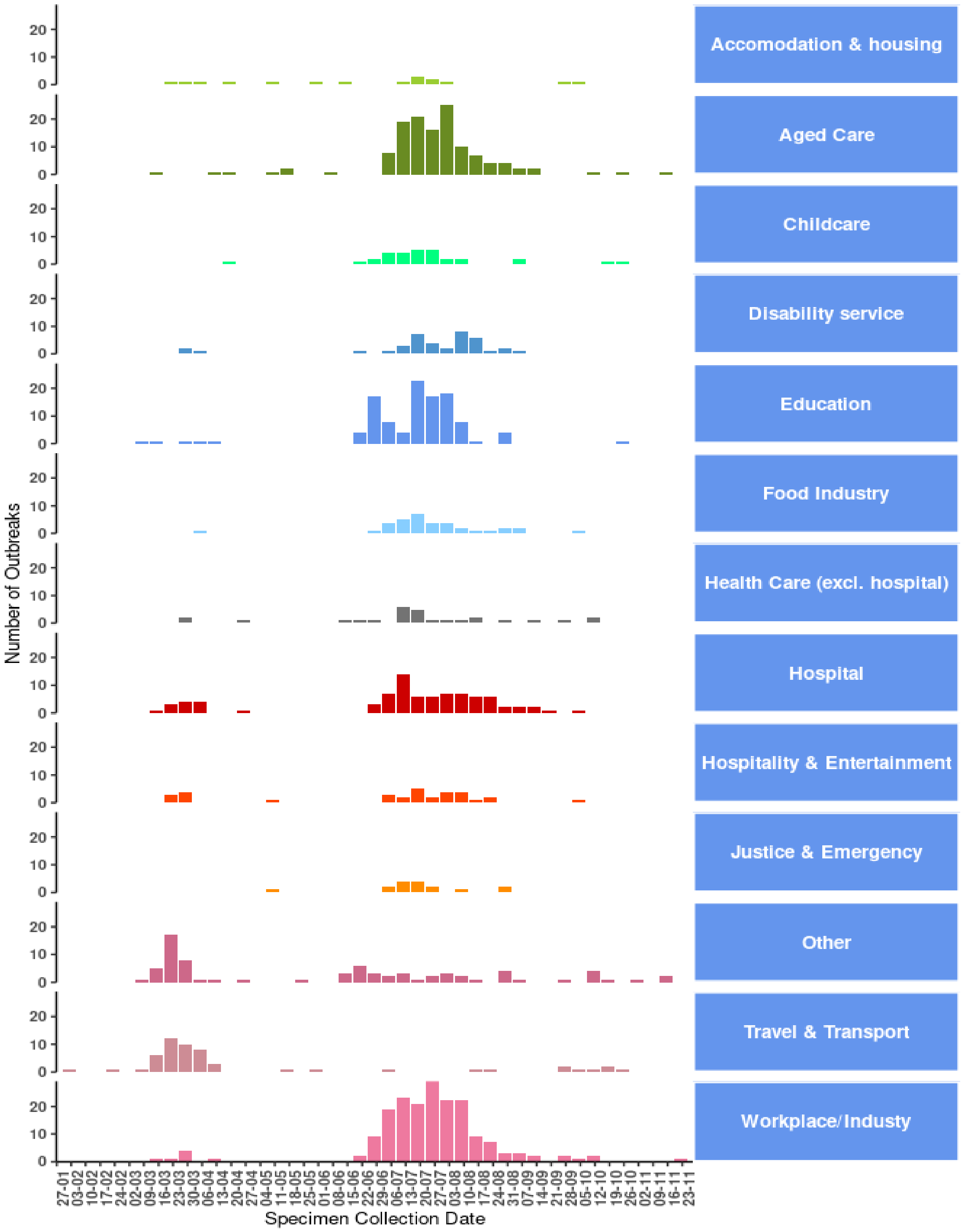

Figure 2. Number of COVID-19 outbreaks, by setting and specimen collection date for the index case per outbreak, Australia, 28 January – 27 December 2020

Discussion

Australia exerted a high degree of COVID-19 control early in the pandemic through extensive non-pharmaceutical interventions. Outbreaks alerted health authorities to settings that required specific restrictions, such as international travel and large social gatherings. Outbreak data in the second wave strongly reflects the situation in Victoria. Overall, 81% (691/853) of outbreaks occurred in Victoria, and resulted in additional important transmission settings that were strongly influenced by a change in demographic characteristics of cases in the second wave.

In the first wave, approximately 50% (66/133) of outbreaks were linked to the introduction of infection from someone who travelled to Australia from overseas — including those at sea. SARS-CoV-2 is easily transmitted on board cruise ships due to high population density, crowded communal and living areas, and shared sanitary facilities (15). Initially, infected cruise ships passengers disembarked at a range of ports around Australia—in many instances continuing travel across the country whilst infectious. A coordinated response by state and territory health authorities was required to rapidly detect and investigate COVID-19 cases among passengers of cruise ships where subsequent multi-jurisdictional outbreaks occurred. As at 31 May 2020, approximately one third of outbreak associated cases and one third of deaths were associated with cruise ships. These figures underestimate the actual number of cases associated with cruise ships due to incomplete reporting of outbreak data to COVID-Net during this period.

After initial epidemic control nationally, Victoria experienced a resurgence of COVID-19 from an outbreak associated with a quarantine facility (15). Subsequent community transmission introduced SARS-CoV-2 into high-risk settings such as RACF, disability services, and health care. Outbreaks in education and childcare settings peaked when community transmission was highest during July 2020, suggesting that infections in these settings were likely driven by community transmission. Children less than 10 years old are thought to transmit SARS-CoV-2 less than adults and adolescents (16). Australian and international evidence indicate transmission of the virus within schools is low and child-to-child transmission within the school setting is uncommon (17-20). We did observe a high number of outbreaks in kindergarten, childcare and primary schools when compared to secondary educational settings, while outbreaks in secondary schools were generally larger in size. However, there were exceptions to these finding where a single outbreak in primary-secondary school was associated with 209 cases.

The high number of outbreaks in the workplace and industry settings during the second wave reflects the staging of lockdown measures. Essential workplaces that were not able to close services or transition workers home such as manufacturers, construction sites, and warehouses were disproportionately affected. Confined and shared spaces associated with a lack of physical distance and poor ventilation are known risk factors for outbreaks in workplace settings (21). For example, workers in meat processing factories often socialise outside of work, share transport to work, and work in close proximity in processing lines in poorly ventilated areas (22, 23). Although fewer outbreaks occurred in food industry settings, abattoir and meat processing plant outbreaks were large with a median of 88 cases (range 5–168) and 22 (range 3–212), respectively. The use of surveillance data to explore the role of superspreader events in settings where environmental conditions are conducive to SARS-CoV-2 transmission is limited. Better understanding of transmission in such workplace setting where infectious individuals work closely with many susceptible individuals, will help control the spread of SARS-CoV-2 as well as inform public health guidance (10, 11).

Transmission of SARS-CoV-2 among older people in RACF may result in significant morbidity and mortality due to age and a high prevalence of co-morbidities (24). Early in the response, the Australian Government released national guidelines for COVID-19 outbreaks in RACF (25). During the peak of the second wave, the number of outbreaks had surged to 88 outbreaks associated with 4,763 cases. During this time, facilities deployed major public health strategies to reduce the risk of entry and transmission of SARS-CoV-2 within facilities. Strategies include the development of outbreak management plans, additional infection control training of staff, and restricted visitor entry within facilities. Of RACF outbreaks across both epidemic waves, nearly half (46%, 397/853) involved 5 cases or less (Table 2). Nationally, outbreaks with longer duration were not necessarily those with the highest case numbers or deaths. This may be due to some facilities experiencing two outbreaks or having gaps of at least 14 days between cases.

Limitations

These surveillance data are subject to several limitations. Firstly, NSW did not report data to COVID-Net for the entire surveillance period, and therefore the picture of outbreaks in Australia during the first wave is incomplete. Secondly, we cannot comment on outbreak risk by setting in the absence of denominator data. However, these data do provide insight into highly affected settings. Thirdly, there was potential for variation in the classification of where outbreaks occurred, although we attempted to standardise this through use of a common database with standardised definitions. In addition, the development of national guidance for screening and testing of cases and close contacts changed as understanding of SARS-CoV-2 transmission increased. Higher rates of screening of staff and residents in certain high-risk settings such as in hotel quarantine and RACF, inevitably improved outbreak detection in these settings resulting in a bias towards detecting cases and outbreaks. As surveillance data are subject to change due to reconciliation, outbreaks and case data reported in our report may vary from previously published reports. Finally, our definition of an outbreak requires two or more linked cases. States and territories have gradually moved to the presence of a single case in any setting as an outbreak definition (4).

Conclusions

During 2020, Australia experienced fewer cases and outbreaks than many other higher income countries. This was the result of concerted efforts at all levels of society, including governments and industry, along with extremely high levels of community engagement. Efforts by jurisdictions to maintain robust isolation of cases and contact tracing capability was critical to prevent community transmission. Our findings demonstrate that multi-jurisdictional outbreaks of COVID-19 occurred regularly prior to domestic and international border closures and require a rapid and coordinated response. Strong public health policies on physical distancing and hygiene, particularly in high-risk settings, will assist in the prevention of outbreaks across all settings. As the rollout of COVID-19 vaccines occurs, it is vital outbreak investigation teams prepare to monitor changing transmission within Australia, particularly within closed cohorts of people. Robust outbreak investigations may indicate groups with lower vaccine coverage and will assist with estimating vaccine effectiveness. There are many lessons to learn from Australia's experiences to prepare for and manage COVID-19 outbreaks in this period of high epidemic control. Ongoing surveillance and analysis of COVID-19 outbreaks will provide an important indicator in response to evolving policies and response strategies for Australia and other countries.

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Appendix 1. COVID-Net definition of outbreak settings and sub-settings

Site setting/sub-setting	Definition/scope
ACCOMODATION & HOUSING	
High density housing	Large apartment blocks, long-term serviced apartments. Do not include public housing. Include residents/guests and staff where relevant.
Hostels & Backpackers accommodation	Short term (generally) accommodation that may have multiple beds with mixed occupancy in one room (occupants potentially unknown to each other). May have communal bathroom facilities. Include residents/guests and staff.
Hotels & Serviced apartments	Short term (generally) accommodation where there is usually a relationship between residents in one room. Usually implies ensuite bathrooms. Include guests and staff.
Public housing	Housing owned and maintained by state and territory housing departments - may be low or high rise. May have shared laundry or other facilities.
Rough sleeping	Where people sleep in the open air such as in doorways, parks, bus shelters etc.
Temporary accommodation	Public or private short term accommodation. Usually implies shared bathroom facilities, may include shared dorm-style accommodation.
RESIDENTIAL AGED CARE	Private and public aged care facilities. Include residents and staff.
HEALTH CARE (excluding hospital)	
Allied health services	Includes health services not part of the medical or nursing services. Includes pharmacy, physiotherapy, dietetics, audiology, chiropractor, occupational therapy, optometrist, psychologist, dentist etc.
Primary Care services	General practice and community health services.
laboratory service	Pathology, diagnostic, research etc. Not limited to labs that have contact with patients.
Other Healthcare	May include offsite hospital laundry services, hospital in the home, & non-urgent patient transport services.
HOSPITAL	
Acute Hospital	Establishments which provide at least minimum medical surgical or obstetrical services for inpatient treatment and/or care.
Sub-Acute Hospital, Transitional care & Other hospital	Sub-acute is a term that captures palliative care, rehabilitation, and geriatric evaluation management. The Transition Care Program provides short-term care and services for older people (and sometimes younger people) after they leave hospital.
CHILDCARE	
Childcare	Pre-school childcare services. Does not include educational kindergarten if the facility does not also provide pre-school childcare. If both, categorise as childcare
Family day care	Childcare services provided from a home
EDUCATION	
Primary school	Catholic schools and Independent schools lists. Include staff and students. May include a 3-4-year-old kindergarten.

Primary-Secondary combined school	Catholic schools and Independent schools lists. Include staff and students. May include a 3-4 year old kindergarten.
Secondary school	Catholic schools and Independent schools lists. Include staff and students.
TAFE/University	TAFE and University lists.
Kindergarten	Catholic schools and Independent schools lists
After school care	After school care at a dedicated centre. For children of school age. May include school holiday programs.
Additional needs school	School environment for children with special needs. Include staff, carers, and students.
Other education/training	Includes educational settings not covered in the other sub- categories, such as adult education and other non-accredited training courses.
WORKPLACE/INDUSTRY	
Construction	Sites used in the construction industry. Would usually be commercial (or larger projects) rather than residential sites where multiple staff/contractors are present.
Food Distribution	Sites where food is deposited and distributed to retail outlets etc.
Logistics	Logistics centres such as mail distribution, freight centres etc.
Manufacturing (not food)	Site where good are made such as automotive parts, plumbing supplies etc.
Office or call centre	Standard work office or call centre.
Personal care services	Personal services such as barbers, hairdressers and beauty therapists.
Residential worksite	Workplaces that involve visiting residential homes for extended periods of time. Electricians, painters, plumbers, technicians etc.
Retail (not supermarket)	Retail such as clothing, electronics, toy shops etc. Includes large chains. Does not include foot retail shops.
Supermarket	Supermarkets and other food retail shops.
Utilities	Sites involved with utilities such as sewerage, power and telecommunications.
Warehouse (not food)	Site where goods (excluding food) are stored.
Other workplace	Other workplaces not captured in another settings.
DISABILITY SERVICES	Disability services, includes private accommodation and support for the disabled.
FOOD INDUSTRY	
Abattoir	Location where live animals are slaughtered and undergo some form of processing. Excludes poultry.
Factory based food production	Larger scale food production locations such as milk or cheese factories.
Food production	Includes non-horticultural e.g. Farms for grain, dairy and fish. Commercial fishing is included in this category.
Fruit or vegetable farming	As defined: horticulture.
Meat processing	Facility producing small good and other meat products.

Poultry processing	Facility where meat chickens or ducks are killed and/or processed.
HOSPITALITY & ENTERTAINMENT	
Bars & Music venues	Includes pubs, clubs and venues where live music is performed (including larger venues such as the Concert Hall). Include staff and patrons.
Cinema & Theatre	Includes indoor and outdoor cinemas and theatres. Includes staff and patrons
Food Premises	Defined as a facility that prepares/sells food direct to customers. Includes restaurants, cafes, and takeaway (only) food.
TRAVEL & TRANSPORT	
Cruise ships	Cruise ships.
Mass transport	Public and private transport, road, rail and air. Includes public-facing staff of the service and drivers, as well as patrons.
Cargo ships	Cargo and freight ships.
Travel group	Domestic and international land travel groups, incl. combined sea and land tours.
Transport services	Taxi, Uber - not logistics, and not emergency services; not mass transport
JUSTICE & EMERGENCY	
Emergency services	Includes police, SES, fire brigade and ambulance
Prison	Adult and Juvenile correctional facilities
Other correctional facility	Remand centres, community corrections programs.
OTHER	
Family & Social gathering	2 or more households, without other known acquisition
Places of worship	Mosques, churches, synagogues
Sports & Recreation venues	Large scale (e.g. MCG) and smaller (e.g. local football club) venues, tennis courts, swimming pools, gyms, dance studios etc.
Other	Any outbreak that does not fit one of the other categories.

Appendix 1. Outbreaks of COVID-19 by setting and sub-setting, Australia, 28 January – 27 December 2020

Setting/sub-setting	First wave (28 January – 31 May)				Second wave (1 June – 27 December)				Total	
	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases
Accommodation & housing	**6 (5%)**	**37**	**4**	**2–18**	**11 (2%)**	**109**	**7**	**2–49**	**17 (2%)**	**146**
High density housing	1	3	-	-	2	10	5	3–7	3	13
Hostels & Backpackers accommodation	-	-	-	-	1	8	-	-	1	9
Hotels & Serviced apartments	5	34	5	2–18	6	78	6	2–49	11	112
Temporary accommodation	-	-	-	-	2	13	6.5	5–8	2	13
Residential aged care facility	**6 (5%)**	**92**	**3**	**2–79**	**108 (15%)**	**5,183**	**16**	**2–301**	**114 (13%)**	**5,275**
Health Care (excl. hospital)	**3 (2%)**	**34**	**3**	**2–28**	**24 (3%)**	**111**	**4**	**2–17**	**27 (3%)**	**145**
Primary care service	1	2	-	-	13	72	4	2–17	14	75
Allied health service	1	28	-	-	4	14	3.5	2–5	5	42
Laboratory service	-	-	-	-	2	12	6	5–7	2	12
Other Healthcare	1	3	-	-	5	13	2	2–4	6	16
Hospital	**13 (10%)**	**248**	**4**	**2–149**	**70 (10%)**	**1,078**	**9**	**2–182**	**83 (10%)**	**1,326**
Acute Hospital	12	230	4	2–149	57	913	10	2–182	69	1,143
Sub-Acute Hospital, Transitional Care & Other hospital	1	18	-	-	13	165	8	2–40	14	183
Disability services	**3 (2%)**	**16**	**6**	**3–7**	**41 (6%)**	**286**	**5**	**2–34**	**44 (5%)**	**302**
Childcare	**1**	**2**	**-**	**-**	**30 (4%)**	**264**	**5**	**2–48**	**31 (4%)**	**266**
Childcare	1	2	-	-	27	239	5	2–48	28	241
Family day care	-	-	-	-	3	25	9	5–11	3	25

