

Whole genomes of coronavirus from UK patients sequenced by Sheffield scientists

March 13 2020, by Rebecca Ferguson



This transmission electron microscope image shows SARS-CoV-2 -- also known as 2019-nCoV, the virus that causes COVID-19 -- isolated from a patient in the US. Virus particles are shown emerging from the surface of cells cultured in the

lab. The spikes on the outer edge of the virus particles give coronaviruses their name, crown-like. Credit: NIAID-RML

Scientists at the University of Sheffield, in partnership with Sheffield Teaching Hospitals Virology team, have sequenced their first two genomes of the novel coronavirus (COVID-19), with samples collected from patients treated in the UK.

The genomes have been published to the international viral sequence database [GISAID](#) to help track the virus and investigate how it is spreading throughout the UK population.

Increasing the amount of sequence data available will provide crucial information to scientists around the world about the origins of [coronavirus](#) cases in the UK, revealing how the virus may change over time.

Following the success of the first two samples, the team will now sequence more samples in the coming days.

The University of Sheffield's Department of Infection, Immunity and Cardiovascular Disease, Florey Institute for Host Pathogen Interactions, and its Sheffield Institute for Translational Neuroscience (SITraN) are working collaboratively to respond to the rapidly evolving outbreak of the virus.

Dr. Thushan de Silva, Wellcome Trust Clinical Fellow and Consultant in Infectious Diseases, is leading the work taking place at the University of Sheffield.

He said: "As a virus travels we know it can mutate as it reacts to the

genetics of localised populations, creating different strains which may behave in different ways to treatments, vaccines and our body's immune response. Generation of sequence data is vital to track this process.

"This data, used alongside published samples from our international partners will be crucial for us to see the trends in these mutations."

The University is working with Consultant Virologist Dr. Caraid Evans, from Sheffield Teaching Hospitals NHS Foundation Trust's Department of Virology, who is leading the regional NHS virology laboratory's rapid response to the urgent requirement to support Public Health England in creating national capacity for diagnostic services.

Sequenced in less than 24 hours, the team used the Oxford Nanopore Technologies GridION capabilities under the guidance of Matthew Wyles, a research technician, based at SITraN, by using an Artic Network protocol for real-time sequencing and analysis of viral genomes.

Matthew Parker, a Clinical Bioinformatics Scientist at the National Institute for Health Research (NIHR) Sheffield Biomedical Research Centre and the analyst for the study at SITraN, said: "The facilities and expertise we have here at SITraN mean that we are able to quickly sequence and analyse these samples. Co-localisation of sequencing equipment and scientists who have expertise in [data analysis](#) in the region are key to a successful project like this.

"The capabilities we have developed here at SITraN are crucial for Sheffield to expand our sequencing of the virus and to continue to contribute timely, accessible data that will help in the global management of the current outbreak."

Currently, 32 countries have contributed to the global effort to tackle the

outbreak by uploading samples to a public database GISAID.

Dr. de Silva said: "Collecting and sharing standardised global clinical data and samples on patients infected with coronavirus is a critical process in how the [health research](#) community can contribute to our understanding outbreaks of new infectious diseases."

Provided by University of Sheffield

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