

25 Jul 2023

≡ The New York Times Magazine

# The Ongoing Mystery of Covid's Origin

We still don't know how the pandemic started. Here's what we do know — and why it matters.



David Quammen

“A team of researchers, including Worobey, detected a pattern in the data: strong proximity between samples containing raccoon dog DNA and others containing SARS-CoV-2 fragments (and some samples that contained both), from stalls in the southwest corner of the market where wild animals had been sold as food. “

<https://web.archive.org/web/20230725093300/https://www.nytimes.com/2023/07/25/magazine/covid-start.html/>  
<https://www.nytimes.com/2023/07/25/magazine/covid-start.html>

21 Aug 2023

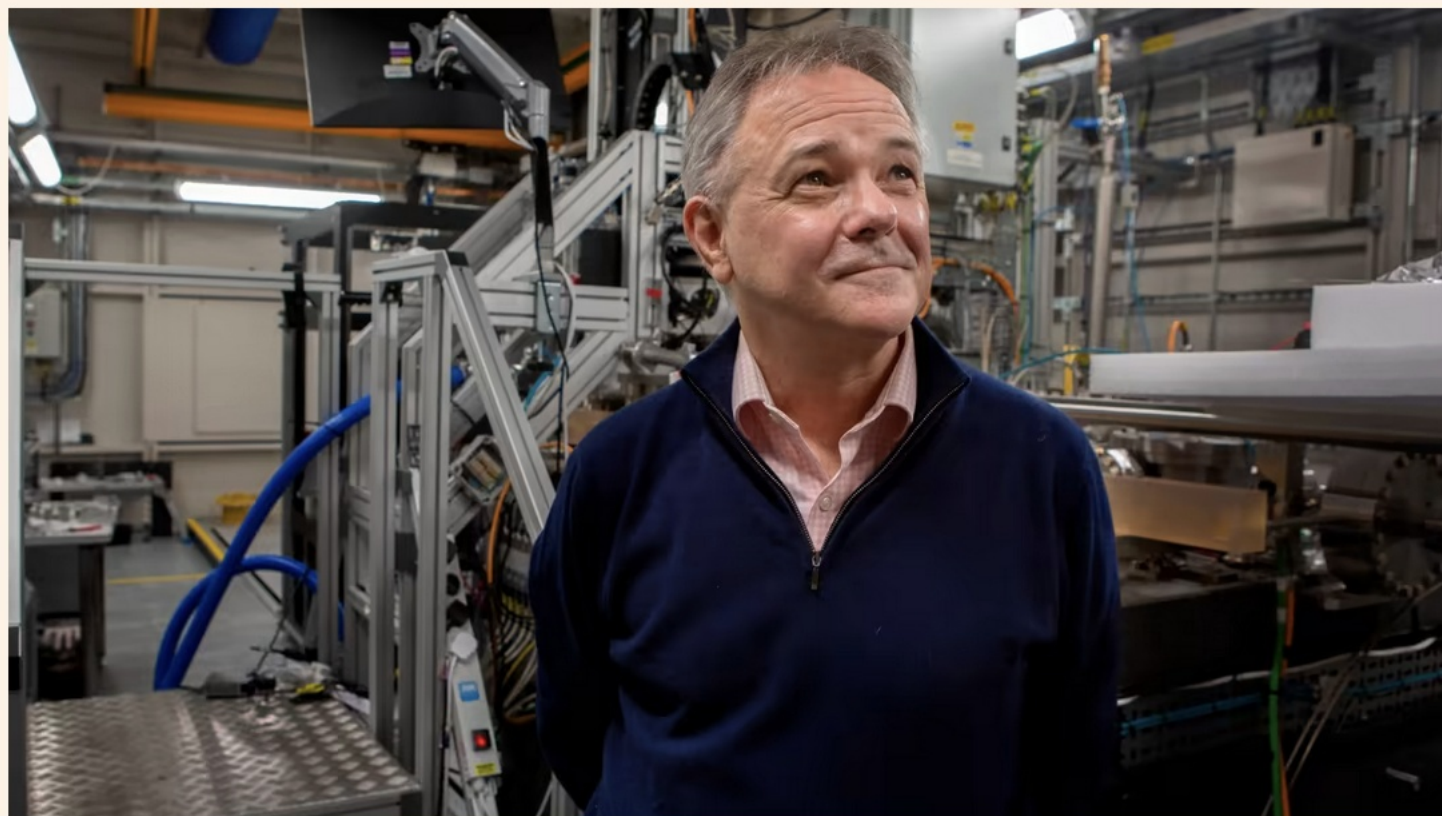
Financial Times

# WHO's chief scientist urges greater collaboration against dangerous pathogens

Joint work would avoid 'deep scars' caused by unequal access to drugs during Covid-19

“Farrar said he was still open to all hypotheses on Covid's origins”

“is increasingly that actually the natural origin is much more likely”.



21 Aug 2023

Fortune

whether  
COVID  
accidentally  
leaked from  
Wuhan virus  
lab.

“We should  
get to the  
bottom of it,”  
Farrar told  
the paper.



