

MEGAN MOLteni SCIENCE 01.23.2020 07:53 PM

Snakes?! The Slippery Truth of a Flawed Wuhan Virus Theory

One paper advanced a controversial theory about the disease's origin. Other scientists aren't biting.



PHOTOGRAPH: XIAOLU CHU/GETTY IMAGES

Sharing data during an outbreak is vital for public health. But it can also lead to sensational, and even spurious, research, like a controversial new paper claiming that people probably picked up a novel coronavirus from snakes.

One of the many mysteries behind the outbreak of a new respiratory-tract-attacking

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—a place where people sell both live and dead animals, including exotic species, from snugly-abutting stalls.

Though nothing has been confirmed, epidemiologists suspect that the novel coronavirus crossed over into humans somewhere inside the market, which has been shuttered since January 1. Tracking down the right viral culprit is paramount to preventing future interspecies spillover. In 2003, when SARS ripped through the same area of China, the outbreak was fully contained only when civet cats, which had passed the virus along to humans, were removed from the region's markets.

A national task force of Chinese researchers working swiftly to isolate and sequence the virus shared a draft of its genome in a public database earlier this month. That enabled labs all over the world to design diagnostic tests to flag cases as they spread outside of China. So far, fewer than a dozen cases have been confirmed in other countries, including Japan, Korea, Singapore, Thailand, Vietnam, and the US. The release of genetic data has also spurred a flurry of new research findings in recent days, including one paper published by a team of Chinese researchers last night in the *Journal of Medical Virology* that claims to have used the viral sequence to find the most likely source of the emerging outbreak. Their theory: snakes.

After being amplified by a press release and a widely syndicated editorial written by three senior editors of the journal, you can guess what happened next. Stories about China's "snake flu" began to spread through social media alongside official reports about new confirmed cases. There's just one problem: Other researchers think it's probably not true.

"It's complete garbage," says Edward Holmes, a zoologist at the University of Sydney's Institute for Infectious Diseases and Biosecurity, who specializes in emerging RNA viruses, a class that includes coronaviruses like 2019-nCoV. Holmes, who also holds appointments at the Chinese CDC and Fudan University in Shanghai, is among a number of scientists who are pointing out—in virology forums, science Slacks, and on Twitter—what they deem to be major flaws in the paper, and calling on the journal to have it retracted. "It's great that viral sequence data is getting shared openly in real

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Preliminary analyses of the genetic data released by Chinese authorities suggest that 2019-nCoV is most closely related to a group of coronaviruses that typically infect bats. But for a variety of reasons—including that it's winter and bats are hibernating—many scientists suspect that some other animal moved the virus from bats to humans.

The Chinese team, led by Wei Ji, a microbiologist at Peking University Health Science Center's School of Basic Medical Sciences, set out to find the identity of this unknown intermediate host. One way is using genetic data to look at codons—triplets of DNA or RNA letters that are the instructions for making proteins. Every organism has its own bias for which codon it uses to make its proteins. Some viruses adapt to new hosts by adopting their codon bias. Wei's team compared the codons preferred by 2019-nCoV to those preferred by a handful of potential hosts: humans, bats, chickens, hedgehogs, pangolins, and two species of snakes.

They reported finding the most overlap in codon bias between 2019-nCoV and those two kinds of snakes—the Chinese cobra and the many-banded krait. Taken together, these results “suggest for the first time that snake is the most probable wildlife animal reservoir for the 2019-nCoV,” the authors wrote. “New information obtained from our evolutionary analysis is highly significant for effective control of the outbreak caused by the 2019-nCoV-induced pneumonia.”

But Holmes says that this approach has a number of issues. For one thing, comparing codon bias is a very indirect way of identifying an animal host. For another, it works best when looking at species from wildly different corners of the taxonomical hierarchy. Plant and mammal viruses have really distinct codon patterns. So do insect and bird viruses. But within more closely related groups, it's much harder to tease apart meaningful patterns—especially when the authors only sampled a few species. “There could easily be other species out there that are more similar than snakes, but we don't know because they just haven't been put in the analysis,” says Holmes.

