

Genome sequencing and genomic clustering to SARS-CoV-2 in Victoria

Report date: 29 January 2021

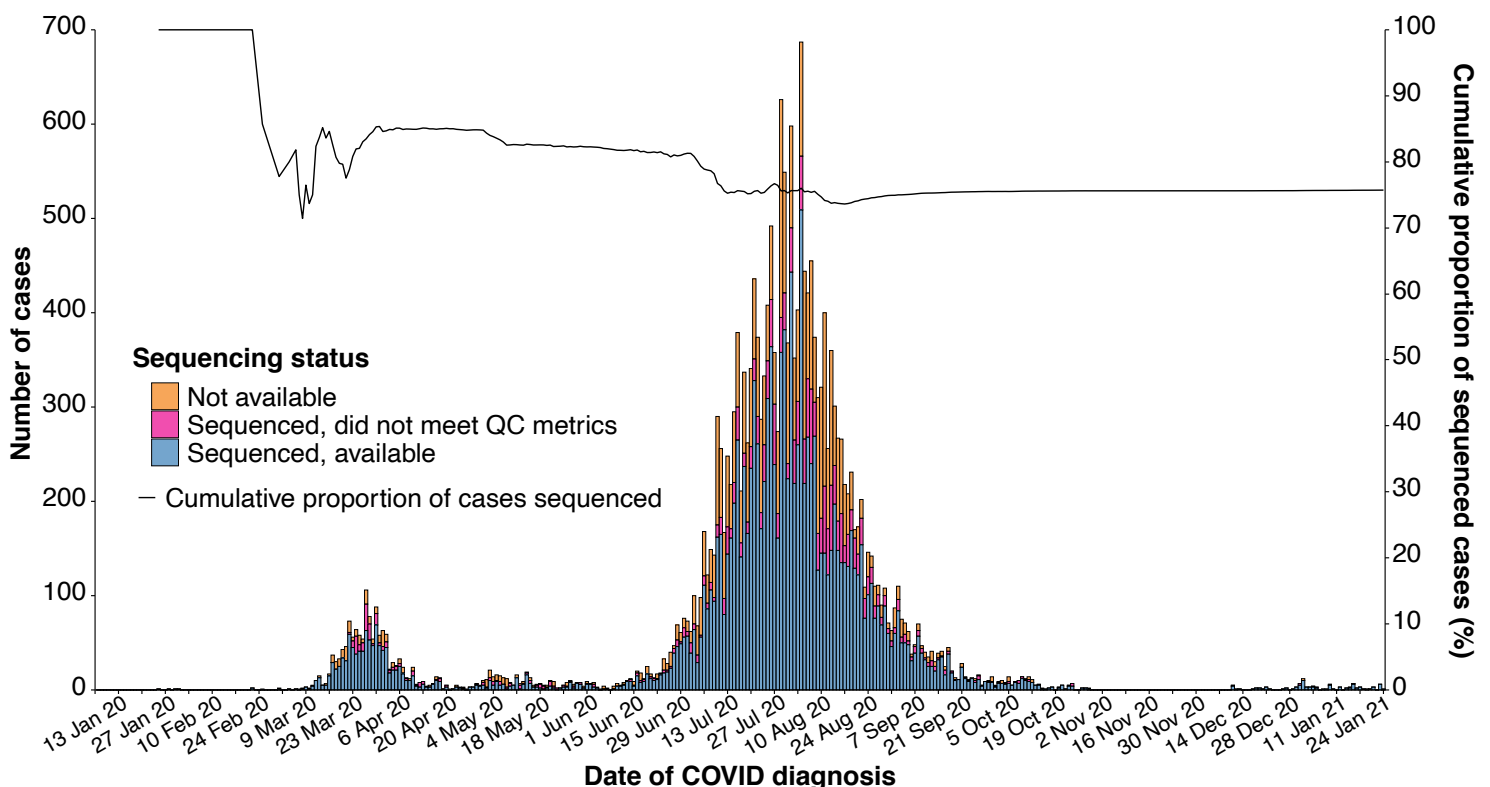
Report period (4 weeks): 29 December - 25 January 2021

Published date: 18 February 2021

The public health genomic sequencing laboratory at The Doherty Institute (the Microbiological Diagnostic Unit Public Health Laboratory) aims to perform genome sequencing of all COVID-19 cases in Victoria. Identifying genomic clusters and linking this information with epidemiological data captured by the Department of Health (DH) can help identify outbreaks, potential sources of infection, and determine which people are more likely to have transmitted the virus to each other. Sharing the data internationally can help understand the evolution of the virus globally.

Figure 1: Epidemic curve of Victorian COVID-19 cases diagnosed between 15 January 2020 and 25 January 2021.

As of 29 January 2021, sequence data was available for 15,477 (75.7%) Victorian COVID-19 cases diagnosed up to and including 25 January 2021, included in the following analysis.



