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## COVID-19 Australia: Epidemiology Report

Last updated 28 June 2022

COVID-19 National Incident Room Surveillance Team

# Communicable Diseases Intelligence

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# COVID-19 Australia: Epidemiology reporting

Last updated 28 June 2022

COVID-19 National Incident Room Surveillance Team

## Summary

This supplement to the series of regular Australian coronavirus disease 2019 (COVID-19) epidemiological reports describes the technical background to the surveillance data reported through Communicable Diseases Network Australia (CDNA) as part of the nationally-coordinated response to COVID-19.

## Background

Coronavirus disease 19 (COVID-19), caused by the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first identified in humans in Wuhan, China, in December 2019. The disease subsequently spread rapidly, leading to a global pandemic.<sup>1</sup> The predominant modes of transmission for COVID-19 are through direct or close contact with an infected person via respiratory droplets, or indirectly via contact with contaminated fomites.<sup>2</sup> The median incubation period of COVID-19 is 5–6 days, ranging from 1 to 14 days.<sup>3,4</sup> The infectious period remains uncertain; however, it is estimated to be from 48 hours before symptoms develop until two weeks after symptom onset.<sup>3,5</sup> The predominant symptoms reported in COVID-19 cases are cough, sore throat, fatigue, runny nose and fever.<sup>6</sup> The majority of cases recover from the disease without clinical intervention; however, approximately 20% of global cases result in more severe outcomes, such as shortness of breath and pneumonia, necessitating hospitalisation and the requirement of additional oxygen or ventilation.<sup>7,8</sup> Severe or fatal outcomes are generally more common among elderly cases or those with comorbid conditions.<sup>8</sup> A visual depiction of the severity spectrum of COVID-19, and of the data sources that we use in this report to measure aspects of severity, is provided in Figure 1.

