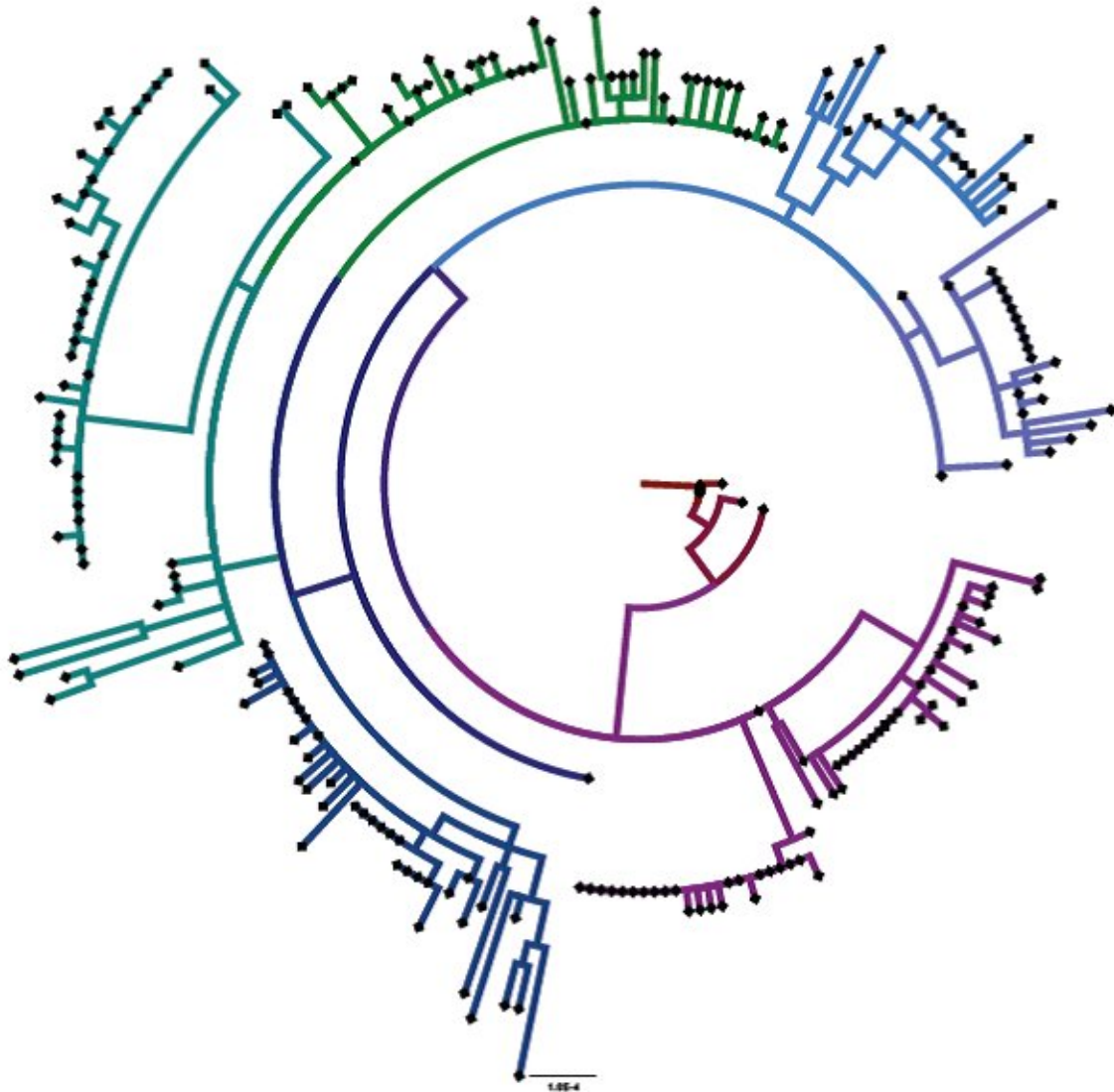


Researchers develop rapid genomics strategy to trace coronavirus

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Phylogenetic 'family' tree of a subset of coronavirus cases in Australia, demonstrating how different strains of the virus are related. 'Second wave'

strains isolated in NSW and Victoria are indicated in teal. Credit: A/Prof Rowena Bull

Thanks to cutting-edge 'Nanopore' genome sequencing technology, researchers at the Garvan Institute of Medical Research and the Kirby Institute at UNSW Sydney have developed the most rapid coronavirus genome sequencing strategy in Australia to date. The technological advance has the potential to provide critical, timely clues on how cases of SARS-CoV-2 infection are linked.

