Australian Government
Department of Health and Aged Care

Australian Centre for Disease Control

Technical supplement –

Australian Respiratory Surveillance Report

Summary

This supplement to the series of Australian Respiratory Surveillance Reports (ARSR) describes the technical background to national surveillance of coronavirus disease 2019 (COVID-19), influenza, and respiratory syncytial virus (RSV) in Australia. The technical supplement includes a description of each of the data sources used in the ARSR and any associated data considerations for COVID-19, influenza and RSV surveillance data. Further information on the goals and objectives of Australia's national surveillance of these viruses is detailed in the Australian National Surveillance Plan for COVID-19, Influenza and RSV.[1]

Background

COVID-19, influenza, and RSV are acute viral respiratory infections that spread from person to person by infectious respiratory particles that are transmitted through the air after an infected person breathes, coughs, sneezes, or talks. Although there are similarities in the symptoms of these infections, they are distinct viruses with differences in their epidemiology, including who is most at risk for infection and severe disease.[2]

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus responsible for the COVID-19 pandemic, emerged in Wuhan, China, in late 2019.[3] Since that time, COVID-19 transmission in Australia has occurred in waves, with no strong seasonal trend.[4] Usually, people experience the onset of COVID-19 symptoms anywhere from two to five days, but sometimes up to 14 days, after infection. The most common COVID-19 symptoms are fever, chills, cough, loss of taste or smell, runny nose, sore throat and tiredness.[5,6] Some people are asymptomatic (they do not experience any symptoms) but can still spread SARS-CoV-2 to other people.[5] Most people experience a mild illness and recover without needing treatment in a hospital.[2,5,6] Some people experience more severe disease, such as difficulty breathing or pneumonia (an infection of the lungs), and will need treatment in hospital or intensive care.[2,5] Severe illness associated with COVID-19 is more common among adults aged 70 years or older, Aboriginal and Torres Strait Islander people, people who are not vaccinated against COVID-19, people who are pregnant, and people living with disability or chronic health conditions including immunocompromise.[2,6,7] People who have had COVID-19, even if they were asymptomatic or their illness was mild, can also experience longer-term effects, such as long COVID.[6]

Influenza is an acute respiratory infection caused by influenza viruses.[8] There are three subtypes of influenza viruses known to infect people: subtypes A, B and C. At present, influenza A and B viruses circulate, causing seasonal epidemics in Australia, especially during autumn and winter.[2,8] Usually, people experience the onset of influenza symptoms one to four days after infection.[2] Influenza symptoms include aches, chills, cough, fever, headaches, runny or stuffy nose, sore throat and tiredness. Vomiting and diarrhoea can occur, particularly in children. Most people experience a mild illness and recover within a week without requiring medical attention. In some people, severe influenza can worsen symptoms of other chronic diseases, or lead to pneumonia and sepsis (the immune system's response to an infection which causes the body to damage its own tissues and organs).[2,8] Severe diseases or complications (hospitalisation, intensive care admission, or death) associated with influenza are more common in at-risk population groups including, but not