## Data sources

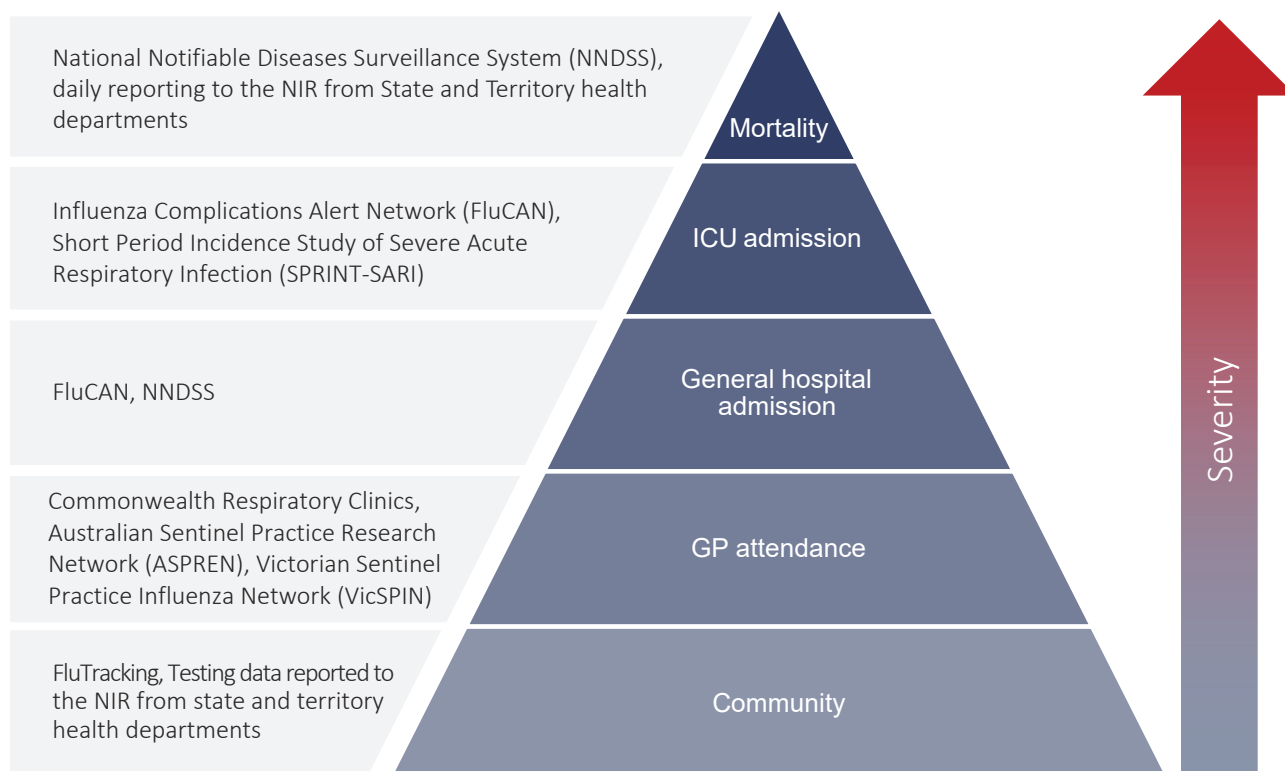
### Notifications to health departments

The majority of data presented in the latest COVID-19 epidemiology report were derived from the National Interoperable Notifiable Diseases Surveillance System (NNDSS). COVID-19 is a notifiable disease under public health legislation in all states and territories and is listed on the National Notifiable Diseases List under the *National Health Security Act (2007)*.<sup>9</sup> Accordingly, all jurisdictions report confirmed and probable cases of COVID-19 through the NNDSS. The national case definition for surveillance is available in the COVID-19 Series of National Guidelines.<sup>10</sup> As of report 62 onward, the case data provided in the reports includes both polymerase chain reaction (PCR) confirmed and rapid antigen test (RAT) probable cases reported to the NNDSS, unless otherwise specified.

Due to the dynamic nature of the NNDSS, numbers presented in the latest report may be subject to revision and may vary from numbers previously reported and from case notifications released by states and territories. Case numbers for the most recent dates of illness onset may be subject to revision, due to reporting delays. Data for the latest report, unless otherwise indicated, have been extracted from the NNDSS within



**Figure 1: Severity spectrum of COVID-19 cases and data sources used to measure severity in Australia**



48 hours after the end of the reporting period, for notifications received up to the end of the reporting period.

### Acute respiratory illness

We report data from surveillance systems that monitor trends in the number of people reporting symptoms of mild respiratory illnesses in the community and in primary care settings. These systems gathered information from across Australia and include the online FluTracking syndromic surveillance system,<sup>11</sup> the Commonwealth General Practice (GP) Respiratory Clinics, and the Australian Sentinel Practice Research Network (ASPREN) and Victorian Sentinel Practice Influenza Network (VicSPIN) GP sentinel surveillance systems. These systems capture data on any respiratory illness experienced by participants, including pathogens such as SARS-CoV-2.

### Hospitalisations

To report on COVID-19 disease severity, we draw on hospitalisations and intensive care

unit (ICU) admissions data provided from two sentinel surveillance systems: the Influenza Complications Alert Network (FluCAN)<sup>12</sup> and the Short Period Incidence Study of Severe Acute Respiratory Infection Study (SPRINT-SARI),<sup>13</sup> as well as NNDSS. FluCAN is a real-time hospital sentinel surveillance system for acute respiratory disease requiring hospitalisation. Established to monitor for seasonal influenza, FluCAN has been modified to include surveillance for COVID-19. Participating sites collect detailed clinical and laboratory information from all hospitalised patients with a confirmed diagnosis of COVID-19. SPRINT-SARI is a sentinel system that collects detailed data on the characteristics and outcomes of and interventions for patients admitted to ICUs or High Dependency Units (HDUs) with COVID-19 at participating sites across Australia. Data presented from both sentinel surveillance systems may be subject to retrospective adjustments following publication. Data on hospitalisations and ICU admissions from the NNDSS is also presented in the report. This is based on data from jurisdictions which have reliable data

across both hospital and ICU data fields, and which do not routinely hospitalise cases for isolation purposes.

## Viral genomics

From Report 36 onwards, information on viral genomics is included in every second report, and has been included in all reports from Report 57 onwards. This information is provided by the National Analysis Team of the national pathogen genomic sequence and analysis platform, AusTrakka,<sup>i</sup> and from jurisdictional pathogen sequencing laboratories. Reporting periods are based on sample collection date, not date of 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 RNA degradation). Quality control for consensus sequences included: requiring  $\geq 90\%$  of the viral genome to be recovered;  $< 50$  single nucleotide polymorphisms (SNPs) from the MN9008947.3 reference genome; and  $< 50$  ambiguous or missing bases. Sequences with 50–90% genome recovery are assessed for potential inclusion.

Report 35 and earlier used data from the Global Initiative on Sharing All Influenza Data (GISAID), an international virus sequence database that provides open access to SARS-CoV-2 genomic data.<sup>14</sup>

SARS-CoV-2 genomic lineages are defined using the Phylogenetic Assignment of Named Global Outbreak (PANGO) lineage nomenclature.<sup>15</sup> 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 within 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. Only three sub-levels are permitted under this nomenclature system and sub-lineages under this will be assigned the next available alpha symbol (e.g. B.1.1.25.1 was reassigned to D.2 and B.1.1.28.1 was reassigned to P.1).

Lineage classifications can change retrospectively as new sequences are added and lineages diversify over time.<sup>ii</sup> Sequences that have been assigned higher-level lineage designations (e.g. B or B.1), where there are sub-lineages defined within the dataset (e.g. B.1.1, B.1.23 or B.1.1.25), may indicate a poor quality sequence; for example, a lower proportion of the genome recovered. Poor sequence quality can lead to uncertainty about the placement of the sequence into sub-lineages.

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 labelled as “variants of concern” (VOCs) and given specific identifiers (e.g. VOC-202012/01). However, as VOCs are usually defined not just by the unique set of mutations, but by membership of distinct lineage groups, they are often referred to by the lineage name. So VOC-202012/01 is often just referred to as B.1.1.7. It should be noted, though, that the lineage naming convention refers to evolutionary aspects of the virus, while the VOC-ID also takes into account the epidemiological behaviour of the virus.

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i [www.cdgn.org.au/austrakka](http://www.cdgn.org.au/austrakka).

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ii Additional detailed information on SARS-CoV-2 lineages can be found at <https://cov-lineages.org/descriptions.html>.

On 31 May 2021 the WHO announced new nomenclature for key variants using letters of the Greek alphabet.<sup>16</sup> This system was developed to assist with public discussion of variants, and aimed to provide labels that were easier to pronounce and non-stigmatising. The VOCs monitored in this reporting series will henceforth note both the genetic Pangolin lineage and the WHO label (if named).

On 27 September 2021, Kappa (B.1.617.1), which had been classified as a VOC in Australia, was reclassified as a “variant of interest” (VOI) by the Communicable Diseases Genomics Network (CDGN) VOC Taskforce. On 31 January 2022, the CDGN VOC Taskforce demoted three further previously-designated VOCs (Alpha (B.1.1.7); Beta (B.1.351) and Gamma (P.1)) due to the sustained absence of any cases in Australia, and very limited prevalence globally. On 23 May 2022, the Taskforce similarly demoted the previously-designated VOC Delta (B.1.617.2) to a VOI, again due to the sustained absence of any cases in Australia.

While these variants are no longer included in this reporting series, detail on these lineages is retained in Appendix B, which retains otherwise-deprecated content of relevance to past publications in this reporting series.

#### **B.1.1.529 (Omicron)**

Lineage B.1.1.529 emerged in South Africa in November 2021,<sup>17</sup> and was designated a VOC by the WHO on 26 November 2021.<sup>18</sup> This VOC contains more than 30 mutations in the spike protein, many of which have been seen in other VOCs.

