

study included only about 350 people, it is probably still too small to provide a definitive conclusion.

Small-scale trials

Researchers are hoping to find out whether more treatments can reduce the risk of long COVID. A large UK-based trial called HEAL-COVID is testing two drugs that target the cardiovascular system in people who have been hospitalized with COVID-19. One, called apixaban, is an anticoagulant. The other, atorvastatin, is a cholesterol-lowering medication thought to reduce inflammation in blood vessels.

The study will investigate whether either treatment reduces hospitalizations and deaths in the year after people are first discharged from hospital. Nearly one-third of people who are discharged after treatment for COVID-19 are re-admitted within six months, and 12% die within six months of their initial discharge. “And when we looked at what was most plausibly leading to death after hospitalization, it was probably the cardiopulmonary effects,”

says Summers, who is leading the study.

At the University of Chicago in Illinois, pulmonologist and critical-care physician Ayodeji Adegunsoye has observed a possible increase in the accumulation of scar tissue, called fibrosis, in the lungs well after the acute infection in people who were hospitalized with COVID-19 and required supplemental oxygen. He is now testing a drug called sirolimus – an immune-suppressing drug that is sometimes given to organ-transplant recipients – in such people, in the hope that it will prevent the migration of cells that promote fibrosis in the lung.

By their nature, long-COVID studies require patience: one commonly accepted definition of long COVID is the persistence of certain symptoms for more than 12 weeks after the acute infection. Altmann is optimistic that this year will yield advances, but cautions against reading too much into small trials that might not yield statistically meaningful results. “There’s such pressure,” he says. “There’s this incredibly pressing and desperate need – we all feel that anxiety.”

diversity of bats in southeast Asia and find standardized ways of identifying them. So she and her colleagues captured bats in southern China and southeast Asia between 2015 and 2020. They took measurements and photographs of the bats’ wings and noseleaf – “the funky set of tissue around their nose”, as Hughes describes it – and recorded their echolocation calls. They also collected a tiny bit of tissue from the bats’ wings to extract genetic data.

To map the bats’ genetic diversity, the team used mitochondrial DNA sequences from 205 of their captured animals, and another 655 sequences from online databases – representing a total of 11 species of Rhinolophidae. As a general rule, the greater the difference between two bats’ genomes, the more likely it is that the animals represent genetically distinct groups, and therefore different species.

The researchers found that each of the 11 species were probably multiple species, possibly including dozens of hidden species across the whole sample. Hidden, or ‘cryptic’, species are animals that seem to belong to the same species but are actually genetically distinct. For example, the genetic diversity of *Rhinolophus sinicus* suggests that the group could be six separate species. Overall, the authors estimated that some 40% of the species in Asia have not been formally described.

“It’s a sobering number, but not terribly surprising,” says Nancy Simmons, a curator at the American Museum of Natural History in New York City. Rhinolophid bats are a complex group and there has been only a limited sampling of the animals, she says.

However, relying on mitochondrial DNA could mean that the number of hidden species is an overestimate. That is because mitochondrial DNA is inherited only from the mother, so could be missing important genetic information, says Simmons. Still, the study could lead to a burst of research into naming new bat species in the region, she says.

The findings corroborate other genetic research suggesting that there are many cryptic species in southeast Asia, says Charles Francis, a biologist at the Canadian Wildlife Service, Environment and Climate Change Canada, in Ottawa. But, he says, the estimates are based on a small number of samples.

Hughes’ team used the morphological and acoustic data to do a more detailed analysis of 190 bats found in southern China and Vietnam and found that it supported their finding that many species had not been identified in those regions. The study makes a strong argument for “the use of multiple lines of evidence when delineating species”, says Simmons.

DOZENS OF UNIDENTIFIED BAT SPECIES COULD HOST NEW VIRUSES

Study suggests some 40% of horseshoe bats in Asia have yet to be formally described.

By Smriti Mallapaty

A genomic analysis suggests that there are probably dozens of unknown species of horseshoe bat in southeast Asia¹.

Horseshoe bats (*Rhinolophidae*) are considered the reservoir of many zoonotic viruses – which jump from animals to people – including the close relatives of the viruses that caused severe acute respiratory syndrome and COVID-19. Identifying bat species correctly might help pinpoint areas with a high risk of zoonotic disease, says Shi Zhengli, a virologist at the Wuhan Institute of Virology in China. “This work is important,” she says.

The study was published in *Frontiers in Ecology and Evolution* on 29 March.

Better identification of unknown bat species could also support the search for the origins of SARS-CoV-2 by narrowing down where to look for bats that may harbour close relatives of the virus, says study co-author Alice Hughes, a conservation biologist at the University of Hong Kong. The closest known relatives of

SARS-CoV-2 have been found in *Rhinolophus affinis* bats in southwestern China², and in three species of horseshoe bat in Laos³.

Hughes wanted to better understand the



There could be more species of horseshoe bat than previously thought.

1. Chornelia, A., Jianmei, L. & Hughes, A. C. *Front. Ecol. Evol.* **10**, 854509 (2022).

2. Zhou, P. et al. *Nature* **579**, 270–273 (2020).

3. Temmam, S. et al. *Nature* <https://doi.org/10.1038/s41586-022-04532-4> (2022).