COVID-19 HIV INSERTS
RETRACTED RESEARCH PAPER
Unnatural Inserts in the Genome Sequence

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The purpose of this study is to review an example of the various write-ups already made that insinuate the fact that according to the discoverer of the HIV virus back in 1983, Dr. Luc Montagnier, the COVID-19 has at least 4 HIV coded inserts that do not occur naturally and therefore that the COVID-19 virus was man-made. He specifically stated that, 'HIV RNA fragments are believed to have been found in the SARS-CoV-2 Genome.' One particular article of this most compelling assertion came from Robert Miller who first published his findings on April 16, 2020 and then reviewed by Gilmore Health later on.

The article goes on to emphatically state that Dr. Montagnier, who won the Nobel Peace Prize in Physiology in 2008 for his discovery insists that the COVID-19 virus came out of the Wuhan Bio Lab in China. The actions of the Chinese immediately after the identification and reaction speaks to this claim. China allowed travelers from Wuhan to all parts of the world, Italy, Iran, the USA, Europe, in particular, etc. And then the pattern resulted in the hotspots that eventually become the 'Pandemic' or was it in reality a plandemic? It has been revealed that Fauci's research labs gave $3.7 million twice to the Wuhan Lab for Corona Virus research with his institute providing the Wuhan Lab with samples via secret shipments to and from the Canadian Winnipeg Level 4 Lab.

In comparison, viruses such as the MERS and SARS were actually more deadly than COVID-19, so why would not 'manipulators' make the already more deadly virus leak or just manufacture that one to spread easier? In the article, it addresses this to state that more than 100,000 deaths have been recorded worldwide as of the article due to COVID-19. However, many argue that it has not justified the worldwide lockdown of the entire planet. As it has been reported in many news outlets, the National Italian Institute of Statistics reveals that in Italy in the 1st Quarter of 2020 there were 20,600 deaths due to COVID-19 victims, which was less than in same period when compared to 2019. The ramification and consequences are far more serious.

There is a marked increase in suicides, depression, mental health, disruption in the food chain, and a general erosion of civil liberties that are preventing people from making a living. What is alarming is that the article goes on to state that Dr. Montagnier along with other top world renowned Virologists such as Dr. Jean-Claude Perez acknowledged that Indian Doctors have already tried to publish the results and their analysis that shows that the COVID-19 virus Genome contains 4 code sequence inserts of the HIV virus. They were immediately forced to withdraw their finding even though the paper only sought to investigate and prove or disprove their hypothesis.

Scientific Objectivity?
Afterall, is this not what the ‘Scientific Method’ is all about? Apparently not. Despite the science provided for all to replicated, the arbiters of ‘Science’ deemed it ‘junk science’ and the cohort of Indian Scientists were ostracized for even insinuating such a hypothesis. What is disturbing is that despite other research from other nations such as in Australia that had compared such viruses before already, many detractors who are ‘Scientists’ have instead attacked the personality and ‘mental state’ of Dr. Montagnier for his other theories that came subsequently. However, Dr. Montagnier has stood by his statements and evaluation about the COVID-19 virus. It could have only been bio-engineered in a lab due to this segments of the HIV coded inserts. How is this possible or why? According to Dr. Montagnier, such a code sequence could not occur naturally nor have come from a person infected with the HIV virus.

He determined, medically that this could have only occurred under a laboratory condition. What is also being suppressed like the research paper from India is that although it was a theory, in that ‘it appeared’ to have HIV extracts, that alone was sufficient to have the paper retracted. It would appear then that certain scientific questions cannot be asked, or topics investigated. What does that say about the ‘trust in Science’ to seek the ‘truth’? Is that not the objective of Science? Is not Science to be impartial of politics, religion or biases? Apparently not, unfortunately. And now this vein of questioning will never come to light as it will be suppressed. This is now the new reality in that what is not in line with the ‘Official Scientific Orthodoxy’, is now considered ‘blasphemy’. And those non-conformists are to eventually be ‘burned at the stake’; once again as in medieval times.