Prevalence of Omicron rose sharply in South Africa, with the variant rapidly spreading internationally and accounting for an increasing proportion of cases in several countries. 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 the Omicron strain, or is a consequence of vac-

cination or prior infection. Some of the mutations are predicted to affect its susceptibility to neutralising antibodies, innate immunity, and monoclonal antibody therapies.

Significant community transmission in Australia means that there is a possibility for further evolution of Omicron (B.1.1.529 and BA.\* sub-lineages) within Australia. The evolution will be very closely monitored by the CDGN VOC Working Group, through representative sequencing of Omicron cases in Australia for genomic surveillance via the CDGN and AusTrakka.

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.

### **Testing data**

Testing data by demographic breakdown were reported on a weekly basis by jurisdictions.

### **Denominators**

Population data from the Australian Bureau of Statistics (ABS) Estimated Resident Population are used to estimate rates of infection by jurisdiction, age group, sex and Indigenous status. From Report 37 onwards, Estimated Resident Population data as at June 2020 is used. Previous reports used Estimated Resident Population data as at December 2019.

### **International**

All data reported in the international section were extracted from the World Health Organization (WHO) Dashboard on the last day of the reporting period unless otherwise specified.<sup>19</sup>

## Definitions

**“Cluster”** in relation to COVID-19 refers to two or more cases (who do not reside in the same household) that are epidemiologically related in time, place or person where a common source (such as an event or within a community) of infection is suspected but not yet established.

**“COVID-19”** is the disease caused by a novel coronavirus—SARS-CoV-2—that emerged in China in late 2019. ‘CO’ stands for corona-, ‘V’ stands for virus, ‘ID’ stands for infectious disease, and ‘-19’ refers to the year that this disease was first reported.

**“COVID-19 associated death”** is defined for surveillance purposes as a death in a probable or confirmed COVID-19 case, unless there is a clear alternative cause of death that cannot be related to COVID-19 (e.g. trauma).<sup>20</sup> There should be no period of complete recovery from COVID-19 between illness and death. Where a Coroner’s report is available, these findings are to be observed.

**“Diagnosis date”** is derived from data collected by the NNDSS and represents the reported true onset of disease date. If unknown, the earliest of specimen collection date, notification date or notification received date is used.

**“Initial investigation”** refers to the process of determining whether an infection was acquired locally (within Australia) or overseas. Cases under initial investigation have yet to be classified as locally or overseas acquired.

**“Notification received date”** is reported in the NNDSS and represents the date the notification of the disease was first received by the communicable disease section of the health authority. As notification can only occur after testing is completed and information processed, counts for a defined period will vary according to the date type used.

**“Ongoing investigation”** refers to the process of determining the definitive source of infection

for locally-acquired cases. Cases under ongoing investigation are known to be locally acquired but require further follow-up to determine the precise source of infection.

**“Outbreak”** in relation to COVID-19 refers to two or more cases (who do not reside in the same household) among a specific group of people and/or over a specific period of time where illness is associated with a common source (such as an event or within a community). Some states and territories may report a single case associated with a residential aged care facility as an outbreak.

**“SARS-CoV-2”** is the virus that causes the disease COVID-19. It is a betacoronavirus genetically related to the 2003 Severe acute respiratory syndrome coronavirus (SARS-CoV).

**“True onset date”** (previously “date of illness onset”) is reported in the NNDSS and represents the earliest date the case exhibited symptoms.

## Acknowledgements

This supplement describes the technical background to the surveillance data reported through Communicable Diseases Network Australia (CDNA) as part of the nationally-coordinated response to COVID-19. We thank public health staff from incident emergency operations centres and public health units in state and territory health departments, and the Australian Government Department of Health, along with state and territory public health laboratories. We thank those who have provided data from surveillance systems, such as Commonwealth respiratory clinics, ASPREN, Flutracking, SPRINT-SARI, FluCAN, Communicable Disease Genomics Network, AusTrakka and jurisdictional sequencing laboratories.