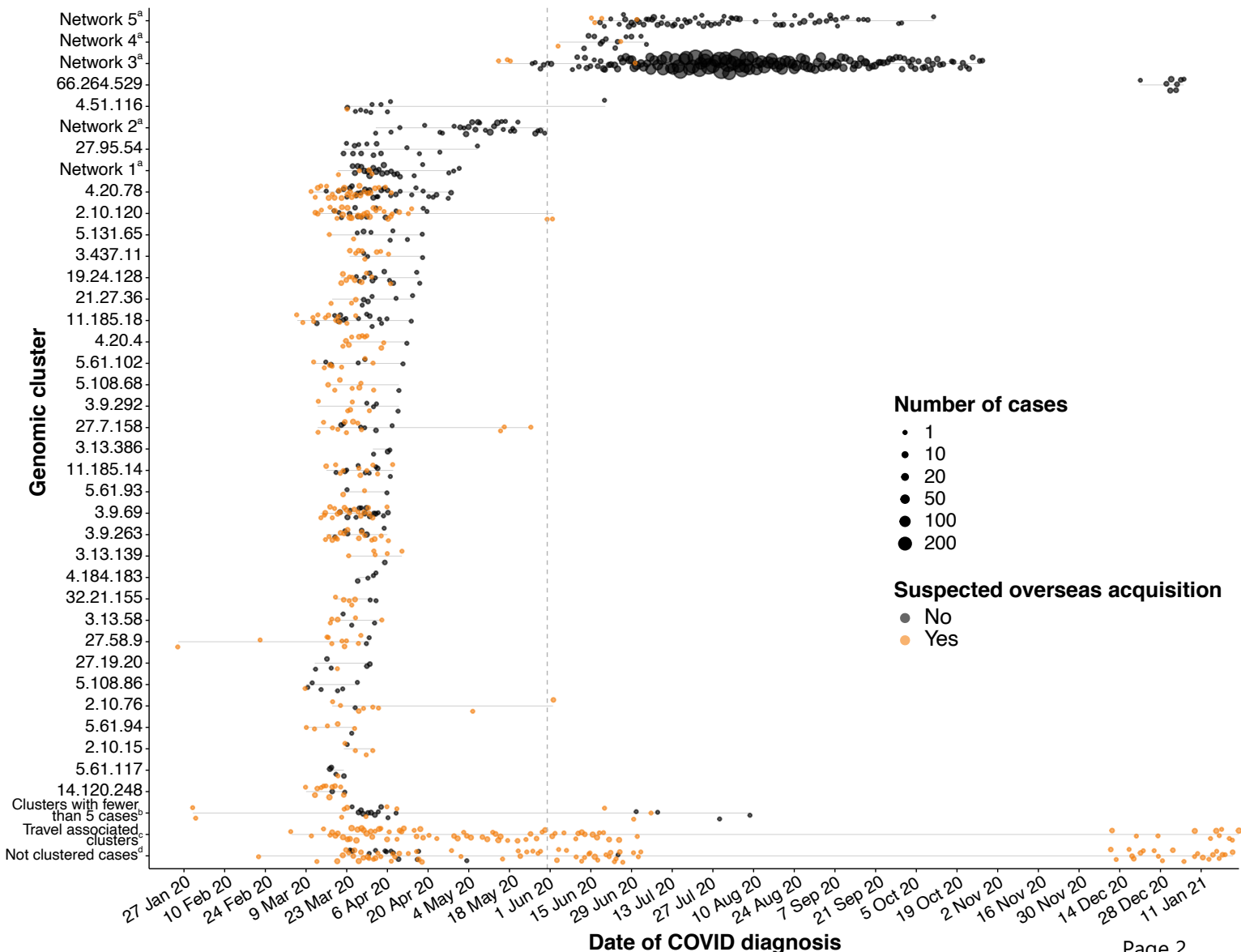
Not available Recently identified cases without available sequence data may include those currently undergoing and/or pending sequencing, and the proportion of cases with available sequence data may increase as sequencing is completed. Cases from the first and second waves where sequence data is not available are unlikely to become available.

Genome sequencing and genomic clustering to SARS Victoria continued

Figure 2: Timeline of Victorian COVID 19 genomic clusters, including cases diagnosed between 15 January 2020 and 25 January 2021.

A group of genome sequences that are more closely related to each other and represent a group of cases more likely to have transmitted it to each other, is referred to as a 'genomic cluster'.

In the past 4 weeks (29 December 2020 – 25 January 2021) there were 65 sequenced cases of COVID 19 in Victoria. Of these, 39 (60%) were travel associated, and 26 (40%) were a locally acquired cluster (66.264.529) epidemiologically linked to the Black Rock Outbreak.



Genome sequencing and genomic clustering to SARS-CoV-2 in Victoria continued

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^aNetwork 1, Network 2, Network 3, Network 4 and Network 5 are discrete transmission networks. In this context, a transmission network represents a group of very closely related genomic clusters. Each transmission network is thought to represent a separate but single importation of the virus into Victoria, with genomic diversity arising as the virus has circulated locally. Genomic clusters within these transmission networks have been grouped and collapsed to enable visualisation.

^bGenomic clusters with fewer than five cases and ^cgenomic clusters involving only cases suspected to have acquired their infection overseas have been grouped as 'Fewer than 5 cases' and 'Travel associated' respectively. ^dCases not currently found within a genomic cluster grouped as 'Not clustered'.

Genomic cluster names are arbitrary and do not reflect relationships between clusters.