

# It's Official Corona Virus is Man Made Bio Weapon

Corona virus a result of China's bio-warfare experiment, says Israeli biological warfare analyst.

<https://www.organiser.org/Encyc/2020/1/29/Corona-virus-a-result-of-China-s-bio-warfare-experiment-says-Israeli-biological-warfare-analyst.html>

In a startling revelation that could have huge consequences on world of biowarfare, an Israeli biological warfare analyst has said that the deadly animal-borne coronavirus spreading globally may have originated in a laboratory in the city of Wuhan linked to China's covert biological weapons program, reports Washington Times.

Dany Shoham, a former Israeli military intelligence officer who has studied Chinese biological warfare, has said that China's most advanced virus research laboratory, known as the Wuhan Institute of Virology, is linked to Beijing's covert bio-weapons program. Mr. Shoham holds a doctorate in medical microbiology. From 1970 to 1991, he was a senior analyst with Israeli military intelligence for biological and chemical warfare in the Middle East and worldwide. He held the rank of lieutenant colonel.

"Certain laboratories in the institute have probably been engaged, in terms of research and development, in Chinese [biological weapons], at least collaterally, yet not as a principal facility of the Chinese BW alignment," Mr. Shoham told The Washington Times. He also informed that work on biological weapons is conducted as part of dual civilian-military research which is definitely covert.

Though China has denied having any link to biological weapons, a US State Department report last year has suspected covert biological warfare work in China. The report had cited Gao Fu, director of the Chinese Center for Disease Control and Prevention, as telling Chinese state-controlled media that initial signs indicated the virus originated from wild animals sold at a seafood market in Wuhan.

### Dubious past of China's biological warfare

The Wuhan facility was reported to have studied Corona viruses in the past, including the strain that causes Severe Acute Respiratory Syndrome, or SARS, the H5N1 influenza virus, Japanese encephalitis, and dengue. The SARS virus had escaped from high-level containment facilities in Beijing multiple times, reported newsmag.com Jan 25, citing Richard

Ebright, a molecular biologist at Rutgers University in Piscataway, NJ, and the Nature magazine.

The China Global Television Network has reported that 46 of the deaths were in the mainland, with the remaining 10 being in Hong Kong, Macao and Taiwan. Also, there were 49 cured cases and 2,684 suspected ones.

President Xi Jinping has said Jan 25 that his nation was facing a “grave situation” as the death toll from the coronavirus had risen to 56 with 1,985 cases of infection. Wuhan, a transport hub, has been placed on lockdown since Jan 23. Presently, 15 Chinese cities in Hubei province, of which Wuhan is the capital, are in lockdown, impacting more than 57 million people, the CGTV report said.

More:

<https://www.zerohedge.com/geopolitical/coronavirus-contains-hiv-insertions-stoking-fears-over-artificially-created-bioweapon>

Now, a respected epidemiologist who recently caught flack for claiming in a twitter thread that the virus appeared to be much more contagious than initially believed is pointing out irregularities in the virus's genome that suggests it might have been genetically engineered for the purposes of a weapon, and not just any weapon but the deadliest one of all.

In "Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag", Indian researchers are baffled by segments of the virus's RNA that have no relation to other coronaviruses like SARS, and instead appear to be closer to HIV. The virus even responds to treatment by HIV medications.

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The theory is that the virus, which was developed by infectious disease experts may have originated in the Wuhan-based lab of Dr. Peng Zhou, China's preeminent researcher of bat immune systems, specifically in how their immune systems adapt to the presence of viruses like coronavirus and other destructive viruses. Somehow, the virus escaped from the lab, and the Hunan fish market where the virus supposedly originated is merely a ruse.

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Why do the authors think the virus may be man-made? Because when looking at the above insertions which are not present in any of the closest coronavirus families, "it is quite unlikely for a virus to have acquired such unique insertions naturally in a short duration of time." Instead, they can be

found in cell identification and membrane binding proteins located in the HIV genome.

Since the S protein of 2019-nCoV shares closest ancestry with SARS GZ02, the sequence coding for spike proteins of these two viruses were compared using MultiAlin software. We found four new insertions in the protein of 2019-nCoV- “GTNGTKR” (IS1), “HKNNKS” (IS2), “GDSSSG” (IS3) and “QTNSPRRA” (IS4) (Figure 2). To our surprise, these sequence insertions were not only absent in S protein of SARS but were also not observed in any other member of the Coronaviridae family (Supplementary figure). This is startling as it is quite unlikely for a virus to have acquired such unique insertions naturally in a short duration of time.

The insertions were observed to be present in all the genomic sequences of 2019-nCoV virus available from the recent clinical isolates. To know the source of these insertions in 2019-nCoV a local alignment was done with BLASTp using these insertions as query with all virus genome. Unexpectedly, all the insertions got aligned with Human immunodeficiency Virus-1 (HIV-1). Further analysis revealed that aligned sequences of HIV-1 with 2019-nCoV were derived from surface glycoprotein gp120 (amino acid sequence positions: 404-409, 462-467, 136-150) and from Gag protein (366-384 amino acid) (Table 1). Gag protein of HIV is involved in host membrane binding, packaging of the virus and for the formation of virus-like particles. Gp120 plays crucial role in recognizing the host cell by binding to the primary receptor CD4. This binding induces structural rearrangements in GP120, creating a high affinity binding site for a chemokine co-receptor like CXCR4 and/or CCR5.

And some visuals, which lead the paper authors to conclude that "this structural change might have also increased the range of host cells that 2019-nCoV can infect":

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But the 'smoking gun' in this case are pieces of the virus's genetic code that Indian researchers, led by Prashant Pradhan at the Indian Institute of Technology, found may have been 'embedded' from HIV, which belongs to an entirely different family of viruses.

16. UPDATE ON GENOME : a very intriguing new paper investigating the aforementioned mystery middle segment w/ “S” spike protein: likely origin from HIV. “Uncanny similarity of unique inserts in the 2019-nCoV spike

protein to HIV-1 gp120 and Gag” from <https://t.co/QAX3usr7vw>  
[pic.twitter.com/WeVA948xin](https://t.co/WeVA948xin)

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

17. ...WHOA- the authors said the finding was “Unexpectedly” related to genes from HIV virus. Notably there were 4 gene insertions (see figure in above post #16). And so, which HIV gene proteins were found in the new #coronavirus? Gag protein and Gp120- key HIV proteins...  
[pic.twitter.com/epN66WcObj](https://t.co/epN66WcObj)

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

18. Notably, in S, authors say for HIVinsertions: “Gag protein of HIV is involved in host membrane binding, packaging of the virus and for the formation of virus-like particles. Gp120 plays crucial role in recognizing the host cell by binding to the primary receptor CD4”

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

19. Again, these are new express published findings and not peer reviewed yet. Let’s not draw conclusions yet. But evidence suggest that 2 different HIV genes are present in the #coronavirus S gene region (that didn’t map to any other coronavirus, according to other studies).

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

20. Further the authors add that “This indicates that these insertions have been preferably acquired by the 2019-nCoV, providing it with additional survival and infectivity advantage. Delving deeper we found that these insertions were similar to HIV-1.”

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

21. Paper piles on: “these insertions are present at binding site of 2019-nCoV. Due to presence of gp120 motifs in 2019-nCoV spike glycoprotein at its binding domain, we propose that these motif insertions could have provided an enhanced affinity towards host cell receptors.”

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

22. The authors dunked this final conclusion: “This uncanny similarity of novel inserts in the 2019- nCoV spike protein to HIV-1 gp120 and Gag is unlikely to be fortuitous”. Wow, they sure just went straight there! What a bold paper... I don’t know what to say [pic.twitter.com/KWcDdknMO4](https://t.co/KWcDdknMO4)

— Dr. Eric Feigl-Ding (@DrEricDing) January 31, 2020

February 7, 2020

Joy of Satan Forums Contributions