

So my name is Judy Breuer. I'm Professor of Virology at UCL, and Consultant virologist at Great Ormond Street Hospital. So the HOCl study, which is the hospital onset COVID infection study, took place during the pandemic. Starting in 2020. The autumn of 2020.

And the study was actually asking the question if we give sequences of COVID of SARS-CoV2 back to the infection control teams in a rapid manner, does it alter how they manage outbreaks of COVID-19 in hospital? Does it improve the management? And the theory was that previously people had started to sequence SARS-CoV2. And were sort of sharing the sequences with their infection control teams. And anecdotally were saying that this was helping to understand better where infections were coming from in the hospital, and how to stop them. And so we decided to measure that in the HOCl study.

It was critical because we were aiming for 48 hours. Very few samples actually did manage to get back to the teams within 48 hours. But we were able to show that if the results got back within five days, then that impacted on infection prevention control decisions in about 20% of cases. So it was the first time that the speed of sequencing, and the speed of return of results to the team had been shown to have an impact on the decisions that were made. The infection prevention control decisions that were made. So we think it's critical that the timing is as fast as possible.

Yes. It was open source. So the sequence data was uploaded to the GISAID database, and was made available for public health use immediately. The metadata was linked a separate exercise. So the data on the patients was linked to the sequences in a separate database, which was not open source because obviously that contained confidential information about patients, and where they were located, and whether they'd become infected in hospital, and things like that. So the actual sequence data was available immediately, or as soon as we could upload it. And that then went on to form part of the public health analysis of SARS-CoV2 in the UK.

The whole of the COG UK Public Health effort depended on people sequencing, and making their sequences available freely to be analysed to help control the pandemic. And we now know that these sequences made a huge difference. It influenced the timing of lock downs. The timing of coming out of lock downs. It influenced planning of the pandemic. Influenced when borders were shut. How long borders were shut for.

And if we hadn't all just made our data available immediately, that couldn't have happened. So it's absolutely critical for public health. And it's critical to make sequence available generally so we can learn about new viruses, or about existing viruses or existing pathogens. So it's critical.

I mean, what is more difficult is to make available the data on the patients from whom those sequences come from. And that usually is kept confidential because, of course, we don't want to identify individuals and make that data publicly available. But the sequence data is critical because you can't do any of the analysis that can lead to lives being saved unless you have the sequence data.