CHAPTER 2

COVID-19 — The science

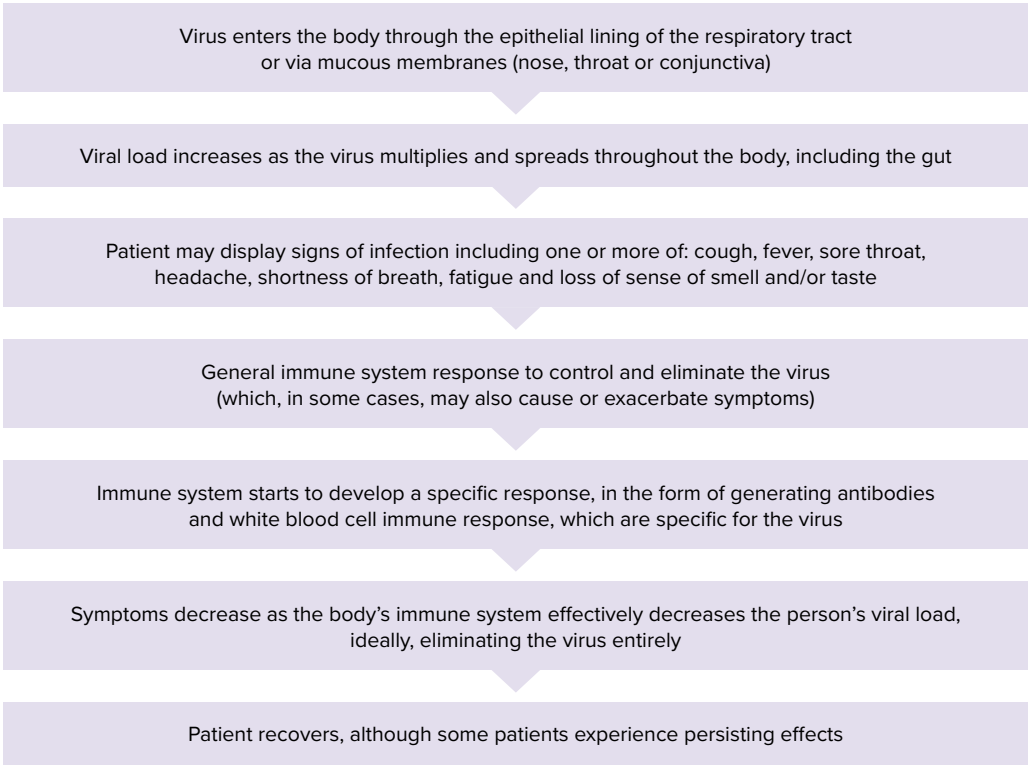
2.1 Introduction

1. As highlighted in the Background section of this report, SARS-CoV-2 is a new virus and information about it continues to emerge as the pandemic progresses. While the scientific and medical communities across the world work to learn more about the virus, the current general understanding of what it is, how it spreads and how it can broadly affect people is useful to set out here, particularly to give context as to why it was that the Hotel Quarantine Program was considered necessary.
2. Further, to assist in ascertaining the links between what has become known as the 'second wave' of COVID-19 cases in Victoria and the Hotel Quarantine Program, it was necessary to understand the science behind the COVID-19 virus, as it is currently understood, and the appropriate mechanisms for managing and controlling it.
3. To do that, evidence was called on 17 and 18 August 2020 from three scientific and medical experts regarding the nature of the COVID-19 disease, infection control, epidemiology and genomic sequencing.
4. The scientific and medical experts were:
    A. Professor Lindsay Grayson — a clinical physician specialising in infectious diseases and infection control. Prof. Grayson provided evidence based upon his years of clinical experience, current scientific and medical information and his first-hand experience managing infection control for COVID-19 at Austin Health as Director of the Infectious Diseases Department, a role he has held since 2000[1]
    B. Professor Ben Howden — a medical microbiologist with expertise in genomic sequencing. Since 2014, Prof. Howden has been the Director of the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) at the University of Melbourne. In his role as Director, he leads a team of scientists, computer scientists and epidemiologists who conduct genomic sequencing and analyse and report on genomic sequencing data in Victoria[2]
    C. Dr Charles Alpren — an expert epidemiologist. Since June 2019, Dr Alpren has been employed by the Department of Health and Human Services (DHHS) as an epidemiologist and is one of the leads in the Intelligence Section (Intelligence) of the COVID-19 Public Health Incident Management Team. His role is to oversee the entry, management, epidemiological analysis, interpretation and reporting of data pertaining to COVID-19 that is collected through the DHHS notifiable diseases surveillance system. He reports to the Deputy Public Health Commander for Intelligence.[3]
5. The evidence and expertise of these three witnesses was not contested during the Inquiry's hearings. I accept their evidence regarding genomic sequencing, the nature of COVID-19, quarantine and associated testing and infection control protocols relating to COVID-19.

2.2 The nature of COVID-19

6. The proceeding paragraphs summarise the current state of knowledge about the COVID-19 virus, how it spreads, for how long people are infectious, the effect on different age groups and what is currently known about immunity. It must be noted, however, as was observed regularly during the Inquiry, that state of knowledge is still developing.

Figure 2.1: Lifecycle of the virus



Source: Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 5 [23].

What is COVID-19?

7. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the strain of coronavirus that causes coronavirus disease 2019 (COVID-19). Prof. Grayson gave evidence that coronaviruses are a family of viruses thought to only affect mammals.[4]

8. COVID-19 is considered to be highly infectious, particularly as it can be transmitted before the onset of symptoms and because those who are infectious may be entirely asymptomatic or have only trivial symptoms.[5]

9. Prof. Grayson's evidence was that COVID-19 is in the same family of viruses as SARS and MERS-CoV, the Middle Eastern coronavirus. He explained that SARS in 2003 was different to the current COVID-19 virus strain in that almost all patients who contracted the virus were very symptomatic and it had a substantially higher death rate.[6] Likewise, while MERS exhibited some asymptomatic carriage, person-to-person transmission was relatively low.[7]

Symptoms of COVID-19

10. It was Prof. Grayson's evidence that respiratory symptoms are a common feature of COVID-19 and can include fever, dry cough, sore throat, tiredness and shortness of breath.[8] An additional, unique symptom is the loss of both smell and taste. Prof. Grayson noted that a loss of sense of smell is common when one has any upper respiratory tract viral infection, but to lose sense of smell *and* taste is definitive of this particular infection. While it does not occur in all cases, when it does, it has been shown in various studies to be highly suggestive of COVID-19.[9]

11. Dr Alpren stated that approximately 17.9 per cent of cases experience asymptomatic infection. This means that some people who are infected will not experience any symptoms and may not know they are sick. He explained that, as symptomology can vary throughout the course of the infection, the overall proportion of cases that remain asymptomatic throughout the course of infection is unknown.[10]

What is known about the infectious nature of COVID-19?

12. Prof. Grayson's evidence was that, for COVID-19 illness to occur, a person must be exposed to a sufficient amount (the viral load) of the SARS-CoV-2 (also referred to as the COVID-19 virus). Exposure occurs through *viral shedding*.[11]

13. He stated that viral load is a measure of the number of virus particles in a given sample. For example, it may refer to the amount of virus present in a person's tissues or bodily fluids (such as respiratory droplets) or the amount of virus to which a person is exposed.[12]

14. He explained that viral shedding occurs when a person who has the virus present in their body expels infectious fluid from their body; for example, by sneezing or coughing.[13]

15. Those with the virus are thought to be at their most infectious (the maximum point of viral load) for up to 48 hours before they show any symptoms, for those who have symptoms. However, Prof. Grayson noted that this timeframe is variable amongst different people; some may be infectious for a longer period before symptom onset and others for a shorter period. Notwithstanding this variability, 48 hours is considered to be a reasonable average timeframe and is similar to many other viral infections.[14]

Incubation period

16. Prof. Grayson agreed with the generally-held medical opinion that the COVID-19 virus has an incubation period of up to 14 days, with an average incubation period of about five to seven days.[15] This means that for those who are exposed to the virus, the majority will develop symptoms (where symptoms show) within 14 days of exposure to the virus. He explained that there have been reports of some individuals not showing symptoms for up to 24 days after exposure to the virus, but 14 days is considered the upper limit for the majority of patients.[16]

17. Prof. Grayson stated that most symptomatic COVID-19 patients resolve their symptoms in approximately 10–14 days and are considered likely to be non-infectious at the end of that time.[17] As noted by Prof. Grayson, '[a]lthough statistics vary from country to country, present data suggests that, for every 100 Australians who test positive for the virus, up to 20 per cent may require admission to hospital, up to 10 per cent may require intensive care support, and between 1.4 to 3.4 per cent may die'.[18]

Modes of transmission

18. The issue of the modes of transmission of the virus is still the subject of varying expert opinions, particularly as between aerosol and fomite transmission. Fomites are defined by Prof. Grayson as surfaces or objects (including hands) which may become contaminated (e.g. through contact with an infected person) and serve as an intermediary vehicle for transmission. According to Prof. Grayson, COVID-19 enters the body through mucous membranes, including the conjunctiva of the eyes and the membranes of the nose and the mouth, and via the lining of the lungs.[19]

19. He explained that the COVID-19 virus can be transmitted through direct contact with infected people via respiratory secretions (droplets and aerosols). It can also be transmitted through fomites. Examples of fomites cited by Prof. Grayson included thermometers or other shared equipment.[20]

20. Prof. Grayson explained in evidence that COVID-19 is a predominantly respiratory virus.[21] That is, it mainly transmits when 'a person inhales droplets or particles that have been expelled by an infected person, either from coughing, sneezing, talking, singing or by breathing. In each case, the virus particle is suspended in the saliva or mucous particles (in droplet or aerosol form) which are ordinarily expelled by each of these actions'.[22]

21. He stated that while the COVID-19 virus may be airborne (particularly when expelled in aerosol format), it appears to have less potential for distant transmission (for example, via an air conditioning system where air is partially recirculated such as in large office buildings, hospitals or hotels). There have been reports of airborne transmission in places that are crowded and likely to be inadequately ventilated, such as restaurants and fitness classes, but Prof. Grayson noted that short-range aerosol transmission cannot be ruled out in these instances. It was his view that were the COVID-19 virus capable of substantial distant airborne transmission, localised outbreaks that are larger than what have been experienced would likely have occurred.[23]

22. Prof. Grayson stated that, regarding fomites, studies have demonstrated that the COVID-19 virus could survive on certain surfaces (such as plastic, cardboard and stainless steel), outside of a body, for up to 72 hours. As an example of how transmission may occur via a fomite, Prof. Grayson said that 'an infected person may cough on a door handle, which is then touched by another person. Should that second person then touch their mouth, there is transmission from the infected person to the second person'.[24]

23. It is relevant to note that, while medical and scientific experts are continuing to develop an understanding of the COVID-19 virus and its modes of transmission, the evidence provided to the Inquiry about the possible modes of transmission of COVID-19 was known as of 29 March 2020, at the time the Hotel Quarantine Program was established. Guidance provided by the WHO on 29 March 2020 and titled 'Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations: scientific brief' was drawn upon by DHHS staff to inform their knowledge of COVID-19.[25]

24. The WHO guidance stated:

> According to current evidence, COVID-19 virus is primarily transmitted between people through respiratory droplets and contact routes … Droplet transmission occurs when a person is in close contact (within 1 m) with someone who has respiratory symptoms (e.g. coughing or sneezing) and is therefore at risk of having his/her mucosae (mouth and nose) or conjunctiva (eyes) exposed to potentially infective respiratory droplets. Transmission may also occur through fomites in the immediate environment around the infected person. Therefore, transmission of the COVID-19 virus can occur by direct contact with infected people and indirect contact with surfaces in the immediate environment or with objects used on the infected person … In the context of COVID-19, airborne transmission may be possible in specific circumstances and settings in which procedures or support treatments that generate aerosols are performed … [26]

Rate of transmission — the concept of R_0

25. Prof. Grayson explained the concept of R_0 in his witness statement as follows:

> R_0 is the average number of people who are likely to contract a contagious disease, from one other person with that disease, within a sample population. For a contagious disease to maintain spread throughout a population, R_0 needs to be greater than 1. A R_0 of 1 means that, in a community of people, one person is likely to infect only one other person. If that occurs, the virus remains in the community, as it is passed along a chain of infected persons. Where the R_0 is greater than 1, the infection is spreading.[27]

26. Essentially, R_0 provides a value to assess transmissibility in the broader community to guide decisions about what precautions and policies should be implemented. Precautions taken in the community are considered fundamental to reducing the R_0 value for COVID-19.[28]

27. The COVID-19 virus is considered to have a potential R_0 value of approximately 2–3, noting that this can vary based on region, health standards and controls. As at 1 August 2020, the R_0 value for COVID-19 in Australia was estimated to be about 1.05, although the R_0 value for Victoria, where the pandemic was changing rapidly, was not publicly available as of that date.[29]

28. As a comparison, Prof. Grayson stated in his witness statement that measles is considered to have an R_0 value of between 12 and 18. That is to say, that for every one person who has measles, an average of between 12–18 other people will be infected (where they are not vaccinated).[30]

29. The evidence was that the R_0 represents an average rate of transmission in the community. It does not define an individual's actual potential for infecting others. Some individuals will have a rate of transmissibility that is higher than the average.[31] These individuals are referred to as 'super spreaders' as defined in paragraphs 30–32 below.

'Super spreaders' and asymptomatic transmission

30. The concept of 'super spreaders' refers to individuals who infect a disproportionately large number of contacts.[32] These individuals may have a higher viral load, and are therefore likely to be more infectious, or they may be asymptomatic and therefore less likely to self-isolate as they may be unaware that they have COVID-19. Prof. Grayson stated that some recent overseas studies have suggested that possibly 10–20 per cent of COVID-19 infected patients may be responsible for 80 per cent of all cases.[33]

31. Super spreaders are not unique to COVID-19. In his witness statement, Prof. Grayson highlighted that during the SARS-CoV outbreak in 2003, the index patient of the Hong Kong epidemic was associated with at least 125 secondary cases.[34]

32. The concept of asymptomatic super spreaders raises important issues that go to the complexity of COVID-19 from an infection control and testing perspective, particularly in a quarantine environment. Prof. Grayson noted that testing for COVID-19 is crucial given that up to approximately 20 per cent of cases can be asymptomatic.[35]

33. The rationale for a 14-day quarantine period, as noted above, is that most people will develop symptoms within 14 days of exposure to the virus, although some individuals have not shown symptoms until up to 24 days after exposure.[36] This variation in incubation period, and given what is known about asymptomatic COVID-19 cases, led Prof. Grayson to conclude that it would be sensible to test all people at the end of their quarantine period to see whether they were infected with the virus, irrespective of symptoms. He noted that if the sole determinant for whether people were released from quarantine was that they were not showing symptoms after 14 days, a proportion of those who were infected with the virus and potentially infectious, but who remained asymptomatic, could be released into the community.[37] The testing regime that developed throughout the course of the Hotel Quarantine Program is discussed in more detail in Chapter 10.

34. It is important to note that, while knowledge of COVID-19 continues to develop, and evidence of asymptomatic transmission has developed more recently, there was knowledge of asymptomatic transmission as early as 29 January 2020.[38] Indeed, an AHPPC statement on COVID-19, published on 29 January 2020, indicated knowledge of 'very recent cases of novel coronavirus who are asymptomatic or minimally symptomatic' and 'reports of one case of probable transmission from a pre-symptomatic case to other people, two days prior to the onset of symptoms'.[39]

Effect of COVID-19 on different age groups

35. In general terms, Prof. Grayson stated that the current state of learning is that children are less affected by COVID-19 (asymptomatic or experience mild symptoms) compared with adults. Observations suggest that about a third of younger people may be asymptomatic or only trivially symptomatic'.[40]

36. As noted by Prof. Grayson, adults and those with a weakened immune system appear to be more affected in terms of symptoms and associated severity of illness. The older one is, the more one's mortality is impacted. But Prof. Grayson stated that it is unclear, at this stage, whether COVID-19 affects older members of the community simply due to age or whether the immune system in general weakens as one gets older.[41]

Immunity

37. According to Prof. Grayson, an immune response is triggered when there is a foreign substance in the body. He explained that, generally speaking, antibodies interact with proteins on the surface of the foreign particles, known as antigens, which are specific to the type of foreign substance detected. Once the body recognises an antigen (either as new or because it has already been exposed to it in the past) it triggers the production of antibodies and enlists the assistance of key white blood cells to fight the infection and develop immunity.[42]

38. Prof. Grayson noted that antibodies also remain in the body to enable it to continuously detect the antigen and eliminate future infections. This is why the body is generally more effective in eliminating foreign particles to which it has been exposed in the past (either via infection or vaccination).[43]

39. The evidence is that work continues to be undertaken to understand the nature and spread of the COVID-19 virus (including asymptomatic transmission), and the body's immune response (including possible reinfection), to support vaccine development.[44]

