

U.S. and Chinese Scientists Trace Evolution of Coronaviruses in Bats

Researchers whose canceled U.S. grant caused an outcry from other scientists urge preventive monitoring of viruses in southwestern China.



By James Gorman

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An international team of scientists, including a prominent researcher at the Wuhan Institute of Virology, has analyzed all known coronaviruses in Chinese bats and used genetic analysis to trace the likely origin of the novel coronavirus to horseshoe bats.

In their report, posted online Sunday, they also point to the great variety of these viruses in southern and southwestern China and urge closer monitoring of bat viruses in the area and greater efforts to change human behavior as ways of decreasing the chances of future pandemics.

The research was supported by a U.S. grant to EcoHealth Alliance, a New York-based nonprofit, that was recently canceled by the National Institutes of Health. The grant, for more than \$3 million, was well on its way to renewal, and the sudden reversal prompted an outcry in the scientific community.

Thirty-one U.S. scientific societies signed a letter of protest on May 20 to the N.I.H., and 77 Nobel laureates sent another letter to the N.I.H. and the Department of Health and Human Services seeking an investigation of the grant denial. The Nobelists said the cancellation appeared to be based on politics rather than a consideration of scientific merit.

The report on the research, which has been accepted by the journal *Nature Communications*, was posted on the BioRxiv (pronounced bio-archive), where scientific research is often released before publication.

The report gives a glimpse of the work the grant had supported.

The researchers, mostly Chinese and American, conducted an exhaustive search for and analysis of coronaviruses in bats, with an eye to identifying hot spots for potential spillovers of these viruses into humans, and resulting disease outbreaks.

The genetic evidence that the virus originated in bats was already overwhelming. Horseshoe bats, in particular, were considered likely hosts because other spillover diseases, like the SARS outbreak in 2003, came from viruses that originated in these bats, members of the genus *Rhinolophus*.

None of the bat viruses are close enough to the novel coronavirus to suggest that it jumped from bats to humans. The immediate progenitor of the new virus has not been found, and may have been present in bats or another animal. Pangolins were initially suspected, although more recent analysis of pangolin coronaviruses suggests that although they probably have played a part in the new virus's evolution, there is no evidence that they were the immediate source.

The new research includes an analysis of bat and viral evolution that strongly supports the suspected origin of the virus in horseshoe bats, but isn't definitive, largely because a vast amount about such viruses remains unknown.

The report also adds detail to what scientists know of coronaviruses in bats, how they have evolved and what kind of threat they pose. Renewal of the grant would have supported a continuation of this work.

N.I.H. canceled the grant shortly after President Trump was asked at a news conference about money erroneously described as going to the Wuhan institute. That lab has been the target of conspiracy theorists who promote the idea that the novel coronavirus was made in a lab. Scientists and U.S. intelligence agencies agree that the overwhelming likelihood is that the virus evolved in nature.

Richard Ebright, a microbiologist and biosafety expert at Rutgers University, has argued that there could have been an accidental leak of a naturally evolved virus that was present in the lab, and that lab safety should be investigated. Many scientists view the leak scenario as unlikely given the many opportunities for infection in the wildlife trade, markets and farming.

There is also no reported evidence that the new virus was ever present at the Wuhan Institute of Virology. It was first discovered after numerous human cases appeared in late December, most in people with connections to a wet market in Wuhan.

Zheng-Li Shi, the director of the Center for Emerging Infectious Diseases at the institute, known for work tracking down the source of the original SARS virus in bats and identifying SARS-CoV-2, as the novel coronavirus is known, is one of the authors of the new paper, along with Peter Daszak, the president of EcoHealth Alliance.

The researchers collected oral and rectal swabs, as well as fecal pellets from bats in caves across China from 2010 to 2015, and used genetic sequencing to derive 781 partial sequences of the viruses. They compared these to sequence information already documented in computer databases on bat and pangolin coronaviruses.

The Coronavirus Outbreak ■

Frequently Asked Questions and Advice

Updated June 5, 2020

- **How does blood type influence coronavirus?**

A study by European scientists is the first to document a strong statistical link between genetic variations and Covid-19, the illness caused by the coronavirus. Having Type A blood was linked to a 50 percent increase in the likelihood that a patient would need to get oxygen or to go on a ventilator, according to the new study.

- **How many people have lost their jobs due to coronavirus in the U.S.?**

The unemployment rate fell to 13.3 percent in May, the Labor Department said on June 5, an unexpected improvement in the nation's job market as hiring rebounded faster than economists expected. Economists had forecast the

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They found evidence that the novel coronavirus may have evolved in Yunnan Province, but could not rule out an origin elsewhere in Southeast Asia outside China.

The family of bats that included the horseshoe genus, *Rhinolophus*, seems to have originated in China tens of millions of years ago. They have a long history of co-evolution with coronaviruses, which the report shows commonly jump from one bat species to another.

Dr. Daszak said that the region where China, Laos, Vietnam and Myanmar converge may be “the real hot spot for these viruses.”

He said the region was characterized not only by bat and coronavirus diversity, but by urbanization, population growth and intense poultry and livestock farming, all of which could lead to viruses jumping from one species to another, and to the spread of human disease.

Not only bats should be monitored, Dr. Daszak said, but humans. “People are farming wildlife all across Southern China, tens of thousands of people involved in the industry, they should be getting regular tests, not just for Covid-19, but for what other viruses they are picking up.”

He acknowledged that such an effort would be very costly, but said that compared to the cost of a pandemic, “You’re definitely getting a good return on investment.”