

# EXHIBIT 16

Investigations

India

# Looks like we found our Highly Variable SARS-like COV: Ralph Baric to Peter Daszak



Savio Rodrigues • 5 hours ago 🔥 217 📖 5 minutes read



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The truth behind the science around the origin of the SARS-CoV-2 lies with Ralph Baric of the University of North Carolina, Peter Daszak of EcoHealth Alliance and Prof Shi Zhengli of the Wuhan Institute of Virology (WIV).

**To:** Baric, Ralph S[rbaric@email.unc.edu]  
**Cc:** Alison Andre[andre@ecohealthalliance.org]  
**From:** Peter Daszak[daszak@ecohealthalliance.org]  
**Sent:** Mon 1/13/2020 7:55:43 PM (UTC-05:00)  
**Subject:** RE: Call with NIH tomorrow

OK - great. It sounds like we're on the same call!

And my thoughts exactly re. the highly variable SARS-like CoV. I've told journalists about it, but it's a complicated story for them to get across..

Cheers,

Peter

Peter Daszak  
President

EcoHealth Alliance  
460 West 34th Street – 17th Floor  
New York, NY 10001

Tel.  
Website: [www.ecohealthalliance.org](http://www.ecohealthalliance.org)  
Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

-----Original Message-----

**From:** Baric, Ralph S [mailto:rbaric@email.unc.edu]  
**Sent:** Monday, January 13, 2020 6:50 PM  
**To:** Peter Daszak  
**Subject:** RE: Call with NIH tomorrow

Hi Peter, I have to participate on an NIH call tomorrow at 10. I believe it's a strategic meeting designed to help craft a NIH response plan to the WU-CoV. Hope things are going well. Looks like we found our highly variable SARS-like CoV! Ralph

-----Original Message-----

**From:** Peter Daszak <daszak@ecohealthalliance.org>  
**Sent:** Monday, January 13, 2020 6:43 PM  
**To:** Baric, Ralph S <rbaric@email.unc.edu>; Sims, Amy C <sims0018@email.unc.edu>  
**Cc:** Alison Andre <andre@ecohealthalliance.org>  
**Subject:** Call with NIH tomorrow

Ralph - I'm having an informational call with our program officer re the Wuhan outbreak tomorrow at 10am - do you want to join and are you available?



According to the email obtained by the US Right To Know organization and in the possession of GoaChronicle, on January 13, 2020, in an email to Peter Daszak at 6.50 pm, Ralph Baric, states:

*Hi Peter, I have to participate in an NIH call tomorrow at 10. I believe it's a strategic meeting designed to help craft an NIH response plan to the WU-CoV. Hope things are going well. **Looks like we found our highly variable SARS-like CoV!** Ralph*

In reply to Ralph Baric's email, Peter Daszak at 7.55 pm states:  
*It sounds like we're on the same call!*

***And my thoughts exactly re. the highly variable SARS-like CoV. I've told journalists about it, but it's a complicated story for them to get across***

On January 13, 2020, before China or the World Health Organisation (WHO) made any official statement on the nature of the coronavirus both Ralph Baric and Peter Daszak in their emails appear to be confident that the coronavirus in China is a 'highly variable SARS-like CoV'. Most importantly, Ralph Baric refers to the coronavirus as 'Our' highly variable SARS-like COV, displaying a familiarity with the virus.

Reportedly, in 2013, the American virologist Ralph Baric approached Zhengli Shi at a meeting. Baric was a top expert in coronaviruses, with hundreds of papers to his credit, and Shi, along with her team at the Wuhan Institute of Virology, had been discovering them by the fistful in bat caves. In one sample of bat guano, Shi had detected the genome of a new virus, called SHC014, that was one of the two closest relatives to the original SARS virus, but her team had not been able to culture it in the lab.