Setting/sub-setting	First wave (28 January – 31 May)				Second wave (1 June – 27 December)				Total	
	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases
Education	**5 (4%)**	**25**	**4**	**2–9**	**117 (16%)**	**1,164**	**6**	**2–209**	**122 (14%)**	**1,189**
Primary school	2	5	2.5	2–3	29	196	5	2–19	31	201
Primary-Secondary school	1	7	-	-	17	350	8	2–209	18	357
Secondary school	1	9	-	-	51	494	8	2–53	52	503
TAFE/University	-	-	-	-	6	26	5	2–6	6	26
Additional needs school	-	-	-	-	2	26	13	6–20	2	26
After school care	-	-	-	-	1	8	-	-	1	8
Kindergarten	-	-	-	-	3	29	6	6–17	3	29
Other Education	1	4	-	-	8	35	4	2–8	9	39
Workplace/Industry	**7 (5%)**	**65**	**5**	**2–34**	**183 (25%)**	**1,495**	**5**	**2–69**	**190 (22%)**	**1,560**
Construction	1	5	-	-	17	108	3	2–27	18	113
Food Distribution	-	-	-	-	14	211	8.5	3–69	14	211
Logistics	-	-	-	-	18	172	4.5	2–64	18	172
Manufacturing (not food)	-	-	-	-	26	228	6.5	2–64	26	228
Office or call centre	3	17	5	4–8	28	213	6	2–29	31	230
Residential worksite	-	-	-	-	1	8	-	-	1	8
Retail (not supermarket)	-	-	-	-	22	109	4	2–15	22	109
Supermarket	1	7	-	-	17	151	3	2–39	18	158
Warehouse (not food)	-	-	-	-	12	88	4.5	2–17	12	88
Other	2	36	18	2–34	26	197	5	2–30	28	233
Food Industry	**1 (1%)**	**111**	**-**	**-**	**33 (5%)**	**1,018**	**10**	**2–212**	**34 (4%)**	**1,129**
Abattoir	1	111	-	-	4	297	62	5–168	5	408

Setting/sub-setting	First wave (28 January – 31 May)				Second wave (1 June – 27 December)				Total	
	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases
Factory food production	-	-	-	-	10	105	4.5	2–40	10	105
Food production	-	-	-	-	2	7	3.5	2–5	2	7
Fruit or vegetable farming	-	-	-	-	1	2	-	-	1	2
Meat processing	-	-	-	-	10	450	11	3–212	10	450
Poultry processing	-	-	-	-	6	157	22.5	6–55	6	157
Hospitality & Entertainment	**8 (6%)**	**161**	**14**	**6–59**	**34 (5%)**	**358**	**8**	**2–39**	**42 (5%)**	**519**
Bars & Music venues	1	59	-	-	11	152	11	3–26	12	211
Cinema & Theatre	-	-	-	-	1	11	-	-	1	11
Food Premises	7	102	13	6–31	22	195	6.5	2–39	29	297
Travel & Transport	**44 (33%)**	**985**	**6**	**2–331**	**12 (2%)**	**104**	**4**	**2–25**	**56 (7%)**	**1,089**
Cargo ships	1	21	-	-	9	62	2	2–25	10	83
Cruise ship	14	752	23.5	2–331	-	-	-	-	14	752
Mass transport	7	46	6	2–16	2	24	12	4–20	9	70
Transport services	1	3	-	-	1	18	-	-	2	21
Travel Group	21	163	4	2–29	-	-	-	-	21	163
Justice & Emergency	**1 (1%)**	**4**	**-**	**-**	**15 (2%)**	**149**	**7**	**2–26**	**16 (2%)**	**153**
Emergency services	-	-	-	-	8	69	7	2–19	8	69
Prison	1	4	-	-	5	72	13	6–26	6	76
Other correctional facility	-	-	-	-	2	8	4	4–4	2	8
Other	**35 (26%)**	**256**	**6**	**2–23**	**42 (6%)**	**602**	**10**	**2–45**	**77 (9%)**	**858**
Family & social gatherings	27	205	6	2–23	23	377	15	4–45	50	582
Places of worship	1	4	-	-	2	47	23.5	23–24	3	51

Setting/sub-setting	First wave (28 January – 31 May)				Second wave (1 June – 27 December)				Total	
	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases	Median size (persons) per outbreak	Range (min–max)	No. of outbreaks N (%)	Total no. of cases
Sports & recreation venues	2	11	5.5	4–7	13	159	7	2–34	15	170
Other	5	36	7	5–11	4	19	2	2–13	9	55
Total	**133 (100%)**	**2,036**			**720 (100%)**	**11,921**			**853 (100%)**	**13,957**

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Chapter 4. Investigation of an acute public health problem

A multi-jurisdictional investigation of a COVID-19 outbreak in attendees of wedding events in Bali, Indonesia, March 2020

Table of Contents

Prologue

Study rationale

On 24 March 2020, Newcastle Public Health Unit (PHU) in the Hunter New England Local Health District (HNELHD), was notified of a case of overseas acquired Coronavirus 2019 (COVID-19). The case was an Australian resident who had attended a wedding event in Bali, Indonesia. Subsequently, health departments in other jurisdiction identified cases among returned attendees. The wedding day was 20 March 2020, 5 days after the Australian Government ordered a 14-day isolation for anyone arriving in Australia to slow the spread of COVID-19. At the time, accumulating evidence suggested that large social events such as weddings and family gatherings were implicated in the spread of COVID-19, however, transmission dynamics and epidemiological features were not well understood. Newcastle PHU conducted an investigation to identify risk factors associated with transmission in this cohort.

My role

I attended the first videoconference with the Newcastle PHU study team on 12 April 2020. My early responsibility in the investigation team was to ascertain the extent of the outbreak. This involved identifying confirmed primary cases in guests who returned to Queensland (Qld), Northern Territory (NT), and internationally, and if there were further secondary cases. The National Incidence Centre (NIC) at the Australian Government Department of Health had been activated since November 2019 in response to the national bushfires, and then COVID-19. From the NIR, I collaborated with epidemiologists in state and territory health departments to gain permission for the study and access case interview information. Through the National Focal Point (NFP), we were able to confirm the COVID-19 status of Australian wedding guests residing abroad. The NFP liaises with states and territories for the purposes of giving effect to the International Health Regulations in relation to public health events of national significance.

As an investigator on the study, I met with the study group via videoconference at least weekly to discuss study progress and findings. My role involved conducting hypothesis generating telephone interviews and subsequently designing questionnaires for study participants. I was then responsible for telephone interviewing wedding attendees in Qld and the NT. The questionnaire was built into REDCap by the HNELHD planning team, and we were able to enter data directly into the database during the interviews. Following case interviews, my main role in the study team was writing the data analysis plan for the study and cleaning and analysing the data in the Stata statistical program. Along with the lead investigator at Newcastle PHU, I drafted the manuscript for publication, with my focus being on the interpretation of results and presentation of epidemiological findings. In addition, I wrote a plain language summary that was distributed to study participants to communicate our findings (Appendix 1).

Lessons learnt

The study was conducted in the first month of commencing the MAE program and proved to be a huge learning opportunity. I learned about the responsibilities of jurisdictions in contact tracing during investigation of an outbreak, and the role the Australian Government can play in the coordination of multijurisdictional outbreak investigations. This was a benefit of working at the national level, and an example of where state and territory health departments did not have complete information available to investigate and connect a cluster.

This was an outbreak in the early stage of the first Australian wave of the global COVID-19 pandemic. Cases travelled at a time when international travel was against Government advice, but not yet banned. At the time of the study, there were many sensitivities around returned travellers who acquired COVID-19 overseas and returned to Australia while infectious. A story of our study cohort’s trip to Bali hit the media to local news media outlets the week we commenced interviews. The news articles implied that guests irresponsibly broke government international travel warnings to attend the wedding, and that several became infected with COVID-19. As a result, there was a general reluctance among guests to participate in interviews, and some were suspicious that we were hoax callers when we rang to interview them. In addition, those who agreed to an interview were often unwilling to provide the names of other guests they travelled and spent time within Bali. The situation increased my awareness of the importance of maintaining full confidentiality and disclosure agreements between myself and the participants, both for the benefits of the participants themselves and study success. Consequently, I dealt with the challenges associated with inconsistencies in participant responses, and it took time to validate information that was missing or inconsistent with original sources. Missing data was a challenge in the analysis, particularly in trying to ascertain interactions between guests and participation in risk behaviours (i.e. sharing cigarettes, shisha, and drinks).

The most valuable thing I learned in this outbreak investigation was designing and developing interview questions that could then be statistically analysed. It was also an introduction to the use of REDCap for data collection, which I subsequently used again in establishing a surveillance system for COVID-19 outbreaks (Chapter 2). This project was my first-time using Stata for data analysis and I really enjoyed learning some basic commands with a small data set. I initially thought working with a small dataset would be more straightforward but soon realised that was not the case. Because of the missing data, shifting denominators, and low statistical power of the dataset, I was limited in the analyses I could undertake. Initially, I assumed if diseased persons were over-represented in a cohort study with a low participation rate, the relative risk would be biased toward the null. However, I learnt that response rate is a form of bias that could not be addressed by a change in the method of calculating associations. Based on the response rate, we chose to use relative risk because we were analysing a cohort. Odds ratios are typically used in case-control analyses or an output from a cohort using regression analysis. I learnt that an odds ratio generally exaggerates the measure of association compared to a relative risk in a cohort of high disease incidence. Therefore in our study, use of odds ratio could have exaggerated the potentially biased point estimates.

This project also challenged me to think about ways to communicate findings, including the appropriate use of *p*-values and confidence intervals. We chose not to present *p*-values in our study, since we believe our data did not meet the assumptions of most common null hypothesis significant tests due to dependency of our comparison groups and lack of random sampling. We chose to present confidence intervals to convey the direction of the effect and uncertainty about our point estimates. Importantly, I learnt how to communicate these statistical findings in tables and figures in a clear and effective way.

As a nurse I am acutely aware of challenges affecting health literacy. While I have had plenty of experience synthesising complex medical issues to patients and their families, I found writing a plain language statement summarising study findings to participants surprisingly difficult (Appendix 2.). Mostly I found epidemiological terminology not easily translatable to simple terms and feared substituting language would render the summary inaccurate. I worked through this by reviewing and simplifying drafts until I accurately expressed statistics and associated uncertainty in a way that did not generalise results or mislead readers.

Public health implications

On 11 March 2020, the World Health Organization announced the COVID-19 outbreak a pandemic. In these early stages, much of what was known about SARS-CoV-2 was based on that of Middle East respiratory syndrome coronavirus (MERS-CoV-2) and severe acute respiratory syndrome (SARS-CoV). At this time, outbreaks that occurred in Australia were linked to the introduction of infection from someone who travelled to Australia from overseas — including at sea. A number of studies suggested that large gatherings posed a risk of transmission of SARS-CoV-2, particularly when there were asymptomatic spread amongst large groups. This outbreak affected healthy young adults and provided early evidence of asymptomatic and low-symptomatic spread. The study supported public health messaging at the time that highlighted the importance of physical distancing, particularly during group gatherings, to control the spread of COVID-19. In addition, it supported advice that people should not share drinks, food or other vehicles that may support the transmission of pathogens.

MAE course requirements

The following MAE core competency requirement was completed with this project: the investigation of an acute public health problem.

Acknowledgements

I would like to acknowledge my supervisors, Rose Wright, Prof Martyn Kirk, Dr Craig Dalton, and Ben Polkinghorne for their guidance and support. I would also like to thank jurisdictions and public health units for collecting the case data and conducting contact tracing of the cases to prevent further spread of COVID-19. I would like to thank my colleagues (Dr Kirsten Williamson and Dr Bhavi Ravindran) at Newcastle PHU, for their valuable input and dedication to the investigation. Finally, I would like to thank the study participants, who provided us with sensitive information in a difficult context.

Chapter Structure

The body of this chapter consists of a paper I co-authored on the investigation into the Bali wedding outbreak (Appendix A). The paper was published in *Communicable Disease Intelligence* on 16 September2020. The study was co-investigated by Kirsten Williamson (2nd year MAE Scholar and Public Health Registrar) and led by Dr Bhavi Ravindran (Medical Officer at Newcastle PHU). The plain language summary I developed summarising the study findings for participants is included at Appendix B.

Abstract

Introduction

On 24 March 2020, Newcastle Public Health Unit (Newcastle PHU), in New South Wales (NSW), was notified of a confirmed novel coronavirus disease 2019 (COVID-19) diagnosis in an Australian resident who had attended a wedding in Bali, Indonesia, from 15–21 March 2020. Initial case investigations by Newcastle PHU revealed further cases in attendees from NSW, as well as other jurisdictions and internationally. The National Incident Room (NIR) at the Australian Government Department of Health was contacted to assist in the outbreak investigation.

Methods

The cluster was investigation via a retrospective cohort study of attendees of the wedding events in Bali. The rationale for this study was to understand transmission dynamics and risk factors associated with of SARS-CoV-2 at the wedding events. We designed an interview questionnaire based off semi-structured hypothesis generating interviews. Of the 41 attendees, 17 participated in a structured telephone interview that included history of illness, risk exposures and event attendance. We obtained data for the remaining 24 participants through corroborative histories and public health unit case investigations.

Data were collected using REDCap and analysed in Stata.13 (StataCorp, USA). We performed univariate analysis to calculate relative risks and risk difference and associated 95% confidence intervals to examine associations between event attendance or activities and subsequent SARS-CoV-2 infection.

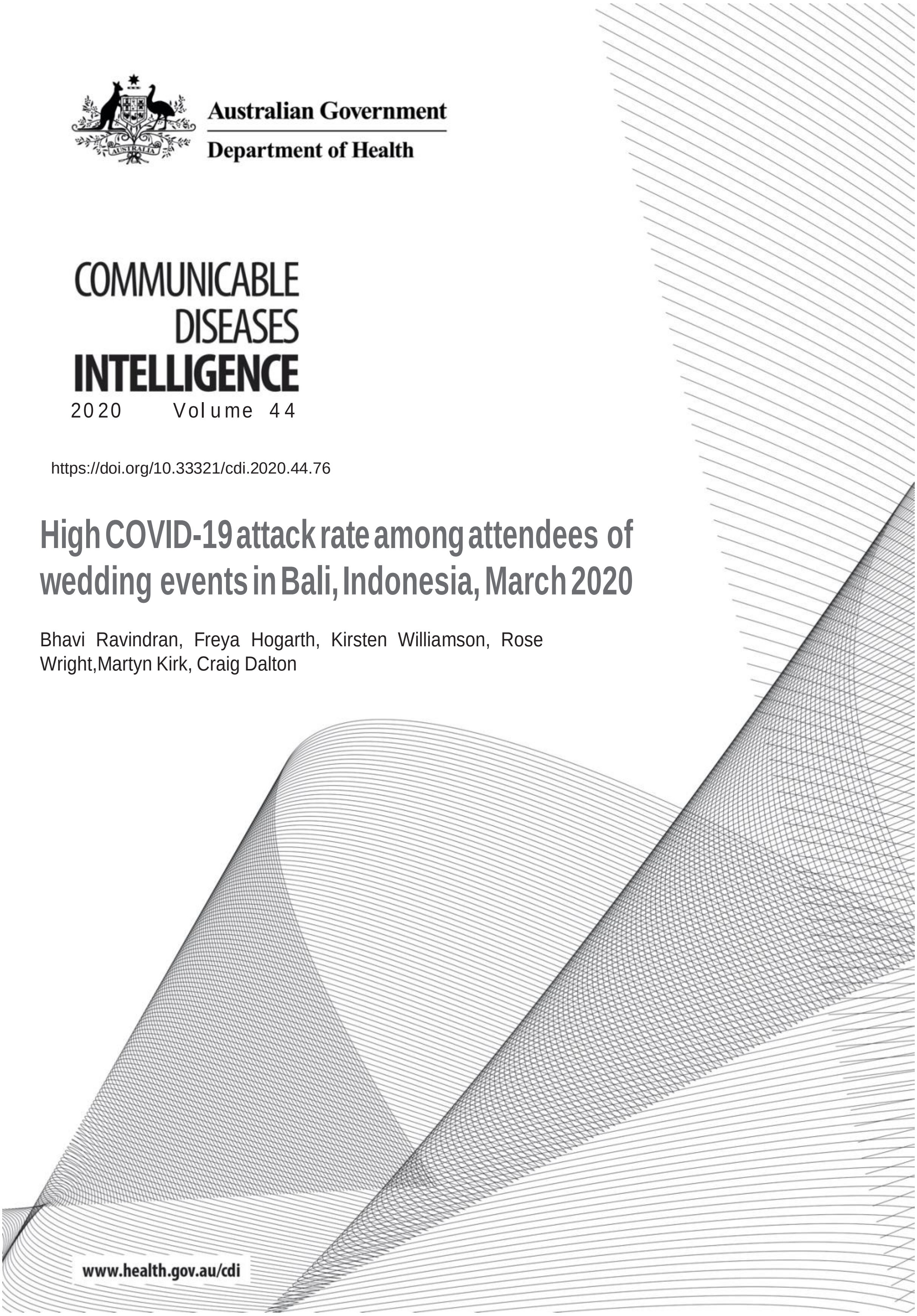
Results

The guest attendance to wedding events during the study periods varied. Of attendees, 56% (23/41) were confirmed COVID-19 cases, along with one secondary case who was a close contact. The median age of cases was 31 years (range 3–64) and all reported a mild illness with no deaths. No cases occurred among six guests who left prior to the actual wedding day. Guests attended multiple events and participated in high-risk transmission behaviours such as shaking hands, kissing, dancing, sharing drinks and sharing shisha (waterpipes); attack rates ranged from 64–87% for different exposures. Attendees sharing shisha at least once over the wedding events were twice as likely to be cases (RR = 2; 95% CI: 0.99–4.75).

Conclusion

Our investigation identified a very high transmission of SARS-CoV-2 among a cohort of young wedding attendees. We did not identify a single risk factor, but attendees engaged in close physical contact, sharing drinks and smoking paraphernalia, and shared spaces during the wedding, which may have contributed to the high attack rate. This outbreak highlights the significant role social gatherings can play in transmission of COVID-19 and underscores why it is important to limit gatherings and close physical contact to control the spread of COVID-19.

Appendix A – Published manuscript



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High COVID-19 attack rate among attendees of wedding events in Bali, Indonesia, March 2020

Bhavi Ravindran, Freya Hogarth, Kirsten Williamson, Rose Wright, Martyn Kirk, Craig Dalton

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Surveillance summary

High COVID-19 attack rate among attendees of wedding events in Bali, Indonesia, March 2020

Bhavi Ravindran, Freya Hogarth, Kirsten Williamson, Rose Wright, Martyn Kirk, Craig Dalton

Abstract

Background

Large gatherings are associated with the spread of coronavirus 2019 disease (COVID-19); however, transmission dynamics are not well understood. We investigated a cluster of COVID-19 cases in returning Australian residents who attended wedding events in Bali, Indonesia, during 15–21 March 2020. Attendees participated in various social events and were in close proximity, providing multiple opportunities for transmission.

