



Jeffrey Sachs: Covid-19 may have originated in US biolabs

Description

USA: VT has published numerous articles pointing out that there is strong evidence that suggests that Covid 19 could have originated in US biolabs. Now we have enough evidence which confirms this theory.

IN AN ARTICLE published Thursday, economist Jeffrey Sachs called for an independent investigation of information held by U.S.-based institutions that could shed light on the origins of the Covid-19 pandemic. Writing in the [Proceedings of the National Academy of Sciences](#), Sachs and his co-author, Neil Harrison, a Columbia University professor of molecular pharmacology and therapeutics, said that federal agencies and universities possess evidence that has not been adequately reviewed, including virus databases, biological samples, viral sequences, email communications, and laboratory notebooks.

Sachs and Harrison also highlighted a tantalizing scientific detail that may be an indication that SARS-CoV-2, the coronavirus that causes Covid-19, originated in a laboratory: a sequence of eight amino acids on a critical part of the virus's spike protein that is identical to an amino acid sequence found in cells that line human airways.

Sachs and Harrison are hardly the first to suggest that SARS-CoV-2 might have been created in a lab. Since its genetic sequence was first published in February 2020, scientists have puzzled over the furin cleavage site, an area on the virus's spike that allows it to be cleaved by a protein on the membrane of human cells and makes the coronavirus particularly dangerous to people.

Once split, the virus releases its genetic material into the cell and reproduces. While attaching to cells and spike cleavage is part of how all coronaviruses work, SARS-CoV-2 is the only one of its class, sarbecoviruses, that can use furin for the cleavage.

As with past discussion of a possible lab origin of SARS-CoV-2, this latest theory has already been met with considerable pushback. Even some scientists who are open to the idea that a lab accident could have sparked the pandemic remain unconvinced by the particular trail of evidence laid out by Sachs and Harrison.

The journal article offers a scientific road map for how this unusual sequence of amino acids could have made its way into the furin cleavage site, or FCS, of the virus. Sachs and Harrison acknowledge that the sequence could have arisen naturally. But they also lay out another possibility: that scientists might have purposefully inserted this particular string of amino acids into a bat coronavirus in the course of their work. They focus particularly on scientists who submitted an unfunded grant proposal to a division of the Defense Department called the Defense Advanced Research Projects Agency, or DARPA, laying out plans to insert a furin cleavage site into a bat coronavirus.

“We do not know whether the insertion of the FCS was the result of natural evolution — perhaps via a recombination event in an intermediate mammal or a human — or was the result of a deliberate introduction of the FCS into a SARS-like virus as part of a laboratory experiment,” Sachs and Harrison write. “We do know that the insertion of such FCS sequences into SARS-like viruses was a specific goal of work proposed by the EHA-WIV-UNC partnership within a 2018 grant proposal (“DEFUSE”) that was submitted to the US Defense Advanced Research Projects (DARPA).”

EHA is a reference to EcoHealth Alliance, a nonprofit research group based in New York City that has received more than \$118 million in grants and contracts from federal agencies. WIV, or the Wuhan Institute of Virology, is a Chinese research organization that collaborated with EcoHealth Alliance in the past and was listed as a subcontractor on the DARPA grant. UNC is mentioned because Ralph Baric, a molecular biologist at the University of North Carolina, Chapel Hill, was to have conducted part of the work pitched to DARPA. The grant proposal touted Baric’s “two-decade track record of reverse engineering [coronavirus] and other virus spike proteins.”

The intent of the DARPA proposal was to prevent emerging pathogenic threats, but the work, if conducted, could have created a novel virus capable of infecting humans. “We will introduce appropriate human-specific cleavage sites and evaluate growth potential in [a type of mammalian cell commonly used in microbiology] and [human airway epithelial cell] cultures,” the proposal stated.

Several scientists interviewed about the DARPA proposal in September told The Intercept that scientists often begin research before seeking funding and thus that some of the experiments described in the proposal could have already been completed. But when asked about that possibility in an [interview](#), Peter Daszak, the president of EcoHealth Alliance, rejected it: “The DARPA proposal was not funded. Therefore, the work was not done. Simple.”