The researchers today published an analytical validation and best practice guidelines for Nanopore sequencing of SARS-CoV-2 in *Nature Communications*, which they hope will enable a greater uptake of the fast sequencing technology for health initiatives in Australia and overseas.

"Every time the SARS-CoV-2 virus passes from person to person, it may make copying errors that change a couple of its 30,000 genetic letters. By identifying this genetic variation, we can establish how different cases of coronavirus are linked—to know where a case was potentially picked up from and who they may have given it to," says co-first author A/Prof Rowena Bull, from UNSW's Kirby Institute.

A/Prof Bull says [genomic testing](#) is crucial for tracking virus transmission in cases where the source remains unclear from investigating known epidemiological contacts alone.

"By reconstructing the virus's evolutionary history, or 'family tree', we can understand the behaviours that help spread COVID-19 and identify so-called 'super-spreaders'," she says.

"When a new 'mystery' coronavirus case is identified, every minute

counts. At Garvan, we have repurposed our genomic sequencing capabilities to enable a rapid analysis of a coronavirus genome in just a few hours," says senior author Dr. Ira Deveson, Head of the Genomic Technologies Group at Garvan's Kinghorn Centre for Clinical Genomics.

"We've been thrilled to collaborate with the Garvan and Kirby Institutes to develop unparalleled speeds of coronavirus genome testing. Rapid methods such as this provide a way forward, as a potential future option for contact tracing through real time genomic transmission studies," says Prof Bill Rawlinson AM, from UNSW Sydney and NSW Health Pathology Randwick.

"This technical advance is a testament to what's possible when public pathology collaborates with Research Institutes for a common goal," says Prof Sebastiaan van Hal, from NSW Health Pathology—Royal Prince Alfred Hospital.

Pioneering rapid genomics

Pinpointing SARS-CoV-2 transmission quickly is crucial. NSW Health Pathology has collaborated with the Garvan Institute and Kirby Institute to develop faster SARS-CoV-2 genome sequencing capabilities, potentially enhancing the ability of contact tracers to take rapid action to quarantine and monitor potential contacts. Garvan researchers have fine-tuned the protocols for cutting-edge Oxford Nanopore Technologies to sequence SARS-CoV-2 in less than four hours. Garvan's Kinghorn Centre for Clinical Genomics is the first facility in Australia to establish and apply this Nanopore technology for genomic surveillance of SARS-CoV-2.

Highly accurate emerging technologies

The current gold-standard method reads short genetic sequences of just 100-150 genetic letters at a time, whereas Nanopore technologies have no upper limit to the length of DNA fragments that can be sequenced and are able to more rapidly determine the complete sequence of a viral genome.

"However, as with many emerging technologies, there have been concerns about the accuracy of Nanopore sequencing. We addressed these concerns in our paper where we report the outcomes of a rigorous analytical evaluation of our protocols for sequencing the coronavirus genome," says Dr. Deveson.

The researchers' analysis revealed the Nanopore sequencing method to be highly accurate (variants were detected with >99% sensitivity and >99% precision in 157 SARS-CoV-2-positive patient specimens) and provides best practice guidelines, which the researchers hope will promote the uptake of the technology by other teams globally.

The researchers say Nanopore sequencing even has the potential to enhance SARS-CoV-2 surveillance by enabling point-of-care sequencing and improved turnaround times for critical cases.

"Nanopore devices are cheaper, faster, portable and don't require the lab infrastructure needed by current standard pathogen genomics tools," says Dr. Deveson. "We hope our validation of this protocol will help other public health teams around the world adopt this technology."

More information: *Nature Communications* (2020). [DOI: 10.1038/s41467-020-20075-6](https://doi.org/10.1038/s41467-020-20075-6)

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