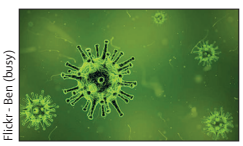
Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

COVID-19: from rapid genome sequencing to fast decisions



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Nucleic acid amplification tests are invaluable tools for rapid and accurate detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections,[1,2] but they are of limited use when identifying transmission events and infection clusters.[3]

In *The Lancet Infectious Diseases,* Luke Meredith and colleagues present an innovative combination of rapid full-genome sequencing of SARS-CoV-2 with epidemiological data to track health-care associated SARS-CoV-2 infections in their hospital and in health-care associated community settings.[4] Within 6 weeks, the authors were able to obtain 747 full SARS-CoV-2 genomes from 1009 PCR-positive patient samples. To obtain rapid results, sequencing was done by direct (nanopore) sequencing of amplicon libraries, which were generated with use of a multiplex PCR approach.[5,6] On a weekly basis the sequenced samples underwent bioinformatic analysis and were combined with epidemiological data. Although the genetic diversity of SARS-CoV-2 is currently low, the combination of genetic, clinical, and epidemiological data was highly effective. With this approach, the authors could identify two infection clusters in their hospital, one in an outpatient dialysis unit and another one in a care home, which would not have been detected without full-genome sequencing. The results were reported back to infection control and management teams and were used to improve patient isolation, ward cleaning procedures, use of personal protection equipment, and staff physical distancing behaviour. Therefore, the combination of rapid genomic and epidemiological analyses in near real time allows the rapid optimisation of countermeasures in ongoing ward and community outbreaks of COVID-19.

The study by Meredith and colleagues convincingly shows the power of direct sequencing as a tool to track SARS-CoV-2 transmission in a very short timeframe and could be a blueprint for tracing of other viral pathogens. We believe that the presented study provides a first glimpse into the point-of-care sequencing revolution provided by novel third-generation technology based on nanopores. Although current protocols are done in a central laboratory, further technological advances in both sequencing and sample preparation technology will enable highly decentralised workflows directly at the bedside or ward level. By contrast with sequencing-by-synthesis approaches, nanopore technology can directly sequence DNA and RNA molecules in the kilobase range, making it potentially suitable for the direct detection of viral genomes without the need for a time consuming PCR step. An additional benefit of this approach is the possibility to theoretically detect any viral pathogen. However, further increases in sensitivity are needed for this approach to be suitable for real clinical samples.[7,8]

Before true viral pathogen detection by amplification-free direct sequencing will be possible, it is probable that small integrated library preparation devices will be developed. These devices are likely to be based on microfluidic technology and will enable the clinical end user to do third-generation sequencing directly from samples such as nasopharyngeal swabs without specialised training. In addition, software tools will be needed to automate what has been done manually in the present study—integrate sequencing and epidemiological data to derive action plans for outbreak control.

We declare no competing interests.

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