40. Indeed, as Prof. Grayson noted in his witness statement, current data seems to indicate that some of the vaccines in development may only be effective (in terms of an adequate antibody response) for a limited period of some months, but this varies with the nature of the candidate vaccine, the number of 'booster' doses given and the adequacy of the recipient's immune system to respond to the vaccine. After that time, the immune system's 'memory' wanes, meaning that the COVID-19 specific antibodies may not remain in the body at adequate immediate concentrations and need either time to recover (via immune 'memory mechanisms') or further 'booster' vaccinations.[45]

41. Prof. Grayson stated that it is not yet clear whether a person who has been infected with, and recovered from, COVID-19 will not be infected again. Some examples have arisen where an individual has been infected with the virus, recovered and contracted the virus again with the same symptoms. However, further work needs to be undertaken on whether, in these cases, the infected people caught the same virus strain twice.[46]

42. Prof. Grayson highlighted in his evidence that each virus and each disease is different, which makes vaccine development an interesting but complex field. In terms of vaccine development for COVID-19, he explained that part of the challenge is creating a vaccine that is effective for the relevant strain and any subsequent variants, and provides immunity for an extended period of time.[47]

43. The next step in understanding the science of COVID-19 for the Inquiry's purposes related to epidemiology and genomic sequencing.

2.3 Epidemiology

What is it and why is it undertaken?

44. Dr Charles Alpren, epidemiologist, defined epidemiology, in a general sense, as the study of the patterns and determinants of disease in specific populations. Medically speaking, he noted that epidemiology and public health medicine are different from patient-specific medicine 'as they advise and implement broad interventions on large groups of people to achieve overall health benefit'.[48]

45. Dr Alpren stated that epidemiologists play a role in both understanding and controlling the spread of communicable diseases (diseases that can spread from person-to-person) by:

    A. analysing data to look for patterns that can forecast the trajectory of disease

    B. informing interventions to alter that trajectory.[49]

46. As outlined by Dr Alpren, epidemiologists integrate key facts about a disease, including mechanisms of transmission, incubation and the infectious period, with the spatial and temporal patterns observed within a population.[50]

47. As an example, Dr Alpren noted that the work of epidemiologists could 'involve a group of infected people in a defined location with disease onset between set dates. An analysis of that group and the circumstances of their interactions can reveal how diseases spread, which can then allow us to understand and inform changes ..'.[51] By understanding how and why disease is spread, advice can be provided on how to interrupt the spread of disease.[52]

48. Dr Alpren explained that epidemiology informs an understanding of the risk factors that are characteristic of people or environments that place individuals at higher risk of acquiring or becoming affected by disease. It can, therefore, make broad predictions about people or circumstances that present a higher risk of disease. It can also predict disease trajectory under known parameters and assumptions, and outline what could happen if, for example, restrictions are placed on a population.[53]

What are epidemiological methods used for?

49. Epidemiology supports the detection, surveillance and control of communicable diseases. This involves the collection and analysis of information and data, with the outcomes of this analysis informing contact and communications with people affected by an outbreak, advising next steps and required actions.[54]

50. Dr Alpren explained that inside DHHS, broadly in Victoria, this work is split into streams including: (1) Intelligence and (2) Case, Contact and Outbreak Management. At a high level, Intelligence is responsible for data collection, entry and classification, undertaking data analysis and modelling, and providing associated advice within the Department and to government to support decision-making and planning.[55]

51. Work undertaken by Intelligence supports the work of the Case, Contact and Outbreak Management Team where contact tracing is undertaken. Contact tracing involves the 'identification, assessment and management of people who have potentially been exposed to disease and are at a higher risk of developing and spreading disease'.[56]

52. Dr Alpren explained that contact tracers work with people to interrupt the spread of a disease by ascertaining who might have been exposed to a disease (via interviews with possible contacts and examination of data sources, such as employment rosters) and informing them of their responsibility to quarantine. Contact tracers also work with epidemiologists to identify patterns and risk factors involved in disease transmission.[57] Difficulties with contact tracing in the context of Victoria's hotel quarantine outbreaks is discussed in more detail in Chapter 9.

2.4 Genomic sequencing

What is genomic sequencing?

53. Prof. Howden gave evidence about the science of genomic sequencing, a process by which the whole genetic signature of a pathogen is recovered. A pathogen is defined as a microorganism that can cause a disease, such as a virus.[58]

54. A genome is defined by Prof. Howden as an organism's complete set of genes or genetic material, comprising DNA or RNA. COVID-19, which is a viral genome, is made up of RNA, whereas the human genome, bacterial genomes and some viral genomes are made up of DNA.[59]

55. As outlined in Prof. Howden's statement, whole genome sequencing is the process to determine the complete sequence (DNA or RNA) of an organism's genome and can be broken down into two distinct processes:

    - first, there is an analytical process undertaken in a specialised genome sequencing laboratory, using sophisticated laboratory hardware, to determine the complete genome of an organism in a single reaction
    - then, this genome sequence is investigated and compared with other genome sequences using bioinformatic software.[60]

56. Regarding COVID-19, Prof. Howden explained that this virus has a genome size of approximately 30,000 bases, which is effectively 30,000 letters in a row. When undertaking genomic sequencing of the virus, the aim is to recover the majority of the 30,000 letters in their correct sequence, providing the genetic code.[61] He explained that the sequencing process can recover and reconstruct up to 99.8 per cent of the SARS-CoV-2 genome, but this percentage varies based on several biological and testing factors.[62]

Why is genomic sequencing undertaken?

57. Through the process of genomic sequencing, inferences can be made about genomic clusters and the presence of any mutations.[63] This creates an understanding of where a virus sample may have originated and relationships between virus samples. Further, for COVID-19, there is no alternative to genomic sequencing to identify, and discriminate between, clusters.[64]

58. As explained by Prof. Howden, if there are two virus samples that have the same sequence, they would cluster together during the analysis stage. In a genomic context, this means that the samples are identical or highly related.[65] Where sequences are highly genomically related, then an epidemiological link is likely; for example, cases where the virus has been transmitted between members of a household.[66] The interaction between genomic sequencing and epidemiology is discussed from paragraph 67.