Methods

We conducted a retrospective cohort study of the 41 attendees, of whom 17 participated in a structured interview that included history of illness, risk exposures and event attendance. We obtained data for the remaining 24 participants through corroborative histories and public health unit case investigations.

Results

COVID-19 was identified in 56% of attendees (23/41), with illness onset between 21 March and 2 April 2020. One secondary case was identified in a household contact of an attendee. The median age of cases was 31 years (range 3–64). One case was hospitalised and did not require critical care. There were no deaths. No cases occurred among six attendees who left prior to the actual wedding day. Guests attended multiple events and participated in high-risk transmission behaviours such as shaking hands, kissing, dancing, sharing drinks and sharing shisha (water pipes). Attack rates ranged from 64% to 87% for different exposures. We could not identify a single risk exposure that accounted for all cases; it is therefore likely there were multiple episodes of transmission.

Conclusion

Our investigation identified a high attack rate of COVID-19 among a cohort of wedding event attendees. Attendees engaged in close physical contact, shared drinks and shisha, and were in close proximity during the wedding events, which may have contributed to the high attack rate. This outbreak highlights the significant role social events can play in transmission of COVID-19 and underscores why it is important to limit gatherings and close physical contact to control the spread of the virus.

Keywords: Smoking, shisha, SARS virus, risk factors, Indonesia, coronavirus disease 2019 (COVID-19), Australia, public health, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), outbreak

Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), first identified in Wuhan, China in December 2019, has resulted in a pandemic of the associated disease, coronavirus disease 2019 (COVID-19).[1] Accumulating evidence suggests that large social events such as weddings,[2] church services,[3] and choir practices[4] are implicated in the spread of SARS-CoV-2; however, public health agencies are still learning about transmission dynamics and epidemiological features.

On 24 March 2020, we were notified of a confirmed COVID-19 case in an Australian resident who had recently attended a wedding in Bali, Indonesia. Investigations by health departments in other Australian states and territories identified a cluster of cases amongst attendees of the same wedding. Early case interviews revealed that attendees stayed in close proximity and socialised together before and after the wedding day, thus providing multiple opportunities for SARS-CoV-2 transmission.

We conducted a retrospective cohort study of the 41 attendees of the wedding events. The report examines the risk factors associated with transmission at the wedding events.

Methods

Study design

We conducted a retrospective cohort study of attendees who participated in at least one event that was (a) associated with the wedding and (b) took place during 15–21 March in Bali. All attendees were non-residents of Bali, Indonesia, and travelled only to attend the wedding events.

Semi-structured, hypothesis-generating interviews were conducted via telephone with a subset of four attendees. A structured questionnaire was designed using the *OzFoodNet* salmonella and NSW Health COVID-19 case questionnaires,[5,6] informed by the initial public health case investigation and aforementioned hypothesis-generating interviews. Questions encompassed: demographic information; history and duration of illness; event attendance; potential risk activities; and protective behaviours, such as handwashing.

Respondents either were interviewed via telephone or completed an online questionnaire. Study data was collected and managed using REDCap electronic data capture tools hosted at Hunter New England Health.[7] Information on attendees who were unable to be interviewed was obtained from initial case investigations; from contact tracing interviews; and from attendees whom we were able to contact, through corroborative histories. Public health units actively monitored all close contacts for symptoms of COVID-19, and they were tested if they became symptomatic.

Case definition

We defined a primary case as any person who attended the wedding events in Bali Indonesia during 15–21 March 2020 and who tested positive to a SARS-CoV-2 real-time reverse transcription-polymerase chain reaction (RT-PCR) assay within 14 days of 21 March 2020 (the upper limit of one incubation period for COVID-19).[8] A secondary case was defined as any person who tested positive on SARS-CoV-2 RT PCR assay after the 14 day period and who was a close contact of a COVID-19 case from the wedding events. A close contact was defined as face-to-face contact for greater than 15 minutes cumulative in the period extending from 48 hours before onset of symptoms in a confirmed case; or sharing of a closed space with a confirmed case for a prolonged period of time in the period extending from 48 hours before onset of symptoms in a confirmed case.[9]

Data analysis

We conducted data analysis using Stata version 13 (Statacorp., USA). We calculated proportions and attack rates (AR). We performed univariate analysis to calculate relative risks (RR), risk difference (RD) and associated 95% confidence intervals (CI) to examine associations between event attendance or activities and subsequent SARS-CoV-2 infection.

Ethical considerations

The investigation was undertaken as part of the public health emergency response under the *NSW Public Health Act 2010*;[10] therefore, ethics approval was not required. Informed consent was obtained from all participants prior to interviews. Permission was granted from relevant jurisdictions for use of case data collected by public health units. The Australian National University Human Research Ethics Committee (Protocol 2017/909) has a standing approval for outbreak investigations involving staff and students.

Results

A total of 41 people attended wedding events from 15 to 21 March 2020, with guest attendance varying for each of the seven events. Among the attendees, 56% (23/41) met the primary outbreak case definition. There was one secondary case in a household contact of a primary case, after that case had returned to Australia. None of the six guests who left Bali the day prior to the wedding day contracted COVID-19. All attendees who returned to Australia after 15 March 2020 were required to undertake 14 days of quarantine.[11]

The majority of attendees (78%, 32/41) were aged 20–39 years; 75% of cases (18/24) were in this age group. The median age of cases was 31 years (range 3–64 years), which was similar to non-cases at 30 years (range 3–71 years). There was no difference in attack rates between males and females.

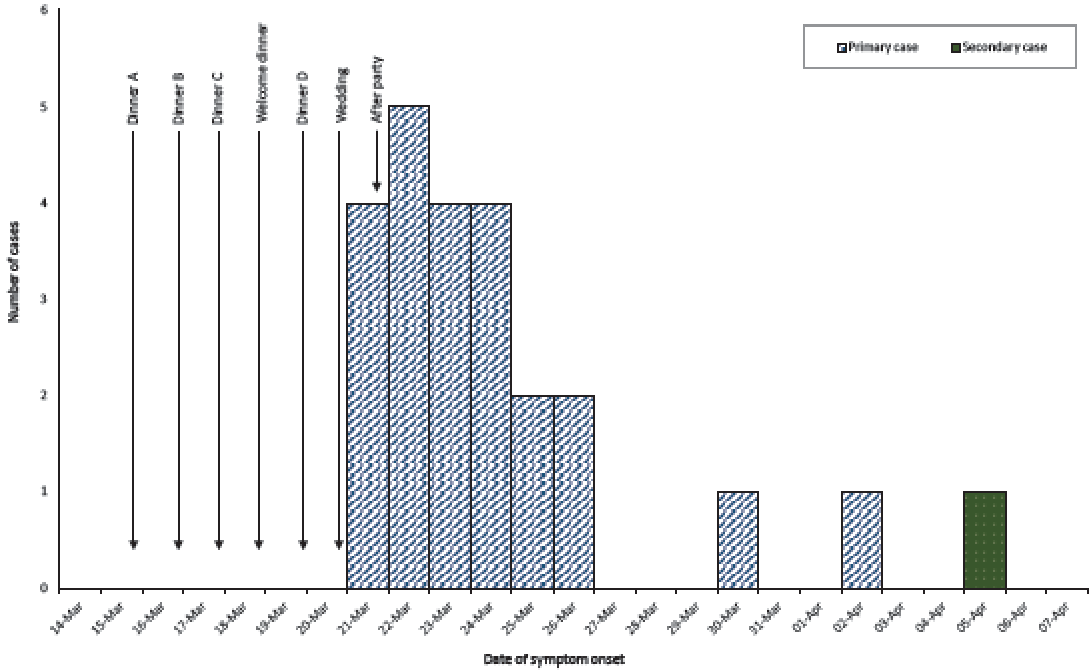
Demographic and limited exposure information was available for 41 attendees. Seventeen attendees (11 cases and 6 non-cases) participated in the study interview (14 attendees) or online questionnaire (3 attendees). Varying symptom data were available for the 12 of the remaining 13 cases, from public health unit case investigation

Table 1: Symptom profile of 23 confirmed cases[a] of COVID-19 among attendees of the wedding event, Bali, 15–21 March 2020

Symptom	Frequency	Percent (%)
Cough	19/23	83
Chills/rigors	16/20	80
Loss of taste	10/13	77
Headache	16/23	70
Loss of smell	9/13	70
Fatigue	14/20	70
Fever	12/23	52
Arthralgia or myalgia	10/23	44
Sore throat	9/23	39
Rhinorrhoea	7/23	30
Shortness of breath	6/23	26
Diarrhoea	6/23	26
Chest pain	4/23	17
Vomiting	0/23	0
Diagnosed with pneumonia	0/23	0

a No clinical symptom information was available for one of the 24 cases.

Figure 1: Epidemic curve of COVID-19 cases by onset date at wedding events in Bali, Indonesia, 15–21 March, 2020



forms. Of the cases, 83% (19/23) reported cough, 80% (16/20) chills/rigors, 77% (10/13) loss of taste, 70% (10/13) loss of smell, 70% (16/23) headache, and 52% (12/23) fatigue (Table 1).

The median time from onset of any symptom to the onset of loss of taste was 4.5 days (range 1–7), and from any symptom onset to the onset of loss of smell was 4 days (range 1–7). The median duration of illness was 10.5 days (range 3–23 days). One case was hospitalised but did not require critical care, and there were no deaths.

The estimated attack rates at the different wedding events ranged from 61 to 77% (Table 2). The excess risk for COVID-19 among those who attended the wedding day was 66% (95% CI 50–81%). All attendees participated in activities resulting in potential exposure, such as shaking hands, kissing, dancing, sharing drinks and sharing shisha (smoking water pipes), with estimated attack rates ranging from 64 to 87% (Table 2). Attendees sharing shisha at least once over the wedding events were twice as likely to be cases (RR = 2; 95% CI: 0.99–4.75).

During their trip to Bali, approximately 88% (15/17) of attendees reported hand washing always before meals, 24% (4/17) used a facemask at least once, and none (0/17) of the attendees used gloves.

Discussion and conclusion

We describe transmission of SARS-CoV-2 among a cohort of people attending wedding events involving multiple high-risk activities. Guests attended several social gatherings where they engaged in close physical contact, shared drinks and smoking utensils, and shared indoor and outdoor spaces for prolonged periods during the wedding events. We postulate that these repeated exposures contributed to the high attack rate amongst attendees. Our findings are consistent with other reports suggesting physical contact during social gatherings poses a risk for rapid transmission.[12] Indirect contact (e.g. via fomite and sharing drinks) is thought to facilitate transmission of COVID-19.[13]

Table 2: Estimated attack rates of COVID-19 among attendees at wedding events, Bali, Indonesia, 15–21 March 2020[a]

Exposure activity	Exposed			Unexposed			RR	95% CI
	Cases	Total	AR%	Cases	Total	AR%		
Shared shisha	13	15	87	4	10	40	2.2	[0.99–4.75]
Kissed	10	13	77	0	3	0	–	–
Shared drinks	9	13	69	1	4	25	2.8	[0.49–15.71]
Danced	9	14	64	1	3	33	1.9	[0.37–10.01]
Shook hands	8	12	67	2	4	50	1.3	[0.46–3.84]
Event attendance								
Dinner A	7	9	78	7	13	54	1.4	[0.82–2.68]
Dinner B	5	7	71	9	15	60	1.3	[0.70–2.22]
Dinner C	7	9	78	7	13	54	1.4	[0.82–2.68]
Welcome party	23	41	56	0	0	–	–	–
Dinner D	14	22	64	0	6	0	–	–
Wedding day	23	35	66	0	6	0	–	–
After party	11	18	61	5	12	42	1.5	[0.68–3.15]

a Exposure and event attendance information were obtained from questionnaires and corroborative histories.

We hypothesise that smoking shisha, which is considered a possible transmission vehicle of infectious disease[14] such as tuberculosis,[15] may have assisted SARS-CoV-2 transmission and therefore contributed to the high attack rate. To date, there is limited evidence documenting the contribution of shisha use in the spread of COVID-19. Our results represent the poor understanding of risks and preventative measures to minimise the spread of COVID-19 amongst the wedding attendees.

In this cohort, we observed a high attack rate of a relatively low-severity illness. Importantly, 11 cases questioned specifically about loss of taste (77%) and smell (70%) reported these as symptoms. Although these symptoms are known predictors of mild and early SARS-CoV-2 infection,[16,17] our findings support limited evidence that loss of taste and loss of smell develop later in illness.[18]

Based on the shape of the epidemic curve and the known serial interval,[19] it is possible that multiple points of infection occurred within the cohort in Bali and it remains unlikely there was a single point-source exposure. Australia's mandatory quarantine of returned travellers, and attendees' compliance with these regulations, minimised ongoing transmission from the cases in our cohort to the broader Australian community.

Our investigation findings are subject to some limitations. Firstly, we had only a moderate response rate for follow-up interviews, meaning we had insufficient power to assess the importance of some risk behaviours and subsequent SARS-CoV-2 infection. Secondly, initial case interviews were conducted by multiple public health units that collected differing symptom and exposure information. Thirdly, participant interviews were conducted up to 4 weeks after the wedding; recall bias may have affected the quality of the data collected. Hotel and event staff in Indonesia were not tested or interviewed to identify potential source cases for the wedding cluster. We were also unable to investigate whether any of the cohort were asymptomatic cases, due to Australia's testing criteria at the time that limited testing to persons with symptomatic illness. Despite these limitations, we still demonstrate that frequent and prolonged interactions can contribute to the high attack rates of COVID-19 in this cohort.

Our study highlights the important role which social gatherings play in transmission of COVID-19 and underscores the importance of physical distancing to control the spread of COVID-19. The findings support Australian public health recommendations at this point in the epidemic to not shake hands or exchange physical greetings, and wherever possible for persons to stay 1.5 metres apart to reduce SARS-CoV-2 transmission.[20] We emphasise the importance of public health messaging to discourage sharing of smoking utensils, drinks, food and other vehicles that may transmit SARS-CoV-2.

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Appendix B – Plain Language Summary for Bali wedding study participants

In March 2020, there was an outbreak of novel coronavirus disease 2019 (COVID-19) in a group of people attending a wedding in Bali, Indonesia. The Hunter New England Public Health Unit interviewed people who had participated in many activities and stayed close together during the wedding period.

COVID-19 primarily spreads from one person to another through close contact with an infected person, mainly through contact with droplets from coughing or sneezing. Among people travelling to Bali to attend the wedding, 56% (23/41) became infected with COVID-19. It was important to understand why such a high proportion of people were infected.

The investigation captured information from participants and State and Territory health department interviews. The investigation team conducted a series of phone interviews with some of the people who attended the wedding. People were asked whether they had been ill, what events they attended, what activities they took part in, and any measures taken to protect themselves against COVID-19.

There was little difference in the age and gender of those infected with COVID-19 and those who were not. People infected with COVID-19 had a mild illness and no one required hospitalisation for COVID-19 illness. None of the guests who left Bali prior to the wedding day were infected with COVID-19.

A single cause of infection among the group was not identified. Guests attended multiple activities where they engaged in close contact, sharing drinks and shisha, and occupying shared spaces for long time periods across all wedding events. This may have contributed to the spread of the virus. The Australian requirements that all international travellers complete quarantine on return to Australia minimised spread of the virus to other people.

This investigation shows the important role that social gatherings can play in the spread of COVID-19. It highlights why it is important to limit gatherings and minimise close physical contact to control the spread of COVID-19 among people. This study will help guide public health approaches to prevent further spread of this disease.

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Chapter 5. Data analysis

Effect of the COVID-19 pandemic and public health measures on salmonellosis in Australia, 2020

Table of Contents

Prologue

Study rationale

In Australia, the initial public health response to the Coronavirus disease 2019 (COVID-19) pandemic started near the end of January 2020 and was followed by the implementation of public health measures and restrictions on people's ability to work, travel, gather and interact from March 2020. A preliminary analysis of nationally notifiable salmonellosis data conducted by the Department of Health reported lower than average case notifications in the first half of 2020. The reported incidence of other infectious diseases under surveillance in 2020 had also been observed to be reduced, particularly for respiratory infections and influenza. Non-typhoidal *Salmonella* infection (salmonellosis) is one of the leading causes of hospitalisation and deaths due to foodborne disease Australia. This project aimed to assess the potential impact of the COVID-19 pandemic and the associated public health measures on salmonellosis in Australia in 2020.

My role

This data analysis project was identified by the Communicable Disease Epidemiology and Surveillance Section at the Department of Health as a priority research project for a Master of Applied Epidemiology (MAE) student. The preliminary analysis suggested observed changes may reflect a combination of reduced exposure to *Salmonella* due to restrictions on travel and closure of restaurants and the hospitality sector, which highlighted an important question related to the extent of the impact these measures had on salmonellosis during 2020. In this project, I conducted a literature review, prepared the research plan, applied for Human Research Ethics Committee approval, collated the data sets, and conducted data cleaning and analysis.

Lessons learnt

Originally, when scoping this project, I had planned to use Health Services Australia data to examine the activity of gastroenteritis related calls to Healthdirect Australia during 2020 as an indicator of community level incidence of *Salmonella* illness. While there is some evidence that gastroenteritis calls to telephone based help advice services correlates with actual gastroenteritis activity in general practices, emergency departments (ED) and the community, a previous MAE scholar, Mica Hartley (2018), investigated the utility of conducting surveillance at Healthdirect for gastroenteritis illness through comparing the incidence of calls to the Australian Sentinel Practices Research Network, the New South Wales (NSW) ED and the Western Australia (WA) ED. While Hartley found that building a case definition using the symptoms of *Diarrhoea* OR *Vomiting* had the strongest correlation between the data sets, these findings were limited without further comparison data sources. Once I extracted the data from the Department of Health's REDCap database using a series of patient symptoms, I subsequently cleaned and analysed the data to then realise it was not completely representative of Victoria (Vic), Queensland (Qld), and Tasmania (Tas). I subsequently learnt that these states predominantly use alternative Nurse Triage services and general practitioner helplines. While this experience was a useful process because I learnt about the analytic challenges in using syndromic surveillance, it's a good idea to investigate the data sources and available materials prior to starting a project.