A Rational Choice

Sachs and Harrison note, the part of a protein on the cell membrane that shares its amino acid sequence with the bat coronavirus is critical for lung function. Known as an epithelial sodium channel-alpha, or ENaC-alpha, it is found in human airway cells, as well as in human kidneys and colons. Intriguingly, like SARS-CoV-2, ENaC-alpha, which facilitates the absorption of fluid in cells, is also activated by the unusual furin cleavage site. Harrison, a physiologist affiliated with Columbia’s Department of Molecular Pharmacology and Therapeutics, studies ion channels, the larger category to which ENaC-alpha belongs.

Other scientists have already pointed out the match between the amino acid series in the furin cleavage site of SARS-CoV-2 and the ENaC-alpha found in human airways. In 2020, a team from the

biomedical company Nference [suggested](#) that the overlap between the virus and the sequence found in human lungs is part of the reason that Covid-19 is so damaging to the respiratory system. Those scientists described the sequence as having evolved naturally.

Sachs and Harrison, in contrast, suggest that researchers may have inserted the string of amino acids into a bat coronavirus precisely because of its known importance to lung function. “For a research team assessing the pandemic potential of SARS-related coronaviruses, the FCS of human ENaC — an FCS known to be efficiently cleaved by host furin present in the target location (epithelial cells) of an important target organ (lung), of the target organism (human) — might be a rational, if not obvious, choice of FCS to introduce into a virus in order to alter its infectivity, in line with other work performed previously,” they write.

Such a choice, they point out, would have been in keeping with another viral research project on which EcoHealth Alliance, the Wuhan Institute of Virology, and UNC’s Baric collaborated: a 2014 grant from the National Institute of Allergy and Infectious Diseases that involved increasing the transmissibility and pathogenicity of bat coronaviruses.

Growing List of Coincidences

The intriguing theory of viral engineering hinges on two observations: that the amino acid sequences match and that experts in both the [ENaC-alpha furin cleavage site](#) and the insertion of genetic sequences into bat coronaviruses happen to work at the same academic institution: the University of North Carolina, Chapel Hill.

Baric, whose work aims to prevent and create treatments for viral outbreaks, has previously [inserted](#) segments of DNA and RNA into viruses and created an infectious clone of SARS using his own [patented “No See’m”](#) method of inserting genetic materials without a trace. He has also [collaborated](#) on coronavirus research with scientists from a center for lung studies at UNC-Chapel Hill who are knowledgeable about ENaC-alpha. In one 2016 [study](#), the scientists created a new virus using the spike of a bat coronavirus that had been [isolated and characterized](#) by the Wuhan Institute of Virology. The experiment found that the new virus “replicated efficiently” in human airway cells that were cultured in a lab.

In another paper, published a year earlier, Baric, along with the Wuhan Institute of Virology’s Shi Zhengli and a lung expert at UNC-Chapel Hill’s lung institute, described creating a hybrid virus using a SARS-like virus from a bat and a “mouse-adapted” coronavirus. The new virus caused mice to get sicker than those exposed to the original virus. The goal of these experiments was to prepare for the possibility that a virus might jump naturally from animals to humans, as SARS had in 2003. But even before the pandemic, the experiment drew criticism from other scientists, who were concerned because the researchers had created a virus that was able to spread in humans.

Sachs and Harrison note that the scientists who co-authored the DARPA grant proposal would have been aware of research on coronavirus furin cleavage sites, including one 2006 [experiment](#) in which a furin cleavage site was inserted into a coronavirus. “The research team would also have some familiarity with the FCS sequence and the FCS-dependent activation mechanism of human ENaC, which was extensively characterized at UNC,” they write.

Still, both the overlap in the amino acid sequence and the fact that experts in the furin cleavage site of the ENaC-alpha and insertion of genetic material into bat coronaviruses work at the same university could be coincidental, as Harrison and Sachs acknowledge. Some virologists, though, say that the coincidence strains credulity.

“Could be,” Richard Ebright, a molecular biologist at Rutgers University, wrote in an email to The Intercept when asked about the possibility that these things are both chance occurrences. “But the list of coincidences is getting verrrrrrrrrry long.”

Ebright, a proponent of investigating the origin of SARS-CoV-2 and of investigating both natural-spillover and research-related-spillover, whom Harrison and Sachs thank “for helpful commentary on the manuscript,” spelled out some of the other Covid coincidences that he considers questionable, including its initial outbreak in a city that, [well](#) before [2019](#), had already been pegged as a biosafety risk. Ebright also noted Wuhan’s 1,000-mile distance from the nearest wild bats that carry the type of SARS-related coronaviruses that caused the pandemic. And he pointed to the particular coding of the amino acids in the furin cleavage site of SARS-CoV2.