59. Prof. Howden explained that, by contrast, sequences that have different patterns of mutations are not closely related by genomics; for example, as seen with returned travellers who acquired COVID-19 in different countries.[67]

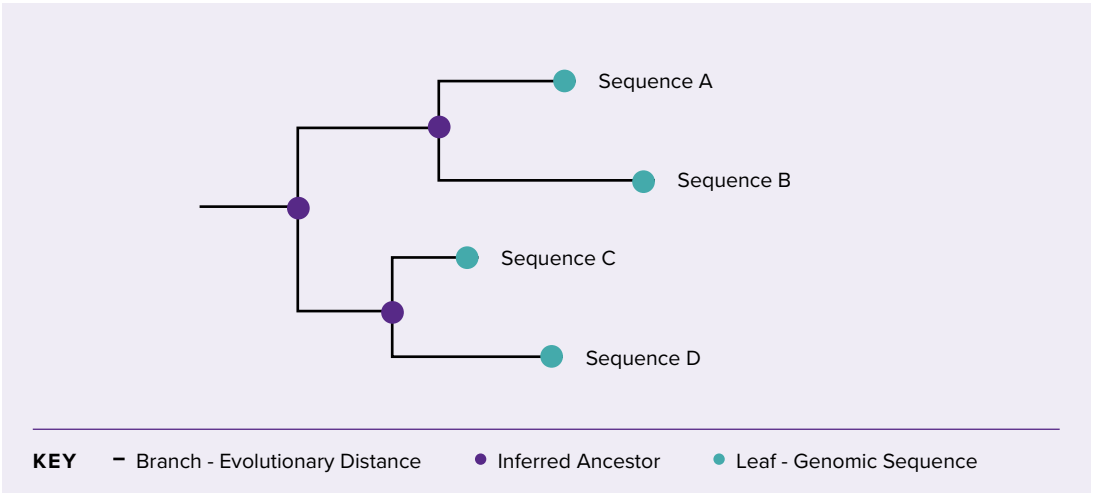
60. A genetic mutation is a permanent alteration in the genetic makeup of an organism and plays a role in the evolution of the organism.[68] All pathogens acquire mutations over time at different rates.[69]

61. As an example of genetic mutation, Prof. Howden explained that if one exposes bacteria to an antibody it will develop a mutation that helps it survive in the case of an antibiotic.[70] With COVID-19, mutations could occur at any point in the 30,000 letters of the genome. As mutations accumulate over time, and Prof. Howden notes that mutations in the COVID-19 genome have been occurring slowly,[71] they can act like a 'passport stamp' for the virus. This allows bioinformatic analysis to determine where a virus sample may have been previously.[72]

62. Prof. Howden outlined that 'once a mutation occurs in the genome of a virus, it is copied to and shared by all its descendant copies, creating groups of viruses that share a mutation because of their shared ancestry ....[73]

63. This shared ancestry informs phylogenetic analysis, used to understand the evolutionary history of an organism.[74] Figure 2.2, provided by Professor Howden, is an example of a phylogenetic tree, which is a visual representation of the likely evolutionary relationships between samples or sequences.

Figure 2.2: Annotated phylogenetic tree describing the evolutionary relationships between sequences



Source: Exhibit HQI0005_P Witness Statement of Prof. Ben Howden, 8 [46].

64. In Figure 2.2, the green dots are explained by Prof. Howden as the leaves of the tree and represent a sample or a sequence. The branches represent the genetic distance between the sequence and its inferred ancestral or parent sequences. The distance between the leaves (samples) on the horizontal lines represents the genomic distance between the samples. In this example, sequence A has a much shorter horizontal distance from sequence B, compared with sequences C or D. This means that sequence A is much more closely related, at a genomic level, to sequence B than it is to sequence C or D.[75]

What is genomic sequencing used for?

65. Prof. Howden explained that MDU PHL uses genomic sequencing of SARS-CoV-2 to identify genomic clusters that are likely to be epidemiologically linked.[76]

66. More broadly, as explained by Prof. Howden, genomic sequencing is used for pathogen surveillance and outbreak detection and investigation. It also supports findings around the resistance of a pathogen to antibiotics, how a pathogen is evolving, whether a pathogen is bringing in new genes and what the disease-causing potential is of a given pathogen.[77]

The interaction between genomic sequencing and epidemiology

67. Dr Alpren and Prof. Howden explained that genomic sequencing and epidemiology go hand-in-hand, and genomic sequencing data is not fully informative without epidemiological data. Genomic sequencing supports the identification of possible transmission networks and the likely origin of cases. Epidemiological investigations support the hypotheses generated by genomic sequencing.[78]

68. Incorporating information from epidemiological investigation (contact tracing) with genomic science allows further inferences to be drawn about transmission networks and the mechanisms and risks associated with viral transmission. As an example, Dr Alpren stated healthcare workers are known to be at higher risk than others in the community for acquisition of COVID-19.[79]

69. Identifying genomic and epidemiologic clusters supports targeted investigation of cases within the cluster to identify and remove the source of infection or disrupt transmission chains. In this context, a cluster refers to a group of people or samples with a condition or disease that share some similarity, suggesting they may have acquired the condition from each other, from a common source or due to a common cause.[80]