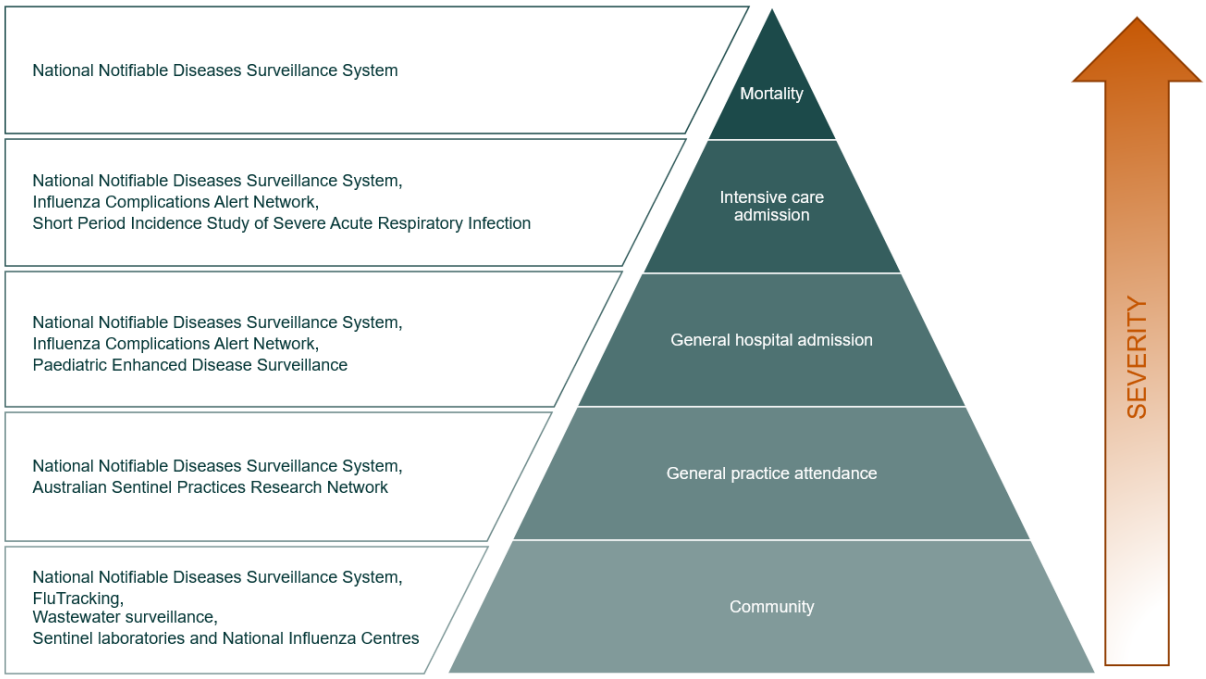
limited to, children aged under five years, adults aged over 65 years, people who are pregnant, and people living with chronic health conditions including immunocompromise.[2,8,9]

RSV is one of the most common viral infections in children, partly due to the lack of long-term immunity after infection, meaning re-infection can be frequent.[10,11] Almost all children will have been infected with RSV within the first two years of life.[11] There is one serotype of RSV, classified into two subtypes: A and B.[10] Usually, people experience the onset of RSV symptoms four to six days after infection. The most common RSV symptoms include cough, fever, runny or stuffy nose, and wheezing or difficulty breathing. Most people experience a mild illness and will recover in a week or two weeks.[2,10,11] Infants aged 12 months or under are especially likely to experience severe illness with complications such as bronchiolitis (an inflammation of the small airways in the lungs) and pneumonia. RSV can worsen symptoms of chronic health conditions like asthma.[11] Severe illnesses are generally more common among infants aged 12 months or under, and young children or older adults with chronic health conditions.[2,10,11]

Data Sources

No one single system, including national notification data, provides the full picture on the epidemiology of COVID-19, influenza, or RSV. The epidemiology of these acute respiratory infections are informed by a number of different systems based in the community, primary care, hospitals and laboratories, as well as notifiable diseases data, which includes officially reported deaths. All data sources have strengths and limitations, so they need to be used in combination to provide comprehensive information for public health decision-making.[1] A visual depiction of the severity spectrum for acute respiratory infections, and the data sources that are used in Australia to measure aspects of activity, severity and at-risk populations, is provided in Figure 1.[12] The information in the ARSR is reliant on the surveillance data sources available to the interim Australian Centre for Disease Control at the time of production.

Figure 1. Severity spectrum of acute respiratory infections and data sources used to measure severity in Australia adapted from Technical supplement – COVID-19 Australia: Epidemiology reporting[12]



- The **National Notifiable Diseases Surveillance System (NNDSS)** coordinates the national surveillance of more than 70 communicable diseases. In Australia, COVID-19, influenza and RSV are notifiable diseases under public health legislation in all states and territories and are listed on the National Notifiable Diseases List under the *National Health Security Act (2007)*. Accordingly, state and territory health authorities report notified cases of COVID-19, influenza and RSV to the Australian Government Department of Health and Aged Care via the NNDSS for national collation, analysis and to assist in the coordination of public health responses.[13] This includes notifications of COVID-19, influenza and RSV based on the Australian national surveillance case definitions.[14] Data from the NNDSS are analysed and reported based on diagnosis date, which is the true onset date of a case if known, otherwise it is the earliest of the specimen date, the notification date, or the notification received date.[13] In the NNDSS:
  - True onset date (previously “date of illness onset”) represents the earliest date the case exhibited symptoms
  - Specimen date represents the date when the first laboratory specimen was taken
  - Notification date represents the date when health professional signed the notification form, or the laboratory issued the results
  - Notification received date represents the date the notification of the disease was first received by the communicable disease section of the health authority.[13]
- **FluTracking** is an online syndromic surveillance system which aims to monitor respiratory illness activity, including influenza-like and COVID-19-like illness in the community. FluTracking provides consistent community level surveillance of respiratory illness activity in all jurisdictions and over time. FluTracking enables year-to-year