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# New WHO chief scientist backs fact-finding mission to China to examine whether COVID accidentally leaked from Wuhan virus lab

BY **CHRISTIAAN HETZNER**

August 21, 2023 at 2:43 PM GMT+2



<https://fortune.com/2023/08/21/covid-lab-leak-china-who-chief-scientist-jeremy-farrar/>

<https://web.archive.org/web/20230825065744/https://fortune.com/2023/08/21/covid-lab-leak-china-who-chief-scientist-jeremy-farrar/>



# FEDERAL REGISTER

The Daily Journal of the United States Government



 Notice

## **Request for Information; Potential Changes to the Policies for Oversight of Dual Use Research of Concern (DURC) and the Potential Pandemic Pathogen Care and Oversight (P3CO) Policy Framework**

A Notice by the [Science and Technology Policy Office](#) on [09/01/2023](#)



This notice from the Federal Register by the Office of Science and Technology Policy (OSTP) seeks comments by 16 October.

<https://www.federalregister.gov/documents/2023/09/01/2023-18906/request-for-information-potential-changes-to-the-policies-for-oversight-of-dual-use-research-of>



[nature](#) > [nature microbiology](#) > [articles](#) > article

Article | [Open access](#) | [Published: 25 September 2023](#)

# Host range, transmissibility and antigenicity of a pangolin coronavirus

[Yixuan J. Hou](#), [Shiho Chiba](#), [Sarah R. Leist](#), [Rita M. Meganck](#), [David R. Martinez](#), [Alexandra Schäfer](#), [Nicholas J. Catanzaro](#), [Vishwaraj Sontake](#), [Ande West](#), [Catlin E. Edwards](#), [Boyd Yount](#), [Rhianna E. Lee](#), [Samuel C. Gallant](#), [Seth J. Zost](#), [John Powers](#), [Lily Adams](#), [Edgar F. Kong](#), [Melissa Mattocks](#), [Aleksandra Tata](#), [Scott H. Randell](#), [Purushothama R. Tata](#), [Peter Halfmann](#), [James E. Crowe Jr](#), [Yoshihiro Kawaoka](#) & [Ralph S. Baric](#) 

[Nature Microbiology](#) **8**, 1820–1833 (2023) | [Cite this article](#)

PgCoV GD reconstructed in vitro, capacity for airborne spread in hamsters (previously pseudotyped viruses, showed that PgCoV GD spike can utilize human ACE2 receptor for entry)

SCIENCE

## The Banality of Bad-Faith Science

Not every piece of published research needs to be heartfelt.

By Benjamin Mazer

<https://archive.ph/Wz7Ki>

## The Peer-Review Dilemma

Scientific publication can be a constraining, flattening, and maddening process—but that’s not necessarily a bad thing.

By Benjamin Mazer

<https://www.theatlantic.com/science/archive/2023/09/scientific-research-papers-covid-lab-leak/675464/>

“The editor of Nature Medicine, the journal that published Andersen’s paper, said that retraction was unwarranted.”

## Erratum for the Research Article “The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2” by J. E. Pekar *et al.*

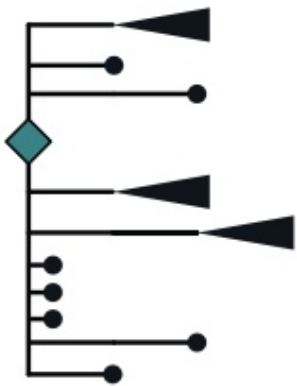
SCIENCE • 13 Oct 2023 • Vol 382, Issue 6667 • DOI: 10.1126/science.adl0585

↓ 1,864

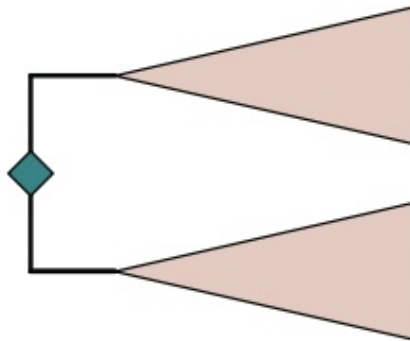


In the Research Article “[The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2](#),” the frequency of simulated topologies matching phylogenetic structures arising from a single introduction was incorrectly reported because of an **error in the code**, which has been corrected. Correspondingly, the Bayes factors in favor of multiple introductions of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) into the human population relative to a single introduction were **overestimated**. The text now represents the corrected Bayes factors and topology frequency (Fig. 2C), which **still favors the multiple introduction scenario**. Bayes factor significance cutoffs from Kass and Raftery (1995) are now used throughout the text, including Table 1, where the probability of inferred ancestral haplotypes is reported. These cutoffs highlight the disagreement between the rooting inferred when using only human viruses (lineage B rooting) by comparison with incorporating the bat viruses through the recombinant common ancestor (lineage A rooting). This analysis independently supports the conclusion that lineages A and B were most likely the result of at least two cross-species transmissions of SARS-CoV-2.