70. A detailed definition of epidemiological and genomic clusters was provided by Prof. Howden, as follows:

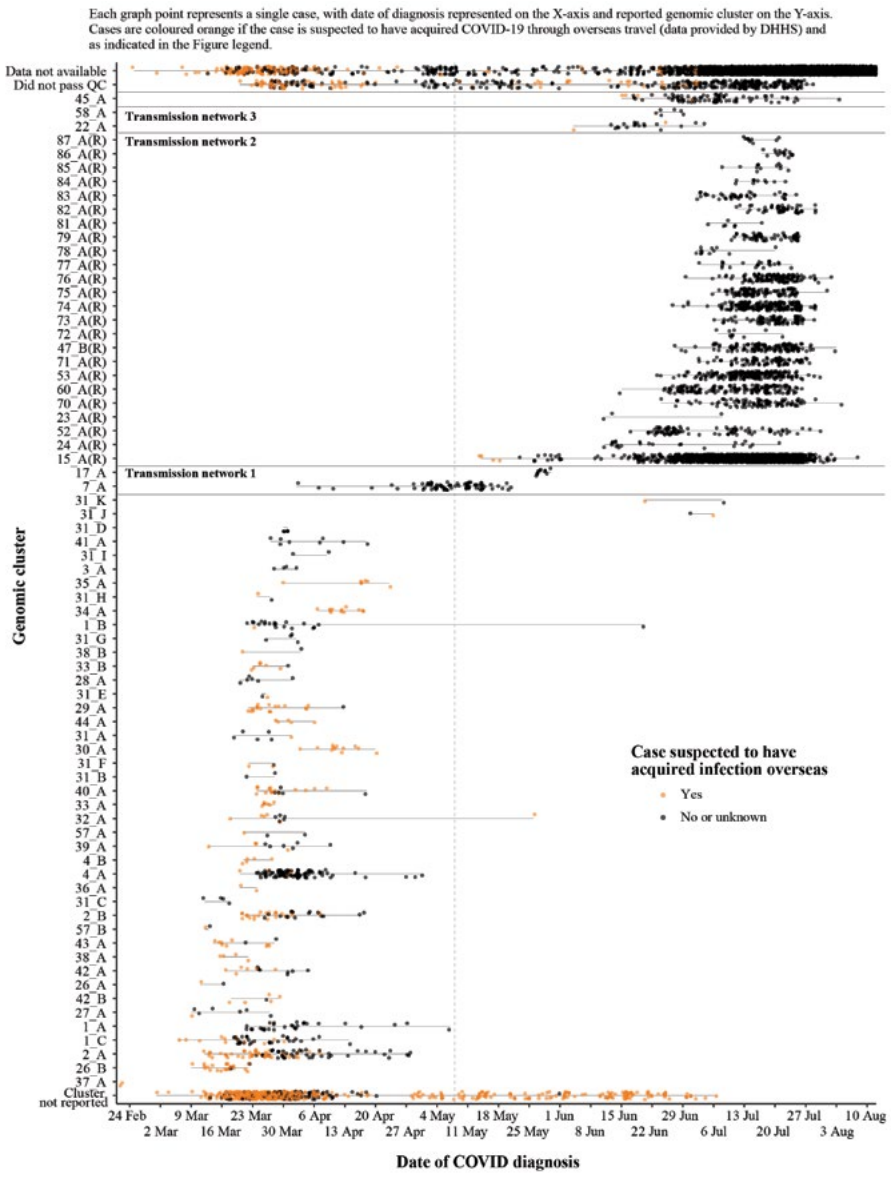
    - **Epidemiological clusters** are based on similarity in the epidemiological characteristics of person (for example, demographics), place (for example, attending the same location) and time or a combination of these.
    - **Genomic clusters** are based on the degree of genomic similarity between the pathogens (such as a virus or a bacteria). Genomic clusters indicate the sequences contained within the cluster are more related to each other than they are to any other sequences in the dataset.[81]

2.5 Genomic sequencing, epidemiology and COVID-19 cases in Victoria

71. Prof. Howden provided his uncontested expert opinion as to the results of the genomic sequencing completed by the MDU PHL of COVID-19 cases in Victoria between 21 February and 11 August 2020.

72. Figure 2.3 below, produced by Prof. Howden, represents COVID-19 cases in Victoria during this timeframe. Prof. Howden explained that each dot represents a case, with orange dots representing cases likely to have acquired infection overseas and the black dots representing cases that are likely to have been locally acquired (via community transmission). The date of diagnosis for each case is located on the X-axis and the reported genomic cluster is located on the Y-axis.

Figure 2.3: Genomic clustering of Victorian COVID-19 cases diagnosed between 21 February and 11 August 2020



Note: A transmission network, in this context, represents a group of very closely related genomic clusters with a most recent common ancestor. Each transmission network is thought to represent a separate but single importation of the virus into Victoria, with genomic diversity, which is well supported but small in magnitude, arising in Victoria as the virus has circulated within the community and resulting in mutliple closely related genomic clusters.

73. Figure 2.3 was provided by Prof. Howden when giving his oral evidence on 17 August 2020 and is an updated version of the graph that appeared in his witness statement (dated 4 August 2020), which contained data from 21 February to 23 July 2020. As at 29 July 2020, 65 genomic clusters had been identified, ranging in size from 2 to 1,071 cases (with a median of 10 cases per cluster).[82]

74. As at 14 August 2020, 72 genomic clusters had been identified (as located on the Y-axis in Figure 2.3 above), with the additional seven clusters included since 29 July linked to transmission network 2.

75. Reported genomic clustering on the graph is broadly categorised into two periods, represented by the vertical dotted line running through the graph:

    A. **Period 1** — which contains cases from 1 March to 7 May and is characterised by many diverse genomic clusters with each cluster containing a small number of cases.

