

February 2019

Zheng-Li Shi and colleagues:

“It is highly likely that future SARS or MERS like coronavirus outbreaks will originate from bats, and there is an increased probability that this will occur in China.”






viruses



Review

Bat Coronaviruses in China

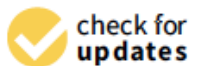
Yi Fan ^{1,2} , Kai Zhao ^{1,2}, Zheng-Li Shi ^{1,2}  and Peng Zhou ^{1,2,*} 

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9 December 2019

Peter Daszak:

"Now, the logical progression for vaccines is, if you are going to develop a vaccine for SARS, people are going to use pandemic SARS, but let's try to insert these other related diseases and get a better vaccine."



Vincent Racaniello (left), Peter Daszak (right). (YouTube, TWiV 615 screenshot)

<https://www.taiwannews.com.tw/en/news/4104828>

https://youtu.be/IdYDL_RK--w

2 February 2020



Shi Zhengli about COVID-19 outbreak:

Shi Zhengli said on her social media "the virus was the result of "nature punishing the uncivilized habits and customs of humans", and she is willing to "bet my life that [the outbreak] has nothing to do with the lab."



石正丽

欢迎转发：2019新型冠状病毒是大自然给人类不文明生活习惯的惩罚，我石正丽用我的生命担保，与实验室没有关系。奉劝那些相信并传播不良媒体的谣传的人、相信印度学者不靠谱的所谓“学术分析”的人，闭上你们的臭嘴。同时转发这个打脸消息：印度学者已经决定撤回这篇预印本文章。他本人说："It was not our intention to feed into the conspiracy theories...we appreciate the criticisms...and will get back with a revised version"

收起

1分钟前

当代恩格斯



<https://lh3.googleusercontent.com/proxy/cJQmNIqss34EMilHThDbDILR0xztMYFaLOs7bjC-Jz5kpvb17mOAB7sSvnKFYl8vFgmEaOHE>

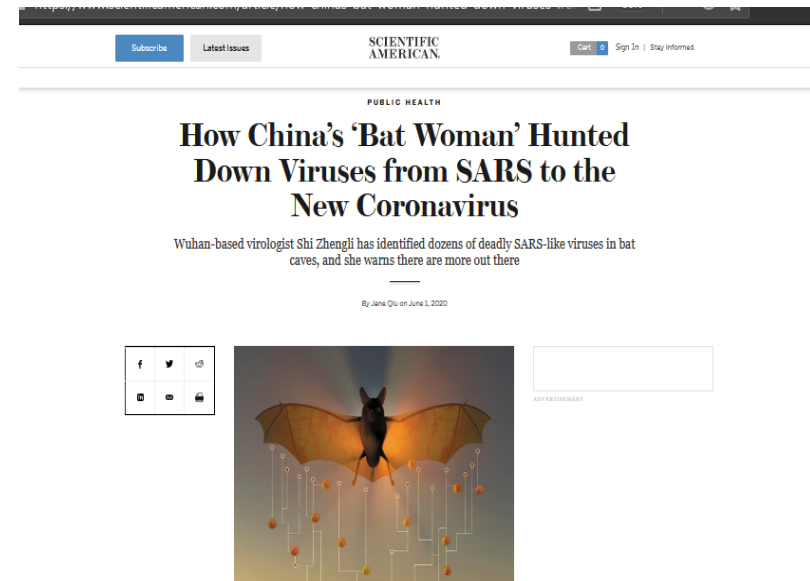
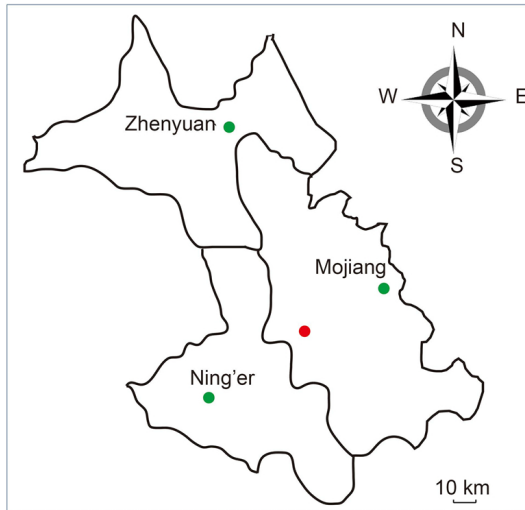
<https://global.chinadaily.com.cn/a/202002/02/WS5e36b2b7a31012821727432e.html>

4 March 2020

Shi Zhengli about the Mojiang mine:

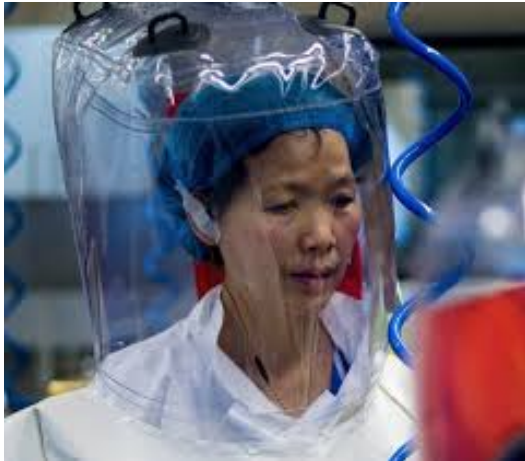


““The mine shaft stunk like hell,” says Shi, who, like her colleagues, went in wearing a protective mask and clothing. “Bat guano, covered in fungus, littered the cave.” Although the fungus turned out to be the pathogen that had sickened the miners, she says it would have been only a matter of time before they caught the coronaviruses if the mine had not been promptly shut.”



