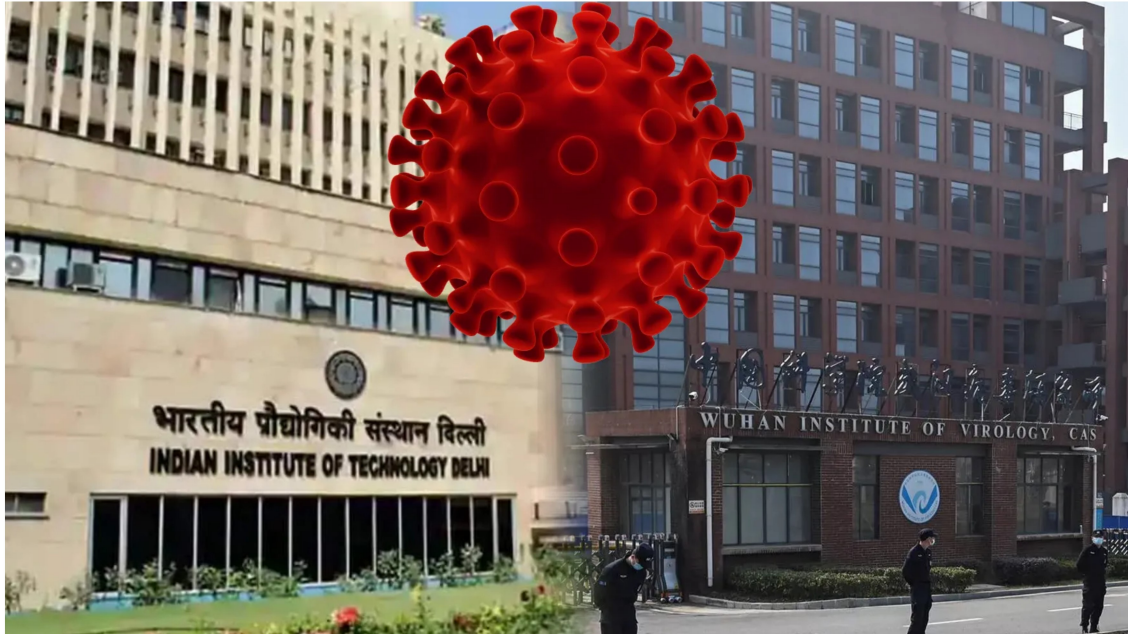


Covid-19 lab leak theory: Indian scientists had flagged 'unnatural insertions' in its genome, were forced to withdraw study

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After vehemently rejecting the possibility of the SARS-CoV-2 virus being leaked from a lab in China for more than a year, suddenly the American left-liberal has started to consider the possibility. When former president Donald Trump had suggested the possibility, it was dismissed as his wild imagination, but now that president Biden has **ordered** a probe into the possibility, the media is forced to wake up and question the national origin theory of the virus.

The lab-leak theory got another boost after thousands of **mails** of Dr Anthony Fauci were obtained under Freedom of Information Act revealed that Wuhan Institute of Virology was researching on increasing the infectious nature of the Coronavirus obtained from bats. The mails, and other studies that have **surfaced** recently, suggest that several people, including researchers, people in US administration and intelligence, wanted to probe the role of the Chinese lab, but they were overruled



by Dr. Fauci and other, who had vested interests in the issue as they themselves were instrumental in US govt funding the study on the virus in the Wuhan lab.

One of such studies that was brought to the notice of Fauci was a research paper by some scientists from India. In January last year, researchers from Kusuma School of Biological Sciences in IIT Delhi and Acharya Narendra Dev College under Delhi University had published a paper, where they had found that the spike glycoprotein (S) of SARS-CoV-2 had four insertions which are not found in any other Coronavirus, and the insertions are similar to those found in HIV virus. The study had raised that possibility that SARS-CoV-2 may have been bio-engineered using the existing Coronavirus and HIV virus.

