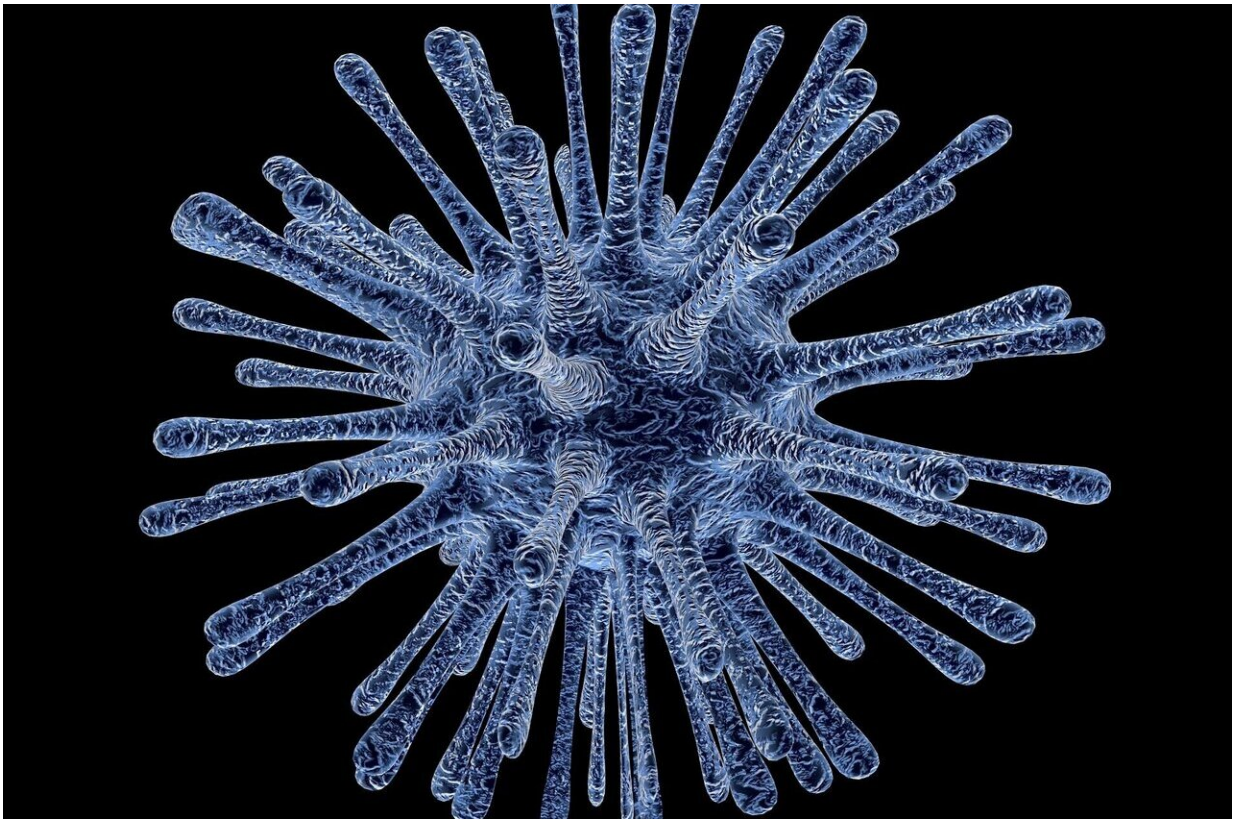


Genomic tracking reveals rise and fall of COVID-19 in Guangdong Province

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A new study led by researchers at Oxford and Guangdong Centre for Diseases Control and Prevention describes the epidemiology and genetic make-up of the COVID-19 outbreak in China's most populous region,

and shows how early and intensive testing and tracing helped to interrupt local transmission of the virus.

The study combines genome sequencing and epidemiology to reveal three phases of the outbreak in Guangdong Province, China, in January and February this year: the introduction of new cases into Guangdong from other Chinese provinces, the rise and fall of local transmission within Guangdong, and finally the import of new cases into Guangdong from international travelers. The epidemic in Guangdong was the second largest in China except for Hubei, where Wuhan is located.

In Guangdong, a region of >100 million people, testing was mobilized quickly. By 19th March a total of 1.6 million tests for COVID-19 had identified 1,388 positive cases. Enhanced surveillance started at the end of January aimed to monitor all travelers returning from Hubei and other provinces experiencing outbreaks, their close contacts, and all hospitalized patients in clinics, even if they did not have symptoms and no known exposure to infected individuals.

Analysing genomes generated from infected individuals, the researchers establish that the outbreak in Guangdong was not caused by one large chain of transmission, but instead there were hundreds of independent introductions from outside the Province. Locally-transmitted chains of infection are shown by their [genetic information](#) to be limited in size and duration. This, the researchers say, illustrates that the screening and interventions implemented in Guangdong were effective in interrupting local transmission of the [virus](#).

The study also shows that the genome of SARS-CoV-2 (the virus that causes COVID-19) could be rapidly sequenced and analyzed in near-real time. Due to the speed and nature of this outbreak, different experimental approaches were attempted. Good results were obtained using the handheld MinION sequencing device (developed by Oxford

Nanopore Technologies) and a sequencing protocol developed by the ARTIC Network.

The authors are confident that this approach to study the early COVID-19 epidemic in China can be scaled-up and applied to other COVID-19 outbreaks world-wide.

Senior author Professor Oliver Pybus of the Department of Zoology and the Oxford Martin School and other authors are now key members of the COVID-19 Genomics UK Consortium. This consortium has already sequenced >3000 genomes from the UK and analyzing them to track transmission and to understand how the virus is evolving.

Professor Oliver Pybus says: "We know already that changes to the COVID-19 genome accumulate more slowly than for other viruses such as influenza. This means the COVID-19 virus is moving and transmitting faster than it mutates. So it's crucial to analyze the virus genomes in combination with detailed epidemiological information, which is what we achieved in this study."

Going forward, this genomic data will not only be used to understand how the virus is spreading among locations, it will also be used to track various virus [genetic variation](#), knowledge that is vital for researchers working on vaccines and anti-viral drugs.

Dr. Jing Lu, from Guangdong Provincial Institution of Public Health, Guangdong Centre for Disease Control, says: "To get the best and most powerful insights we need to combine virus [genome](#) information with epidemiology and other data. Our work in Guangdong Province shows that high levels of very early testing, together with active case tracing and strict isolation, can bring an [outbreak](#) under control."

More information: *Cell*, [DOI: 10.1016/j.cell.2020.04.023](https://doi.org/10.1016/j.cell.2020.04.023)

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