comparisons of trends in the incidence and severity of COVID-19 and influenza in the community. FluTracking participants are given the option to opt-out over the summer period and as a result there is a reduced sample size from October to April of the following year.

- **Sentinel laboratories**, including **National Influenza Centres** are a surveillance network of laboratories that collect data on diagnostic respiratory pathogen testing. This includes the number of tests undertaken, the number of positive results, and the detected viruses. Sentinel laboratories are not intended to capture all diagnostic testing occurring, rather, sentinel laboratories aim to provide a representative sample of people tested for respiratory viruses in Australia. In addition, sentinel laboratories aim to provide an indication of circulating respiratory virus activity. Sentinel laboratory site testing data are influenced by jurisdictional and laboratory testing practices and should be interpreted with caution. Sentinel laboratories include laboratory networks in South Australia and Tasmania, and the National Influenza Centres. In Australia, the National Influenza Centres are:
  - Institute of Clinical Pathology and Medical Research in New South Wales
  - PathWest Laboratory Medicine in Western Australia
  - Victorian Infectious Diseases Reference Laboratory in Victoria.

  The National Influenza Centres are also part of the World Health Organisation (WHO) Global Influenza Surveillance and Response System, contributing testing data and sending representative clinical specimens and isolated viruses to the World Health Organization Collaborating Centre (WHOCC) for Reference and Research on Influenza for advanced antigenic and genetic analysis.
- **Wastewater surveillance** for SARS-CoV-2 involves the sampling and testing of wastewater to detect the SARS-CoV-2 virus. Analysis of the amount of viral load of SARS-CoV-2 in wastewater catchment areas are used to indicate changes in the prevalence of COVID-19 within communities. Wastewater surveillance for SARS-CoV-2 can be used to detect the SARS-CoV-2 variants, as well as estimate the relative abundance (or distribution) of specific SARS-CoV-2 variants within communities. At present, there are no national wastewater surveillance data for SARS-CoV-2, influenza, or RSV. Wastewater surveillance data for SARS-CoV-2 are reported separately by states and territories. For further detail refer to the SARS-CoV-2 Wastewater Surveillance CDNA National Strategy.[15]
- The **Australian Sentinel Practices Research Network (ASPREN)** is a year-round network of sentinel general practices in which general practitioners and nurse practitioners report de-identified information on the number of influenza-like illness (ILI) patient presentations seen in participating practices each week. ASPREN uses the WHO ILI case definition which is defined as an acute respiratory infection with measured fever of ≥ 38°C and cough with an onset within the last 10 days.[16] Data from ASPREN are used for acute respiratory infection surveillance nationally, and general practice research, including providing annual vaccine effectiveness estimates. It should be noted that in addition to the overarching impacts of COVID-19 on influenza surveillance systems, interpretation of ASPREN's data from 2020 onwards should consider the following COVID-19 impacts:

  - Changes in the health seeking behaviour at ASPREN sentinel sites due to the availability of telehealth and respiratory clinics may result in fewer presentations to general practice; and
  - Changes to swabbing practices at ASPREN sentinel sites, due to the availability of telehealth and respiratory clinics, may result in a lower number of swabs being taken.
- The **Influenza Complications Alert Network (FluCAN)** is a real-time, hospital-based surveillance system for severe acute respiratory illness. FluCAN was initially established to monitor seasonal influenza hospitalisations. Since 2014, the Paediatric Active Enhanced Disease Surveillance (PAEDS) network has partnered with FluCAN to contribute data on paediatric admissions with influenza at PAEDS sentinel hospital sites. FluCAN has been modified to include surveillance data for COVID-19 from 2020 at sentinel hospitals across Australia, including paediatric admissions with COVID-19 at PAEDS sentinel hospital sites via FluCAN. From 2023, FluCAN piloted the collection of surveillance data for RSV and in 2024 FluCAN commenced comprehensive surveillance data collection for RSV, including paediatric admissions with RSV at PAEDS sentinel hospital sites via FluCAN. Participating sites collect detailed clinical and laboratory information from all hospitalised patients with a confirmed diagnosis of COVID-19, influenza or RSV.
  - When interpreting data from FluCAN it is important to note these data reflect the sickest patients with severe acute respiratory illnesses who are hospitalised or admitted to intensive care; data are therefore not generalisable to all cases or patients in hospital.
  - When interpreting data from FluCAN it is important to note that date of admission is used for all patients admitted to a FluCAN sentinel hospital, except where the patient acquired their infection in hospital. For those patients who acquired their infection in hospital, date of onset is used. In addition, for length of stay data from FluCAN these data exclude patients that acquired their infection in hospital.
  - The distribution of demographic characteristics for hospital admissions in the FluCAN sentinel surveillance system may not reflect the distribution of demographic characteristics for severe acute respiratory infection admissions nationally. It should be noted that hospital admissions in children 16 years of age or less are overrepresented to provide enhanced surveillance on this at-risk population. In addition, some jurisdictions are overrepresented amongst participating sites, and the majority of sites are in major cities, thereby underrepresenting activity in regional and remote areas.
- The **Paediatric Active Enhanced Disease Surveillance (PAEDS)** network, established across eight major children's hospitals in Australia, is a hospital-based surveillance system for selected serious paediatric conditions and adverse events following immunisation. The PAEDS network aims to better understand these serious paediatric conditions; inform policy and practice under the National Immunisation Program[17]; and enable public health responses. While the overall risk for severe complications of COVID-19 in children in Australia remains extremely low, the PAEDS network continues to monitor rare, but clinically significant, complications of COVID-19. This includes Paediatric Inflammatory Multisystem Syndrome Temporally associated with SARS-COV-2 (PIMS-TS), also known as Multisystem Inflammatory Syndrome in Children associated

with COVID-19 (MIS-C). The PIMS-TS case definition for surveillance in Australia is available from PAEDS.[18]

  - When interpreting data from the PAEDS network it is important to note these data reflect the sickest paediatric patients with adverse outcomes post SARS-CoV-2 infection who are hospitalised or admitted to intensive care; data are therefore not generalisable to all paediatric cases or patients in hospital.
  - The distribution of demographic characteristics for paediatric hospital admissions in the PAEDS network may not reflect the distribution of demographic characteristics for paediatric severe acute respiratory infection admissions or PIMS-TS admissions nationally.

- **Short Period Incidence Study of Severe Acute Respiratory Infection (SPRINT-SARI) Australia** is a national, multi-centre, prospective, short period incidence observational study that collects detailed data on the characteristics, outcomes, and interventions for patients admitted to participating intensive care units or high dependency units with severe acute respiratory infections. From March 2020 to May 2022, data were collected only on patients with an admission to intensive care associated with COVID-19. From June 2022 onwards, data collection began for all other severe acute respiratory infection patients with an admission to intensive care for the management of acute respiratory failure or a complication and who were positive for a viral respiratory pathogen. SPRINT-SARI Australia is managed at the Australian and New Zealand Intensive Care Research Centre (ANZIC-RC) and Monash University.
  - When interpreting data from SPRINT-SARI Australia it is important to note these data reflect the sickest patients with severe acute respiratory illnesses who are admitted to intensive care; data are therefore not generalisable to all cases or patients in general hospital wards or intensive care.

