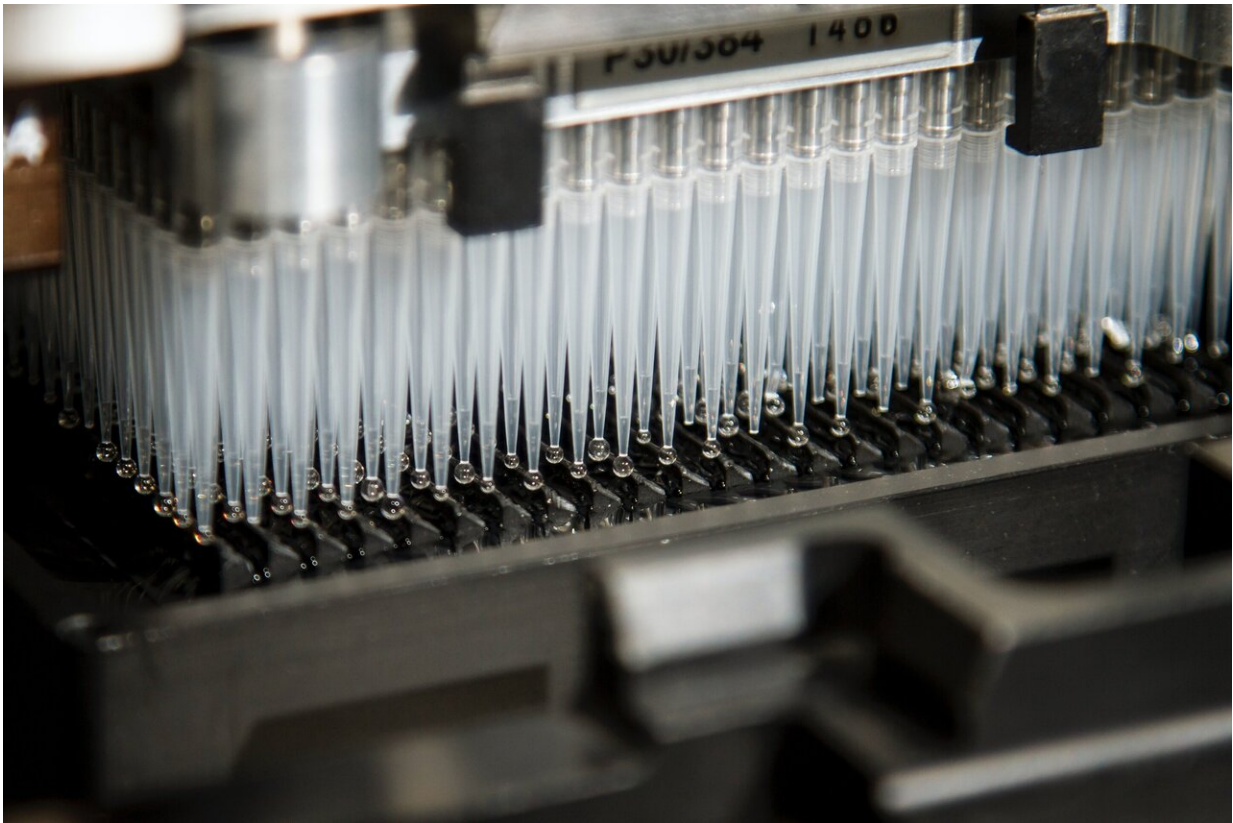


Tracking the COVID-19 pandemic in Australia using genomics

May 21 2020, by Catherine Somerville



Whole genome sequencing of pathogens in real-time is an important tool in managing public health responses to infectious diseases outbreaks. Credit: Unsplash

Using genome sequencing to identify genetic mutations in SARS-CoV-2

cases in Victoria, researchers have identified clusters and transmission networks which has helped limit the spread of the virus, painting an important picture of transmission in Victoria.

Whole-genome sequencing of pathogens in [real-time](#) is an important tool in managing public health responses to infectious diseases outbreaks.

A dedicated SARS-CoV-2 multidisciplinary genomic response team from the Victorian Infectious Diseases Reference Laboratory (VIDRL) and the Microbiological Diagnostic Unit Public Health Laboratory (MDU-PHL) at the Peter Doherty Institute for Infection and Immunity (Doherty Institute), and the Victorian Department of Health and Human Services (DHHS) was formed to link epidemiological and genomic data of Victoria's [coronavirus](#) (COVID-19) cases and assess the impact of social restrictions.

University of Melbourne Professor Benjamin Howden, Director of MDU-PHL at the Doherty Institute, said the team sequenced 75 percent of Victoria's cases.

"Our sequencing showed that Victoria's cases were representative of the global diversity of SARS-CoV-2. Consistent with epidemiological findings, we found that most of Victoria's cases were imported with limited onward transmission," Professor Howden said.

"Sequencing allowed us to identify large clusters from social venues, [healthcare facilities](#) and cruise ships, and importantly see how enforced social restrictions impacted transmission.

"Finally, we are able to demonstrate how the application of genomics will become critically important to rapidly identify SARS-CoV-2 transmission chains as social restrictions ease globally."

Victoria's Chief Health Officer, Professor Brett Sutton said public health responses to emergent cases of SARS-CoV-2 must be swift, highly focused and effective.

"Genomic sequencing is an incredibly powerful tool for our disease detectives to identify SARS-CoV-2 cases and clusters, which will be an ongoing challenge in Victoria and Australia," Professor Sutton said.

"Working so closely with the team at Doherty Institute, who rapidly shared the sequences they found has had a huge, positive impact on Victoria's successful response to limiting [transmission](#) of SARS-CoV-2."

This research has been submitted for peer-review and was conducted under strict protocols in a well-established research program. However it has not been evaluated by the scientific research community.

More information: Torsten Seemann et al. Tracking the COVID-19 pandemic in Australia using genomics, *medrxiv* (2020). [DOI: 10.1101/2020.05.12.20099929](#)

Provided by University of Melbourne

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