



HAL
open science

An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2

Jacques van Helden, Colin Butler, Guillaume Achaz, Bruno Canard, Didier Casane, Jean-Michel Claverie, Fabien Colombo, Virginie Courtier-Orgogozo, Richard Ebright, François Graner, et al.

► To cite this version:

Jacques van Helden, Colin Butler, Guillaume Achaz, Bruno Canard, Didier Casane, et al.. An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. *The Lancet*, 2021, 398 (10309), pp.1402-1404. 10.1016/S0140-6736(21)02019-5 . hal-03358748

HAL Id: hal-03358748

<https://amu.hal.science/hal-03358748>

Submitted on 20 Oct 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Copyright

An appeal for an objective, open and transparent scientific debate about the origin of SARS-CoV-2

Jacques van Helden^{1,*}, Colin D Butler^{2,*}, Guillaume Achaz³, Didier Casane⁴, Jean-Michel Claverie⁵, Fabien Colombo⁶, Virginie Courtier⁷, Bruno Canard⁸, Richard H. Ebright⁹, François Graner¹⁰, Milton Leitenberg¹¹, Serge Morand¹², Rossana Segreto¹³, Nikolai Petrovsky¹⁴, Etienne Decroly^{15,*}, José Halloy^{16,*}

1. Aix-Marseille Univ, INSERM, Lab. Theory and Approaches of Genome Complexity (TAGC), Marseille, France. Email Jacques.van-Helden@univ-amu.fr. ORCID [0000-0002-8799-8584](https://orcid.org/0000-0002-8799-8584)
2. National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia. Email colin.butler@anu.edu.au. ORCID [0000-0002-2942-5294](https://orcid.org/0000-0002-2942-5294).
3. Université de Paris, Muséum National d'Histoire Naturelle, Collège de France, France. Email: guillaume.achaz@mnhn.fr ORCID [0000-0003-4514-5935](https://orcid.org/0000-0003-4514-5935)
4. Université de Paris, CNRS, Laboratoire Evolution, Génomes, Comportement, Ecologie, Gif-sur-Yvette, France. Email: didier.casane@egce.cnrs-gif.fr ORCID [0000-0001-5463-1092](https://orcid.org/0000-0001-5463-1092).
5. Aix-Marseille University, France. Email: claverie@igs.cnrs-mrs.fr ORCID [0000-0003-1424-0315](https://orcid.org/0000-0003-1424-0315)
6. Université Bordeaux Montaigne, MICA, EA 4426, Pessac, France. Email: fabien.colombo@u-bordeaux-montaigne.fr
7. Ecole Polytechnique, Université de Paris, CNRS, Institut Jacques Monod, France. Email: virginie.courtier@ijm.fr ORCID [0000-0002-9297-9230](https://orcid.org/0000-0002-9297-9230)
8. Architecture et Fonction des Macromolécules Biologiques, Centre National de la Recherche Scientifique, Aix Marseille University, Marseille, France. Email: bruno.canard@univ-amu.fr ORCID [0000-0003-4924-1991](https://orcid.org/0000-0003-4924-1991).
9. Department of Chemistry and Chemical Biology and Waksman Institute, Rutgers University, Piscataway NJ, USA. Email: ebright@waksman.rutgers.edu ORCID [0000-0001-8915-7140](https://orcid.org/0000-0001-8915-7140).
10. MSC, Université de Paris, CNRS UMR 7057, 10 rue Alice Domon et Léonie Duquet, 75205 Paris Cedex 13, France. Email: francois.graner@univ-paris-diderot.fr ORCID [0000-0002-4766-3579](https://orcid.org/0000-0002-4766-3579)
11. University of Maryland, School of Public Affairs, USA. Email: mleitenberg@cs.com
12. Montpellier University, CNRS, Institut des Sciences de l'Evolution, France. Email: serge.morand@umontpellier.fr ORCID [0000-0003-3986-7659](https://orcid.org/0000-0003-3986-7659)
13. University of Innsbruck, Austria. Email: rsegreto@protonmail.com ORCID [0000-0002-2566-7042](https://orcid.org/0000-0002-2566-7042).
14. College of Medicine and Public Health, Flinders University, Adelaide Australia. Email: nikolai.petrovsky@flinders.edu.au ORCID [0000-0002-1580-5245](https://orcid.org/0000-0002-1580-5245).
15. Architecture et Fonction des Macromolécules Biologiques, Centre National de la Recherche Scientifique, Aix Marseille University, Marseille, France. Email: etienne.decroly@univ-amu.fr. ORCID [0000-0002-6046-024X](https://orcid.org/0000-0002-6046-024X)
16. Université de Paris, LIED, CNRS UMR 8236, Paris, France. Email: jose.halloy@u-paris.fr. ORCID [0000-0003-1555-2484](https://orcid.org/0000-0003-1555-2484).