What was alarming is the scorn that come from those of ‘Science’ and the proponents of the ‘Official Scientific Narrative’. They labeled the more than a dozen Indian Researcher’s work as ‘pseudo-science’. And this coming from a country of top Mathematicians and Physicians. Obviously, they asked the ‘wrong question’. Unbeknown to most, there is a war on Science in full effect presently concerning the ‘science’ of viruses and the need for their corresponding forced vaccinations upon an uninformed and unsuspecting populace. This is the endgame. And the question is then, who is to say that HIV coded inserts will not also be part of the COVID-19 vaccine? In the meanwhile, the battle of what ‘Science’ will prevail is now like a political and/or religious movement of which denomination or party is to win-out.

And thus, any deviation from what is the desired outcome has to be kept in check. What is the difference now with the COVID-19, in comparison to its manufactured cousins of the MERS and SARS? Although they were far more deadly or lethal, they were not readily contagious as COVID-19 is. And here is the difference. The COVID-19 virus does not kill. It is highly contagious, mucal targeting, and an RNA virus type. What kills are the compromising pre-existing conditions whereby the immune system is weakened. The virus attacks the lungs that are the most vulnerable part of the human body. It is when pneumonia sets in, that then ultimately causes organ failure and then death. The mass media is not reporting, nor those who are preparing to make billions on vaccines that Corona Viruses in their natural state cannot penetrate the human cells.

Indian Research Paper

This is why the HIV inserts are required and other codes in the form of proteins are needed. It is only after a protein 'spike' is introduced that the human cells absorbs a Corona Virus and its respiratory payload. It was Shi Zhengli of the Wuhan Institute, also known as the 'Bat Lady' that was responsible for this added protein to the Corona Virus and has published, no less than 4 papers on the subject. It just so happens that the quick-test kit just conveniently comes from researchers with direct involvement in the Wuhan Institute who have cornered the market on virus testing.

In another example, as far back as in 2015, an Italian State TV report from TGR Leonardo about the Corona Virus clearly stated that it was not prudent to cultivate artificially any COVID strands. Concerning the latest release of the COVID-19, the data shows that the Corona Virus is less lethal than the MERS and SARS of the past years. What the Indian Lab did was to analyze through reverse engineering the COVID-19 DNA or its Genome sequence. As noted, the Indian Lab's e-published findings were roundly condemned and dismissed despite the information being quite clear and well referenced. The following are the excerpts from the actual Indian Scientists' Abstract.

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Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag by Prashant Pradhan, Ashutosh Kumar Pandey, Akhilesh Mishra, Parul Gupta, Praveen Kumar Tripathi, Manoj Balakrishnan Menon, James Gomes, Perumal Vivekanandan and Bishwajit Kundu Kusuma School of biological sciences, Indian institute of technology, New Delhi-110016, India. Acharya Narendra Dev College, University of Delhi, New Delhi-110019, India email: bkundu@bioschool.iitd.ac.in

Abstract:

We are currently witnessing a major epidemic caused by the 2019 novel coronavirus (2019- nCoV). The evolution of 2019-nCoV remains elusive. We found 4 insertions in the spike glycoprotein (S) which are unique to the 2019-nCoV and are not present in other coronaviruses. Importantly, amino acid residues in all the 4 inserts have identity or similarity to those in the HIV- 1 gp120 or HIV-1 Gag. Interestingly, despite the inserts being discontinuous on the primary amino acid sequence, 3D-modelling of the 2019-nCoV suggests that they converge to constitute the receptor binding site. The finding of 4 unique inserts in the 2019-nCoV, all of which have identity /similarity to amino acid residues in key structural proteins of HIV-1 is unlikely to be fortuitous in nature.
This work provides yet unknown insights on 2019-nCoV and sheds light on the evolution and pathogenicity of this virus with important implications for diagnosis of this virus.