The technical aspects of the project were interesting to me as I had planned to try to advance my data analysis skills and use a negative binominal regression to estimate incidence rate ratios by state and territory. However, since there was a large salmonellosis outbreak in the first half of 2020, I needed to account for outbreak cases in my line-listed data. Unfortunately, on review of the NNDSS I found poor completeness of the outbreak reference field and I could not account for outbreak cases, and consequently limited this analysis.

Overall, I found this project refreshing since it exposed me to foodborne disease epidemiology. I developed an understanding of the importance of assessing changes in testing methods to determine their impact on surveillance of enteric diseases. I also learnt that the level of completeness of extended typing fields for *Salmonella* varied depending on the reporting state or territory and the level of laboratory investigations conducted. This was important when interpreting results, and I found it useful to detail these caveats in my data cleaning log in R. I also learnt using both the percentage and number of notifications for surveillance provides a broader understanding of data trends. Finally, in detailing these trends, I built on my data visualisation skills in R utilising the ggplot packages.

Public health implications

The COVID-19 pandemic and associated public health measures present challenges to explaining changes in salmonellosis incidence. Given surveillance data is used to monitor the effectiveness of health prevention measures in limiting transmission of *Salmonella* and decreasing illness, any significant increase or decrease in notifications should be investigated. Findings of this analysis could be used to guide future pandemic planning for surveillance of salmonellosis, particularly at the community level.

MAE course requirements

Analysis of a public health dataset.

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I wish to acknowledge the following persons and organisations for their assistance with this project: Rose Wright, Stacey Kane, Ben Polkinghorne, Katie Glass, and OzFoodNet

Abstract

Background

The 2019 coronavirus pandemic (COVID-19) and consequent public health measures have had an indirect influence on other infectious diseases. Salmonellosis is one of the leading causes of foodborne gastrointestinal illness in Australia. Early in 2020, national surveillance data suggested a decrease in the trend of *Salmonella* infections. The pandemic had direct impacts on health seeking behaviours, diagnostic laboratory testing strategies, the workload of public health units, and may have led to a change in transmission dynamics of other infectious diseases. I aimed to assess the impact of the pandemic and associated public health measures on salmonellosis under surveillance in Australia in 2020.

Methods

I conducted retrospective analyses of nationally collected salmonellosis surveillance data reported to the National Notifiable Disease Surveillance System in Australia in 2020 compared with the 5-year historical average (2015-2019). Monthly, quarterly, and annual salmonellosis notifications per 100,000 population for each state and territory in 2020 were compared with the previous 5-year average. Notification rates by age, sex, place of acquisition, and serovar were also examined. Medicare Australia claim data for pathology services was used as the denominator in a separate analysis to assess the potential impact of changes to testing practices for *Salmonella*.

Results

The salmonellosis notification rate in Australia was 27% lower in 2020 than the historical 5-year average. Reductions were observed across all age groups and both sexes, with substantial declines in international travel associated cases (99%) from Q2-Q4 where reported. From Q2, states and territories with the application of longer COVID-19 public health measures reported greater reductions in salmonellosis incidence, while demographic and environmental factors in the Northern Territory and Western Australia may have had more of an impact on high salmonellosis rates in these jurisdictions.

Conclusion

The observed changes in salmonellosis incidence in the context of the COVID-19 pandemic suggest reduced exposure to *Salmonella* due to restrictions to social gatherings and international travel, closure of dine-in restaurants and the hospitality sector, and changes in health-seeking behaviours that impacted diagnostic testing for salmonellosis. Continued surveillance may improve the understanding of how COVID-19 public health measures target *Salmonella* transmission.

Introduction

Salmonellosis is an acute gastrointestinal disease caused by infection with *Salmonella enterica*, a gram-negative bacteria that can infect humans through the ingestion of contaminate food or water. Other less common routes of transmission include direct contact with the environment, contact with infected animals, and human-to-human spread.[1] There are more than 2,500 serotypes of *Salmonella* enterica, less than 100 are responsible for most human infections.[2] Typhoidal *Salmonellae* (*Salmonella* Typhi and *Salmonella* Paratyphi A, B, and C, not including *Salmonella* Paratyphi B var Java) are human-adapted serotypes causing enteric fever after ingesting contaminated food or water.[3] Non-typhoidal *Salmonella* serotypes have a variety of hosts and reservoirs and cause a spectrum of illnesses in humans known as salmonellosis.[2]

Salmonellosis is typically characterised by the acute onset of diarrhoea, abdominal pain, nausea, and fever.[4, 5] Symptom onset usually starts 6 to 72 hours after infection and symptoms typically last for 2 to 7 days.[6] While most people with salmonellosis recover without specific treatment, high-risk groups including infants and the elderly are more likely to develop severe illness that can lead to hospitalisation or death.[4, 6] In addition, it has been estimated that approximately 8.8% of people infected with non-typhoidal *Salmonella* develop irritable bowel syndrome (IBS) and 8.5% develop reactive arthritis (ReA).[7, 8]

Salmonellosis in Australia

In Australia, *Salmonella* infections are a leading cause of hospitalisation and death from gastrointestinal illness.[9] While the reported incidence of salmonellosis has been declining since 2016, at 56.6 cases per 100,000 population in 2018, the rate was still substantially higher than the European Union (19.6/100,000)[10] and USA (16.67/100,000).[5] In Australia circa 2015, it was estimated that 90,833 cases, 4,312 hospitalisations, and 19 deaths occurred from salmonellosis, at direct cost of AUD 23.8 million and a total cost of AUD 124.4 million.[8] Foodborne infections were estimated to be responsible for AUD 88.9 million from acute salmonellosis and 10.4 million when IBS and ReA were included.[8] These costs extend beyond the health care system to affect the economy, industry, and community.

Weather is a key influence on salmonellosis as higher temperatures enable faster replication of *Salmonella* in environment and food.[11, 12] In Australia, non-typhoidal serotypes are predicted by climatic and geographical factors,[13, 14] and rates and trends differ between and within state and territories.[11, 15, 16] While infections display a strong seasonal trend, fluctuations in salmonellosis incidence can result from indirect effects of season as consumption of certain foods change seasonally.[11, 12]

Nationally, it is estimated that 72% of *Salmonella* infections are transmitted through contaminated food.[1, 16] Infection from contaminated foods is an important cause of both sporadic cases and outbreaks (responsible for 53% of all foodborne outbreaks in 2013–2015), and outbreaks are of economic importance because of the widespread impacts for industry and food regulators.[9] Common foods associated with salmonellosis outbreak investigations and source attribution studies include egg, poultry, pork, and dairy products.[9]

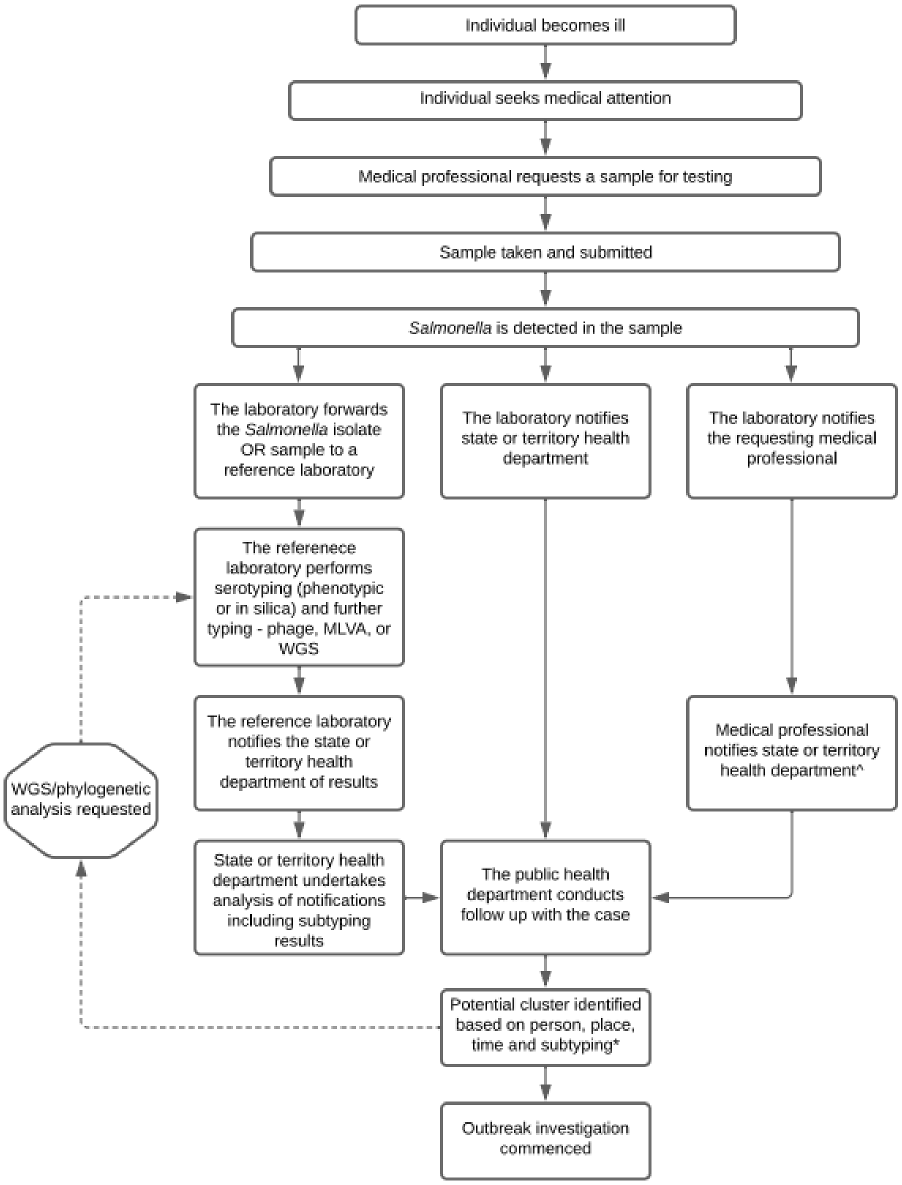
Salmonella Typhimurium (*S*. Typhimurium) is the most commonly notified serovar in Australia, accounting for 48% of all typed notifications during 2013-2015, and was the most frequently identified aetiological agent in foodborne outbreaks (90%).[9, 17] Of *S*. Typhimurium outbreaks during this period, 55% were associated with raw egg-based dishes (e.g. mayonnaise, dressings and desserts).[9] *Salmonella* Enteritidis (*S*. Enteritidis) is an important serotype because it can infect poultry and has the unique ability to infect the internal content of eggs.[9, 17, 18] While the majority of reported cases are associated with overseas travel [9, 17, 18], there have been recent foodborne outbreaks in humans and detections of *S*. Enteritidis in Australian egg layer flocks.[19, 20]

Public health surveillance of *Salmonella*

Salmonellosis is a nationally notifiable disease, and all state and territory public health departments are required to nationally report cases to the Nationally Notifiable Disease Surveillance System (NNDSS) under the *National Health Security Act 2007*.[9] The steps involved in the surveillance of *Salmonella* in Australia differ by state and territory. The steps are shown in Figure 1 and briefly described below.

Salmonellosis surveillance begins when a person becomes ill, seeks medical attention, and submits a stool, urine, or blood specimen to test for *Salmonella* infection. A confirmed case requires the isolation or detection of *Salmonella* species (excluding serotypes captured under the case definitions for typhoid and paratyphoid).[21] Once *Salmonella* is detected in a sample, isolates may be forwarded from pathology laboratories to a state reference laboratory to confirm *Salmonella* using biochemical identification and complete serological identification. Other specific subtyping such as multi-locus variable number tandem repeat analysis (MLVA) and/or whole genomic sequencing (WGS) can also be performed.[22] Until recently MLVA was routinely performed for *S*. Typhimurium in most jurisdictions to identify related isolates for investigation.[22-24]

The state reference laboratory notifies the health department of the results. Some smaller jurisdictions (i.e. NT, ACT, Tas) send samples interstate for subtyping. Epidemiological information is obtained by the department through interviewing cases and contact tracing.



^Requirement depends on state public health department of health
** In most states/territories, cases are interviewed at this point, while ACT often interview all cases on initial notification of Salmonella species*

Figure 1. Steps involved in surveillance of salmonellosis in Australia

When there is an increase above the expected number of cases of a particular serotype in a given population and geographical area, public health departments initiate an outbreak investigation. Early detection of *Salmonella* outbreaks is essential to control the source of infection and prevent further cases of illness. At this point, whole genome sequencing (WGS) may be requested to characterise microbial genomes to rapidly differentiate *Salmonella* isolates.[25] WGS is a highly discriminative subtyping method and has proven usefulness for identifying smaller foodborne outbreaks that may otherwise not have been identified as well multi-state outbreaks, and even outbreaks that cross international borders. However, like all typing methods WGS must be interpreted in an epidemiological context, and identifying common exposures between cases through interview is a vital step to generate a hypothesis regarding the source of infection.[26]

Public Health response to COVID-19 in Australia

Since the first case of Coronavirus 2019 (COVID-19) was identified in Australia on 25 January 2020, all state and territories have reported cases of COVID-19. The epidemiology of COVID-19 in Australia is discussed in detail in Chapter 2. From March 2020, state and territory governments implemented a range of public health measures to limit the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). A 14-day mandatory hotel quarantine was introduced for all returned travellers on March 29; regional lockdowns began in April, followed by stay-at-home recommendations, physical distancing policies and mandatory mask wearing. These restrictions had a serious impact on the Australian society by limiting people's ability to work, travel, gather and interact (Table 1). The timing of key events and restrictions are summarised in Appendix A.

The COVID-19 pandemic placed a substantial burden on the Australian public health system, including health departments, diagnostic laboratories, and hospitals to respond and manage thousands of cases and close contacts. While Australia had significantly less cases and severe health impacts seen in many other countries[27], the direct and indirect effects of COVID-19 on the health system were immense. Even in areas where COVID-19 case numbers were relatively low, preparation and planning for major outbreaks resulted in significant changes to routine services.[28] Some health services were restricted at various times (i.e. non-urgent and elective surgeries), there was a decreased need for others (i.e. injury, emergency services), and services in the community increased due to changes to health-seeking behaviours of different groups in the population.[29] Commencing 13 March 2020, temporary COVID-19 Medicare Benefits Schedule (MBS) telehealth and phone consolation numbers were available to a range of health care professionals to reduce the risk of community transmission of COVID-19 and provide protections for patients and health care providers.[30]

Table 1. Public health restrictions implemented in response to the COVID-19 pandemic, 2020

Stage 1 restrictions
• Closure of pubs, clubs, hotels, gyms and indoor sporting venues, cinemas, entertainment venues, casinos, and night clubs • Restaurants and cafes restricted to takeaway and/or home delivery • No religious gatherings in places of worship, or funerals in enclosed spaces and where the 1 person per 4 square metre rule cannot apply • Non-essential gatherings limited to < 500 people outside or < 100 people inside • Avoid non-essential travel • Schools and childcare open
Stage 2 restrictions
• Outdoor private and public gatherings, and outdoor recreation activities limited to a maximum of 20 people • Religious gatherings, places of worship or funerals limited to 50 people if indoors • Beauty venues and hairdressers limited to ≤ 20 people • Work and school from home where possible
Stage 3 restrictions
• Indoor and outdoor gatherings limited to 2 people • Leave home for essential purposes only (food, work, education, exercise) • Mandatory face coverings in public (indoor and outdoor) • Essential workers only [31]
Stage 4 restrictions
• Leave home for essential reasons in a 5km radius (food, work, exercise, and caregiving) • Exercise with one another person from the same household • Closure of schools

Aims and objectives

In Australia, salmonellosis is a substantial public health problem, and prior to 2020 the incidence of *Salmonella* infection has been decreasing at a steady rate. Globally, there is a growing body of evidence indicating that the COVID-19 pandemic and implemented control measures have had direct and indirect impacts on salmonellosis incidence. The reasons behind changes in surveillance data are multifactorial, and changes to health seeking behaviours – how and when people seek healthcare – and uptake of telehealth services may have influenced subsequent diagnosis and reporting.

In this study, I aim to assess the impact of the COVID-19 pandemic and associated public health measures on salmonellosis under surveillance in Australia during 2020. The study has the following objectives:

- To summarise and describe trends in the epidemiology and reported incidence of salmonellosis during 2020 when compared to the historical 5-year average (2015-2019);
- To assess whether changes in trends might be influenced by faecal culture testing rates by comparing rates in 2020 to the historical 5-year average (2015-2019); and
- To identify the timing and implementation of COVID-19 public health measures and uptake of telehealth services in relation to the observed trends.

Methods

I conducted a descriptive analysis of three main data sources as summarised below. All analyses were performed R Statistical Software[32] version 4.0.01. Ethics approval was obtained from the Australian National University Human Research Ethics Committee [protocol 2021/185].

National Notifiable Diseases Surveillance System

All confirmed notifications of salmonellosis with diagnosis dates from 1 January 2015 to 31 December 2020 (inclusive) were extracted from the NNDSS on 29 April 2021. Fields extracted included state, diagnosis date, age of onset, sex, organism, serogroup, and country of acquisition. Diagnosis date was used for all analyses, which was derived from the date of disease onset, or, when not available, the earliest recorded date amongst the following dates: data of specimen collection, date of notification or date the notification was received. I reported the incidence of salmonellosis during 2020 by month and quarters (Q1-Q4) compared to the historical 5-year average (2015-2019) over the same periods. Rates were calculated using mid-year Australian Bureau of Statistics data.[33] The direct method was used to calculate age standardised rates.