In addition, the interim Australian Centre for Disease Control works with several other systems to measure aspects of health system impact and to understand which viruses are circulating in Australia. These systems include, but are not limited to:

- The **Critical Health Resource Information System (CHRIS)** is a real-time national system which provides data to monitor intensive care activity, capacity, and resourcing. In response to rising numbers of COVID-19 associated intensive care admissions in late March 2020, CHRIS was developed as a collaboration between the Australian and New Zealand Intensive Care Society (ANZICS) and Ambulance Victoria, funded by the Australian Government Department of Health. CHRIS, which has been in use since 1 May 2020, receives data from all 191 adult and paediatric intensive care units (over 2,300 intensive care beds) across Australia twice daily. Throughout the COVID-19 pandemic, CHRIS was used to facilitate the transfer of critically ill patients and enable early diversion of ambulance presentations to hospitals with intensive care capacity.
- **AusTrakka** serves as Australia's national pathogen genomic sequence and analysis platform for SARS-CoV-2 and coordinator of genomics outbreak investigations across jurisdictions. Most state and territory public health laboratories upload genomic sequences and agreed epidemiological metadata to AusTrakka for nationally aggregated genomics analysis and visualisation of sequences. Genomic surveillance data in

AusTrakka have been used to track transmission within and between jurisdictions, identify emerging clusters to inform public health responses, and for in the surveillance of SARS-CoV-2 lineages. Please refer to Appendix A: Viral genomic surveillance for further details on genome sequencing.

- In Australia, the **World Health Organization Collaborating Centre (WHOCC) for Reference and Research on Influenza** is hosted by the Victorian Infectious Diseases Reference Laboratory. The WHOCC for Reference and Research on Influenza is part of the WHO Global Influenza Surveillance and Response System, that was established to monitor the changes in influenza and reduce the impact of influenza viruses. Together with other WHOCCs, the Centre is responsible for analysing influenza viruses currently circulating in the human population. These data are used by the WHO to make recommendations on appropriate influenza subtypes to be included in annual seasonal influenza vaccines for the northern and southern hemispheres.

Lastly, the **Australian Bureau of Statistics (ABS)** Estimated Resident Populations (ERP) are used for population denominators. As at 1 April 2024, national rates and rates by age, sex, or jurisdiction use ABS ERP National, state and territory population estimates for the reference period 30 June 2023, released on the 14 December 2023.[19]

Data Considerations

When interpreting disease notification data, it is important to note that changes in notifications over time may not solely reflect changes in disease prevalence or incidence. Depending on the disease, the number of notifications may be influenced by changes in testing policies; changes in case definitions; changes in testing practices and screening programs; the use of less invasive and more sensitive diagnostic tests; periodic awareness campaigns; and the use of other public health and social measures.

When interpreting data included in the Australian Respiratory Surveillance Report, it is important to note both the data considerations provided for each data source and those specific to each disease.

COVID-19

- The Australian COVID-19 surveillance case definition was last updated in July 2024.[14]
- The Australian COVID-19 surveillance case definition was embedded in the COVID-19 CDNA National Guidelines for Public Health Units,[20] from 23 January 2020 to 12 June 2024.
- As the COVID-19 pandemic has progressed in Australia, the proportion of cases reported through traditional surveillance has decreased. For this reason, the availability and reliability of particular metrics, such as COVID-19 case information, has decreased over time.
  - From late 2021 onwards, there was a transition away from test, trace, isolate and quarantine practices to supress transmission of COVID-19 at a population level. Due to the vast number of COVID-19 cases, testing strategies and surveillance practices changed considerably, and case ascertainment was reduced across Australia. COVID-19 case notifications in the NNDSS are now a considerable underestimate of the true incidence of COVID-19 in Australia.[4]
  - From 2023 onwards, seven jurisdictions have stopped collecting self-reported rapid antigen tests results; Victoria ceased collection on 1 July 2023, Queensland on 1 September 2023, New South Wales on 1 October 2023, Western Australia on 9 October 2023, the Northern Territory on 21 October 2023, the Australian Capital Territory on 22 December 2023; and Tasmania on 12 April 2024. Rapid antigen tests administered in healthcare or aged care settings continue to be reported to the NNDSS by several jurisdictions.[4] For this reason, from Report 5 onward only laboratory-confirmed COVID-19 cases are included in the Australian Respiratory Surveillance Reports.
  - The completeness and reliability of particular indicators such as hospitalisations, intensive care admissions or deaths associated with COVID-19 varies, as data are sourced in different ways by state and territories based on their local surveillance system capabilities, definitions, priorities, and needs.
  - Data should be interpreted with caution as the way states and territories source and report these indicators has also changed throughout the pandemic, and may continue to change further, in particular for reporting deaths associated with COVID-19. For example, New South Wales previously used a linkage method for ascertaining deaths from late 2022 through to 2023, where death records that mentioned COVID-19 were