He and others are also skeptical that snakes could be the intermediate host, because there aren't any documented cases of reptiles hosting coronaviruses that can transmit

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“I’m not saying it can’t happen. It could. Nature does weird things,” says Nathan Grubaugh, an epidemiologist at the Yale School of Public Health, whose lab specializes in using genomic data to track emerging diseases. But Grubaugh argues there’s no evidence it did. “There’s about as much justification for snakes being the intermediate hosts as me saying on a whim right now that it’s birds,” he says.

Editors of the *Journal of Medical Virology* told WIRED they stand by the publication, which they say went through a formal peer-review process that found the authors’ methods were solid. That process was expedited—the reviewers were given 24 hours to comment and the authors had three days to respond. But given the need for public health information, they believe the speed-up was appropriate. “With this serious situation, with people dying, holding this paper up in review would be criminal,” says Shou-Jian Gao, the journal’s editor-in-chief. “This is intended to just open the scientific dialogue.” He invited any researchers with dissenting assessments to submit them to the journal as written commentaries.

At the time of publication, Wei’s team had not yet responded to emails from WIRED seeking comment on the paper and the criticism it has received.

One thing everyone does agree on is that there’s only one way to conclusively, definitively, undeniably establish which animal served as the bridge to humans—and that’s collecting blood from every winged, webbed, and scaled creature that was in the wet market and analyzing it for the virus. Finding antibodies would be a strong clue, but the live virus would be even better. Those investigations are currently underway, according to World Health Organization officials who [spoke at a news conference](#) Wednesday. Until they turn something up, any guesses are just that.

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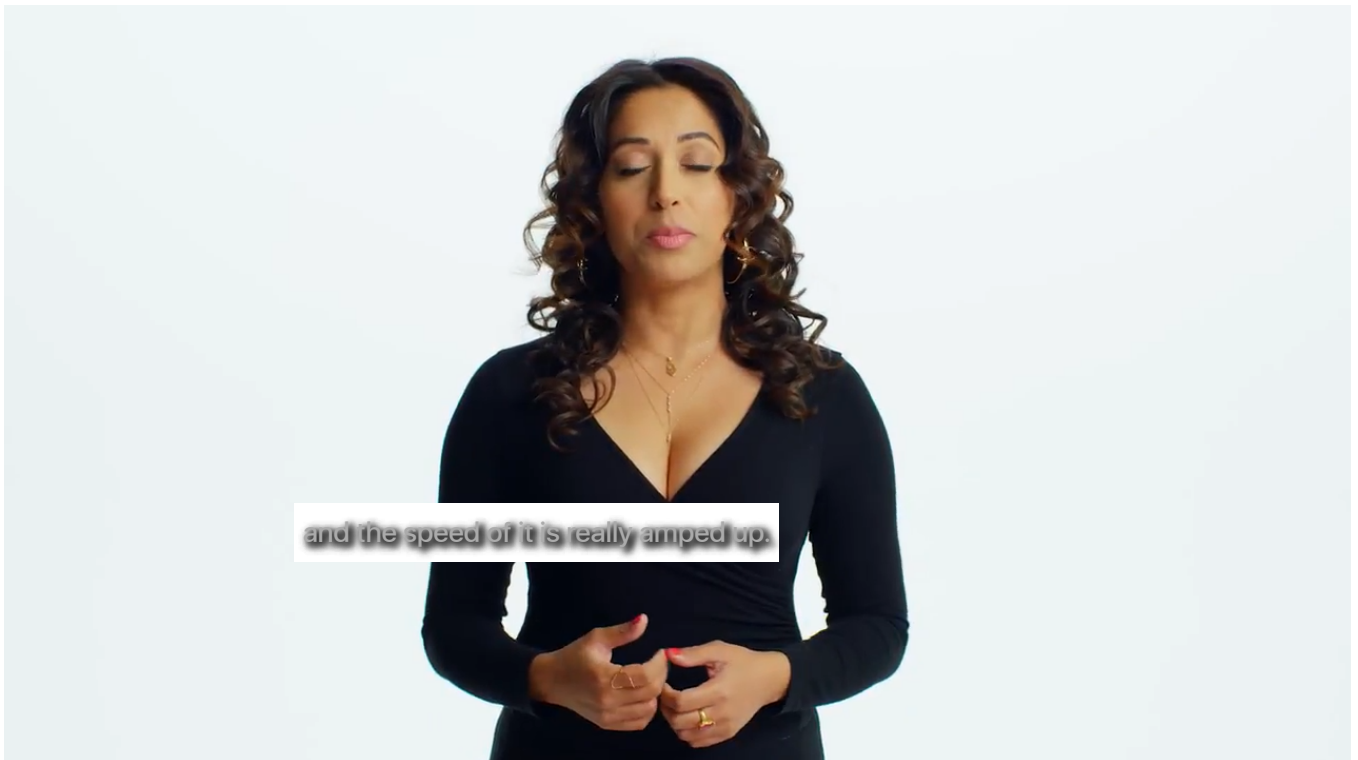
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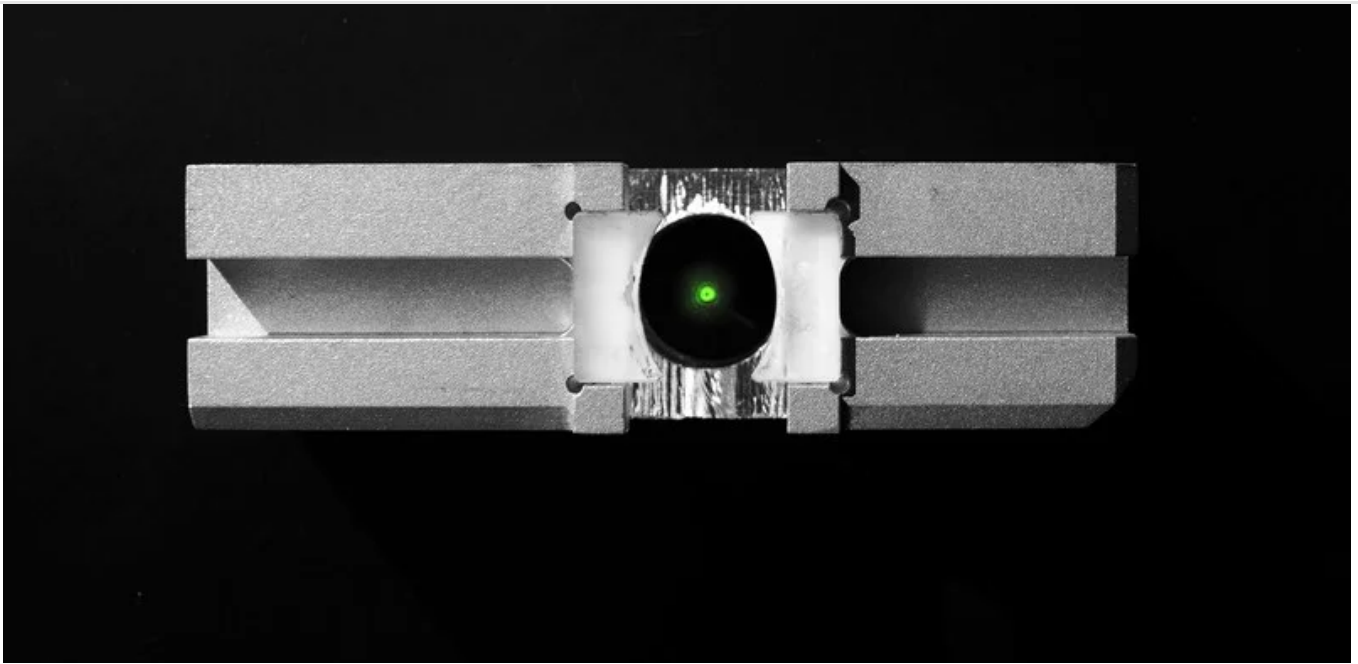
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