Medicare Benefit Schedule

Data on Medicare Benefit Schedule (MBS) item 69345, by month for the reporting period 1 January 2015 to 31 December 2020 were obtained from the MBS Statistical Reports published online by Medicare Australia.[34]

The definition of MBS item number 69345 is as below:

Culture and (if performed) microscopy without concentration techniques of faeces for faecal pathogens, using at least 2 selective or enrichment media and culture in at least 2 different atmospheres including (if performed):

(a) pathogen identification and antibiotic susceptibility testing; and
(b) the detection of clostridial toxins; and
(c) a service described in item 69300.[35]

Fields extracted include state/territory and month. State/territory was determined according to the address (at the time of claiming) of the patient to whom the service was rendered.[34] Month was determined by the date the service was processed by Services Australia, not the date the service was provided.[34]

The number of tests performed, and testing rate were calculated by month of sample receipt. The number of tests was used as a denominator to calculate the *Salmonella* positivity rate (infection rate per 1,000 tests performed) by month and quarter.

Results

Overview of trends in 2020

There were 12,034 confirmed cases of salmonellosis reported to the NNDSS with a diagnosis date from 1 January 2020 to 31 December 2020 inclusive, which was 25% lower than the 5-year average (2015-2019) (n=16,018), and 18% lower than 2019 (n=14,674). The national monthly rate peaked in February at 9.9 per 100,000, 30% higher than the previous 5-year average for that month (Table 2). Salmonellosis incidence decreased substantially from Q2-Q4 of 2020 (-41%) when compared to 5-year average over the same quarters, with a low of 6 notifications per 100,000 population in Q3 representing a 45% decrease (5-year average: 11/100,000) (Supplementary

Table 1). The rate increased to 9.6/100,000 in Q4 following the seasonal trend for salmonellosis activity despite remaining lower than historical figures (5-year average: 15.2/100,000; 37% decrease).

The reduction in salmonellosis rate varied between state and territories. Figure 2 shows that in February 2020 there was a sharp increase in salmonellosis rates in Northern Territory (NT), Qld, WA, Tas and NSW. From Q2-Q4, rates sharply decreased below the 5-year average in all jurisdictions and remained substantially lower than historical figures except for small peaks in WA in June and September (Supplementary Table 1). The Australian Capital Territory (ACT) and South Australia (SA) had large reductions in notifications from Q2-Q4 of 2020 compared to the average for the same quarters in 2015-2019 period (59% and 56% respectively). In Victoria the rate was 61% lower than the 5-year average, with the greatest reductions occurring in April and July 2020 coinciding with the two epidemic waves in COVID-19 cases and public health restrictions (Figure 2).

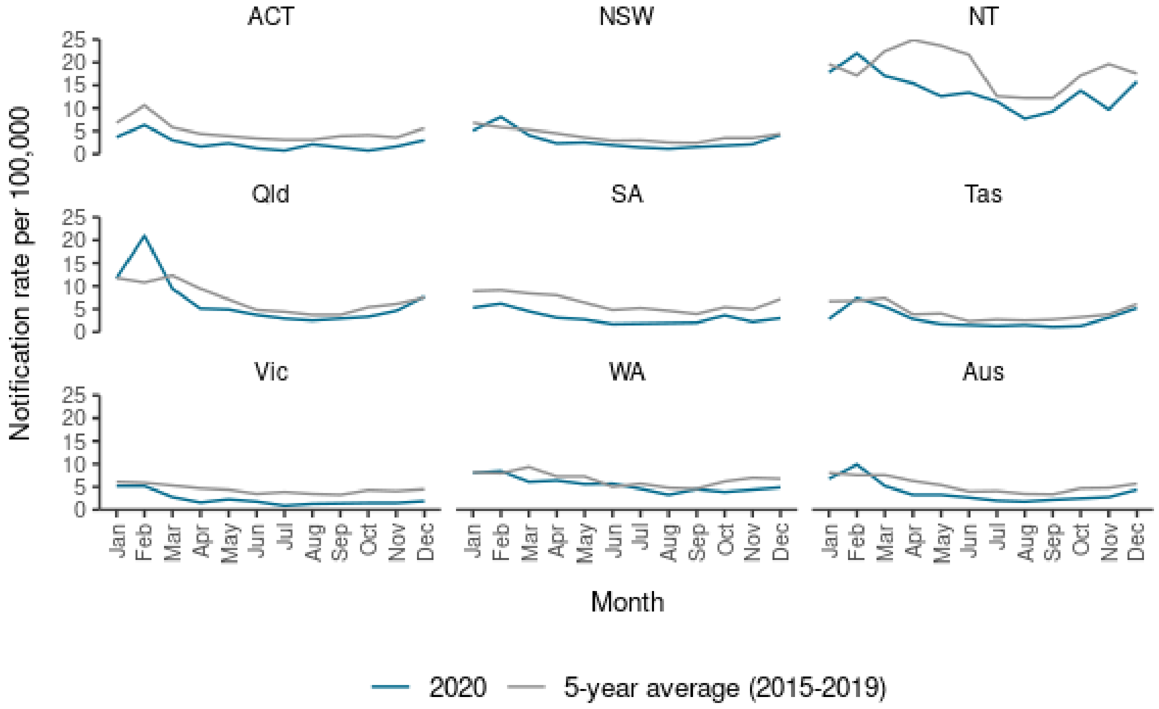


Figure 2. Rate of salmonellosis notifications in Australian states and territories, by month, 2020 vs 5-year average (2015-2019)

Demographics

Of salmonellosis notifications in 2020, 99% (12,021/12,034) included both age and sex data. The sex profile of notifications remained similar over time, in 2020, 52% (6,299/12,034) of notifications were for females, which was the same as the 5-year average (52%, 8,185/15,730). The proportion of cases among age groups also remained similar from 2015-2020. Reductions in notifications were observed across all age groups and both sexes in 2020 compared to the 5-year average, varying from a reduction of 11% in females <1 year, to reductions of 34% and 36% in males and females aged 20-29 years respectively (Figure 3). Age-specific rates for all age groups sharply decreased below historical figures from Q2, except for a rate increase comparable to historical figures in June and August of 2020 in the 80+ year age group, and September in the 5–9-year age group. Rates in the <1 year and 5–9-year age groups increased to comparable figures during Q4.

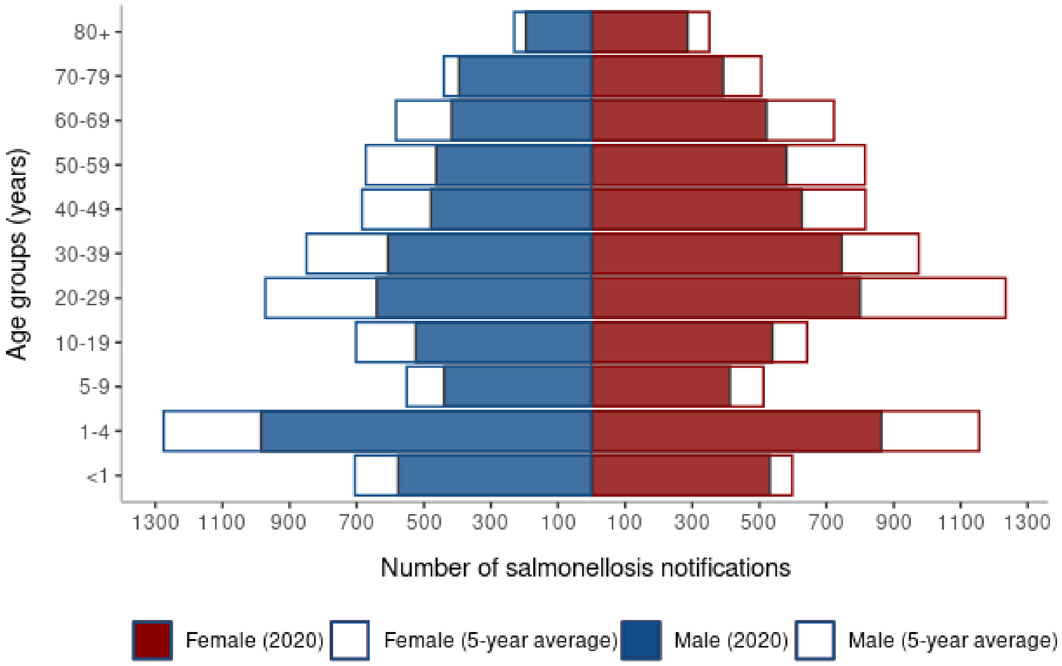


Figure 3. Salmonellosis notifications in 2020 Vs 5 -year average (2015-2019), by age group and sex

Incidence trends of *Salmonella* serovars

Of salmonellosis notifications in 2020, 91% (10,997/12,034) included serovar data. Compared to the 5-year average, there were substantial reductions in the number of notifications for commonly reported *Salmonella* serovars nationally and in states and territories in 2020 (Supplementary Table 2). Overall, the incidence was highest for *S*. Typhimurium (19.4/100,000), followed by *S*. Saintpaul (2.9/100,000), *S*. Virchow (2.3/100,000), *S*. Wangata (1.6/100,000), and *S*. Enteritidis (1.2/100,000). Rates of *S*. Stanley, *S*. Subsp I Ser 4,5,12:I:-, and *S*. Virchow showed low plateaus throughout 2020, with reductions of 77%, 62%, and 21% respectively (Figure 4). Rates of *S*. Enteritidis and *S*. Paratyphi B bv Java were substantially lower from Q2–Q4 of 2020 when compared to the previous 5-year average, with reductions of 88% and 83% respectively. Overall, the incidence of *S*. Wangata was 60% higher in 2020 comparable to the 5-year average and remained comparable to historical figures for *S*. Saintpaul.

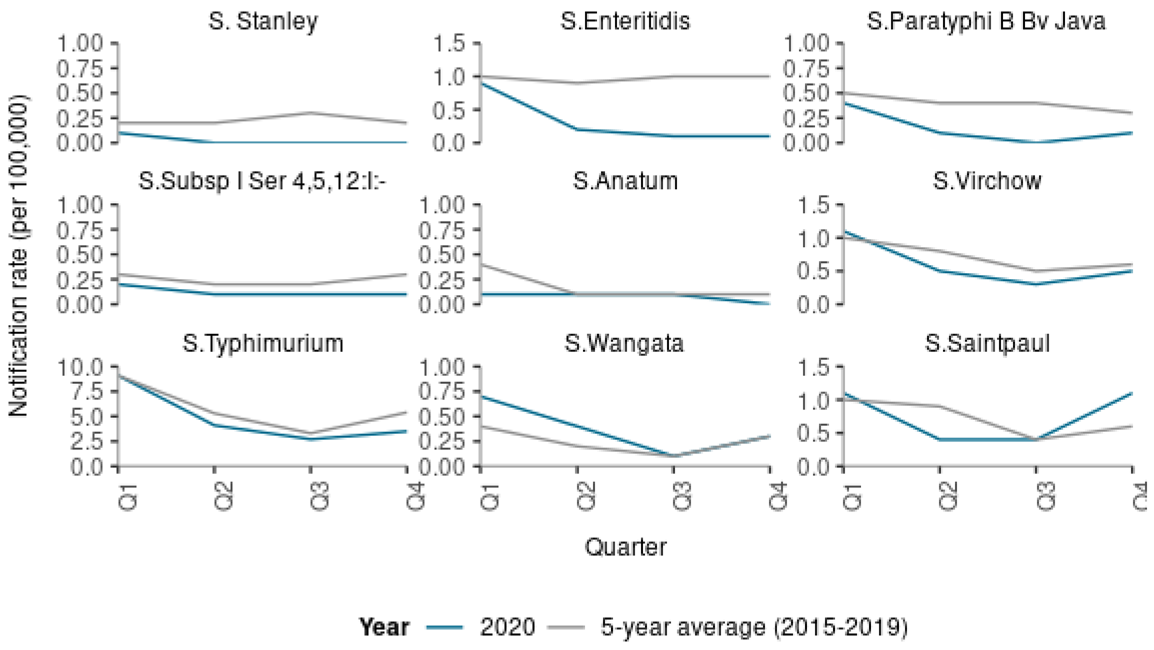


Figure 4. Notification rate per 100,000 population of the 9 common *Salmonella* serovars in Australia, by quarter, 2020 vs 5-year average (2015-2019).

The rate of *S*. Typhimurium peaked in February at 6.0 per 100,000 population, 94% higher than 5-year average for that month (3.1/100,000). *S*. Typhimurium incidence decreased notably after March 2020; in Q2, Q3 and Q4 the incidence decreased by 23%, 18% and 36% respectively, compared to the average for the same quarters of 2016-2019 (Supplementary Table 3). Large rate reductions during this period were noted in SA, Vic, ACT, and NT (Supplementary Table 3). In Qld and NT the rate of *S*. Typhimurium peaked in Q1 (increases of 81% and 49% respectively), before dropping below historical figures. In WA the rate of *S*. Typhimurium peaked in Q2 and

Q3, with increases of 40% and 47% respectively, compared to the 5-year average over the same quarters.

The incidence of non-Typhimurium *Salmonella* (27.4/100,000) in 2020 was 33% lower when compared to the previous 5-year average (41.0/100,000). Compared to *S*. Typhimurium, the rate of non-Typhimurium *Salmonella* in Q2, Q3, and Q4 of 2020 compared to the 5-year average was notably lower (50%, 57%, and 37% respectively) (Supplementary Table 4). During this period, ACT, SA, Vic, NSW, and Qld had large rate reductions of non-Typhimurium *Salmonella* compared to the 2015-2019 average, with notable reductions in Q3 in Vic (79%), ACT (68%), WA (63%), and NSW (64%) (Supplementary Table 4).

Travel related serovars

In 2020, place of acquisition was reported for 24% (2,934/12,034) of salmonellosis notifications, which was similar to 30% (4,405/14,674) in 2019 and the 5-year average of 28% (4,558/16,018). During 2020, 9% (276/2,934) of *Salmonella* infections were reported to be associated with international travel compared with the 5-year average of 31% (1,593/5,146). In 2020, the majority of these infections occurred during January-March (97%, 267/276) (Figure 6). From Q2-Q4 international travel associated cases declined by 99% compared to 5-year average in the same quarters and accounted for 4% of travel associated infections in 2020.

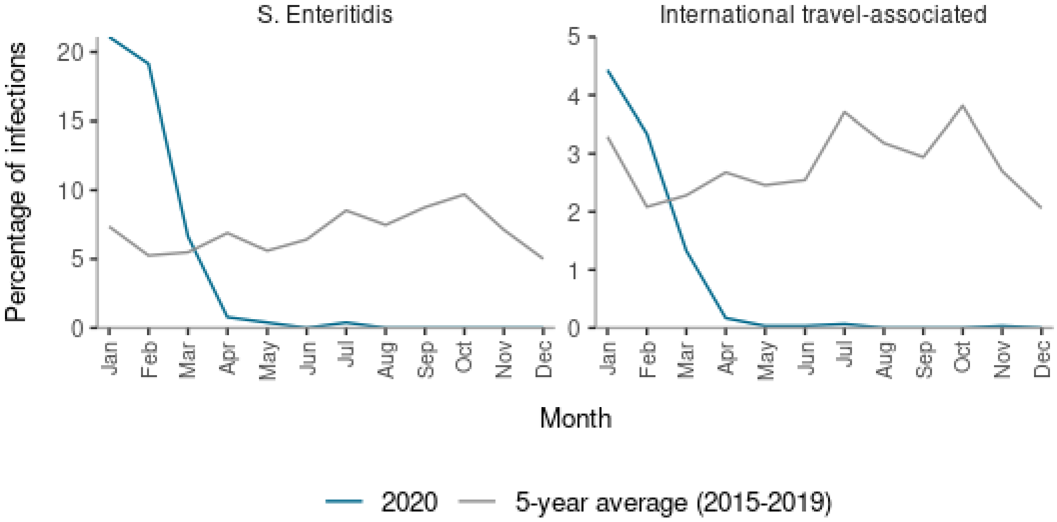


Figure 6. Percentage of *S*. Enteritidis infections with associated with international travel, and all salmonellosis notifications associated with international travel, by month, 2020 Vs 5-year average (2015-2019)

During 2020, 48% (124/256) of *S*. Enteritidis infections were associated with international travel compared with the 5-year average of 84% (716/856). The majority (97%, 120/124) of these infections were notified in Q1 (Figure 4). Similarly, 43% (30/70) of *S.* Paratyphi B bv Java infections in 2020 were associated with international travel compared with the 5-year average (70%, 160/228). In 2020, all *S.* Paratyphi B bv Java infections associated with international travel were notified in Q1 of 2020 compared with the 5-year average of 25% (40/160) (Table 4).

Culture rates

There were 515,672 subsidised tests for MBS item number 69345 for culture of faeces for faecal pathogens performed from 1 January 2020 to 31 December 2020, of which 12,034 (2.3%) had *Salmonella* detected. When the trends in tests performed and percentage of tests positive for Salmonella were examined in 2020 and compared to those in 2015-2019, a decline in the positivity rate was observed (Table 2).

In Q1 of 2015-2019, the average number of tests performed was 151,391, comparable to 154,647 tests in 2020 . Similarly, the *Salmonella* positivity rate did not differ appreciably, from an average of 3.8% in 2015-2019 to 3.6% in 2020. In February, the number of salmonellosis notifications sharply increased, and the positivity rate peaked at 4.8% (2,553/52,769) which was 30% higher than the 5-year average of 3.7% (1,861/50,339). In Q2 and Q3 of 2020 when the number of samples tested and salmonellosis notifications declined, the Salmonella positivity rate dropped when compared to the 5-year average by 15% and 32% respectively.

Table 2. Average number of subsidised tests for culture of faeces for faecal pathogens performed in Australia and the *Salmonella* positivity rate for 2015-2019, compared to 2020

Month	**2015-2019**			**2020**		
	Number of specimens tested	Number of specimens with *Salmonella* detected	*Salmonella* positivity rate (%)	Number of specimens tested	Number of specimens with *Salmonella* detected	*Salmonella* positivity rate (%)
Q1	151,391	5,729	3.8	154,647	5,637	3.6
Q2	148,948	3,847	2.6	108,869	2,384	2.2
Q3	145,410	2,698	1.9	122,979	1,541	1.3
Q4	152,602	3,744	2.5	129,177	2,472	1.9
Total	598,351	16,018	2.7	515,672	12,034	2.3

Discussion

Since March 2020 in Australia, a notable decrease in the incidence of salmonellosis reported nationally was observed among all age groups, coinciding with the implementation of COVID-19 pandemic public health measures aimed at reducing transmission of SARS-CoV-2. In February 2020, rates were above historical figures in six states and territories due to a large multi-jurisdictional outbreak of *Salmonella* Typhimurium.[36] Rate reductions in states and territories were notable in Q2–Q4 of 2020, after widespread control measures were introduced. Jurisdictions such as Victoria reported greater reductions that coincided with the application of longer and stringent public health measures, while demographic and environmental factors in the Northern Territory and Western Australia may have had more of an impact on salmonellosis rates in these jurisdictions.