Introduction

Coronaviruses (CoV) are single-stranded positive-sense RNA viruses that infect animals and humans. These are classified into 4 genera based on their host specificity: Alphacoronavirus, Betacoronavirus, Deltacoronavirus and Gammacoronavirus (Snijder et al., 2006). There are seven known types of CoVs that includes 229E and NL63 (Genus Alphacoronavirus), OC43, HKU1, MERS and SARS (Genus Betacoronavirus). While 229E, NL63, OC43, and HKU1 commonly infect humans, the SARS and MERS outbreak in 2002 and 2012 respectively occurred when the virus crossed-over from animals to humans causing significant mortality (J. Chan et al., n.d.; J. F. W. Chan et al., 2015).

In December 2019, another outbreak of coronavirus was reported from Wuhan, China that also transmitted from animals to humans. This new virus has been temporarily termed as 2019-novel Coronavirus (2019-nCoV) by the World Health Organization (WHO) (J. F.- W. Chan et al., 2020; Zhu et al., 2020). While there are several hypotheses about the origin of 2019-nCoV, the source of this ongoing outbreak remains elusive. The transmission patterns of 2019-nCoV is similar to patterns of transmission documented in the previous outbreaks including by bodily or aerosol contact with persons infected with the virus.

Cases of mild to severe illness, and death from the infection have been reported from Wuhan. This outbreak has spread rapidly to distant nations including France, Australia and USA, among others. The number of cases within and outside China are increasing steeply.

Our current understanding is limited to the virus genome sequences and modest epidemiological and clinical data. Comprehensive analysis of the available 2019- nCoV sequences may provide important clues that may help advance our current understanding to manage the ongoing outbreak.

The spike glycoprotein (S) of cornonavirus is cleaved into two subunits (S1 and S2). The S1 subunit helps in receptor binding and the S2 subunit facilitates membrane fusion (Bosch et al., 2003; Li, 2016). The spike glycoproteins of coronoviruses are important determinants of tissue tropism and host range. In addition, the spike glycoproteins are critical targets for vaccine development (Du et al., 2013). For this reason, the spike proteins represent the most extensively studied [aspects of] among coronaviruses. We therefore sought to investigate the spike glycoprotein of the 2019-nCoV to understand its evolution, novel features, sequence and structural features using computational tools.

Methodology

Retrieval and alignment of nucleic acid and protein sequences.

We retrieved all the available coronavirus sequences (n=55) from NCBI viral genome database (https://www.ncbi.nlm.nih.gov/) and we used the GISAID (Elbe & Buckland-Merrett, 2017) (https://www.gisaid.org/) to retrieve all available full-length sequences (n=28) of 2019- nCoV as on 27 Jan 2020.

Multiple sequence alignment of all coronavirus genomes was performed by using MUSCLE software (Edgar, 2004) based on neighbour joining method.

Out of 55 coronavirus genomes, 32 representative genomes of all category were used for phylogenetic tree development using MEGAX software (Kumar et al., 2018). The closest relative was found to be SARS CoV. The glycoprotein region of SARS CoV and 2019-nCoV were aligned and visualized using Multalin software (Corpet, 1988). The identified amino acid and nucleotide sequence were aligned with whole viral genome database using BLASTp and BLASTn. The conservation of the nucleotide and amino acid motifs in 28 clinical variants of 2019-nCoV genome were presented by performing multiple sequence alignment using MEGAX software. The three dimensional structure of 2019-nCoV glycoprotein was generated by using SWISS-MODEL online server (Biasini et al., 2014) and the structure was marked and visualized by using PyMol (DeLano, 2002).

This is why the coming COVID-19 vaccine is dangerous as many qualified and talented top-notch Doctors have been warning the public about. For example, top Pathologist Dr. Roger Hodkinson told Canadian government officials in Alberta that the Corona Virus pandemic is, ‘the greatest hoax ever perpetrated on an unsuspecting public.’ Hodkinson, who is the CEO of a biotech company that makes COVID tests said, ‘there is utterly unfounded public hysteria driven by the Media and Politicians.’ ‘We are seeing politics playing medicine, and that is a very dangerous game.’ He has further stated that ‘positive test results do not mean a clinical infection. All testing should stop because the false numbers they produce are driving public hysteria.’