    B. **Period 2** — which contains cases from 8 May onwards and is characterised by the expansion of three transmission networks and an additional new cluster (45_A). Each transmission network is a group of closely related genomic clusters with a common recent ancestor and is believed to represent a single importation of the virus into Victoria, supported by epidemiological clustering and travel history data.[83]

76. Each transmission network, marked on the graph by the dark horizontal lines, is categorised as follows:

    A. **Transmission network 1** — first identified in March and expanded rapidly throughout May. No further cases have been identified within this transmission network since 30 May 2020

    B. **Transmission network 2** — first identified in mid-May in a group of returned travellers (as identified by the orange dots). Additional cases were identified within this transmission network throughout June and July. This network included 24 clusters that appeared to have originated from the earliest cluster (15_A) based on the data available to date

    C. **Transmission network 3 and cluster 45_A** — both first identified in returned travellers during June, with additional cases identified throughout June and into July.[84]

77. As identified on the graph, and subsequently confirmed by Prof. Howden during his oral evidence, more than 99 per cent of all cases in Victoria as of August 2020, where genomic sequencing data was available, were derived from transmission network 2, predominantly, as well as transmission network 3 and cluster 45_A.[85]

78. Of note was the increase in cases that were likely to have been acquired locally during Period 2 (from 8 May onwards) compared with Period 1 (1 March–7 May), where a significant proportion of cases were attributed to infection acquired overseas.

79. The question that remained was what caused the significant increase in locally acquired cases? The answer lay with the epidemiology and the contact tracing methods used to ascertain the source of a case.

Increase in COVID-19 cases in Victoria and links to the Hotel Quarantine Program

80. Through the combination of genomic sequencing and epidemiological investigation undertaken by DHHS, Dr Alpren concluded that Victorian COVID-19 cases, as at 4 August 2020, were connected with times, transmission events or locations related to the Hotel Quarantine Program, noting that since this transmission occurred further community transmission may also have been exacerbated in additional settings, such as public housing towers and aged care homes.[86]

81. Specifically, Dr Alpren concluded that approximately 99 per cent of COVID-19 cases in Victoria, as at 4 August 2020, had arisen from outbreaks at the Rydges Hotel in Carlton (Rydges) or the Stamford Plaza Hotel (Stamford).

82. What led to the outbreaks, and their impact, is considered in detail at Chapter 9. For present purposes, the outbreak at Rydges can be traced back to a family of four that returned to Australia on 9 May 2020. Each member of that family eventually tested positive to COVID-19 and were moved to Rydges where, 10 days later, two security guards and one member of staff working at Rydges became symptomatic and were subsequently diagnosed with COVID-19.[87]

83. The Stamford outbreak can be traced back to a traveller returning to Australia on 1 June 2020 and entering quarantine at Stamford. That traveller became symptomatic and was diagnosed with COVID-19.[88] On 10 June 2020, a member of staff became symptomatic.[89] A day later, a couple, who were returned travellers quarantining at the Stamford, became symptomatic. Those two travellers and the staff were diagnosed with COVID-19 over the course of 14–16 June 2020.[90]

84. While Dr Alpren noted that he cannot be precise in the exact number or proportion to have arisen from each outbreak separately, he stated that it was likely that the large majority — approximately 90 per cent or more — of COVID-19 infections in Victoria as of 4 August 2020 could be traced to Rydges. It is likely that a small proportion — approximately 10 per cent or less — of COVID-19 infections in Victoria as of 4 August 2020 could be traced to Stamford.[91]

2.6 Conclusions

85. While acknowledging that there is a continuous state of learning with respect to the COVID-19 virus, the weight of the current expert knowledge is that the COVID-19 virus has an incubation period of up to 14 days for the majority of patients, with most patients being non-infectious at the end of that 14-day period. On this basis, the 14-day quarantine period imposed for the purposes of the Hotel Quarantine Program was a reasonable and appropriate period.

86. The evidence established that, while scientific and medical communities continue to develop an understanding of the modes of transmission for the COVID-19 virus, including what asymptomatic transmission may mean in terms of testing in a quarantine environment, there was a general understanding of the modes of transmission of the virus as at 29 March 2020 among the experts. This included that:

    - the virus primarily spread from person-to-person via droplets, aerosols and fomites
    - droplet transmission occurred when a person was in close contact (within one metre) with someone who had the virus
    - airborne transmission may have been possible in specific circumstances and settings in which procedures or support treatments that generated aerosols were performed.[92]

87. These methods of transmission were of critical importance when considering the use of hotels as facilities for mass quarantine, what adaptions needed to be made to ensure the safety of those being placed in quarantine and those working on-site at the hotels, and what needed to be put in place by way of appropriate infection prevention and control standards to address and minimise the risk of the virus spreading in quarantine hotels.

88. Asymptomatic transmission (including by way of super spreaders) led to particular complexities for infection control and testing regimes in the Hotel Quarantine Program. The public health community had knowledge of the risk of asymptomatic transmission of the virus by March 2020.

89. The weight of the current expert evidence to the Inquiry was that between 17 and 20 per cent of cases experienced asymptomatic transmission, which had flow-on impacts in terms of appropriate testing requirements. That evidence led to the conclusion that to address the risk inherent in asymptomatic spread of the virus, it is necessary to require testing of all people at the end of their quarantine period regardless of whether they are reporting symptoms.

Hotel quarantine's link to the 'second wave'

90. Dr Alpren's evidence, based on genomic testing, was that 99 per cent of Victoria's second wave of COVID-19 cases in the community have come from transmission events from returned travellers infected with the virus to people working at the Rydges and the Stamford hotels. The movement of the virus from these infected workers into the community was characterised by high rates of local transmission.[93]

91. Prior to the second wave, Victoria's COVID-19 cases were largely attributable to infection acquired overseas. All cases in transmission network 1 had ceased by 30 May 2020.[94]

Mass quarantining and the science

92. The conclusions that could be drawn from the scientific evidence provided to the Inquiry were that three fundamental safety features needed to be built into any program that sought to house together potentially infected people in a quarantine facility. They were:

    A. the importance of expert advice, input and ongoing supervision and oversight of infection prevention and control

    B. the importance of an evidentiary base for the testing regime

    C. the importance of a rapid and effective contact tracing regime.

93. Each of these areas were important topics in and of themselves and subject to their own conclusions. Accordingly, they are dealt with in more substance throughout this Report:

    A. the importance of expert advice, input and ongoing supervision and oversight of those within the Hotel Quarantine Program, is dealt with in chapters 8 and 9, in the context of the outbreaks at the Rydges and Stamford and the structure and governance of the Program

    B. the importance of a rapid and effective contact tracing regime, is also dealt with in Chapter 9

    C. the importance of an evidentiary basis for the testing regime, is considered in Chapter 10.

Endnotes

1 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 1–3; Exhibit HQI0002_RP Curriculum vitae of Prof. Lindsay Grayson.
2 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 1–4; Exhibit HQI0006_P Curriculum vitae of Prof. Ben Howden.
3 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 1–3.
4 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 3 [9]–[10].
5 Ibid 10–11 [47(c)].
6 Transcript of day 3 hearing 17 August 2020, 33.
7 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 10 [47(b)].
8 Ibid 3 [14].
9 Transcript of day 3 hearing 17 August 2020, 34.
10 Transcript of day 4 hearing 18 August 2020, 100; Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 14 [57(d)].
11 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 3 [12], 4 [17]–[18].
12 Ibid 4 [17].
13 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 4 [18]; Transcript of day 3 hearing 17 August 2020, 35.
14 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 4–5 [20].
15 Transcript of day 3 hearing 17 August 2020, 36; Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 14 [57(b)].
16 Transcript of day 3 hearing 17 August 2020, 36; Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 12 [55].
17 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 4 [20]–[22].
18 Ibid 5 [24].
19 Ibid 3 [11].
20 Ibid 8–9 [38]–[42].
21 Transcript of day 3 hearing 17 August 2020, 39.
22 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 8 [39].
23 Ibid 9 [44]–[45].
24 Ibid 9 [42].
25 Exhibit HQI0106_RP Witness statement of Dr Sarah McGuinness, 7 [27]
26 Ibid, quoting World Health Organization, 'Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations: scientific brief', 29 March 2020 <https://www.who.int/news-room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19-implications-for-ipc-precaution-recommendations>.
27 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 7 [33].
28 Ibid 8 [36]–[37].
29 Ibid 7 [34].
30 Ibid 8 [35].
31 Ibid 8 [36].
32 Transcript of day 3 hearing 17 August 2020, 35.
33 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 4 [19].
34 Ibid, citing Riley et al, 'Transmission Dynamics of the Etiological Agent of SARS in Hong Kong: Impact of Public Health Interventions' (2003) 300(5627) Science 1961.
35 Transcript of day 3 hearing 17 August 2020, 43.
36 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 12 [55].
37 Ibid 12 [55]–[56].
38 Australian Health Protection Principal Committee (AHPPC) statement on novel coronavirus on 29 January 2020 <https://www.health.gov.au/news/australian-health-protection-principal-committee-ahppc-statement-on-novel-coronavirus-on-29-january-2020-0>.
39 Ibid.
40 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 4 [16].
41 Transcript of day 3 hearing 17 August 2020, 34.
42 Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 6 [26]–[28].
43 Ibid 6 [29]; Transcript of day 4 hearing 18 August 2020, 100.
44 Ibid 7 [32].

45 Ibid 7 [31].
46 Transcript of day 3 hearing 17 August 2020, 37–38.
47 Ibid 38, Exhibit HQI0001_P Witness statement of Prof. Lindsay Grayson, 7 [32].
48 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 3 [17].
49 Ibid 3 [18].
50 Ibid.
51 Transcript of day 4 hearing 18 August 2020, 5.
52 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 3–4 [18]–[20].
53 Ibid 4 [21]–[22].
54 Transcript of day 4 hearing 18 August 2020, 95.
55 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 5 [27].
56 Ibid 9 [38].
57 Ibid 9–10 [38]–[44].
58 Transcript of day 3 hearing 17 August 2020, 74–75.
59 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 4 [22].
60 Ibid 4 [24]–[25].
61 Transcript of day 3 hearing 17 August 2020, 76.
62 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 6 [35].
63 Ibid 4 [28].
64 Ibid 5 [30].
65 Transcript of day 3 hearing 17 August 2020, 76.
66 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 7 [39].
67 Ibid 7 [40].
68 Ibid 5 [31]–[33].
69 Transcript of day 3 hearing 17 August 2020, 76.
70 Ibid.
71 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 6 [36].
72 Transcript of day 3 hearing 17 August 2020, 76.
73 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 5–6 [33].
74 Ibid.
75 Ibid 8 [47]; Transcript of day 3 hearing 17 August 2020, 78.
76 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 9 [52].
77 Ibid 9 [51].
78 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 9 [52]–[54]; Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 12–13 [49]–[53]; Transcript of day 4 hearing 18 August 2020, 98.
79 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 12 [50].
80 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 7 [41]–[44].
81 Ibid 7 [42]–[43].
82 Exhibit HQI0005_P Witness statement of Prof. Ben Howden, 18 [95].
83 Ibid 20 [101]–[103].
84 Ibid 21 [104].
85 Transcript of day 3 hearing 17 August 2020, 86.
86 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 19 [78].
87 Ibid 20 [86].
88 Ibid 21 [95].
89 Ibid 22 [97].
90 Ibid 21–22 [96].
91 Ibid 28 [130].
92 Exhibit HQI0106_RP Witness statement of Dr Sarah McGuinness, 7 [27]; World Health Organization, 'Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations: scientific brief' (Brief, 29 March 2020) <https://www.who.int/news-room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19-implications-for-ipc-precaution-recommendations>.
93 Exhibit HQI0008_RP Witness statement of Dr Charles Alpren, 28 [130]; Transcript of day 3 hearing 17 August 2020, 86.
94 Exhibit HQI0006_P Witness statement of Prof. Ben Howden, 21 [104].