linked to COVID-19 case notifications. This method does not differentiate deaths from COVID-19 and deaths with COVID-19. Since early 2024, only COVID-19 deaths reported to New South Wales through mechanisms such as doctor notifications or coroner reports have been notified to the NNDSS. Increasingly with the reduction in COVID-19 testing, attribution of deaths to COVID-19 will significantly underestimate COVID-19 mortality. Hence, assessment of mortality impacts of COVID-19 in New South Wales is now primarily informed by trends in all-cause mortality. For more detail, please refer to reports and data considerations published by individual jurisdictions.

- In this context, COVID-19 data in the Australian Respiratory Surveillance Report should be interpreted with caution, especially where comparisons are made to previous transmission waves when ascertainment and reporting of confirmed and probable COVID-19 cases was higher.
- In addition, data on SARS-CoV-2 genomic surveillance should be interpreted with caution as SARS-CoV-2 sequencing strategies have changed significantly, and the representativeness of sequences uploaded to AusTrakka may be limited by the different sample referral pathways for each jurisdiction, and significant reduction in sequencing across the country.[4] Additional data considerations for SARS-CoV-2 genomic surveillance are provided in Appendix A: Viral genomic surveillance.

Influenza

- The Australian influenza surveillance case definition was last updated in July 2023.[14]
  - From 1 January 2022, the NNDSS surveillance case definition for laboratory-confirmed influenza was updated to remove Point 5: 'Single high titre by complement fixation test (CFT) or haemagglutination inhibition (HAI) to influenza virus' from the list of laboratory definitive evidence. This change has had minimal impact on the interpretation of influenza notification trends, with the change ensuring consistency with the influenza laboratory case definition. For further information, please refer to the Technical supplement – 2022 update to NNDSS laboratory-confirmed influenza case definition.[21]
- It is important to note that due to the COVID-19 epidemic in Australia, data reported from the various influenza surveillance systems may not represent an accurate reflection of influenza activity. Some COVID-19 related public health and social measures (border restrictions, social distancing measures, and face mask use) likely resulted in a true decrease in influenza activity in 2020 and 2021. During this time, there were likely changes in health seeking behaviour in the Australian community, including but not limited to, the introduction of respiratory clinics and focused testing for COVID-19 response activities, access to alternative streams of acute respiratory infection specific health services and telehealth.
  - In this context, influenza data from April 2020 onwards should be interpreted with caution, especially where comparisons are made to previous influenza seasons.
- Due to the reduction in influenza activity in 2020 and 2021, data from these years may reduce five-year means and affect analyses of usual seasonal trends. Therefore, the years 2020 and 2021 are excluded when comparing the current influenza season to

historical periods when influenza virus circulated without public health restrictions. Where referenced, the five-year mean in the 2024 Australian Respiratory Surveillance Reports refers to the average of data from the years 2017, 2018, 2019, 2022, and 2023.

- For influenza, it is difficult to establish severity at the beginning, or during a low activity influenza season. The proportion of confirmed influenza cases with serious outcomes might be skewed initially because there are only a small number of cases notified. This means that the measure of severity will vary substantially fortnight to fortnight until numbers are sufficiently high and there is enough data for measurements to stabilise. An assessment of severity will be provided in the Australian Respiratory Surveillance Report once the signals become clearer.

RSV

- The Australian RSV surveillance case definition was first published in July 2021, and last updated in July 2023.[14]
- In Australia, RSV was added to the *National Health Security (National Notifiable Disease List) Instrument 2018* in July 2021 and then became notifiable in all states and territories on 1 September 2022. However, comprehensive national data for RSV are only available from 2023 onwards.

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Appendix A: Viral genomic surveillance

Nationally, viral genomic information for SARS-CoV-2 is analysed by the National Analysis Team from AusTrakka. Data in the Australian Respiratory Surveillance Report on SARS-CoV-2 genomics should be interpreted with caution as SARS-CoV-2 sequencing strategies and the representativeness of sequences uploaded to AusTrakka have changed significantly over time.