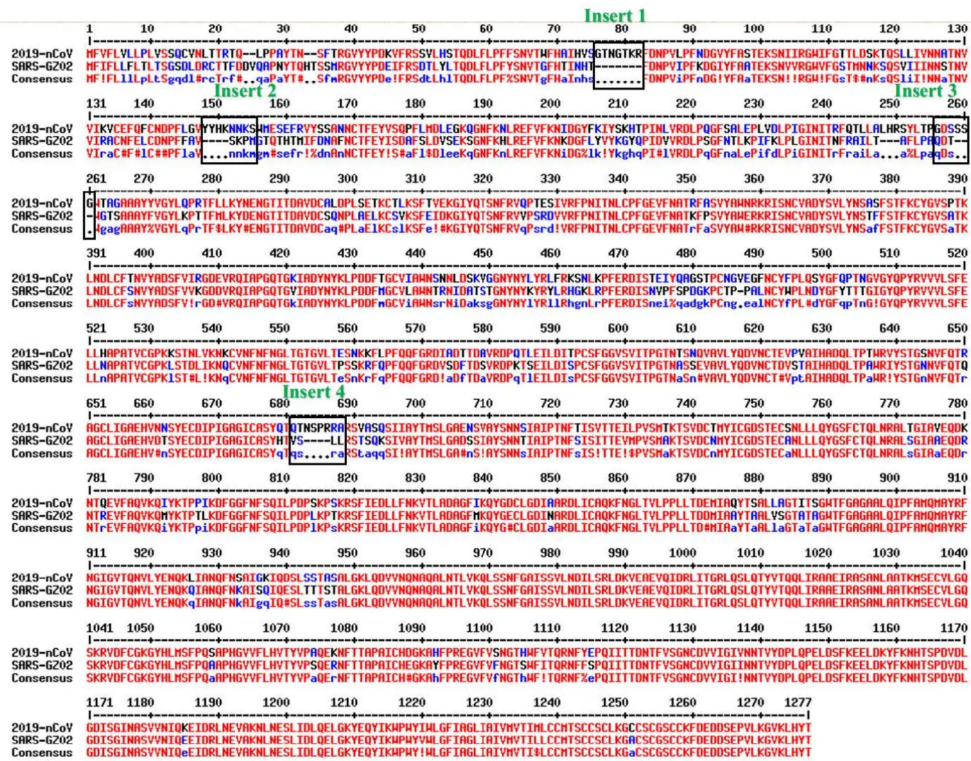
The research [paper](#), Prashant Pradhan, Ashutosh Kumar Pandey, Akhilesh Mishra, Parul Gupta, Praveen Kumar Tripathi, Manoj Balakrishnan Menon, James Gomes, Perumal Vivekanandan and Bishwajit Kundu, had studied the all the available coronavirus sequences which are available at NCBI viral genome [database](#).

The spike (S) glycoproteins enable the Coronavirus to enter the cells of human bodies. Studies have [shown](#) that the glycoprotein has a specific shape that helps them to attach to host cells, and this ability is unique to the SARS-CoV-2, not found in other types of Coronaviruses like SARS-CoV. More specifically, the spike glycoprotein (S) of Coronavirus is cleaved into two subunits, S1 and S2. The S1 helps in binding with the receptor on the target cell, and the S2 subunit facilitates fusion with the cell membrane.

As this splitting of the glycoprotein in SARS-CoV-2 is unique to it, the Indian researchers wanted to study how this evolution happened. To do this study, they compared the spike glycoprotein sequences of the SARS-CoV-2 with SARS-CoV, and analysed the difference in them. On careful examination of the sequence alignment, they found that the SARS-CoV-2 spike glycoprotein contained 4 insertions, or 4 segments that are not found in the earlier less infectious forms of Coronavirus.

The four insertions found in the study are, GTNGTKR, HKNNKS, GDSSSG and QTNSPRRA.





4 insertions at SARS-CoV-2 spike glycoprotein

After finding this, they then studied all available full-length sequences of the virus found in human bodies, and they found that the insertions were present in all of them. But most importantly, they found that these segments were not there in the spike glycoprotein sequence of the same virus found in bats.

When they further analysed these 4 segments to know its possible origin, they found that all four of them match with segments in Human immunodeficiency Virus-1 (HIV-1) proteins. The first 3 segments match with segments of amino acid residues in HIV-1 gp120, while the fourth segment matches with HIV-1 Gag. Among the first two are 100% matches, while the rest two have some gaps. These proteins are critical for the viruses to identify and latch on to their host cells and for assembly of new viruses.

According to the researchers, such matches of proteins in both SARS-CoV-2 and HIV-1 viruses can't be random. They also say that as the segments were not in the same virus found in bats or all other forms of Coronavirus, it is very startling, as it is quite unlikely for a virus to have acquired such unique changes naturally in a short duration of time. It may be noted that it is claimed that the virus jumped to humans from bats, either directly or through an intermediary animal.