The decreases were significant in cases notified with an overseas place of acquisition, which normally account for approximately 10% of cases in the 5-years prior, but after Q2 of 2020 cases reported with an overseas place of acquisition decreased to <1%. A likely factor in this reduction is a decrease in overseas acquired *Salmonella* as a result of international border entry restrictions, preventing non-Australian citizens and permanent residents entering Australia from 20 March 2020 (Appendix A). The rate reductions in international travel associated cases was reflected in the distribution of serovars often associated with international travel. Infection with *S.* Enteritidis and *S.* Paratyphi B bv Java in Australia is commonly associated with international travel (83% (3,389/4,087) in 2015-2019 and 70% (796/1,136) in 2015–2019 respectively). In 2020, *S.* Enteritidis and *S.* Paratyphi B bv Java associated with international travel both reduced by 83% respectively. However, it should also be noted that the significant burden of the pandemic required a re-allocation of many public health resources within all states and territories to support COVID-19 contract tracing and investigation, and therefore the overall reduction in travel associated cases observed in this analysis could also be partially attributed to a decreased capacity to interview salmonellosis cases or reduction in data cleaning of records which could not be accounted for in this study. The reduction in cases with an overseas place of acquisition and reduction in serovars commonly associated with international travel contributed to the overall decrease in cases of salmonellosis.

Victoria had the largest quarterly rate reductions in salmonellosis notifications from Q2 of 2020 and experienced the most severe and longest COVID-19 restrictions (Appendix A). Restaurants are the most commonly-reported food preparation setting for foodborne disease outbreaks in Australia, accounting for 47% (211/452) of foodborne outbreaks and 37% (1,338/639) of cases of illness associates with foodborne outbreaks in Australia from 2013–2015.[9] Closure of dine-in restaurants, cafes, and bars likely reduced large scale exposure to *Salmonella* outbreak incidents.

Restrictions on social gatherings such as large-scale weddings and festivals, and small scale such as barbecues and dinner parties where food and drinks are often cooked by people who are not schooled in food safety, likely also played a large part in the reduction in illness. While people were unable to eat out in restaurants or cafes, food takeaway and delivery services continued and therefore people remained at risk of *Salmonella* infection associated with these food preparation settings noting that takeaway settings accounted for 9% (327/3,639) of cases of illness associated with foodborne outbreaks in Australia from 2013–-2015.[9] Changes to food purchasing and preparation during lockdown have been identified as having significant impacts on food consumption habits in households, including increased purchases of take away foods to support local businesses.[37] However, data from the ABS Household Impacts of COVID-19 Survey [38] showed that in in April 2020, 36% of participants reported decreased consumption of take-away or delivered means than during February 2020. These results complement the findings of the VicHealth Coronavirus Victorian Wellbeing Impact Surveys[39, 40] conducted in April 2020, and repeated in September 2020, which found 34% and 41% of respondents reported consuming fewer takeaway foods than before the pandemic because of enhanced health literacy, and increased time for time for cooking home meals (12% and 37% respectively). While the impact of these food consumption changes on rates salmonellosis during 2020 cannot be fully explained by the analysis of surveillance data, marked reductions in salmonellosis rates in Victoria where longer and widespread public health measures were applied, suggests the importance of behavioural factors associated with these measures in the prevention of *Salmonella* infection. When available, analysis of foodborne outbreak setting data in 2020 will provide further evidence for the impact of restrictions and food consumption behaviours on the incidence of salmonellosis.

These findings build on other Australian reports that suggest the variability in salmonellosis trends observed between states and territories in 2020 reflect locally applied public health measures and staged easing of restrictions.[41, 42] Smaller reductions in quarterly salmonellosis rates from Q2 of 2020 were observed in WA, Qld, and NT, than in Vic, NSW, ACT, and SA. A potential reason for smaller decreases in Qld, NT, and WA could reflect the implementation of less stringent public health measures for these jurisdictions compared to the south-eastern states were longer and more widespread lockdowns were applied. However, in Q2 and Q3 of 2020 Tas had a 39% and 70% reduction in non-Typhimurium *Salmonella*, and experienced similar levels of restrictions to NT and WA. In WA during the same quarters, the rate of *S*. Typhimurium peaked while the rate of non-Typhimurium *Salmonella* decreased by 59% and 63%. This suggests the importance of predominant environmental serotypes in these jurisdictions for which public health measures had less of an impact and potentially outbreaks especially those associated with foods commonly prepared and consumed in the home.[15, 41] Other factors that have varied the influence of COVID-19 public health measures on salmonellosis incidence is the geographical variation and warmer climates in jurisdictions such as NT and Qld, and the higher proportion of young people in NT noting that salmonellosis is known to be more common in younger age groups.[9]

The reduction in salmonellosis incidence from Q2 of 2020 could also be partially attributed to changes in patient health seeking behaviours and physician consultation and referral behaviours leading to decreased testing for *Salmonella*. Capturing salmonellosis notifications in the NNDSS is sensitive to human behaviour because it depends on an individual seeking medical attention to undertake a diagnostic test for *Salmonella*. How and when people seek healthcare likely changed due to COVID-19, and people with symptoms of enteric diseases such as salmonellosis may have refrained from health service attendance due to concerns about the risk of infection and a reluctance to burden the healthcare system.[43, 44] If this is the case, salmonellosis diagnoses may have been missed, especially cases with only mild or moderate symptoms. Some indicators that suggest this could have been the case are provided in an analysis by the Australian Institute of Health and Welfare.[29] Between the weeks starting 9 March and 30 March 2020, emergency presentations decreased by 38% compared to the same period in 2019. While over subsequent weeks the number of presentations slowly increased, they remained lower than the previous year. The fall in presentations generally affected the less urgent categories of patients; and presentations for non-urgent and semi-urgent cases in 2019-2020 financial year were 14% and 11% lower compared with 2019-2020. Decreases in emergency department presentations and fewer hospital admissions were also reported internationally.[45] Moreover, the same report[29] found no decrease in general practitioner consultations which were supported by the uptake of the MBS telehealth items in late March 2020. By April 2020, 36% of GP consultations were delivered by phone or video, a pattern that continued to August 2020 before subsequently declining towards the end of the year.

The impact of the introduction of MBS telehealth items[30] also had potential to contribute to the decrease in subsidised test of culture for faecal pathogens performed in 2020. A decline in face-to-face consultations likely resulted in the opportunity of fewer cases to collect a faecal specimen. Culture data indicated a 14% decrease in the number of specimens submitted for testing in Q2 of 2020 when compared to 5-year average in that quarter, and a 13% reduction in salmonellosis positivity rate (using culture as a denominator). A fall in the salmonellosis positivity rate could indicate a change in testing practices, with those cases with severe symptoms more likely to be infected. While other Australian reports[36, 41] consider the potential de-prioritisation or delays in PCR testing for faecal specimens by some laboratories because of increased demand in testing samples for SARS-CoV-2, it’s assumed to unlikely have a large impact on the observed decreases. Analyses of laboratory testing data in states and territories to obtain a true denominator would provide a more accurate indication of trends in the population, particularly by month in response to implementation of public health measures.

These findings contribute to other reports in Australia and internationally documenting the impact of the COVID-19 pandemic and public health measures on exposures associated with salmonellosis and enteric diseases, with reduced incidence especially among international travel related cases and serovars, and in state and territories where there were longer and widespread applications of pandemic related public health restrictions.[36, 41, 45-50] In Victoria, the enterovirus specimen positivity rate was reduced by 84% in 2020 compared to the previous decade (2010-2019), while the norovirus outbreak positivity rate declined 49% during the same period.[51] A Germany study[45] reported a 45% (range: 83% to 7%) reduction in salmonellosis under surveillance in 2020 compared to the expected numbers over previous years (2010–20160).[45] In the Netherlands, travel related cases of salmonellosis decreased fourfold compared with 2016–2019[50], and *S*. Enteritidis incidence in the United States was 36% lower in 2020 compared with the average incidence during 2017–2019.[49] The consistent findings globally make it plausible that these reduction were influenced by COVID-19 public health measures introduced.

This analysis has several limitations. First, individual COVID-19 mitigation measures (e.g. hand and surface hygiene) could have had an impact on salmonellosis in 2020, and the effect of these measures on reducing transmission of human-to-human transmission of *Salmonella* were not accounted for in this study. Second, foodborne outbreaks of *Salmonella* could not be accounted for in this analysis as line listed data for outbreak cases were unavailable, nor the OzFoodNet Outbreak Register data for 2020 available for analysis of food preparation settings. This consequentially limited the analysis undertaken. Third, this analysis did not measure changes to behaviour in patients and public health staff. An analysis of hospitalisation data could provide an important insight into the incidence since people with severe disease will most likely seek medical attention regardless of behaviour influences. Moreover, the smaller decrease in salmonellosis notifications among the elderly during 2020 supports the hypothesis of differential health seeking behaviours among different population groups. This observation supports similar findings internationally.[50] Fourth, only a subset of pathology testing data for faecal pathogens was available rather than all laboratory tests for salmonellosis including PCR. Last, staged application and easing of mitigation measures by and within state and territories varied, which makes interpretation of trends among states and territories challenging.

Conclusion

In Australia, COVID-19 public health measures to prevent SARS-CoV-2 transmission have likely contributed to a decline in salmonellosis incidence, as suggested by a decrease in the number of infections associated with international travel and below average notification rates in states and territories from Q2 2020. The multifactorial nature of these reductions makes interpretation of findings challenging and highlights the need for ongoing close community level surveillance of salmonellosis during the COVID-19 pandemic. Since key sources of salmonellosis serovars vary in different states and territories, a future analysis would benefit from a detailed examination of changes in serovars within jurisdictions. It is likely that declines in non-travel related serovars were due to an under-diagnosis as a result of changes to health seeking behaviours, eating out patterns, and reduced face-to-face medical practitioner consultations. Additionally, restaurant closures and changes in food consumption habits are likely to have contributed to a true reduction in salmonellosis. This project highlights the effectiveness of the COVID-19 public health measures to prevent transmission of *Salmonella* (albeit unintentionally), which positively affects the associated health and economic burdens on the individual and health care system. Ongoing food safety messaging encouraging proactive hand hygiene to prevent salmonellosis and other food-borne illness should continue. A further analysis of 2020–2021 surveillance data, including the OzFoodNet outbreak data is recommended to improve understanding of the public health measures that target *Salmonella* transmission. Alternatively, a false reduction associated with changes in health seeking behaviour highlights the need for future pandemic planning to guide the development of public health communication during a pandemic to highlight the accessibility of health services at the primary and tertiary level, including the integration of telehealth services. Furthermore, availability of all pathology testing data for salmonellosis would assist in determining whether a true reduction in salmonellosis occurred.

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Appendix A –Timeline of key dates and public health measures in response to the COVID-19 pandemic, 2019–2020

Date	Details
31 Dec 2019	A cluster of cases of pneumonia associated with a seafood market in Wuhan City, Hubei Province, China was notified to the WHO.
25 Jan 2020	Australia reported its first case of COVID-19 in a traveller from Wuhan City.
30 Jan 2020	The WHO declares the COVID-19 outbreak a Public Health Emergency of International Concern.
01 Feb 2020	Travel ban for international arrivals from China.
13 Feb 2020	Australian citizens and permanent residents from China self-isolate 14 days.
29 Feb 2020	Travel ban on international arrivals from Iran.
13 Mar 2020	Introduction of new MBS COVID-19 telehealth and phone consultation item numbers.[30]
11 Mar 2020	The WHO declared the COVID-19 outbreak a pandemic.
15 Mar 2020	Self-quarantine for 14 days for all international arrivals to Australia. Ban on cruise ships from entering Australia from foreign ports
16 Mar 2020	Public gatherings of >500 people prohibited. Australian's advised to 'Do not travel' overseas Restriction for aged care facilities [52]
20 Mar 2020	Travel ban on non-Australian citizens and permanent residents entering Australia. Non-essential indoor gatherings >100 people prohibited. 4 square meter arrangements for indoor and outdoor venues.
21 Mar 2020	Select states and territories close borders to non-essential travel
23 Mar 2020	Stage 1 restrictions on social gatherings (Table 1). Non-essential domestic travel should be avoided.
24 Mar 2020	Travel ban on Australians travelling overseas.
25 Mar 2020	Prohibited activities and venues including cafes, food-courts, retail, beauty and personal care services, entertainment venues, leisure and recreation, residential facilities, outdoor recreation, non-residential institutions [53].
28 Mar 2020	All international arrivals required to undertaken mandatory 14-day quarantine in designated facilities.
29 Mar 2020	Indoor and outdoor gatherings limited to ≤ 2 persons.
30 Mar 2020	Stay home unless shopping for essentials, receiving medical care, exercising, or travelling to work or education.
27 Apr 2020	Start easing of restrictions in select states and territories.
20 Jun 2020	Stage 2 restrictions reinstated in Vic.
01 Jul 2020	Vic implements lockdowns on 'hotspot' suburbs.
08 Jul 2020	NSW/Vic border closes. Stage 3 Lockdown of Melbourne and Mitchell Shire.
02 Aug 2020	Stage 4 restrictions for metro Melbourne. Stage 3 restrictions for regional Vic
13 Sep 2020	Vic commences easing of restrictions against the 'roadmap to re-opening'.[54]
08 Nov 2020	Further easing of restrictions in Vic as third step in the 'roadmap to reopening. [55]
19 Nov 2020	SA implements lockdowns in response to a cluster (revoked on 22 Nov).
22 Nov 2020	Vic moves to the last step in the 'roadmap to reopening'.[56]
20 Dec 2020	NSW restrictions implemented in response to Sydney COVID hotspot.[57]

Supplementary Figures

Supplementary Table 1. Rate of salmonellosis in Australia and Australian states and territories, 2020 vs 5-year average (2015-2019) and percent change compared to the 5-year average

State/ Territory	Q1			Q2			Q3			Q4		
	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change
ACT	13.0	23.2	-44	5.1	11.6	-56	4.2	10.4	-60	5.3	13.3	-60
NSW	17.3	17.9	-3	6.6	11.0	-40	4.0	7.9	-49	8.1	11.4	-29
NT	56.8	58.7	-3	41.4	69.7	-41	28.4	37.1	-23	39.3	54.2	-27
Qld	42.0	34.8	21	13.6	21.3	-36	8.3	11.8	-30	15.6	19.1	-18
SA	16.0	26.4	-39	7.5	19.2	-61	5.7	13.7	-58	8.8	17.5	-50
Tas	15.7	20.9	-25	5.9	10.1	-42	3.9	7.8	-50	9.6	13.1	-27
Vic	13.1	17.4	-25	5.6	12.7	-56	3.6	10.7	-66	4.9	12.9	-62
WA	22.7	25.6	-11	17.7	19.7	-10	12.4	15.2	-18	13.1	20.0	-34
Aus	23.2	23.5	-6	9.3	15.7	-41	6.0	11.0	-45	9.6	15.2	-37

Supplementary Table 2. Salmonellosis notifications in 2020 by top five serovars in Australia, and states and territories, 5-year mean (2015-2020), and percentage increase or decrease compared to 2020

NSW			
Salmonella	2020	5-yr average	% change
S. Typhimurium	1,124	1,263	-11
S. Wangata	264	167	48
S. Saintpaul	156	99	58
S. Enteritidis	114	242	-53
S. Virchow	105	127	-17

Vic			
Salmonella	2020	5-yr average	% change
S. Typhimurium	1,032	1,625	-37
S. Saintpaul	64	76	-16
S. 4,5,12:I:- *	47	109	-57
S. Virchow	46	69	-33
S. Enteritidis	45	220	-80

Qld			
Salmonella	2020	5-yr average	% change
S. Typhimurium	1190	958	24
S. Saintpaul	389	310	25
S. Virchow	324	358	-10
S. Weltevreden	177	163	9
S. Wangata	122	67	82

WA			
Salmonella	2020	5-yr average	% change
S. Typhimurium	1,167	1,009	16
S. Enteritidis	47	206	-77
S. Saintpaul	39	54	-28
S. Infantis	28	31	-10
S. Muenchen	27	27	0

SA			
Salmonella	2020	5-yr average	% change
S. Typhimurium	318	660	-52
S. Hessarek	38	16	138
S. Saintpaul	35	77	-55
S. Virchow	29	46	-37
S. Muenchen	21	12	75

Tas			
Salmonella	2020	5-yr average	% change
S. Mississippi	90	109	-17
S. Typhimurium	47	63	-25
S. Infantis	4	4	0
S. Enteritidis	4	13	-69
S. Saintpaul	3	4	-25

ACT			
Salmonella	2020	5-yr average	% change
S. Typhimurium	69	121	-43
S. Saintpaul	7	5	40
S. Infantis	5	3	67
S. Virchow	3	7	-57
S. Mississippi	2	1	100

NT			
Salmonella	2020	5-yr average	% change
S. Saintpaul	61	80	-24
S. Virchow	55	63	-13
S. Typhimurium	43	46	-7
S. 16:I,V:- ^	20	13	54
S. Ball	15	23	-35

Aus			
Salmonella	2020	5-yr average	% change
S. Typhimurium	4,990	5,745	-13
S. Saintpaul	754	704	7
S. Virchow	584	717	-19
S. Wangata	402	244	65
S. Enteritidis	320	972	-67

* *S*. Subsp I Ser 4,5,12:i:-

^ *S*. Subsp I Ser 16:I,V:-

Supplementary Table 3. Rate of *S*. Typhimurium in Australia and Australian states and territories, 2020 vs 5-year average (2015-2019) and percent change compared to the 5-year average

State/ Territory	Q1			Q2			Q3			Q4		
	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change
ACT	7.4	14.8	-50	3.2	5.6	-43	2.1	3.6	-42	3.2	5.1	-37
NSW	6.0	6.8	-12	3.3	3.6	-8	1.7	1.9	-11	2.7	3.6	-25
NT	8.5	5.7	49	2.0	4.9	-59	2.4	4.1	-41	4.5	3.7	22
Qld	16.3	9.0	81	2.1	4.1	-49	2.0	2.2	-9	2.5	4.0	-38
SA	7.3	15.0	-51	3.6	8.9	-60	2.3	5.7	-60	4.7	8.6	-45
Tas	3.5	4.6	-24	0.9	1.9	-53	2.2	1.9	16	2.0	3.6	-44
Vic	7.1	9.3	-24	3.4	5.8	-41	2.2	4.1	-46	2.8	6.3	-56
WA	11.9	12.9	-8	13.6	9.7	40	9.1	6.2	47	9.1	10.1	-10
Aus	9.1	9.2	-1	4.1	5.3	-23	2.7	3.3	-18	3.5	5.5	-36

Supplementary Table 4. Rate of non- Typhimurium *Salmonella* in Australia and Australian states and territories, 2020 vs 5-year average (2015-2019) and percent change compared to the 5-year average

State/ Territory	Q1			Q2			Q3			Q4		
	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change	2020	5-yr average	% change
ACT	5.6	8.5	-34	1.9	5.8	-67	2.1	6.5	-68	2.1	8.2	-74
NSW	11.2	11.1	1	3.3	7.3	-55	2.3	6.0	-62	5.4	7.7	-30
NT	48.3	53.0	-9	39.3	64.8	-39	26.0	32.6	-20	34.9	50.1	-30
Qld	25.7	25.9	-1	11.5	17.2	-33	6.3	9.6	-34	13.0	15.0	-13
SA	8.5	11.3	-25	3.9	10.3	-62	3.3	8.0	-59	4.0	8.8	-55
Tas	12.0	16.3	-26	5.0	8.2	-39	1.7	5.7	-70	7.6	9.7	-22
Vic	6.0	8.1	-26	2.2	6.8	-68	1.4	6.6	-79	2.1	6.5	-68
WA	10.7	12.7	-16	4.1	10.0	-59	3.3	8.9	-63	4.1	9.9	-59
Aus	12.8	14.1	-9	5.2	10.3	-50	3.3	7.6	-57	6.1	9.7	-37

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Chapter 6. Teaching

Lessons from the field and additional teaching activities

Table of Contents

Prologue

Background

MAE scholars are required to conduct two main teaching exercises. These are a teaching session for the first year MAE cohort and a lesson from the field (LFF).