Baric had developed a way around that problem—a technique termed as "reverse genetics" in coronaviruses. Not only did it

allow him to bring an actual virus to life from its genetic code, but he could mix and match parts of multiple viruses. He wanted to take the "spike" gene from SHC014 and move it into a genetic copy of the SARS virus he already had in his lab. The spike molecule is what lets a coronavirus open a cell and get inside it. The resulting chimera would demonstrate whether the spike of SHC014 would attach to human cells.

Baric asked Shi Zhengli if he could have the genetic data for SHC014. "She was gracious enough to send us those sequences almost immediately," he told media. His team introduced the virus modified with that code into mice and into a petri dish of human airway cells. Sure enough, the chimera exhibited "robust replication" in the human cells—evidence that nature was full of coronaviruses ready to leap directly to people.

It is no surprise that a group of Chinese scientists lobbied through US Professor of the University of North Carolina Ralph Baric to rename 'SARS-CoV-2' given by the Coronavirus Study Group (CSG) of the International Committee on Virus Taxonomy (ICTV) to 2019-nCoV.

In the correspondence, the Chinese scientists feared that the virus would become known as 'Wuhan Coronavirus' or 'Wuhan Pneumonia'.

In an email dated 13/2/2020, Professor Shi Zhengli wrote to Ralph Baric. The subject of the email was 'Virus Name'. The email had an attached document titled, 'A unique and unified name for the novel coronavirus from Wuhan SJ clean'

The email stated:

***"Dear Ralph,***

***We heard that the 2019-nCoV was renamed as SARS-CoV-2. We had a fierce discussion among Chinese virologists.***

***We have some comments on this name, I'm wondering if the CoV study group would consider a revision.***

***I attached the comments from me and my Chinese colleague."***

The document from Prof. Shi Zhengli to Prof. Ralph Baric states:

**"A unique and unified name is needed for the novel coronavirus identified from Wuhan**

An outbreak of 'unusual pneumonia of unknown cause in Wuhan, China was first reported in December 2019. By 5 January 2020, Chinese scientists had quickly identified the causative agent a new type of coronavirus (CoV) belonging to the Betacoronaviruses genus of the Coronaviridae family that also includes severe acute respiratory syndrome (SARS)-CoV and the Middle East respiratory syndrome (MERS)- CoV.

On 12th January 2020, the World Health Organization (WHO) temporarily named the virus as **2019 novel coronavirus(2019-nCoV)**. On 30th January, WHO recommended naming the disease as "2019-nCoV acute respiratory disease". On 8 February 2020, the China National Health Commission (CNHC) announced naming the disease as "**Novel CoronavirusPneumonia**"(NCP). On 11th February 2020, WHO renamed the disease "**coronavirus disease2019**"(**COVID-19**). On 7 February 2020, the Coronavirus Study Group (CSG) of the International Committee on Virus Taxonomy (ICTV) posted a manuscript at bioRxiv and suggested designating the novel coronavirus as "**severe acute respiratory syndrome coronavirus 2(SARS-CoV-2)**" based on the phylogenetic analysis of related coronaviruses.



Zhengli further in her document to Ralph Baric expresses, "By 11th February 2020, the new coronavirus had caused more than 40,000 confirmed infections and more than 1000 deaths, mostly in mainland China, in spite of efforts by the Chinese government and its people to contain the spread of the virus in past weeks. It goes without saying that the effects of the epidemic on all the aspects of Chinese life are devastating and, possibly, irreversible. Consequently, appropriately naming the virus and disease becomes a matter of importance to the Chinese people, in general, and virologists, in specific, and the issue has been fervently discussed and debated among scientists with the outcome, so far, as noted above. We fully agree that the new virus and SARS-CoV belong to the same virus species by classification, However, the consensus opinion of Chinese virologists is that none of the currently proposed names reflects the uniqueness and characteristics of the novel virus and that more consideration is needed for naming the virus. **Based on the following reasons, we propose giving a unique and unified name to the new virus."**

