SARS-like viruses may jump from animals to people hundreds of thousands of times a year

Study pinpoints Asian regions that could spark the next coronavirus pandemic

A horseshoe bat (Rhinolophus affinis) exits a cave at dusk, in Perak state in Malaysia, one of the countries where severe acute respiratory syndrome–related viruses may frequently infect people. FLETCHER & BAYLIS/SCIENCE SOURCE

Only two new coronaviruses have spread globally the past 2 decades: SARS-CoV, which caused an outbreak of severe acute respiratory syndrome (SARS) in 2003, and SARS-CoV-2, the virus that causes COVID-19. But that may just be the tip of the iceberg of undetected infections with related viruses emerging from bats, a new paper claims. In a preprint published yesterday, researchers estimate that an average of 400,000 people are likely infected with SARS-related coronaviruses every year, in spillovers that never grow into detectable outbreaks.
Although that number comes with big caveats, “It should be eye-opening to the entire scientific community that we don’t know very much about the frequency of zoonotic spillover,” says virologist Angela Rasmussen of the University of Saskatchewan, who was not involved in the work. That needs to change, she says, “because otherwise we grossly underestimate it.”

The researchers, including Peter Daszak from the EcoHealth Alliance and Linfa Wang from Duke-NUS Medical School in Singapore, created a detailed map of the habitats of 23 bat species known to harbor SARS-related coronaviruses, the group to which SARS-CoV and SARS-CoV-2 belong, and then overlaid it with data on where humans live to create a map of potential infection hot spots. They found that close to 500 million people live in areas where spillovers can occur, including northern India, Nepal, Myanmar, and most of Southeast Asia. The risk is highest in southern China, Vietnam, Cambodia, and on Java and other islands in Indonesia (see map, below).

“This is a definitive analysis of where on the planet the next SARS- or COVID-like virus is most likely to emerge,” Daszak says. The maps could guide efforts to reduce the likelihood of spillover by changing behaviors in high-risk communities and targeting surveillance to detect new outbreaks earlier, he says. Daszak, a vocal advocate of the hypothesis that SARS-CoV-2 came from the wild instead of a research lab, says the maps could also guide efforts to find the virus’ natural origin. (Several studies are underway or being planned to look for SARS-CoV-2 and its relatives in Rhinolophus [horseshoe] bats and other animals.)

But the researchers went one step further. Small surveys done before COVID-19 erupted have suggested some people in Southeast Asia harbor antibodies against SARS-related coronaviruses. Combining those data with data on how often people encounter bats and how long antibodies remain in the blood, the researchers calculated that some 400,000 undetected human infections with these viruses occur each year across the region.

Daszak says interactions with bats are much more common than people think: “Just living there means you’re exposed: People are sheltering in caves, they’re digging guano out of caves, they’re hunting and eating bats.” The paper does not even address how many people work in the wildlife trade and may be infected indirectly when a bat virus infects another animal first, he says.

Although 400,000 infections annually sounds like a lot, Rasmussen says, “in a region with likely hundreds of millions of bats and nearly half a billion people it isn’t that many.” The confidence interval stretches from one to more than 35 million hidden infections per year, however—big enough to “fly the entire population of Rhinolophid bats through,” Rasmussen quips. Models are only as good as the data that are fed into them, says Vincent Munster, a virologist at the U.S. National Institute of Allergy and Infectious Diseases who studies coronaviruses. The data on antibodies only include a few thousand people, he notes, and the assays used to test for antibodies can easily lead to false positives.

“I think if the seroprevalence estimate is way off, the whole thing collapses,” says David Fisman, an epidemiologist at the University of Toronto, who calls the modeling “shaky.” The high number of hidden infections “doesn’t ring true,” Fisman says, because you would expect regular spillovers to be recognized, as they are for rabies and the Nipah virus.

But Rasmussen says many infections could remain hidden if they are short-lived and don’t lead to onward transmission because the viruses are not well adapted to humans. They might not infect enough cells—or cells of the right type—to be transmitted to another person, or they might not be able to escape humans’ immune defenses. In cases when the virus does spread, sheer chance may keep it confined to a small, isolated community.
“A lot of the viruses are probably unable to be transmitted from one person to another, but I have very little doubt that there have been illnesses due to these viruses that get misdiagnosed or never diagnosed,” Daszak says. “A rural farmer in Myanmar is hardly likely to go to the clinic because they’ve got a bit of a cough.”

The work is part of a nascent effort to try to understand the risk factors for viral spillover from animals into humans, Munster says. Already, one message is clear, he says: “I think for virtually any zoonotic pathogen from wildlife, spillover is more frequent than previously recognized.”

*Update, 16 September, 5:20 p.m.: Comments from Davis Fisman have been added to this story.*
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