I planned, developed, and delivered the teaching session *Introduction to REDCap for data collection* to the first year MAE cohort with two other second-year MAE colleagues' — Kim and Steph (Appendix 1). One of the skills I developed as part of the public health response activities I undertook throughout my MAE was conducting *Salmonella* and COVID-19 case interviews. I decided this was a valuable skill to share with my MAE cohort and I developed *The art of case interviewing* as my LFF.

My role

Combined teaching of first year MAE students

On discussion with my MAE teaching group, we decided to conduct a session on REDCap for data collection. Steph had experience using REDCap in her field placement, while Kim had never used REDCap, but had a keen interest to learn. REDCap is a secure browser-based application for building and managing online surveys and databases. From our experiences, Steph and I found REDCap to be a powerful and intuitive data management tool. I was introduced to REDCap early in my field placement when I was required to build data collection forms. In my outbreak project, I was required to use REDCap to directly enter case interview information, and in my surveillance project, I designed and built a COVID-19 outbreak register in REDCap. Through my work in the NIC, I was aware there were some jurisdictions already using REDCap databases for surveillance data, while others had adopted it for COVID-19 contact tracing. Therefore, we were excited to introduce the first years to REDCap in a session that was designed to be useful and informative. We decided to focus the session on providing the first-year students with a broad overview of REDCap, with the aim to familiarise them with the features of the online designer tool.

All group members were involved in the planning and development of the teaching materials. This was conducted via teleconference leading up to the teaching day. On a shared google drive, we developed the PowerPoint slides and a running sheet for the lesson activity. My primary role was developing and presenting slides on the types of projects and field types available in REDCap. In the teaching session I walked through an example REDCap project used at my field placement. In the breakout group activity, I also facilitated a group to create 5 fields in a REDCap data collection form. The lesson plan, presentation slides, and hand-outs are provided in Appendix A and Appendix B.

Student feedback

On completion of the session, participants were asked to fill out an evaluation form on REDCap rating the session for preparation, content, mode of delivery, knowledge gained, student engagement, and overall satisfaction. Overall, the responses were very positive and the average score (1=strongly disagree, 5=strongly agree) on each item ranged from 4–5 out of a total of 5 (Box 1).

Box 1. 2021 MAE cohort evaluation questions on teaching session

1. The facilitators were organised and well prepared for the lesson.
2. The facilitators delivered lesson materials in a clear manner that facilitated understanding.
3. The virtual mode of delivery aided my learning.
4. The lesson was useful in progress towards a career in field of epidemiology.
5. I would highly recommend this less on to others.

As a free text field, the 2021 MAE cohort were also asked what could be improved, what was done well, and additional comments. The responses are provided in Table 1 below. Of the 18 students in the 2021 cohort who participated, 13 completed the evaluation.

Table 1. 2021 MAE cohort feedback on teaching session

What could be improved?	What was done well?	Additional comments
Nothing	Good to see a real-life example	Really useful session
Time management	Everything	Can’t wait to use it.
Good coverage of the program and feel like I could use it. Thanks. No suggestions.	Topic of choice and going through REDCap online through an example - which was helpful	Scary but great to have such a useful tool at our disposal

Lesson from the field

My lessons from the field teaching session was developed in response to my experience conducting case interviews throughout my MAE and prior to the program as a Registered Nurse. Having just began at my field placement, I investigated a COVID-19 outbreak. While conducting the outbreak hypothesis generating interviews, I came across various challenges in interviewing due to certain personalities in the outbreak group and the nature of sensitivities surrounding being a COVID-19 case at the time. This effected data collection and consequently the development of my hypotheses and ability to conduct appropriate analyses. When I conducted salmonellosis case interviews, I had a profoundly different experience. The use of a tried and tested questionnaire and the lack of social sensitivities of the disease, meant the interviews were much easier. Therefore, I thought it would be useful to conduct a teaching session highlighting interview skills and techniques, especially when faced with some challenging situations.

On consultation with MAE colleagues in my LLF group, I proposed the topic I planned to deliver. Members of our group had differing levels of experience with case interviewing and were pleased with the topic. I developed and disseminated the hand-out (Appendix 3) three weeks before the scheduled LFF.

Reflections

A challenging aspect of preparing the LFF was ensuring the content was useful for all participants and skill sets. Given the fact that interviewing is a very much an applied skill, I feel the session would have benefited from working through more examples and conducting role plays. Given the time allocated to the LFF, this was not feasible.

The lesson was well received by my colleagues and demonstrated by the evaluation question responses as presented in Figures 1 and 2 below.

Figure 1. Was the lesson organised in a manner that helped my learning? Response from LLF participants

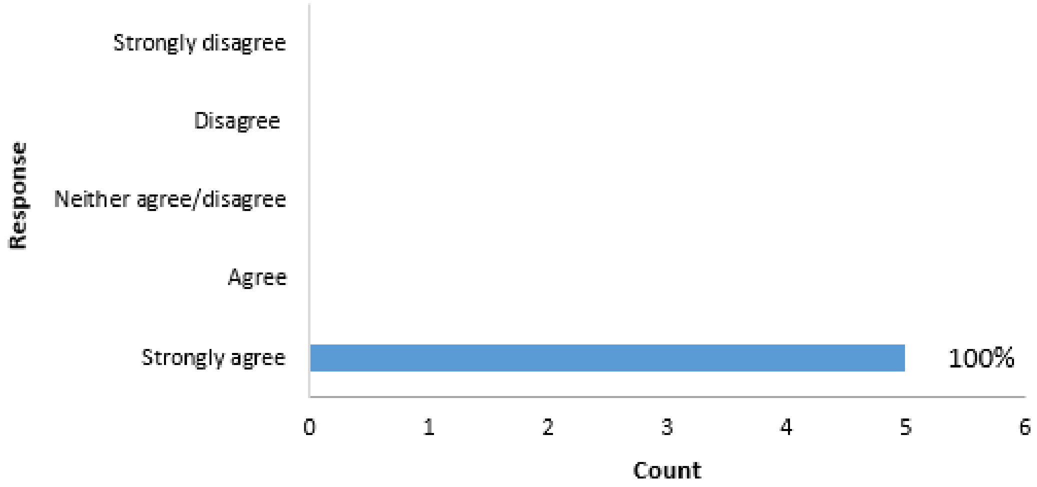
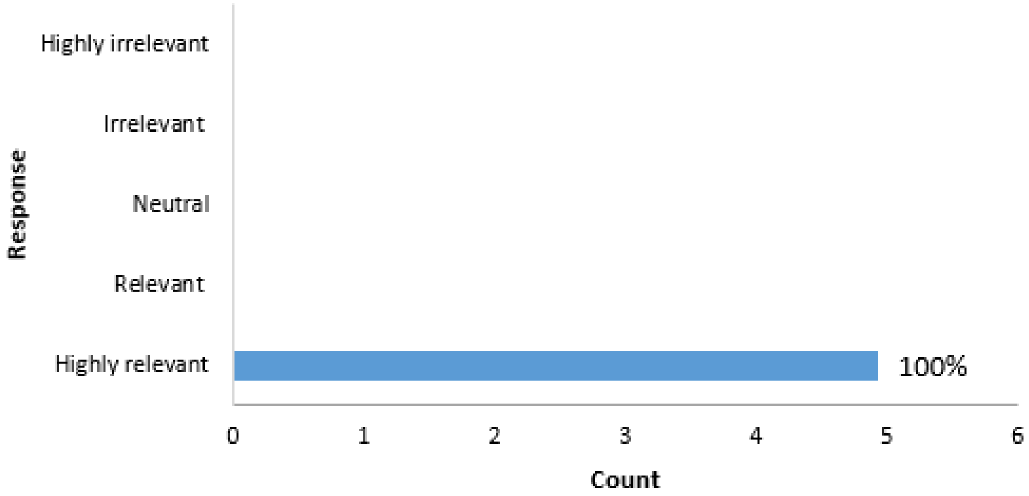


Figure 2. Was the lesson relevant to your needs as future field epidemiologists? Response from LLF participants



Free text responses to the question ‘How would you improve this lesson?’ included the below:

- Time to practice a case interview and discussing other diseases, not just food-borne
- Nothing to improve.
- Thanks for the session!
- Wonderful, helpful session! Really enjoyed it.
- It was fun! Improvements not needed. Thanks Freya! :)
- Maybe some practice interviews to each other.

Lessons learnt

Overall, I found the teaching component of this program to be useful and informative in my development of skills as an educator. In my past experiences, I would often teach in a style that was conducive to my learning style. Teaching virtually forced me to try a range of learning and teaching techniques, including content rich group discussions, and the use of visual aids to support theoretical content.

Appendix A – Lesson plan for teaching session to the first year cohort

Title: Introduction to REDCap for data collection

Time required: 50 minutes

Purpose of session:

1. To introduce REDCap and considerations why it is used for data collection.
2. To provide an example of how a real-life project is used.
3. To provide a practical exercise to demonstrate how a data collection form is built in the online designer feature.

Learning objectives:

- Describe REDCap and benefits of its use for data collection
- Navigate the REDCap interface
- Identify the features of the online designer
- Identify when you would use various functions:
    - Data validation
    - Branching logic
- Identify the data dictionary for building surveys, data reports and data exporting features.

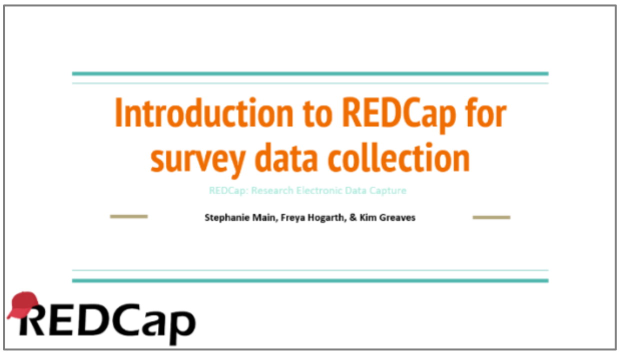
Session structure:

Our group had 40 minutes allocated to our session. The lesson structure in the below table provides an example of the running sheet in conjunction to the power point slide and speaker.

Table. Lesson structure for teaching of the first year MAE cohort

Start Time	Total (min)	Speaker	Content covered	Slide
1350	5	Kim	**Introduction** • Introduction to lesson and presenters • Acknowledgement to country • Learning objectives	1-3
	5	Kim	**Introduction to data collection** • Poll Everywhere x 1 *(Ascertaining experience of MAE2021 cohort in using data collection tools)* • Usual data collection pathway for researchers • Poll Everywhere x 1 (Asking MAE2021 cohort what issues in the pathway could be anticipated/or have been experienced)	4-6
		Kim	**Overview of REDCap** What is REDCap and why is it used?	7-8
1400	7	Freya	**Types of REDCap projects and using the online designer** • Introduction to the 3 types of REDCap projects • Introduction to the 14 field/variable types available in the online designer.	9-10
	3	Freya	**Example of REDCap project** Walk through the OzFoodNet Salmonella Hypothesis generating questionnaire in REDCap	11
1410	20	Steph	**Breakout room exercise** Creating a data collection form and data fields in REDCap	12
		Freya	Facilitation of break out room exercise	N/A
1430	4	Steph	**Data dictionaries** • Overview to REDCap data dictionary • Introduction to building projects in a data dictionary	13-14
1434	3	Steph	**Data reports and exports** • Overview of data reports and stats features • Identify data export options	15-16
1437	3	Steph	Extra resources & Questions	17-18
1440	5	Sera	Close of Session & Evaluation	19

Appendix B – PowerPoint slides for teaching session to the first-year cohort

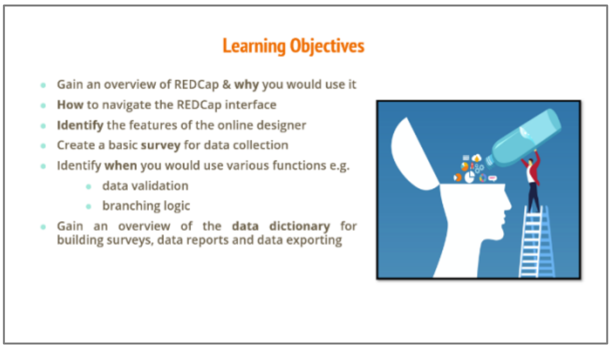


Introduction to REDCap for survey data collection

REDCap: Research Electronic Data Capture

Stephanie Main, Freya Hogarth, & Kim Greaves

REDCap



Learning Objectives

- Gain an overview of REDCap & **why** you would use it
- **How** to navigate the REDCap interface
- **Identify** the features of the online designer
- Create a basic **survey** for data collection
- Identify **when** you would use various functions e.g.
  - data validation
  - branching logic
- Gain an overview of the **data dictionary** for building surveys, data reports and data exporting

Have you worked with data capture tools before?

Top

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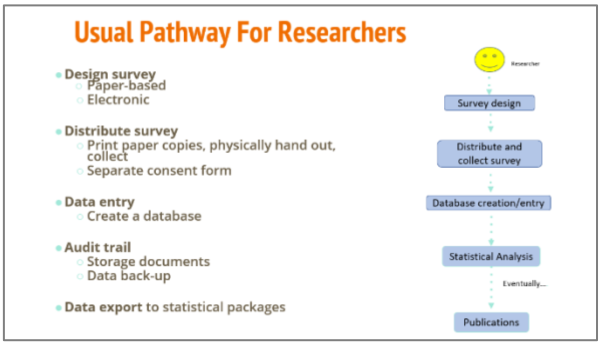

Usual Pathway For Researchers

- **Design survey**
  - Paper-based
  - Electronic
- **Distribute survey**
  - Print paper copies, physically hand out, collect
  - Separate consent form
- **Data entry**
  - Create a database
- **Audit trail**
  - Storage documents
  - Data back-up
- **Data export** to statistical packages

What issues in this pathway could be anticipated, or have you experienced before?

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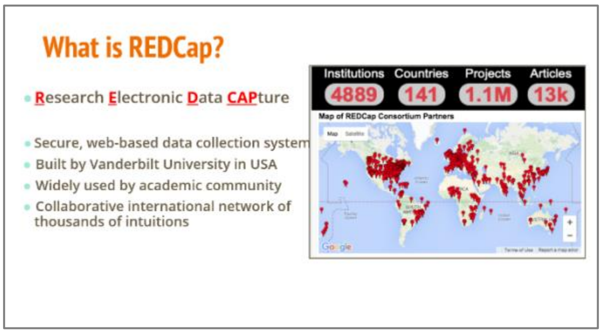
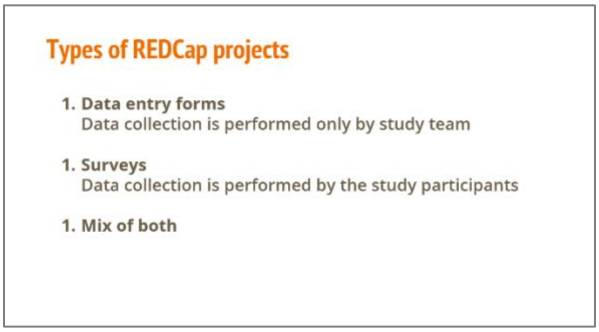
Why use REDCap?

- Web-based and mobile app
- Data security
  - compliant with Australian legislation
  - better than MS excel and Survey Monkey
- View in real-time data entry
- Intuitive & easy-to-use interface
- Many features e.g. longitudinal data collection and multi-site access with user access rights



What is REDCap?