- Since late 2022, the rates of quantitative reverse transcription polymerase chain reaction (RT-qPCR) testing and referrals of positive samples to sequencing laboratories decreased significantly, resulting in changes to sequencing strategies across Australia.[4]
- From 1 July 2023, jurisdictional sequencing strategies for SARS-CoV-2 have changed considerably. Some jurisdictions have ceased SARS-CoV-2 sequencing, while other jurisdictions have reduced the number of SARS-CoV-2 samples being sequenced. For jurisdictions that are continuing SARS-CoV-2 genomic surveillance, SARS-CoV-2 samples which are likely to be prioritised for sequencing include those from cases who are hospitalised or admitted to intensive care, or cases of clinical significance. As a result, these changes are likely to affect the representativeness of sequenced SARS-CoV-2 lineages across Australia.

There are several additional data considerations that should be noted when interpreting SARS-CoV-2 genomic surveillance data.

- Only samples with laboratory-definitive evidence of SARS-CoV-2 are eligible for sequencing. Not all samples will be suitable for sequencing, especially those samples with low amounts of viral nucleic acid (i.e., high RT-qPCR cycle thresholds) such as those collected from cases late in their disease episode (common in returned travellers) or those subjected to storage at suboptimal conditions, causing viral nucleic acid degradation.[12]
- The number of sequences presented in the AusTrakka data are not equivalent to the number of reported cases, as not all cases are sequenced and there may be duplicates in the AusTrakka data.
- Sequencing methodology and protocols vary between jurisdictions.
- AusTrakka uses a combination of consensus sequences (a consensus sequence is an interoperable genomic surveillance unit that can be combined from laboratory sources) publicly available in the Global Initiative on Sharing All Influenza Data (GISAID) repository, consensus sequences uploaded directly to AusTrakka, and consensus sequences generated at the Microbiological Diagnostic Unit Public Health Laboratory for sequences yet to be publicly available.[12]
- Quality control for consensus sequences include: requiring ≥ 90% of the viral genome to be recovered; < 50 single nucleotide polymorphisms from the MN9008947.3 (SARS-CoV-2 Wuhan Hu-1) reference genome; and < 50 ambiguous or missing bases. Sequences with 50–90% genome recovery are assessed for potential inclusion.[12]
- AusTrakka uses a maximum likelihood algorithm for phylogenetic reconstruction.
- AusTrakka defines SARS-CoV-2 genomic lineages using the Phylogenetic Assignment of Named Global Outbreak (Pango) lineage nomenclature.[22] Lineages reflect evolutionary

relationships and are hierarchically organised following the phylogenetic tree structure. The Pango designation describes major lineages with letters of the alphabet (A, B, etc.), with sub- and sub-sub-lineages numbered and separated by dots (“.”). Thus, sub-lineage B.1.1 is contained with sub-lineage B.1, which is itself part of lineage B. The numbers at the same level are not indicative of a phylogenetic relationship. As such, B.1.1 is not necessarily more closely related to B.1.2 than to B.1.5. However, all the sub-lineages under B.1 are closer to each other than they are to B.2, for example.[12,22]

- Lineages and sub-lineage classifications are continuously defined, and lineage classification may change retrospectively as new sequences are added and lineages diversify over time. Sub-sub lineage designations may change with updates to Pangolin, USHER, and NextClade lineage calling software used by AusTrakka. For this reason, numbers and proportions of sub-lineages may be adjusted in future reports.
- A “variant” refers to a set of viruses with the same or similar patterns of mutations, some of which are associated with increased transmissibility or virulence, or decreased effectiveness of public health measures. These are commonly referred to as “variants of concern”. A Pango lineage of SARS-CoV-2 may be designated as a variant of concern if there is evidence of epidemiological, pathological, or immunological features of concern.[23] These may be designated by international bodies like the World Health Organization, or potentially observed and designated as variants of concern locally.
- Since July 2023, AusTrakka has used the World Health Organization designations[24] for any variant of concern, variant of interest, or variant under monitoring designations. Prior to July 2023, the Communicable Diseases Genomics Network Variant of Concern Working Group actively assessed lineages with consideration to the Australian context. Readers are encouraged to consult the COVID-19 Epidemiology Reports and the Technical supplement: COVID-19 Australia[12] published in *Communicable Diseases Intelligence* Journal for historical context information on those lineages previously classified as a variant of concern in Australia.
    - The B.1.1.529 (Omicron) lineage was designated a variant of concern by the World Health Organization on 26 November 2021.[25] There is evidence of higher transmissibility, including higher rates of re-infections. There are some indications of decreased rates of severe clinical disease, but it is unclear whether this can be attributed to biological characteristics of Omicron, or is a consequence of vaccination or prior infection. Considerable community transmission in Australia has since led to further evolution of Omicron (B.1.1.529 and BA.* sub-lineages) within Australia. To date, there have been five major sub-lineages defined under B.1.1.529: BA.1, BA.2, BA.3, BA.4 and BA.5, and a large number of sub-lineages under these; all are designated Omicron.[12]
- Currently, in AusTrakka variants of concern are determined from a viral sequence by using the NextClade Pangolin software and scorpio algorithm, which assigns a sequence to a Pangolin constellation (the presence of a set of characteristic mutations for each variant of concern lineage). Non-variant of concern lineages are determined using the Pangolin software PangoLEARN. This approach is aligned with the World Health Organization position on variant of concern classification and interpretation.

Appendix B: Vaccine terminology

Vaccine coverage

Vaccine coverage refers to the proportion or prevalence of complete immunisation in a population.[26] Vaccine coverage is a widely used performance indicator to determine utilisation of a vaccine program. Vaccine coverage can establish if enough people are being vaccinated so that the spread of diseases will be interrupted. In addition, assessing vaccine coverage in population sub-groups (such as age groups) or local areas can identify specific areas of low coverage so that measures to improve coverage can be appropriately targeted. Vaccine coverage is measured through registries (like the Australian Immunisation Register), routine administrative reports or community-based surveys.

Vaccine efficacy

Vaccine efficacy refers to the reduction in disease, due to vaccination, as shown in research studies carried out under controlled conditions like in randomised controlled trials.[28] While this type of study is considered the gold standard to confirm the protective effects of vaccination, there are important limitations. Clinical trials are often performed in healthy populations, and usually exclude people with medical conditions and pregnant women. For vaccines that need multiple doses, people are more likely to follow the vaccine schedule if they are enrolled in a trial than they would in "real life". Clinical trials usually enrol too few people to see changes in rare but important outcomes, such as hospital admission or death.

Vaccine effectiveness

Vaccine effectiveness refers to the reduction in clinical outcomes due to vaccination in the "real world" after a vaccine program has been implemented.[28] These outcomes may include disease incidence, or other measures such as general practice attendance with disease, or hospital admission with disease. Vaccine effectiveness is often lower than vaccine efficacy, because it includes people in whom the immune responses to vaccines may not be as strong as healthy people in clinical trials, and because adherence to vaccine schedules may not be as good as in clinical trials. In addition, for influenza vaccines, the effectiveness will depend on the match between the vaccine influenza strains and influenza strains circulating in the community and is likely to vary from season to season. Vaccine effectiveness is usually estimated from observational studies.

Vaccine impact

Vaccine impact refers to the reduction in disease incidence in the population attributed to the vaccine.[28] This includes factors such as vaccine coverage and effectiveness, as well as potential indirect protection due to a reduction in disease spread. The degree of indirect protection depends on how infectious the disease is, how different populations come into contact with each other, how many people get vaccinated, and the degree to which vaccination reduces disease spread. The effect of vaccination on disease spread in the population may be different to the protection against the disease in individuals.

Vaccine match

Vaccine match refers to the similarity or match between the virus strains in a vaccine and the virus strains circulating in the community.[27] If the vaccine match to circulating strains is good, there is usually a lower burden of severe illness and severe disease outcomes at a population level. Each year, strains of influenza circulating in the community change, and influenza vaccines are reformulated to match circulating influenza strains as closely as possible. This is why an influenza vaccine is recommended for people aged six months and over each year. Virological surveillance of circulating influenza virus strains during the season can provide an assessment of vaccine match.