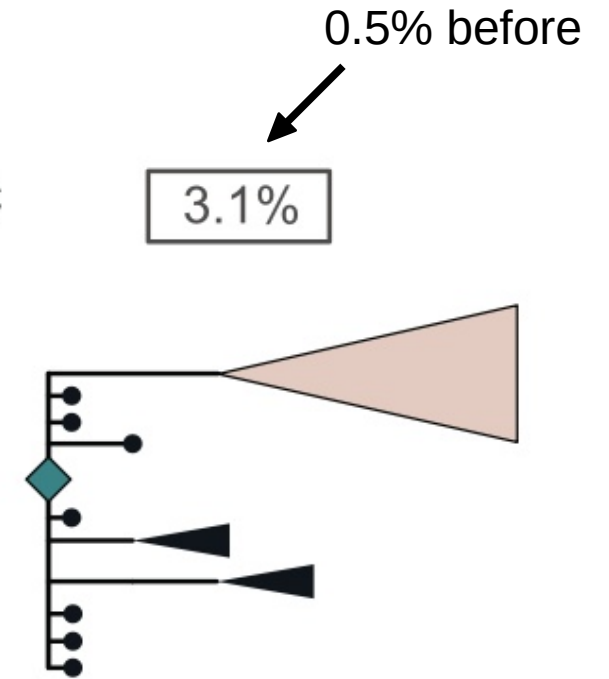
**A** 47.5%



**B** 0.0%



**C** 3.1%



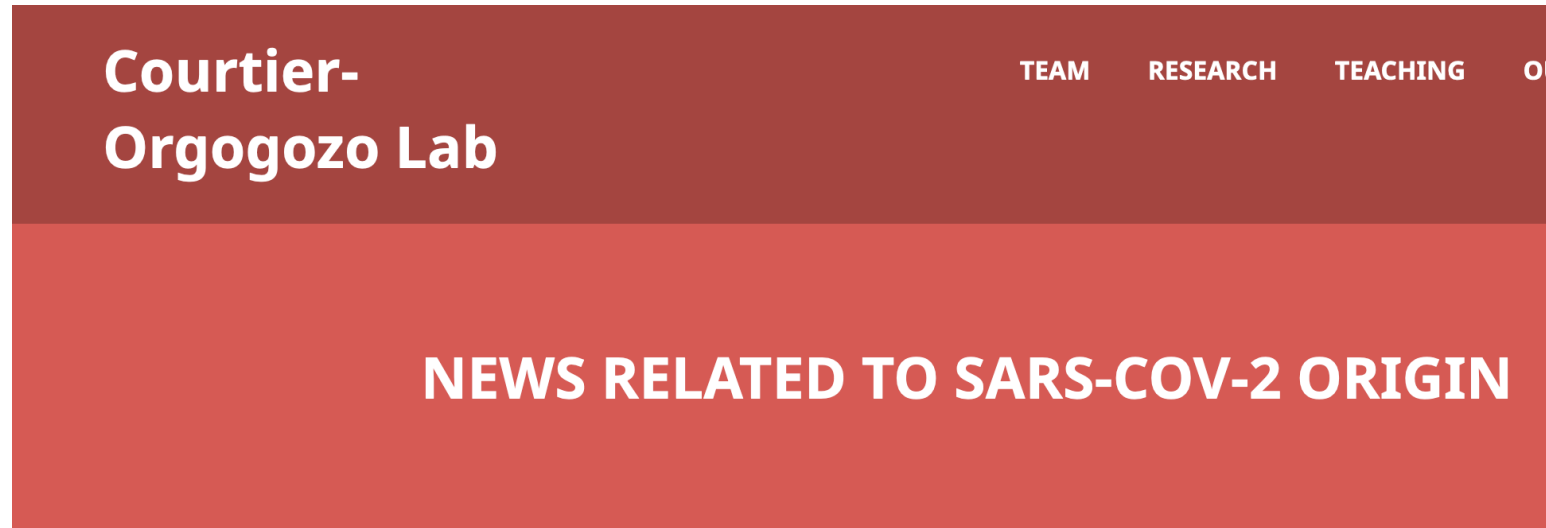
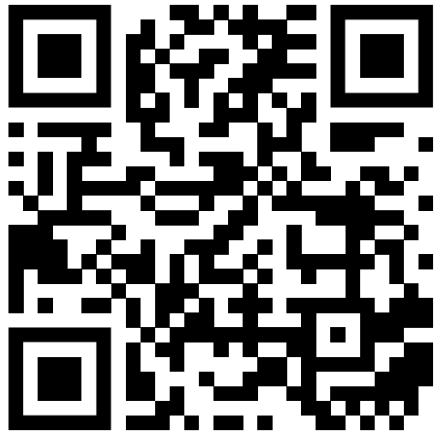
◆ MRCA  
● Sampled taxon

▲ Clade  
▲ Clade w/  $\geq 30\%$   
and  $\leq 70\%$  of taxa

1 mutation



All my introduction slides are available online  
<https://courtier.ijm.fr/news-covid-origin/>



Here are the introduction slides presented at our international workshop entitled "*Evidence-based investigation of SARS-CoV-2 proximal origin*". They present key newspaper articles & scientific papers related to SARS-CoV-2 origin published over the years.

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