- **R**esearch **E**lectronic **D**ata **CAP**ture
- Secure, web-based data collection system
- Built by Vanderbilt University in USA
- Widely used by academic community
- Collaborative international network of thousands of intuitions

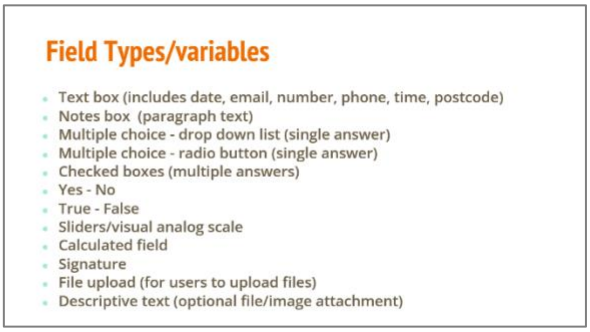


Types of REDCap projects

1. **Data entry forms**
   Data collection is performed only by study team

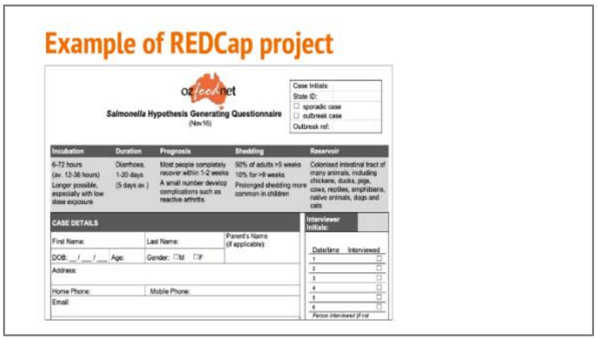
1. **Surveys**
   Data collection is performed by the study participants

1. **Mix of both**



Field Types/variables

- Text box (includes date, email, number, phone, time, postcode)
- Notes box (paragraph text)
- Multiple choice - drop down list (single answer)
- Multiple choice - radio button (single answer)
- Checked boxes (multiple answers)
- Yes - No
- True - False
- Sliders/visual analog scale
- Calculated field
- Signature
- File upload (for users to upload files)
- Descriptive text (optional file/image attachment)



Example of REDCap project

ozfoodnet

***Salmonella* Hypothesis Generating Questionnaire**
(Nov16)

Case Initials:	
State ID:	
☐ sporadic case ☐ outbreak case	
Outbreak ref:	

Incubation	Duration	Prognosis	Shedding	Reservoir
6-72 hours (av. 12-36 hours) Longer possible, especially with low dose exposure	Diarrhoea, 1-20 days (5 days av.)	Most people completely recover within 1-2 weeks A small number develop complications such as reactive arthritis.	50% of adults >5 weeks 10% for >9 weeks Prolonged shedding more common in children	Colonised intestinal tract of many animals, including chickens, ducks, pigs, cows, reptiles, amphibians, native animals, dogs and cats

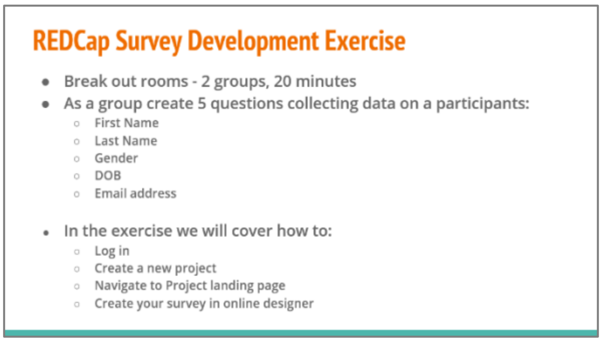
CASE DETAILS

First Name:		Last Name:	Parent's Name (if applicable):
DOB: __ / __ / __	Age:	Gender: ☐M ☐F	
Address:			
Home Phone:		Mobile Phone:	
Email:			

Interviewer Initials:

Date/time	Interviewed
1	☐
2	☐
3	☐
4	☐
5	☐
6	☐

Person interviewed (if not

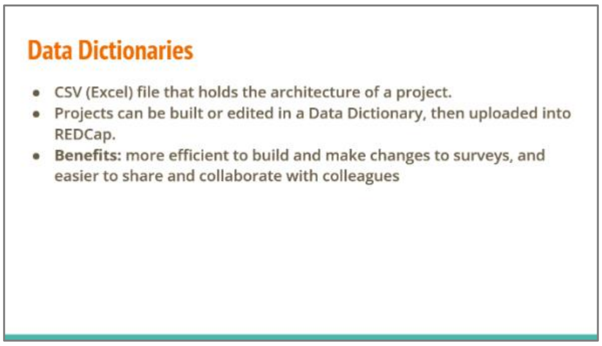


REDCap Survey Development Exercise

- Break out rooms - 2 groups, 20 minutes
- As a group create 5 questions collecting data on a participants:
  - First Name
  - Last Name
  - Gender
  - DOB
  - Email address

- In the exercise we will cover how to:
  - Log in
  - Create a new project
  - Navigate to Project landing page
  - Create your survey in online designer

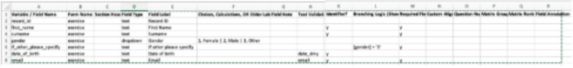
Discussion



Data Dictionaries

- CSV (Excel) file that holds the architecture of a project.
- Projects can be built or edited in a Data Dictionary, then uploaded into REDCap.
- **Benefits:** more efficient to build and make changes to surveys, and easier to share and collaborate with colleagues

Data Dictionary Example

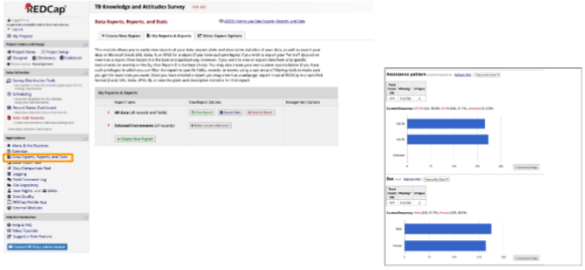


	A	B	C	D	E	F	G	H	K	L	M	N	O	P	Q	R
1	Variable / Field Name	Form Name	Section Heac	Field Type	Field Label	Choices, Calculations, OR Slider Lab	Field Note	Text Validat	Identifier?	Branching Logic (Show	Required Fie	Custom Alig	Question Nu	Matrix Grou	Matrix Rank	Field Annotation
2	record_id	exercise		text	Record ID											
3	first_name	exercise		text	First Name				y		y					
4	surname	exercise		text	Surname				y		y					
5	gender	exercise		dropdown	Gender	1, Female | 2, Male | 3, Other										
6	if_other_please_specify	exercise		text	If other please specify					[gender] = '3'	y					
7	date_of_birth	exercise		text	Date of birth			date_dmy	y							
8	email	exercise		text	Email			email	y		y					

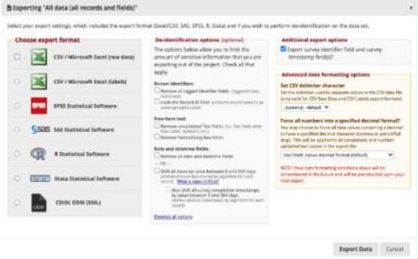
Resources: The Data Dictionary (10 min)

https://healthinstitute.illinois.edu/sites/default/files/How_to_Use_a_Data_Dictionary.pdf

Data Reports & Exports



Data Reports & Exports



Exporting "All data (all records and fields)"

Select your export settings, which includes the export format (Excel/CSV, SAS, SPSS, R, Stata) and if you wish to perform de-identification on the data set.

Choose export format

- ○ CSV / Microsoft Excel (raw data)
- ○ CSV / Microsoft Excel (labels)
- ○ SPSS Statistical Software
- ○ SAS Statistical Software
- ○ R Statistical Software
- ○ Stata Statistical Software
- ○ CDISC ODM (XML)

De-identification options (optional)

The options below allow you to limit the amount of sensitive information that you are exporting out of the project. Check all that apply.

Additional export options

☑ Export survey identifier field and survey timestamp fields?

Advanced data formatting options

Set CSV delimiter character

Force all numbers into a specified decimal format?

Export Data Cancel

Extra Resources

- https://rsph-redcap.anu.edu.au/
- https://redcap.vanderbilt.edu/plugins/redcap_consortium/training_materials.php

Any Questions? Is there anything else you want to know or learn?

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Thank you & Evaluation

Appendix C – Lesson plan for LLF

Title: The Art of Case Interviewing

Background:

Interviewing cases about where and what they ate in the days before they got sick is an essential component to hypothesis generation during an outbreak investigation of foodborne disease. In this lesson you will learn about case interview techniques for investigation of foodborne illness. These types of interviews are often lengthy and detailed and can be a difficult task if the interviewer is not prepared.

Learning objectives:

At the end of the session, you should be able to:

- Demonstrate knowledge of specific techniques to increase effectiveness of case interviews
- Identify strategies that can be implemented to keep an interview on track
- Describe the do's and don'ts when interviewing cases
- List considerations for conducting case interviews for certain communicable diseases.

Lesson Overview:

Prior to the online session, please review the following resources that will help you complete the exercises associated with Part 1 of this lesson. These resources will explain the principles of case interviewing for outbreak investigation and provide key tips on what to do and what not to do!

Resource List:

1. Mejia, G.C. FOCUS on Field Epidemiology: Hypothesis-Generating Interviews. North Carolina Centre for Public Health Preparedness – The North Institute for Public Health. Vol. 2(1). **Available from:** https://nciph.sph.unc.edu/focus/vol1/issue3/1-3Embarking_issue.pdf
2. OzFoodNet: Salmonella Hypothesis Generating Questionnaire (Nov.16).
3. **Available from:** https://www.health.nsw.gov.au/Infectious/Forms/salmonellosis-questionnaire.pdf

4. The DO'S and DON'Ts of Outbreak Interviewing. Available from: https://www.youtube.com/watch?v=O6gKLQpEkfY
5. Online Training Video: The Good, The Bad, and The Ugly. Oregon Public Health Division. **Available from:** https://www.youtube.com/watch?app=desktop&v=8oigheug0L4&feature=emb_title
6. Nelson, A. Rentz, E. FOCUS on Field Epidemiology: Interview Techniques. North Carolina Centre for Public Health Preparedness – The North Institute for Public Health. Vol. 2(3). **Available from:** https://nciph.sph.unc.edu/focus/vol2/issue3/2-3Interviewing_issue.pdf

Part 1: Case interviewing for foodborne disease

This is to be completed in your own time. Please bring your answers to the online session (Part 2).

Please complete the following exercises:

1. Hypothesis generating interviews

You are a 2nd year MAE Scholar working in the Communicable Disease Section at the ACT Department of Health. There is a new outbreak of Salmonella *Typhimurium, and your supervisor has asked you to conduct hypothesis generating case interviews to investigate the possible source. You decide to do some homework to better prepare yourself since this will be your first-time conducting hypothesis generating interviews!!*

Refer to resource 1 and resource 2 to help you answer the following questions.

a) Briefly, explain why hypothesis generating interviews are conducted when an outbreak occurs.

- A hypothesis generating interview gives initial clues to possible sources of exposures.
- From these initial interviews, information can be used to develop a more detailed questionnaire for testing the hypothesis generated through initial interviews.
- They can be used to develop or refine a case definition and develop a demographic profile that helps identify the population at risk.

b) You review the OzFoodNet *Salmonella* Hypothesis Generating Questionnaire. What type of questions will you be asking cases?

- Demographic information (i.e. name, sex, age, occupation, contact information).
- Clinical details (i.e. signs and symptom of disease, date of onset and duration of illness, health care received, comorbidities).
- Laboratory results.
- Reports of compatible illness in household or contacts.
- Activities (e.g. wedding events).
- Details on food consumption (including restaurant exposures and food purchasing information) in the 7 days prior to onset of illness. Exposures that could potentially cause or predispose the case to illness.

c) List some important considerations/tips for conducting interviews?

- Get enough background information.
- Review the literature.
- Act friendly but professional.
- Introduce yourself and the organisation you’re representing.
- Notify the person the length of the interview.
- Do not use abbreviations.
- Record information clearly and accurately.
- Vary between close and open-ended questions where possible.

2. 10 Cardinal Rules for conducting effective case interviews

Watch the video ***The DO'S and DON'Ts of Outbreak Interviewing*** (resource 3) **(9 minutes)** and list the 10 cardinal rules for conducting effective case interviews.

1. Do a practice run
2. Find a quiet place
3. Be non-judgmental
4. Avoid leading the case
5. Accurately record what people say
6. Ensure confidentiality
7. Gently re-direct, as needed
8. Probe if answers are vague
9. Work with epidemiology staff to provide language interpretation
10. Thank interviewee at closing and explain how the information will be used

3. Training Scenario

Watch Scene 1 (only) of the video ***The Good, The Bad, and The Ugly*** (resource 4) **(4.20 minutes).**

The video provides a scenario of a case interview conducted as part of a foodborne outbreak investigation. Make a list of *what was done well* and *what was done not so well* by the interviewer.

What was done well	What was done not so well
• Introduction and explanation of the purpose of the interview. • Clearly specified the exposure time period. • Conversational, interactive. • Closing explanation of how the information will be used. • Asked for best number to contact the interviewee if additional follow-up was necessary. • Thanked the interviewee.	• Request for cookies and coffee during the interview. • Mispronunciation of items from questionnaire (Sashimi, Ceviche). • Did not remain neutral, judgmental about mice and snakes. • The owner of the snake mentioned he purchased mice at a pet store but during the interview question about pet stores, he responded “No” without the interviewer probing further.

4. Common issues experienced by interviewers and proposed solutions

The table below highlights common scenarios experienced in case interviewing for investigation of foodborne illness. Review the issues assigned to your group and scenario relating back to Question 1. Provide possible solutions.

a) Group 1: *Anny, Mik, Khon, Sera*

***Scenario**: You are conducting your first Salmonella hypothesis generating interview. The case (Judy) is a 21-year-old female.*

Issue	Solution
You mispronounced the word "cantaloupe" when reading through the questionnaire. 	• Read the questionnaire carefully and clarify mispronunciation prior to starting the interview. • Become familiar with the flow of the questionnaire.
Judy is convinced the source of her illness was the cantaloupe and becomes frustrated that you continue to question her about other foods.	• Explain that it is important to explore the range of foods consumed to determine the likely source. • Explain each interview needs to be done thoroughly and without bias. • May need to explain the incubation period of the pathogen to highlight it could not be the food of interest and that other food may be involved.
Judy provides contradictory answers when recalling eating the cantaloupe.	• Probe gently. • Re-phrase the responses to highlight the conflicting information and reconfirm the answer provided.

Judy doesn’t want to name the cafe where they ate cantaloupe because it’s their friend’s cafe.	• Reassure that the purpose of the investigation is to prevent further illnesses. • Reassure that the privacy is protected (in addition to reading a privacy clause before commencing the interview). • Explain why the information is needed. • Explain that the restaurant may have done nothing wrong, and it is in their interest to find out the likely source to prevent others becoming unwell.
You begin to become tired and expressed personal disgust for cantaloupe!!	• Focus on the questions and stay neutral. • Use a natural voice. • Avoid comments such as ‘really!’, ‘I totally agree’, ‘I disagree’, and ‘perfect point. • Avoid using jokes to establish rapport.

b) Group 2: *Margie, Steph, Ngoc-Anh*

Scenario: *You are conducting your first* Salmonella *hypothesis generating interview. The case (Bob) is an 85-year-old elderly gentleman, who usually wears hearing aids. His wife always does the cooking and grocery shopping for him.*

Issue	**Solution**
Bob has poor recall of his food history. He responds that he can’t recall a single thing he ate in the days prior to becoming unwell. 	• Prepare a calendar to help prompt Bob with days/dates. • Assist (prompt) the respondent in identifying key events or dates. • Use wife/family for support with information regarding grocery shopping and mean preparation.
You fail to build rapport with Bob, who is becoming increasingly frustrated with the number of questions.	• Keep the interview relaxed and conversational. • Be positive. • Take time to listen and show concern and interest.

	• Don’t cut off responses, redirect if needed.
Bob begins to tell you about his symptoms but becomes angry about becoming ill. He tells you he doesn’t want to talk anymore.	• Show empathy and validate his response. • Stay calm. • Highlight the purpose of the interview and emphasise that the process will help prevent others becoming unwell.
You have difficulty understanding Bob over the phone and misinterpret what he says.	• Repeat responses back to Bob. • Seek clarification if unsure. • Have Bob’s wife present during the interview.
Bob asks for details about the investigation (number of cases, suspected source, etc.).	• Explain that you are limited in the information you can provide due to laws that govern confidentiality and privacy. • Every state/territory is different – often a request of the report of the investigation can be requested through health authorities.

c) Disease sensitivities and considerations

List some specific considerations for interviewing cases for other communicable diseases.

Disease	Considerations
Chlamydia	• Usually done by trained public health nurses. • Often sensitivities around case interviewing surrounding stigmatisation of the disease. • Contact tracing can be difficult, and people are often reluctant to disclose sexual partners. • Providing education about contraception and follow-up is important, in addition to reinforcing risk of chronic reinfection. i.e. PID
COVID-19	• Stigmatisation early in the epidemic. • Now mandatory quarantine enforced by the Biosecurity Act. Cases should understand their legal requirement to quarantine. Often now mandatory to transfer in a managed facility. • Reinforce understanding of testing requirements and release of isolation procedures (i.e. asymptomatic for 72 hrs). • Ensure the case has Help Line number.
Tuberculosis	• Usually done by trained public health nurses. • TB is a chronic disease and new diagnosis on initial interview involves counselling and education. Take time to address cases concerns and questions. • The infectiousness of a case and ability to transmit disease is the main consideration for prioritising the interview. If there is evidence of recent transmission, upstream contact tracing is important because the contact is viewed as the “source,” or the person who transmitted TB infection and not the recipient of TB infection due to prolonged exposure to the index case.

Part 2: LFF Online session

- Discuss the groups experiences of case interviewing (15 minutes)
- Revise and discuss part 1 answers (40 minutes)
- LFF Evaluation (5 min)

Discuss the following issues:

Intro & informed consent – participants cannot give informed consent unless you provide full disclosure about what you are doing and why