“The sequence encoding the FCS of the pandemic virus contained two consecutive CGG arginine codons,” Ebright explained in his email. (A codon, or a combination of three nucleotides, supplies the genetic code for a single amino acid, though most amino acids can be represented by multiple different codons. Each nucleotide is represented by a letter — for RNA, either A, C, U, or G.) “This codon usage is unusual for a natural bat SARS-related coronaviruses (for which fewer than 1 in 30 arginine codons are CGG) but is optimal for humans (for which most arginine codons are CGG codons).”

Still, Ebright said that at first he didn’t see the identical amino acid sequences as particularly suspicious. “I had known for more than a year that there was a perfect match to an eight-amino acid sequence present in human ENaC. What I had not known was that the sequence was known to be a functional furin cleavage site and that it was a sequence extensively studied at UNC,” he said. “The crucial point that the ENaC sequence was a known functional site, not just that there happens to be a match to a protein that happens to be in humans. ... That suddenly turned it from what I thought to be largely irrelevant to being a logical and obvious choice to proceed.”

Ralph Baric and the University of North Carolina did not immediately respond to requests for comment.

Name Calling

Other scientists dismiss the idea that the ENaC sequence might have been purposefully inserted into a coronavirus. Scientists who are already convinced that the new coronavirus emerged naturally are unlikely to be persuaded by Sachs and Harrison’s article, which appears in the opinion section of the esteemed journal. Over the past year, many scientists involved in the debate over the origins of the pandemic have settled into an increasingly acrimonious, coarse, and unyielding opposition.

Some proponents of the natural origin theory became particularly dismissive of those open to the possibility of a lab leak after the February release of two pre-print studies mapping the early spread of the virus at the Huanan market in Wuhan. Angela Rasmussen, one of a team of virologists who worked on the project, [described](#) it on Twitter as “dispositive evidence of a zoonotic origin” that will “drive those

with personal interest in the lab leak hypothesis out of their goddam minds.” In another tweet, Rasmussen [referred](#) to proponents of the lab-leak theory as a “pack of ghouls, who through gullibility, stupidity, & conspiracist thinking have decided this is their thing despite zero expertise.”

Although the pre-prints had not been peer-reviewed and may have simply illustrated the spread of the virus rather than its original outbreak, the New York Times ran a front-page story about them that quoted an epidemiologist as saying that the origins debate “has been settled with a very high degree of evidence.” The story, which was announced by a push notification from the paper, also noted a lack of direct evidence for a lab leak.

Meanwhile, Kristian Andersen, another co-author of the pre-prints and a virologist at the well-regarded Scripps Research Institute, used the “[poop](#)” emoji to criticize a deeply researched article by Katherine Eban about EcoHealth Alliance. On Twitter, Andersen tarred Eban, New York Times columnist Zeynep Tufekci, and others reporting on biosafety issues that could have led to the release of SARS-CoV-2 as “deep in conspiracy theories” and on the other side of “a clear split” from journalists who dismiss the possibility of a lab origin, whom Andersen referred to as “science-based.”

Even some scientists who have been vocal about the possibility that the pandemic may have been sparked by research have expressed skepticism about the theory suggested by Harrison and Sachs. “The pandemic virus might have been genetically engineered. However, this could have been done in various ways not limited to the specific theory by Harrison and Sachs. I’m not convinced that their hypothesis is the most plausible one,” said Alina Chan, a scientist who laid out a number of possible routes for how the coronavirus might have emerged through research-related incidents in her recent book “Viral: The Search for the Origin of Covid-19.”

While she is open to the possibility that the furin cleavage site might have been purposefully inserted into the coronavirus, Chan said there was no reason to think that researchers would mine humans for such material. “These scientists literally had access to hundreds of SARS-like viruses and sequences,” said Chan, referring to the vast collection of coronaviruses from bats and other animals that researchers amassed at the Wuhan Institute of Virology. “There’s no need for them to go hunting inside the human protein catalogue to look for cleavage sites to put into viruses.”

