have pointed to oddities in the data, such as smoking and obesity rates that were reported as nearly equal across all parts of the world studied in the analysis. And because the work relied on proprietary data gathered from medical centres, the raw data were not made available to other researchers.

Following criticisms, Mehra's team has tracked down some errors – the table reporting smoking and obesity rates, for example, erroneously listed modelled data rather than raw data. *The Lancet* will soon issue a correction, Mehra says, but the errors did not affect the conclusions. And the company that gathered the proprietary data, Surgisphere of Chicago, Illinois, says that it will accept proposals from other researchers to analyse its data.

But some remain sceptical about the study's conclusion that hydroxychloroquine is a safety risk to some people with COVID-19. Smith says that he and his collaborators have analysed the data that are available and concluded that people who received hydroxychloroquine in the study were often sicker in the first place than were those who did not. But Mehra says that his team accounted for those differences and still found a small difference in mortality. Furthermore, he says, his study merely highlights an association between the treatment and increased death, but because it is an observational study and not a clinical trial, it cannot exclude the possibility that other factors contributed to that difference in mortality.

GENOMICS USED TO HELP AVOID A SECOND CORONAVIRUS WAVE

Scientists in New Zealand and elsewhere are using sequence data to track infections as lockdowns ease.

By Clare Watson

As many countries emerge from lockdowns, researchers are poised to use genome sequencing to avoid an expected second wave of COVID-19 infections.

Since the first whole-genome sequence of the new coronavirus, SARS-CoV-2, was shared online on 11 January, scientists have sequenced and shared some 32,000 viral genomes from around the world. The data have helped researchers to trace the origin of their countries' COVID-19 outbreaks and pinpoint when community transmission occurred[1].

Now, countries that have successfully suppressed infections are entering the next phase of the COVID-19 pandemic – where there's a risk of new cases appearing as social restrictions ease. Researchers say that genomics will be crucial to quickly track and control these outbreaks. Studies already show that disease outbreaks tend to be shorter and smaller when genomics is used to help contact tracing[2].

"When there are few cases, genomics can very quickly tell you what you're dealing with and therefore guide precision interventions," says Gytis Dudas, a consulting bioinformatician at the Gothenburg Global Biodiversity Centre in Sweden.

Several places are particularly well placed to do that because they invested in genome sequencing early in the pandemic and have a relatively small numbers of cases. Researchers in New Zealand, and at least one state in Australia, decided that they would aim to sequence most coronavirus genomes in their region.

As SARS-CoV-2 spread around the world and viruses circulating in different regions gradually evolved, distinct lineages began to form. By comparing sequences, researchers can quickly rule out possible lines of transmission if two sequences don't match, and can link together cases that do.

"When there are few cases, genomics can very quickly tell you what you're dealing with."

Scientists in the United Kingdom, the United States and other countries are also sequencing SARS-CoV-2 from a large proportion of cases there, but because their epidemics are still ongoing and case numbers are high, genomics is being used to monitor spread and help identify the source of some cases where contact tracing fails.

Before the first reported case arrived in Australia from Wuhan, China, in early January, researchers at a laboratory in Melbourne, Victoria, that usually investigates outbreaks of food-borne illness started preparing to sequence SARS-CoV-2 genomes.

So far, the team has sequenced samples from three-quarters of the state's roughly 1,700 cases[3], thought to be the most comprehensive sequencing coverage in the world for an infectious-disease outbreak.

The data will be used to help identify the probable origin of new cases that arise as Victoria's social restrictions ease. Public-health officials will be able to make decisions to control outbreaks much faster than was possible in the first few weeks of the pandemic, when there were fewer genomes to compare, says Torsten Seemann, a bioinformatician at the Microbiological Diagnostic Unit Public Health Laboratory based at the Peter Doherty Institute for Infection and Immunity in Melbourne.

For example, the sequence data helped to resolve the true source of exposure for one health-care worker, proving that they contracted the virus at a social event and not from a patient in hospital. That information prevented the need for an investigation into a possible outbreak at the hospital, he says.

Genomic data will be particularly important when regional travel resumes. Borders of all states in Australia have been closed since March, but new infections are expected when they reopen. Over the past two months, viral genomes will have mutated just enough to tell whether they come from outside the state, researchers say.

Scientists in New Zealand have so far sequenced 25% of the country's 1,154 reported cases. They're aiming for more than 70% to get the most complete picture practically possible, says Joep de Ligt, lead bioinformatician at the Institute of Environmental Science and Research near Wellington, which is sequencing the country's cases. But the sequence data are already proving useful in responding to outbreaks, he says. Genomic data have identified links between cases that were missed by conventional contact tracing, and have untangled two clusters that were thought to be one.

But using genomics as part of the response to an outbreak has limitations, says de Ligt. With SARS-CoV-2, people who experience asymptomatic infections are unlikely to be tested, creating gaps in the genomic data, he says.

The use of genomic analysis to help contact tracing is also largely restricted to high-income countries, says Meru Sheel, an epidemiologist at the Australian National University in Canberra. She would like to see genomics considered as a tool for outbreak responses in resource-limited countries in the Asia–Pacific region, as it was in the Democratic Republic of the Congo, Sierra Leone and Guinea during the 2014–16 Ebola outbreak.

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3. Seemann, T. *et al.* Preprint at MedRxiv https://doi.org/10.1101/2020.05.12.20099929 (2020).