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## Appendix A: Definitions for outbreak settings

Setting	Inclusions
Accommodation & housing	Includes high-density housing; hostels and backpackers; hotels and serviced apartments; public housing; rough sleeping; and temporary accommodation.
Aged care	Includes residential aged care facilities; commonwealth aged care facilities; and home-care.
Healthcare (excl. hospital)	Includes primary care; and allied health services.
Hospital	Includes inpatient acute and sub-acute hospital (including psychiatric units); day surgeries; and transitional care.
Childcare	Includes preschool child care services; and childcare services provided from home.
Educational facility (excl. childcare)	Includes schools; universities; TAFE; kindergarten; after-school care; other education and training facilities; and higher educational facilities.
Workplace/industry	Includes warehouses (not food); supermarkets; utilities; residential work sites; office spaces; manufacturing; logistics; food distribution centres; construction sites; retail and supermarkets.
Disability services	Includes disability services and private accommodation; and support services.
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 & 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 & emergency	Includes emergency services; correctional facilities; and prisons.
Other	Includes other various settings not captured by the other exposure settings, e.g. extended family gatherings (where two or more separate households come together); religious services; and sports and recreation venues.



## Appendix B: Deprecated content from past versions of this Technical Supplement

### Information on demoted former VOCs

The following descriptions have been extracted from earlier versions of this Technical Supplement, to provide detail on former Variants of Concern (VOCs) which may assist in interpreting earlier reports in the COVID-19 epidemiology reporting series. Extracts provided are of the final form as published in the Technical Supplement prior to VOC demotion; accordingly, some detail given here (such as WHO variant nomenclature using letters of the Greek alphabet) may not have been included in some of the earlier versions of the Technical Supplement describing these variants.

## Former VOCs included in the Technical Supplement from 9 April 2021 to 22 February 2022

### B.1.1.7 (VOC-202012/01, Alpha)

The B.1.1.7 lineage is characterised by 17 mutations, including spike protein mutations N501Y and P681H, and a two-amino-acid deletion of residues 69,70 (IHV68I).<sup>21</sup> Having first emerged in the United Kingdom in September 2020, it has now been detected in more than 90 countries worldwide.

### B.1.351 (501Y.V2, Beta)

The B.1.351 lineage is characterised by nine characteristic mutations, including spike protein mutations K417N, E484K and N501Y.<sup>22</sup> In addition to potentially increased transmissibility, there is concern that the E484K mutation may affect antibody-mediated neutralisation of the virus.<sup>23</sup> This variant was first detected in South Africa in October 2020 and has since been documented in more than 40 countries.

### P.1 (501Y.V3, Gamma)

The P.1 lineage is a sub-cluster within lineage B.1.1.28 that is characterised by 17 mutations, including the same spike protein mutations K417T, E484K and N501Y as B.1.351.<sup>24</sup> The B.1.1.28 lineage was common to Brazil, but in December 2020 reports emerged from Brazil's Amazonas region of a surge in cases associated with the P.1 lineage.<sup>25</sup> In late December, the P.1 variant was reported in four COVID-19 cases in Japan detected during airport screening, and has now been seen in more than 20 countries.

## Former VOCs included in the Technical Supplement from 23 May 2021 to 28 June 2022

### B.1.617.2 (VOC-21APR-02, Delta)

Lineage B.1.617 emerged from India in October 2020.<sup>26</sup> Ongoing genomic surveillance has broken B.1.617 into three sub-lineages—B.1.617.1, B.1.617.2 and B.1.617.3—which vary in mutations in the spike protein.<sup>27</sup> B.1.617.2 has been a particularly successful sub-lineage, with evidence of B.1.617.2 being associated with higher transmissibility and increased risk of hospitalisation.<sup>28</sup>

Public Health England and the World Health Organization (WHO) declared the B.1.617 lineage (PHE designed B.1.617.2 only) as a Variant of Concern on 7 May 2021 and 10 May 2021 respectively.<sup>28,29</sup> With the declaration of new VOC nomenclature by the WHO on 1 June 2021,<sup>30</sup> only the B.1.617.2 lineage was retained as a VOC by the WHO. In Australia, B.1.617.1 (VUI-21APR-01, Kappa) was classified as a VOC until 27 September 2021, when it was demoted to a VOI by the CDGN VOC taskforce.