Jack Nunberg, a virologist at the University of Montana, was also not immediately persuaded by the theory of engineering suggested by Sachs and Harrison. “It’s possible,” Nunberg said of the idea that the ENaC segment was inserted into a bat coronavirus as part of research designed to gauge the pandemic potential of a virus. “But I don’t find their evidence on ENaC compelling because furin cleavage sites have a lot of common amino acids, and therefore it may just have happened by chance.”

Others say that the article adds noteworthy information to the public conversation about the origins of the pandemic. “The defenders of the natural origin indicate that the virus on which this type of experiment could have been done — the backbone — has never been published and that specialists in the furin cleavage sites would have chosen a more commonly used furin cleavage site like RARR rather than PRRAR. The Proceedings of the National Academy of Sciences article contradicts this argument and indicates that specialists knew that the RRAR’SVAS site was efficiently cleaved by furin,” Etienne Decroly, director of virology research at the Aix-Marseille Université in France, wrote in an email to The Intercept.

Decroly added, “It is impossible to decide on the basis of the information currently available and it is

urgent that the WHO Special Advisory Group for the Origins of Novel Pathogens investigate this question.”

On the suggestion of an investigation, Nunberg is in agreement. “You can’t argue with that,” he told The Intercept. “Who’s going to argue for burying one’s head in the sand?”

For their part, Sachs and Harrison emphasize that they’re not saying laboratory manipulation was involved in the emergence of the pandemic virus, only “that it could have been.” They also give a nod to other possibilities, including that an airborne virus might have infected a laboratory worker. Rather than argue that any of these conceivable scenarios happened, they present the clues of the matching amino acid sequences to argue for an independent and transparent scientific investigation of the U.S.-based evidence related to the origins of the virus.

Among the institutions that Sachs and Harrison list as possibly having “knowledge of the detailed activities that were underway in Wuhan and in the United States” are the National Institutes of Health; the Defense Threat Reduction Agency, which has provided grant funding to EcoHealth Alliance; the Department of Homeland Security; DARPA; the U.S. Agency for International Development, which funded the \$200 million PREDICT program that catalogued potential pandemic viruses; and the University of California, Davis, which participated in that program.

The authors suggest that EcoHealth Alliance and UNC may have particularly important untapped resources. “The exact details of the fieldwork and laboratory work of the EHA-WIV-UNC partnership, and the engagement of other institutions in the US and China, has not been disclosed for independent analysis,” they write. “The precise nature of the experiments that were conducted, including the full array of viruses collected from the field and the subsequent sequencing and manipulation of those viruses, remains unknown.”

A Reversal

The publication in the prestigious Proceedings of the National Academy of Sciences marks a reversal of sorts for Sachs, the chair of the Lancet Covid-19 Commission who, in November 2020, appointed Daszak, the EcoHealth Alliance president, to lead a task force to investigate the origins of the pandemic. Earlier that year, Daszak had signed on to a public statement published in The Lancet on behalf of scientists who said they “condemn conspiracy theories suggesting that COVID-19 does not have a natural origin.”

Yet that early certainty about the pandemic’s origins — and the sense of shared civic responsibility among members of the Lancet task force — soon disintegrated. In February 2021, emails revealed that Daszak coordinated the public statement in The Lancet tamping down suspicions of a lab leak. And by June 2021, Sachs was expressing his openness to the possibility of a lab origin, writing that NIH-funded research at the Wuhan Institute of Virology “deserves scrutiny under the hypothesis of a laboratory-related release of the virus.” Three months later, he disbanded the task force that had been organized to “carefully scrutinize the origin of the SARS-CoV-2 virus” in the hopes of preventing future disease outbreaks, explaining that he had concerns that several members of the commission had conflicts of interest because of their ties to EcoHealth Alliance.

After leading the mainstream scientific inquiry into the origins of the pandemic, Sachs is now skewering

it. “A steady trickle of disquieting information has cast a darkening cloud over the agency,” he and Harrison write of the NIH, going on to accuse the entire federal government of not doing enough to explore the possible role of its grantees in the emergence of SARS-CoV-2 and investigate “overlooked details” such as the matching amino acid sequences.

Noting that the NIH has insisted that “the pandemic virus could not have resulted from the work sponsored by” the agency, Sachs and Harrison write that “blanket denials from the NIH are no longer good enough.”

By Sharon Lerner

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