Prof Shi Zhengli, also known as the 'Batwoman' continues to impress upon Ralph Baric on behalf of the group of Chinese scientists, she expresses, "All proposed names are either too generic, or too similar, to previously well-known viruses, or contain an Arabic number. **This makes it hard to remember or recognize, leading to a tendency among the general population and scientists alike to use a shorthand term such as "Wuhan coronavirus" or "Wuhan pneumonia" This has, in fact, been the case since it was named as 2019-nCoV. This practice would, however, stigmatize and insult the people in Wuhan, who are still suffering from the outbreak."**

The document sent by Prof Zhengli to Ralph Baric, further states, "The new virus is still evolving, and it is still too early to predict the outcome of the current outbreak. However, it is already clear that the infection of the new virus has diverse

symptoms, from asymptomatic infection to severe pneumonia and even death. It has less case-fatality rate and higher transmissibility than SARS-CoV, indicating its clear difference from SARS-CoV. Again, therefore, it is not appropriate to designate the new virus as SARS-CoV-2 before we know more properties of the virus.”



**To:** Baric, Ralph S [rbaric@email.unc.edu]  
**From:** zlshi [zlshi@wh.iov.cn]  
**Sent:** Thur 2/13/2020 3:28:25 AM (UTC-05:00)  
**Subject:** vrus name  
A unique and unified name is needed for the novel coronavirus from Wuhan\_SJ\_clean.docx

Dear Ralph,

We heard that the 2019-nCoV was renamed as SARS-CoV-2. We had a fierce discussion among Chinese virologists. We have some comments on this name, I'm wondering if the CoV study group would consider a revision.

I attached the comments from me and my Chinese colleague.

Best regards,  
Zhengli,

SHI Zhengli, Ph. D  
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Peter Daszak and Shi Zhengli published a paper reporting how the Chinese lab had engineered different versions of WIV1 and tested their infectiousness in human cells. The paper announced that the WIV had developed its own reverse-genetics system, following the Americans' lead. But it also included a shocking and troubling detail: the work, which was funded in part by the NIH grant, had been done in a BSL-2 lab. Both Peter Dazsak and Shi Zhengli, experts in this field of science performed highly dangerous experiments in a BSL-2 lab and the US-government funded these experiments.

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View in Publisher's site

American Society for Microbiology  
Journal of Virology  
Volume 90, Issue 14, 15 July 2016, Pages 6572-6582  
<https://doi.org/10.1128/JVI.02079-15>

Virus-Cell Interactions

### Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response

Lei-Ping Zeng<sup>a</sup>, Yu-Tao Gao<sup>a</sup>, Xing-Yi Ge<sup>a</sup>, Qian Zhang<sup>a</sup>, Cheng Peng<sup>a</sup>, Xing-Lou Yang<sup>a</sup>, Bing Tan<sup>a</sup>, Jing Chen<sup>a</sup>, Aleksei A. Chumura<sup>b</sup>, Peter Daszak<sup>b</sup>, and Zheng-Li Shi<sup>b</sup>

<sup>a</sup>Key Laboratory of Special Pathogens, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China  
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**ABSTRACT**

Bats harbor severe acute respiratory syndrome (SARS)-like coronaviruses (SL-CoVs) from which the causative agent of the 2002-2003 SARS pandemic is thought to have originated. However, despite the fact that a large number of genetically diverse SL-CoV sequences have been detected in bats, only two strains (named WIV1 and WIV16) have been successfully cultured *in vitro*. These two strains differ from SARS-CoV only in containing an extra open reading frame (ORF) (named ORFX), between ORF6 and ORF7, which has no homology to any known protein sequences. In this study, we

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The truth behind the science of the coronavirus that led to the COVID-19 pandemic lies with Ralph Baric, Peter Daszak, and Prof Shi Zhengli. It is time all three are investigated.

SHARE



#and Prof Shi Zhengli

#COVID-19 pandemic

#Highly Variable SARS-like CoV

#Peter Daszak

#Ralph Baric