Although the research by the Indian scientists had not claimed that the virus was engineered in a lab, it had concluded that it underwent an “unconventional evolution”. Due to this, the research paper had suggested further investigation on the origin of the virus.

While the preprint of the research paper was published January 31, 2020 on bioRxiv, an open-source portal hosting resources on biological research, it was withdrawn by the researchers on February 2, 2020. The [note](#) of withdrawal says they had intended to revise it in response to comments received from the research community on their technical approach and their interpretation of the results.

While the lab leak theory was strong during the early day of the pandemic, it was not taken seriously by a large section of the scientific community and US administration. Despite President Trump raising the issue time to time, the theory was already by February 19, 2020, when The Lancet [published](#) a statement completely rejecting the possibility that the virus may have leaked from the Wuhan Institute of Virology. Published by such an influential medical journal, the statement signed by 27 scientists had effectively killed any meaningful study into the origin of the virus, as they had shut down one angle completely.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 11:26:13 +0000
To: Collins, Francis (NIH/OD) [E]; Tabak, Lawrence (NIH/OD) [E]; Wolinetz, Carrie (NIH/OD) [E]
Subject: RE: More on evolution of coronavirus

The Indian paper is really outlandish. Agree about [Jon Cohen](#)'s nice summary.

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Sunday, February 2, 2020 5:58 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E] (b) (6); Wolinetz, Carrie (NIH/OD) [E] (b) (6); (b) (6)>
Subject: More on evolution of coronavirus

In case you haven't seen, attached is the Indian paper claiming HIV sequences have been inserted into 2019-nCoV, which has been roundly debunked.

I found Jon Cohen's piece in Science to be a pretty useful summary:

<https://www.sciencemag.org/news/2020/01/mining-coronavirus-genomes-clues-outbreak-s-origins>

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Now the Fauci emails show that when he was asked about this research paper by the Indian scientists, he had dismissed it saying it is “really outlandish”. Several other emails have also shown that Dr Fauci was warned that COVID-19 may have been ‘engineered’, but he had dismissed all of them.

Indian researcher still backs their study, says forced by vested interests to withdraw



OpIndia talked to Ashutosh Kumar Pandey, one of the researchers of the study. Earlier he had commented on Twitter that they stand by their conclusion that the SARS-CoV-2 is not natural. “We said this in Jan 2020, we are saying it again”, he had tweeted.

He reiterated the same while talking to OpIndia, and said that the paper was outlandish for those who wanted to prove the ‘natural origin’ theory for the virus. He said that their study had correctly identified sections of the genome that are giving this virus its speciality. When asked why they had withdrawn the paper, he said that was withdrawn due to the pressure from the people with vested interests.

Pandey also said that this paper was just a section of the different studies that they had conducted and they wanted to include the entire findings in the updated version. But the revised manuscripts were hard-blocked by the publishers. He said that in the revised manuscript, they have provided information on why the virus infection remains asymptomatic and why it infects human beings so easily. But it never was allowed to come out, he said.

Commenting on how a scientific paper is being blocked to favour a particular agenda, he said, “Science is the new medieval church, those who are popes of it censor at their will”.

Virus gene segments cut-paste is not unusual

While the Indian researchers didn’t claim that SARS-CoV-2 virus was created by using segments from HIV virus, and only wanted further study on it, the fact is that such studies are regularly done. In fact, the Wuhan Institute of Virology has done several such experiments in the past on Coronavirus itself.

Between 2007 and 2017, the lab had **created** 8 new chimeric coronaviruses with various receptor binding motifs in spike protein. Such research was still going on in 2019, which was also funded by the US govt. For example, this 2008 **paper** talks about Manipulation of the coronavirus genome using targeted RNA recombination.

A 2019 **paper** by scientists from Wuhan Institute of Virology and University of Minnesota in the USA had said this while describing the objectives of their study on Coronavirus: “In vitro and in vivo characterization of SARS-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify the regions and viruses of public health concern. We will use S protein sequence data, infectious clone technology, in vitro and in vivo infection experiments and analysis of receptor binding”.

It may be noted that “Infectious clone technology” means creating live synthetic viral clones. In vitro means study on micro-organisms done in test tubes, and in vivo means the same study done in lab animals.



