inspired discussions about racism worldwide.

It was produced by a group of six independent reviewers, supported by three experts in racial equality. They reviewed data and documents from the LSHTM, surveyed current and former staff members and students, and had targeted discussions with some participants.

Fifty-two per cent of survey respondents who were people of colour said that they had witnessed or experienced racism at the university, and the review heard of several instances in which the LSHTM had failed to act on complaints about racist behaviour. Staff and students of colour also told the reviewers that they were reluctant to challenge racist acts because they feared causing offence, or were concerned about repercussions.

Institutional data show that staff members of colour have faced greater barriers to career progression than their white counterparts. Two-thirds of white staff members who applied for promotion from assistant to associate professor between 2017 and 2020 were successful, compared with one-third of staff members of colour.

The review makes a number of recommendations for the LSHTM, including mandating anti-racism training for senior leaders. Smeeth said in his statement that the university will revise its equity, diversity and inclusion plan by the end of January 2022.

"It will not be a quick or easy journey, but work is already under way and this review accelerates and strengthens the change that is needed," says Mohamed Osman, who is chair of LSHTM's diversity and inclusion committee. "If, by releasing this report, LSHTM is taking one of many steps to help to create a more inclusive and equitable sector, then that is one positive outcome," he adds.

OMICRON BLIND SPOTS: WHY IT'S HARD TO TRACK CORONAVIRUS VARIANTS

Researchers race to sequence viral genomes, but there are flaws in the global surveillance system.

By Amy Maxmen

Scientists are scrambling to detect Omicron, the latest SARS-CoV-2 variant of concern, by sequencing the genomes of coronaviruses infecting people. But surveillance through genomic sequencing can be slow and patchy, complicating the picture of how and where Omicron spreads.

One positive development is that researchers are sequencing more SARS-CoV-2 genomes than ever before. This is what enabled them to notice Omicron relatively swiftly. Last April — about 16 months into the pandemic — an online database belonging to the GISAID data-science initiative contained one million SARS-CoV-2 genomic sequences. In the roughly eight months since then, researchers have submitted another five million sequences to GISAID — a nearly tenfold rate increase (see 'Genome explosion'). "We are in much better shape to find Omicron or any other emerging variant now," says Kelly Wroblewski, director of infectious diseases at the Association of Public Health Laboratories in Silver Spring, Maryland.

Yet researchers warn that there are still troubling gaps in sequencing data that make any interpretation of a variant's movement fraught. "The numbers are complex, and there are so many caveats," Wroblewski says. For one, some countries don't have the laboratory capacity to sequence pathogen genomes, so it might look as if those places have no variants, when in fact the mutated viruses are spreading under the radar.

Sequencing rates vary within countries, as well, yielding an uneven picture of how a variant is spreading inside a nation's borders. For instance, 10 US states have sequenced coronavirus samples from less than 2% of their inhabitants who tested positive for COVID-19 in the past month, according to sequences posted at GISAID. By contrast, Wyoming, Colorado and Vermont sequenced more than 10% of their positive cases over the same time frame.

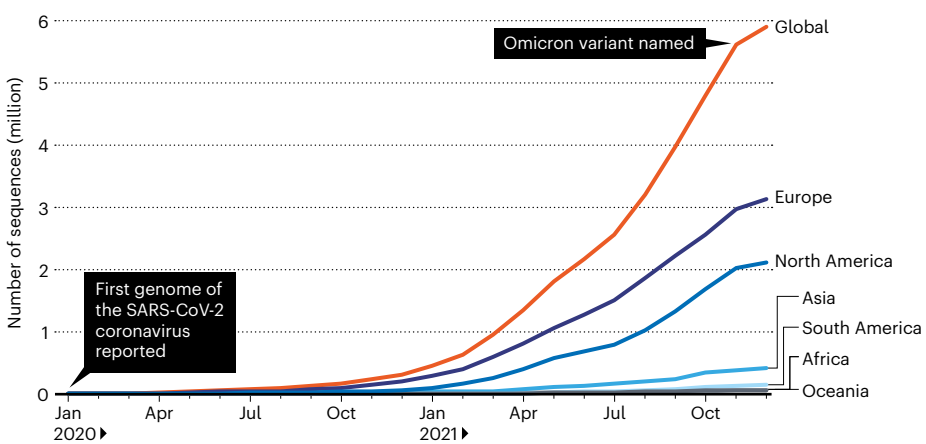
But even if a location is sequencing many of its positive cases, variants could still slip by if testing is poor or biased. "It's easy to sequence 100% of your cases if you only test a few people to begin with," explains Jennifer Nuzzo, an epidemiologist at Johns Hopkins University in Baltimore, Maryland. For example, some countries mainly test international travellers. Even if they sequence all of those samples, they might miss a concerning variant that is circulating domestically.

All of these studies are evolving daily as new Omicron sequences pour in from around the world. A hint of how fast this field is moving can be seen in the rapid rise in genomes reported after the World Health Organization named Omicron a variant of concern on 26 November. Soon after the agency's announcement, 15 countries submitted 187 genomic sequences belonging to Omicron to GISAID. By 14 December, 55 countries had shared 4,265 Omicron sequences. The figures are on course to balloon further — but Dave Luo, a data scientist who advises the Pandemic Prevention Institute at the Rockefeller Foundation in Washington DC, warns that's not necessarily representative of how fast the variant is spreading. Many testing centres are preferentially sequencing samples after a simple, fast genotyping test picks up a possible signal for Omicron — a particular amino acid in the gene for its spike protein. As a result, Omicron might be over-represented among SARS-CoV-2 genome sequences right now.

Genomic information is biased and messy in so many ways, Luo says. "We have to be careful about what we take away from any one source of data."

GENOME EXPLOSION

Scientists have shared about six million SARS-CoV-2 genome sequences on the GISAID data-sharing platform since January 2020, many of them in just the past eight months. Those deposited from Africa proved invaluable in sounding the alarm on the Omicron variant.



SOURCE: GISAID