*These authors contributed equally to the work

The authors have no competing interest

Keywords: COVID-19; SARS-CoV-2 origins; zoonosis; virus escape; gain-of-function;

Commentary

On July 5, 2021, a Commentary was published in these columns, called “Science, not speculation, is essential to determine how SARS-CoV-2 reached humans”.¹ The letter recapitulates the arguments of an earlier letter (February, 2020) by the same authors, called “Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19”² which claimed overwhelming support for the hypothesis that the novel coronavirus causing the Covid-19 pandemic originated in wildlife. The authors associated any alternative view with conspiracy theories by stating: “We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin”. The statement has imparted a “silencing” effect on the wider scientific debate, including amongst science journalists.³ The 2021 letter did not repeat the proposition that scientists open to alternative hypotheses were conspiracy theorists, but did state:

“We believe the strongest clue from new, credible, and peer reviewed evidence in the scientific literature is that the virus evolved in nature, while suggestions of a laboratory leak source of the pandemic remain without scientifically validated evidence that directly supports it in peer reviewed scientific journals.”

In fact, this argument could literally be reversed. As will be shown below, there is no direct support for the natural origin of SARS-CoV-2, and a laboratory-related accident is plausible.

There is so far no scientifically validated evidence that directly supports a natural origin

Among the references cited in the two letters by Calisher et al., all but one simply show that SARS-CoV-2 is phylogenetically related to other betacoronaviruses. The fact that the causative agent of COVID-19 descends from a natural virus is widely accepted, but this does not explain how it came to infect humans. The question of the proximal origin of SARS-CoV-2 – i.e. the final virus and host before passage to humans – was expressly addressed in only one highly cited opinion piece, which supports the natural origin hypothesis,⁴ but suffers from a logical fallacy:⁵ it opposes two hypotheses – laboratory engineering versus zoonosis – wrongly implying that there are no other possible scenarios. The article then provides arguments against the laboratory engineering, which are not conclusive for the following reasons: (1) it assumes that the optimisation of the receptor binding domain (RBD) for human ACE2 requires prior knowledge of the adaptive mutations, whereas selection in cell culture or animal models would lead to the same effect; (2) the absence of traces of reverse-engineering systems does not preclude genome editing, which is currently performed with so-called seamless techniques;^{6,7} (3) the absence of previously known backbone is not a proof, since researchers can work for several years on viruses before publishing their full genome (this was the case for RaTG13, the closest known virus, which was isolated in 2013 and published in 2020).⁸ Based on these *indirect* and questionable arguments, the authors conclude in favour of a natural proximal origin. In the last part of the article, they briefly evoke selection during passage (i.e., experiments aiming to test the capacity of a virus to infect cell cultures or model animals) and acknowledge the documented cases of laboratory escapes of SARS-CoV, but they dismiss this scenario, based on the argument that the strong similarity between receptor binding domains of SARS-CoV-2 and pangolin provides a more parsimonious explanation of the specific mutations. However, the pangolin hypothesis has since been abandoned,⁹⁻¹² so that the whole reasoning should be re-evaluated.

Although considerable evidence supports the natural origins of other outbreaks (e.g. Nipah, MERS and SARS) the evidence for a natural origin for SARS-CoV-2 is missing. After 21 months of investigations, the proximal progenitor of SARS-CoV-2 is still lacking. Neither the host pathway from

bats to humans, nor the geographic route from Yunnan (where the closest viruses have been sampled) to Wuhan (where the pandemic emerged) have been shown. More than 80,000 samples collected from wildlife sites and animal farms in China all proved negative.¹³ In addition, the international research community has no access to the sites, samples, or raw data. Although the China-WHO mission to Wuhan concluded that the laboratory origin was “extremely unlikely”,¹³ WHO Director-General Tedros Adhanom Ghebreyesus declared that all hypotheses remained on the table including the lab leak.¹⁴

A research-related origin is plausible

Two questions need to be addressed: virus evolution and introduction into the human population.