There are now more than a hundred B.1.617.2 sub-lineages defined: AY.1 to AY.127. There are also a number of sub-lineages within the sub-lineages, as well as a few sub-lineages within those in turn. There has been no reported biological difference of the sub-lineages, and these are more reflective of geographical epidemiology. There appears to be some instability in the lineage assignment, with the sub-lineages being sensitive to the proportion of the genome recovered. Therefore, the CDGN VOC Taskforce has decided to report all sub-lineage samples as just B.1.617.2, Delta.

The B.1.617.1 and B.1.617.3 lineages continue to be monitored by AusTrakka, but are not reported.

## Appendix C: Frequently asked questions

### Q: Where can I find more detailed data on COVID-19 cases?

A: We are currently looking into ways to provide more in-depth epidemiological analyses of COVID-19 cases, with regard to transmission and severity, including hospitalisation. These analyses will continue to be built upon in future iterations of the CDI report.

### Q: Can I request access to the COVID-19 data behind your CDI epidemiology reports?

A: National notification data on COVID-19 confirmed cases is collated in the National Notifiable Diseases Surveillance System (NNDSS) based on notifications made to state and territory health authorities under the provisions of their relevant public health legislation.

Normally, requests for the release of data from the NNDSS requires agreement from states and territories via the Communicable Diseases Network Australia (CDNA), and, depending on the sensitivity of the data sought and proposed, ethics approval may also be required.

For information on how to apply to access data from the NNDSS please contact the NNDSS Data Requests inbox.<sup>iii</sup> We can then provide you with further information about the process and the required data request forms. Please note data requests for NNDSS data, including COVID data, will continue to be processed in line with CDNA policies and procedures. The time it takes to process your request may vary depending on the type(s) of data you request and the necessary approval steps.

We will continue to publish regular summaries and analyses of the NNDSS dataset and recommend the following resources be referred to in the meantime:

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iii [nndss.datarequests@health.gov.au](mailto:nndss.datarequests@health.gov.au).

NNDSS summary tables;<sup>iv</sup>

- Daily case summary of cases;<sup>v</sup>
- *Communicable Diseases Intelligence* COVID-19 epidemiology report;<sup>vi</sup>
- State and territory public health websites.

**Q: Can I request access to data at postcode level of confirmed cases?**

A: Data at this level cannot be released without ethics approval and permission would need to be sought from all states and territories via CDNA. As noted above, specific requests for NNDSS data are currently on hold.

Where current or recent reported case numbers are high enough to justify it, a GIS/mapping analysis of cases will be included in the CDI COVID-19 epidemiology report. In order to protect privacy of confirmed cases, data in this map will be presented at SA3 level.

**Q: Where do I find the COVID-19 background information which was included as Appendix A in previous epidemiology reports?**

A: This information was most recently published in Epidemiology Report 24.<sup>vii</sup> Additional information can be found in the CDNA Series of National Guidelines (SoNG) for COVID-19.<sup>viii</sup>

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iv <http://www9.health.gov.au/cda/source/cda-index.cfm>.

v <https://www.health.gov.au/news/health-alerts/novel-coronavirus-2019-ncov-health-alert/coronavirus-covid-19-current-situation-and-case-numbers>.

vi [https://www1.health.gov.au/internet/main/publishing.nsf/Content/novel\\_coronavirus\\_2019\\_ncov\\_weekly\\_epidemiology\\_reports\\_australia\\_2020.htm](https://www1.health.gov.au/internet/main/publishing.nsf/Content/novel_coronavirus_2019_ncov_weekly_epidemiology_reports_australia_2020.htm)

vii <https://doi.org/10.33321/cdi.2020.44.75>.

viii <https://www1.health.gov.au/internet/main/publishing.nsf/Content/cdna-song-novel-coronavirus.htm>.