Hodkinson says the risk of death for people under the age of 65 is, ‘1 in 300,000 and it is outrageous to shut down society for what is merely just another bad flu.’ Sadly, the mainstream media outlets and governments that are controlled are censoring such voices. Why? It is because of such information that HIV inserts are in the COVID-19 virus that cannot have happened naturally must not be confirmed. Any scientific proof that the virus is bio-engineered, if confirmed would unmask the supposed ‘conspiracy’ to force vaccinate everyone on the planet. This is what the Bill Gates types and other world ruling Eugenicists desire. It is about control, not about saving lives.

Then, the vaccine trials for the COVID-19 virus have totally skipped animal trials and gone directly into human trials with dire results and adverse reactions. Other studies suggest that according to some whistleblowers, the vaccinations will lead to sterilization in women. Evidently, even according to Bill Gates, about 10,000 people in a million will statistically die of the vaccine’s adverse side-effects themselves and that is acceptable to them. It will be the most vulnerable that will be vaccinated first. They are the weak, the elderly and/or those with compromising immune systems that will not resist such a coming COVID-19 forced vaccine. And this will be a series of ‘gabs’ as it is called, where at least 2 doses are required within a 21 day period. Then, Dr. Fauci now insists that despite the vaccines, people will still need to social distance and wear masks. What?

He also now has come out to say that once the vaccine is given to ‘everyone’, now the ‘Herd Immunity’ can work. Really? He has been the opponent of natural Herd Immunity or any other possible alternative treatments but his own vaccines. Yet, this is despite the proof that in areas or countries that did not lockdown like Sweden and Belarus, a significant amount of a Herd Immunity has been achieved. Nonetheless, it is well documented that Doctors working on the COVID-19 vaccines have been astonished in how similar the COVID-19 is to HIV. The question everyone should now be asking is if the HIV code inserts are being placed in the vaccine. Why? It is because some people’s bodies naturally rejects COVID, which is when it recognizes the virus as foreign and a person gets a light flu/short fever, etc. So, this makes a person COVID-Negative, but in some bodies, the Immune System accepts the COVID or Positive, etc.

The HIV code inserts essentially ensure the COVID proteins penetrate the membranes of a person’s cells. The question is that the virus may lay dormant, depending on where it manifests itself. The concern is that those Asymptomatic may be COVID Positive and fear that the COVID virus is waiting for the hosts immunity to become weakened. But to reiterate, since Dr. Montagnier came out with this bombshell, along with other prominent Doctors, as with the Indian study, they have been subject to discrediting their work and reputation. Their COIVID-19 HIV connection theories are now labeled, ‘ridiculous’. However, the Press does not take equal responsibility in vetting out the current ‘Official Scientific Narrative’ that the COVID-19 is a ‘pandemic’. The 4th Estate has the responsibility to certify the veracity of the prevailing scientific claims before publishing and broadcasting them as well. There is clearly a double standard at play presently.

Sadly, most journalists in the modern era, especially in the West have taken on an advocacy role that is not impartial but biased. And then most, if not all major news outlets are compromised by CIA Assets as disclosed in Operation Mockingbird. This was and is an operation that has planted CIA Operatives in key positions of editorial positions to dictate information or misinformation, etc. So now a Nobel Prize winner is a ‘Conspiracy Theorists’ for even entertaining a scientific thought or question and the Media defending the ‘Official Scientific Narrative’ are the relevant ones. Such are now the arbitrators of what is or should be discussed in ‘Science’ and be considered ‘Science’. This is what Hitler and Stalin counted on, a blind allegiance by faith in the ‘Official Scientific Narrative’. And in the words of George Santayana, it will come true once again, that ‘those that forget their history are condemned to repeat it’.

Main Sources

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