Since July 2020, several peer reviewed scientific papers have discussed the likelihood of a research-related origin of the virus. Some unusual features of the SARS-CoV-2 genome sequence are suggesting they may have resulted from genetic engineering,^{15,16} an approach widely used in some virology labs.¹⁷ Alternatively, adaptation to humans might result from undirected laboratory selection during serial passage in cell cultures or laboratory animals,^{18,19,5} including “humanized mice”, i.e. genetically modified to display the human receptor for entry of SARS-CoV-2 (hACE2).²⁰ Laboratory research also includes more targeted approaches such as gain-of-function (GOF) experiments relying on chimeric viruses to test their potential to cross barrier species.^{17,21}

A research-related contamination could result from contact with a natural virus during field collection, transportation from the field to a laboratory,²² characterization of bats and bat viruses in a laboratory, or from a non-natural virus modified in a laboratory. There are well-documented cases of pathogen escapes from laboratories.^{23–26} Field collection, field survey, and in-laboratory research on potential pandemic pathogens require high-safety protections and a strong and transparent safety culture. However, experiments on SARS-related coronaviruses are routinely performed at biosafety level 2 (BSL-2),^{21,27} which complies with the current recommendations for viruses infecting non-human animals, but is inappropriate for experiments that might produce human-adapted viruses by effects of selection or oriented mutations.

Overwhelming evidence for either a zoonotic or research-related origin is lacking; the jury is still out

On the basis of the current scientific literature, complemented by our own analyses of coronavirus genomes and proteins,^{5,15,16,18,28,29} we hold that there is currently no compelling evidence to choose between a natural origin (i.e. a virus that has evolved and been transmitted to humans solely via contact with wild or farmed animals) and a research-related origin (which might have occurred at sampling sites, during transportation or within the laboratory, and might have involved natural, selected or engineered viruses).

An evidence-based, independent and prejudice-free evaluation will require an international consultation of high-level experts with no conflict of interest, from various disciplines and countries; the mandate will be to establish the different scenarios, and the associated hypotheses, and then to propose protocols, methods and required data in order to elucidate the question of SARS-CoV-2 origin. Beyond this issue, it is important to continue debating about the risk/benefit balance of current practices of field and laboratory research including gain-of-function experiments, as well as the human activities contributing to zoonotic events.

Scientific journals should open their columns to an in-depth analysis of all hypotheses

As scientists, we need to evaluate all hypotheses on a rational basis, and to weigh their likelihood based on facts and evidence, devoid of speculation concerning possible political impacts. Contrary to the first statement published in *The Lancet*, we don't think that scientists should promote "unity" ("*We support the call from the Director-General of WHO to promote scientific evidence and unity over misinformation and conjecture*").² As shown above, research-related hypotheses are not misinformation and conjecture. More importantly, science embraces alternative hypotheses, contradictory arguments, verification, refutability, and controversy. Departing from this principle risks establishing dogmas, abandoning the essence of science and, even worse, paving the way for conspiracy theories. Instead, the scientific community should bring this debate to a place where it belongs: the columns of scientific journals.^{30,31}

References

- 1 Calisher CH, Carroll D, Colwell R, *et al.* Science, not speculation, is essential to determine how SARS-CoV-2 reached humans. *The Lancet* 2021; : S0140673621014197.
- 2 Calisher C, Carroll D, Colwell R, *et al.* Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19. *The Lancet* 2020; **395**: e42–3.
- 3 Thacker PD. The covid-19 lab leak hypothesis: did the media fall victim to a misinformation campaign? *BMJ* 2021; : n1656.
- 4 Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. *Nat Med* 2020; **26**: 450–2.
- 5 Sallard E, Halloy J, Casane D, Decroly E, van Helden J. Tracing the origins of SARS-COV-2 in coronavirus phylogenies: a review. *Environ Chem Lett* 2021; published online Feb 4. DOI:10.1007/s10311-020-01151-1.
- 6 Yount B, Curtis KM, Fritz EA, *et al.* Reverse genetics with a full-length infectious cDNA of severe acute respiratory syndrome coronavirus. *Proc Natl Acad Sci* 2003; **100**: 12995–3000.
- 7 Cockrell AS, Beall A, Yount B, Baric R. Efficient Reverse Genetic Systems for Rapid Genetic Manipulation of Emergent and Preemergent Infectious Coronaviruses. In: Perez DR, ed. *Reverse Genetics of RNA Viruses*. New York, NY: Springer New York, 2017: 59–81.
- 8 Zhou P, Yang X-L, Wang X-G, *et al.* A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020; **579**: 270–3.
- 9 Choo SW, Zhou J, Tian X, *et al.* Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence? *Conserv Lett* 2020; **13**. DOI:10.1111/conl.12754.
- 10 Frutos R, Serra-Cobo J, Chen T, Devaux CA. COVID-19: Time to exonerate the pangolin from the transmission of SARS-CoV-2 to humans. *Infect Genet Evol* 2020; **84**: 104493.
- 11 Lee J, Hughes T, Lee M-H, *et al.* No Evidence of Coronaviruses or Other Potentially Zoonotic Viruses in Sunda pangolins (*Manis javanica*) Entering the Wildlife Trade via Malaysia. *EcoHealth* 2020; published online Nov 23. DOI:10.1007/s10393-020-01503-x.
- 12 WHO. WHO-convened Global Study of the Origins of SARS-CoV-2: Terms of References for the China Part. World Health Organisation, 2020
<https://www.who.int/publications/m/item/who-convened-global-study-of-the-origins-of-sars-co-v-2>.
- 13 Joint WHO-China Study Team. WHO-convened Global Study of Origins of SARS-CoV-2: China Part. World Health Organisation, 2021.
- 14 WHO. WHO calls for further studies, data on origin of SARS-CoV-2 virus, reiterates that all hypotheses remain open. World Health Organisation, 2021.
- 15 Segreto R, Deigin Y. The genetic structure of SARS-CoV-2 does not rule out a laboratory origin: SARS-COV-2 chimeric structure and furin cleavage site might be the result of genetic

- manipulation. *BioEssays* 2020; : 2000240.
- 16 Deigin Y, Segreto R. SARS-CoV-2's claimed natural origin is undermined by issues with genome sequences of its relative strains: Coronavirus sequences RaTG13, MP789 and RmYN02 raise multiple questions to be critically addressed by the scientific community. *BioEssays* 2021; : 2100015.
 - 17 Menachery VD, Yount BL, Debbink K, *et al.* A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nat Med* 2015; **21**: 1508–13.
 - 18 Sallard E, Halloy J, Casane D, van Helden J, Decroly É. Retrouver les origines du SARS-CoV-2 dans les phylogénies de coronavirus. *médecine/sciences* 2020; **36**: 783–96.
 - 19 Sirotkin K, Sirotkin D. Might SARS-CoV-2 Have Arisen via Serial Passage through an Animal Host or Cell Culture?: A potential explanation for much of the novel coronavirus' distinctive genome. *BioEssays* 2020; : 2000091.
 - 20 Daszak, Peter. Understanding the Risk of Bat Coronavirus Emergence. 2014.
 - 21 Hu B, Zeng L-P, Yang X-L, *et al.* Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLoS Pathog* 2017; **13**: e1006698.
 - 22 Schou S, Hansen AK. Marburg and Ebola virus infections in laboratory non-human primates: a literature review. *Comp Med* 2000; **50**: 108–23.
 - 23 Siengsanon-Lamont J, Blacksell SD. A Review of Laboratory-Acquired Infections in the Asia-Pacific: Understanding Risk and the Need for Improved Biosafety for Veterinary and Zoonotic Diseases. *Trop Med Infect Dis* 2018; **3**: 36.
 - 24 Klotz LC, Sylvester EJ. The Consequences of a Lab Escape of a Potential Pandemic Pathogen. *Front Public Health* 2014; **2**. DOI:10.3389/fpubh.2014.00116.
 - 25 Heymann DL, Aylward RB, Wolff C. Dangerous pathogens in the laboratory: from smallpox to today's SARS setbacks and tomorrow's polio-free world. *The Lancet* 2004; **363**: 1566–8.
 - 26 Sewell DL. Laboratory-associated infections and biosafety. *Clin Microbiol Rev* 1995; **8**: 389–405.
 - 27 Zeng L-P, Gao Y-T, Ge X-Y, *et al.* Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. *J Virol* 2016; **90**: 6573–82.
 - 28 Segreto R, Deigin Y, McCairn K, *et al.* Should we discount the laboratory origin of COVID-19? *Environ Chem Lett* 2021; : s10311-021-01211-0.
 - 29 Piplani S, Singh PK, Winkler DA, Petrovsky N. In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin. *Sci Rep* 2021; **11**: 13063.
 - 30 Relman DA. Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19. *Proc Natl Acad Sci* 2020; **117**: 29246–8.
 - 31 Bloom JD, Chan YA, Baric RS, *et al.* Investigate the origins of COVID-19. *Science* 2021; **372**: 694.1-694.