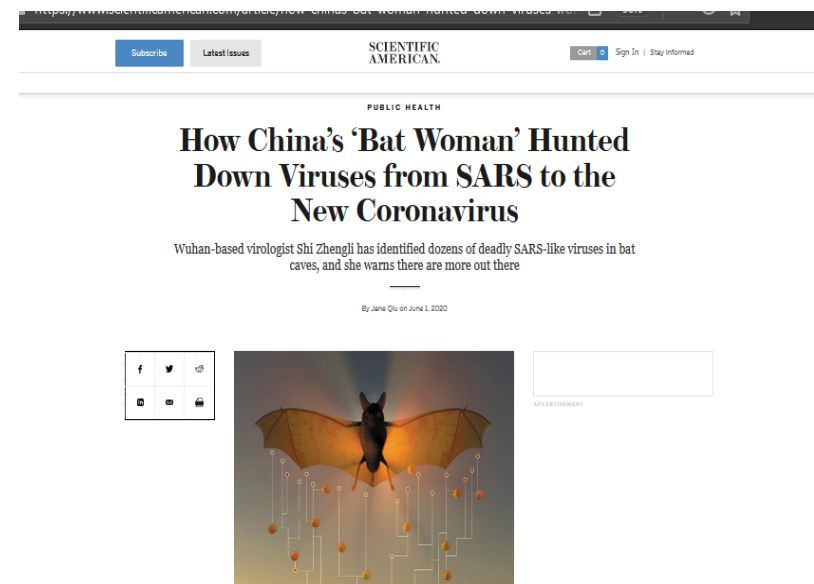
<https://www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus1/>

4 March 2020



Shi Zhengli about lab records:

“Shi instructed her group to repeat the tests and, at the same time, sent the samples to another facility to sequence the full viral genomes. Meanwhile she frantically went through her own lab’s records from the past few years to check for any mishandling of experimental materials, especially during disposal. Shi breathed a sigh of relief when the results came back: none of the sequences matched those of the viruses her team had sampled from bat caves. “That really took a load off my mind,” she says. “I had not slept a wink for days.””



<https://www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus1/>

12 March 2020

Lijian Zhao, Spokesman of
the Chinese Ministry of
Foreign Affairs



Lijian Zhao 赵立坚 
@zlj517



2/2 CDC was caught on the spot. When did patient zero begin in US? How many people are infected? What are the names of the hospitals? It might be US army who brought the epidemic to Wuhan. Be transparent! Make public your data! US owe us an explanation!



 **Voir les faits sur le COVID-19**

3:37 PM · 12 mars 2020



 15,2 k  16,1 k personnes tweetent à ce sujet.

April 2020

Peter Daszak:

"The China bat research project was funded entirely through the NIH grant."



<https://www.npr.org/sections/goatsandsoda/2020/04/29/847948272/why-the-u-s-government-stopped-funding-a-research-project-on-bats-and-coronaviru>

July 2020

Peter Daszak *about RaTG13:*

"went back to that sample in 2020, in early January or maybe even at the end of last year, I don't know."



INSIGHT INVESTIGATION

Seven year coronavirus trail from bat cave via Wuhan lab

• NEW

In 2013, scientists investigating deaths in a disused mine found a coronavirus remarkably similar to that behind the pandemic. They took samples to their lab 1,000 miles away

July 2020

Peter Daszak about RaTG13:

“We found the closest relative to the current SARS-CoV-2 in a bat in China in 2013. We sequenced a bit of the genome, and then it went in the freezer; because it didn’t look like SARS, we thought it was at a lower risk of emerging. With the Global Virome Project, we could have sequenced the whole genome, discovered that it binds to human cells and upgraded the risk. And maybe then when we were designing vaccines for SARS, those could have targeted this one too, and we would have had something in the freezer ready to go if it emerged.”



WHO's stunning failure as coronavirus lay in wait

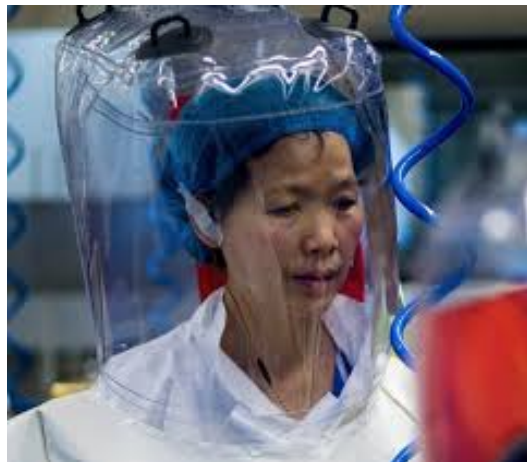
<https://www.theaustralian.com.au/weekend-australian-magazine/coronavirus-how-to-beat-the-next-pandemic/news-story/77989c4bfcb4fc7a120533e159dd35ff>

24 July 2020

Shi Zhengli about RaTG13 :

“Ra4991 is the ID for a bat sample while RaTG13 is the ID for the coronavirus detected in the sample. We changed the name as we wanted it to reflect the time and location for the sample collection. 13 means it was collected in 2013, and TG is the abbreviation of Tongguan town, the location where the sample was collected.”

“In 2018, as the NGS sequencing technology and capability in our lab was improved, we did further sequencing of the virus using our remaining samples, and obtained the full-length genome sequence of RaTG13 except the 15 nucleotides at the 5' end.”



Reply to Science Magazine

1. You have published many papers on coronaviruses and even warned of the possibility of a zoonotic spillover event from animals to humans. Do you feel like your warnings were appropriately heeded and how does what imagined compare to the scale of this pandemic?

A: The risk of cross-species infection always exists. With regards to this issue, China has undertaken scientific research projects, created facilities and equipment, and built team

<https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf>