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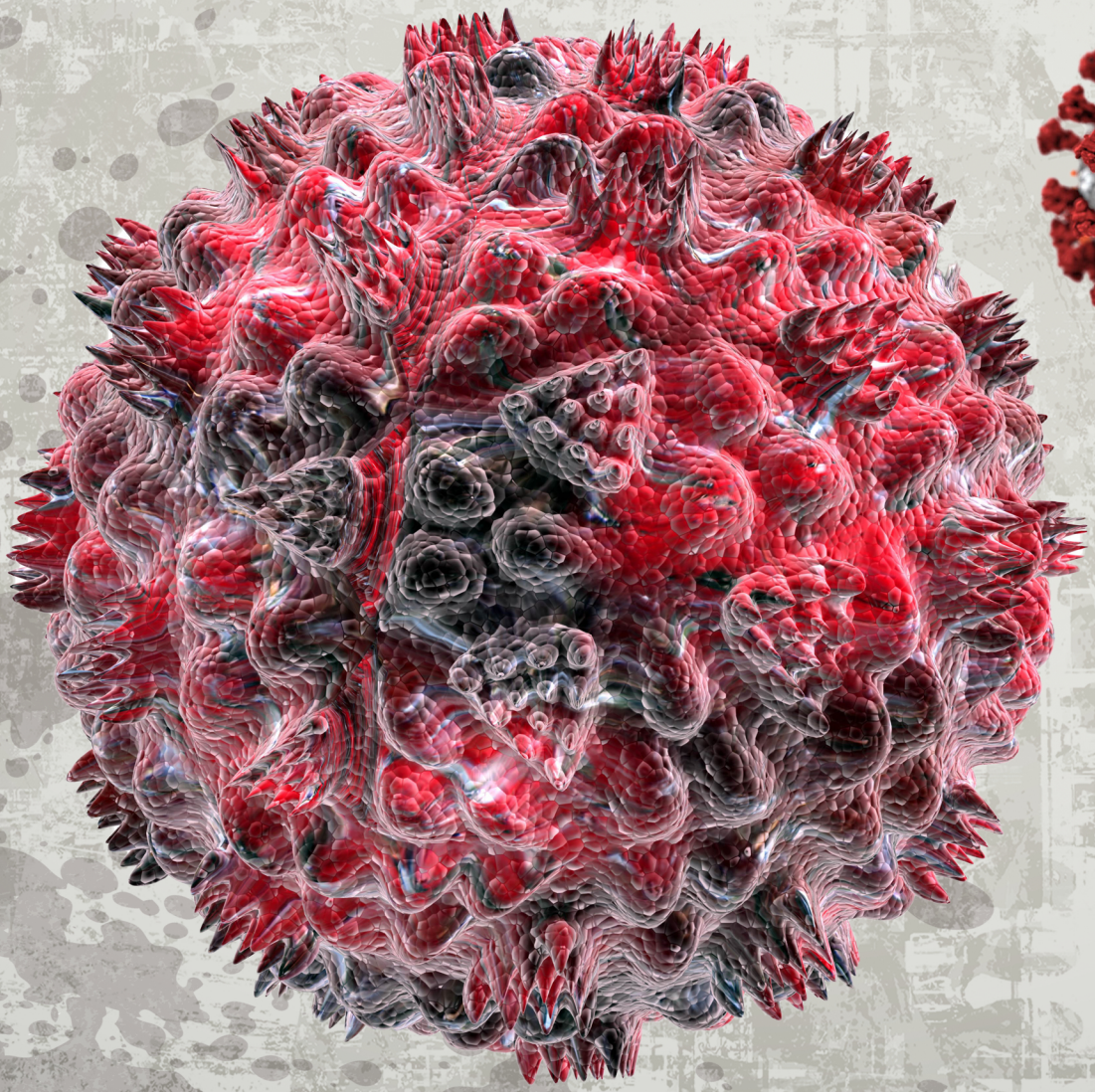
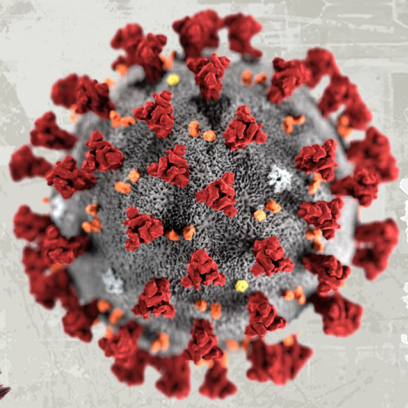
Entangled MAGAZINE

VOLUME-43 DECEMBER 2020

COVID-19 RETROVIRUS



HIV-1



COVID-19

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Introduction

The following explanation is provided in answer to the many questions we have received regarding the genomic fragments of retroviral HIV-1 found within the RNA genome of Covid-19. We have found the clearest depiction is an imaginary of a 'line drawn in the sand'.

On the left is the virus, including the retrovirus HIV-1 fragments. While to the right is the RNA-based vaccine developed from the RNA virus and includes the retroviral HIV-1 fragments.

Persons contracting the Covid-19 virus, do undergo an alteration to the DNA of the infected cell(s), the so-called "host DNA". This is due to the inclusion of retroviral HIV-1 fragments. They do not however contract HIV itself, as the complete genomic sequence of this retrovirus is not present.

Retroviruses are a type of virus that use RNA as their genetic material and a special enzyme called reverse transcriptase to translate the virus's genetic information into DNA. That DNA can then integrate into the host (your) cell's DNA. At this point, the retrovirus can replicate itself using your cells resources. It "goes viral". The HIV-1 fragments act in the normal biological manner as the entire HIV virus itself. Further details are provided later.

To the right of our imaginary line is the RNA-based vaccine. It does contain genomic fragments of the retrovirus HIV-1, and a modified RNA genomic sequence of Covid-19. Likewise, persons inoculated will neither contract HIV, nor Covid-19.

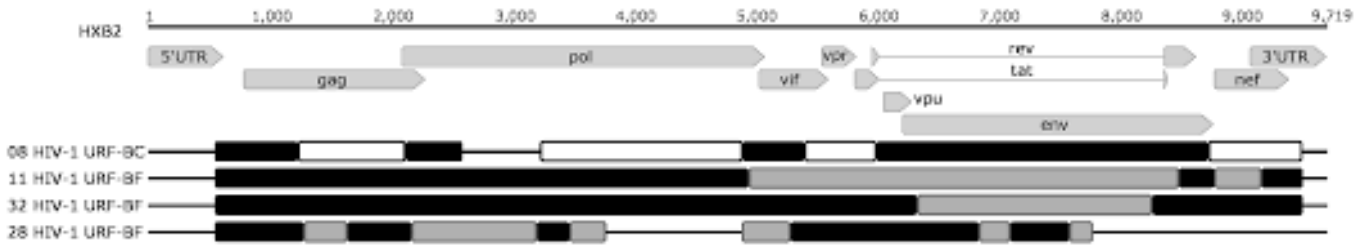
However, and this is the major difference between the virus and the vaccine, the latter does permanently alter a person's entire DNA.

The difference lays within the additional components embedded within the vaccine itself. These are quantum dots, luciferase, hydrogel and nanomaterials such as gold and diamond (functioning as biosensors inside the human body). Working in tadem with the Covid-19 virus, and the fragments of the retrovirus HIV-1, all of the "host DNA" is permanently changed. This exceeds the natural biological changes brought about by a "common" retrovirus.

As a RNA virus, Covid-19 functions as a vector to transmit the HIV-1 fragments into a cell's cytosol. At this point the roles are reversed with the retroviral HIV-1 fragments now acting as a vector for the delivery of the Covid-19 virus into the cell's nucleus.

These fragments of HIV-1 improve the "gain of function" of Covid-19 as a virus, increasing its mobidity, without an increase in mortality. Likewise, this process is detailed later.

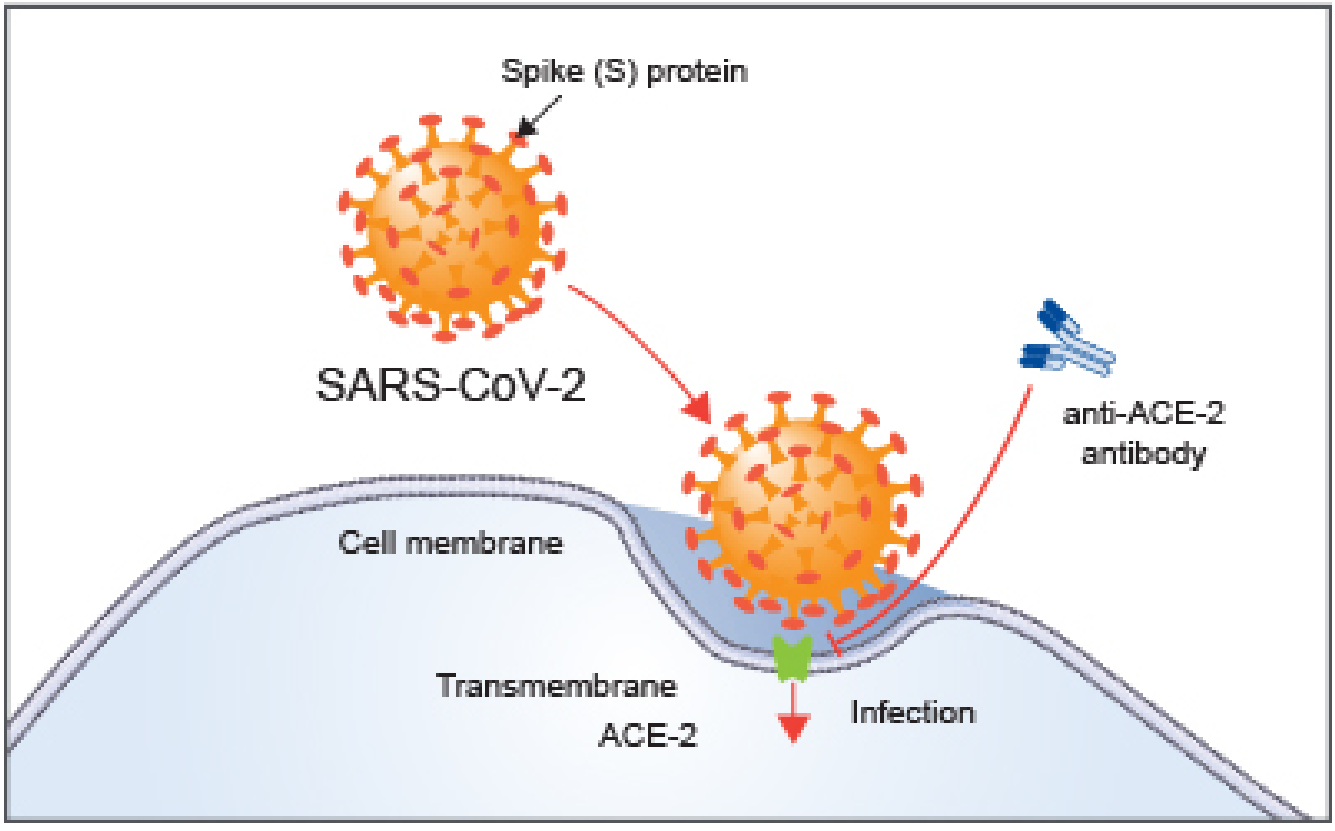
The grand delusion of 2019-nCoV/COVID-19 and its attendant mainstream narrative proclaiming the virus being of natural origin, has obfuscated verified scientific evidence to the contrary. Specifically, not 4, or 6, but 18 genomic fragments (inserts) of HIV-1 (Human Immunodeficiency Virus) have deliberately and artificially been placed within the overall genome of Covid-19, a single-stranded RNA (Ribonucleic acid) virus. A retrovirus.



Characterization of HIV-1 Near Full-Length Proviral Genome

As a retrovirus, these HIV-1 fragments while not forming the entire genome of the HIV virus itself, is directly relevant to every human. As the scientists and their associates prove with their published papers herein, these fragments serve the designed biological objective known as "gain of function" as presented in the following paper.

As will be explained later, the function of the HIV-1 fragments is to promote viral entry into a host cell. Not only entry of HIV-1, but the 2019-nCoV/COVID-19 virus itself. A retrovirus.



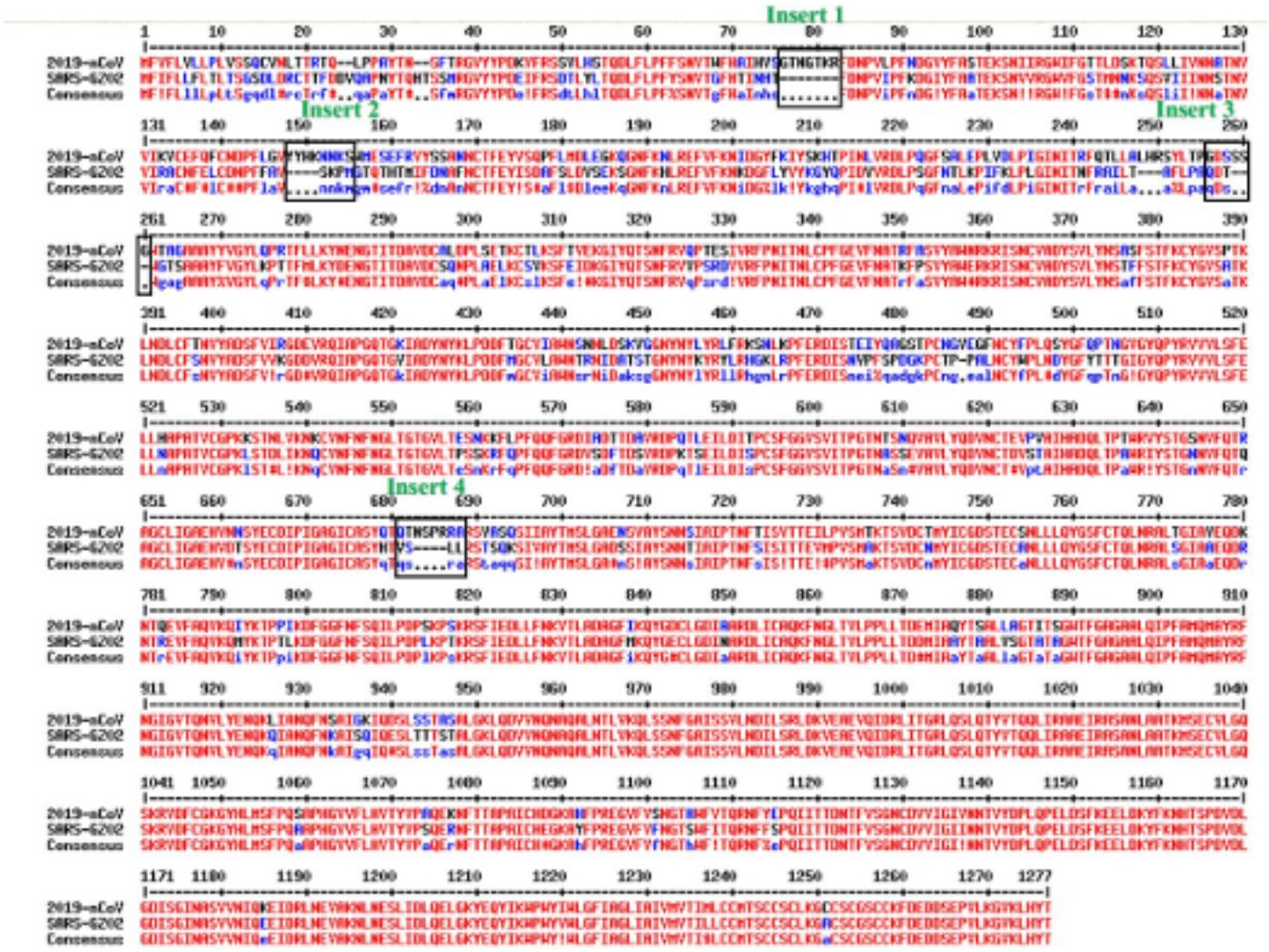
Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag

Prashant Pradhan, Ashutosh Kumar Pandey, Akhilesh Mishra, Parul Gupta, Praveen Kumar Tripathi, Manoj Balakrishnan Menon, James Gomes,Perumal Vivekanandan, Bishwajit Kundu

doi:https://doi.org/10.1101/2020.01.30.927871

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.



Multiple sequence alignment between spike proteins of 2019-nCoV and SARS.

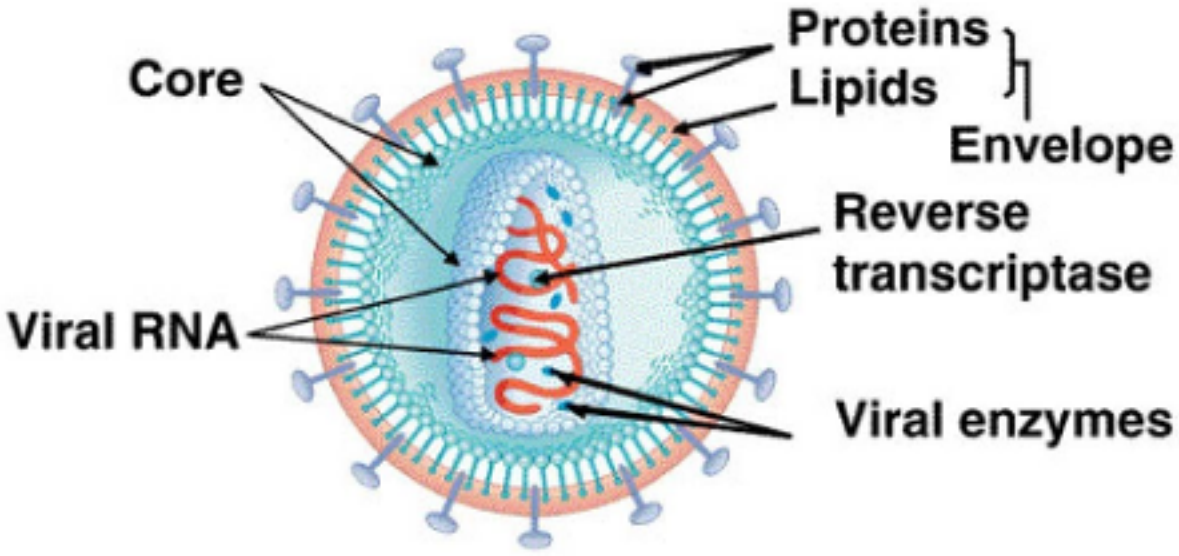
The sequences of spike proteins of 201-nCoV (Wuhan-HU-1), AccessionNC_045512) and of SARS CoV (GZ02, Accession AY390556) were aligned using MultiAlin software. The sites of difference are highlighted in boxes.

Methodology

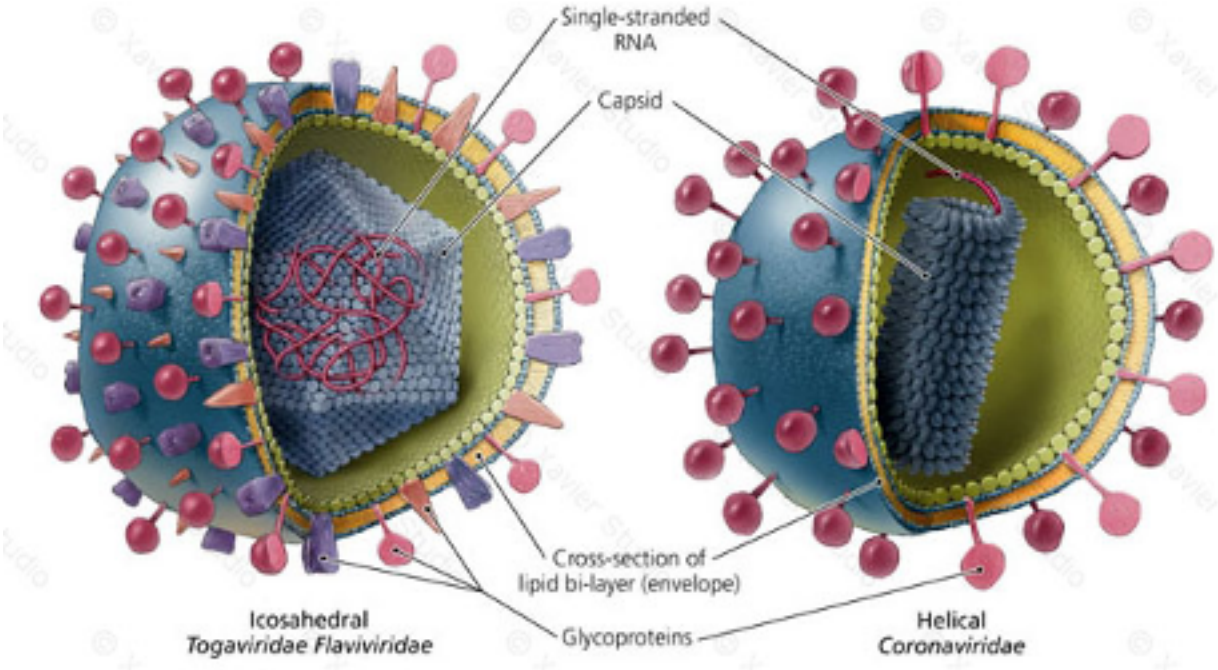
Retrieval and alignment of nucleic acid and protein sequences

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 genome 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).

Structure of a retrovirus

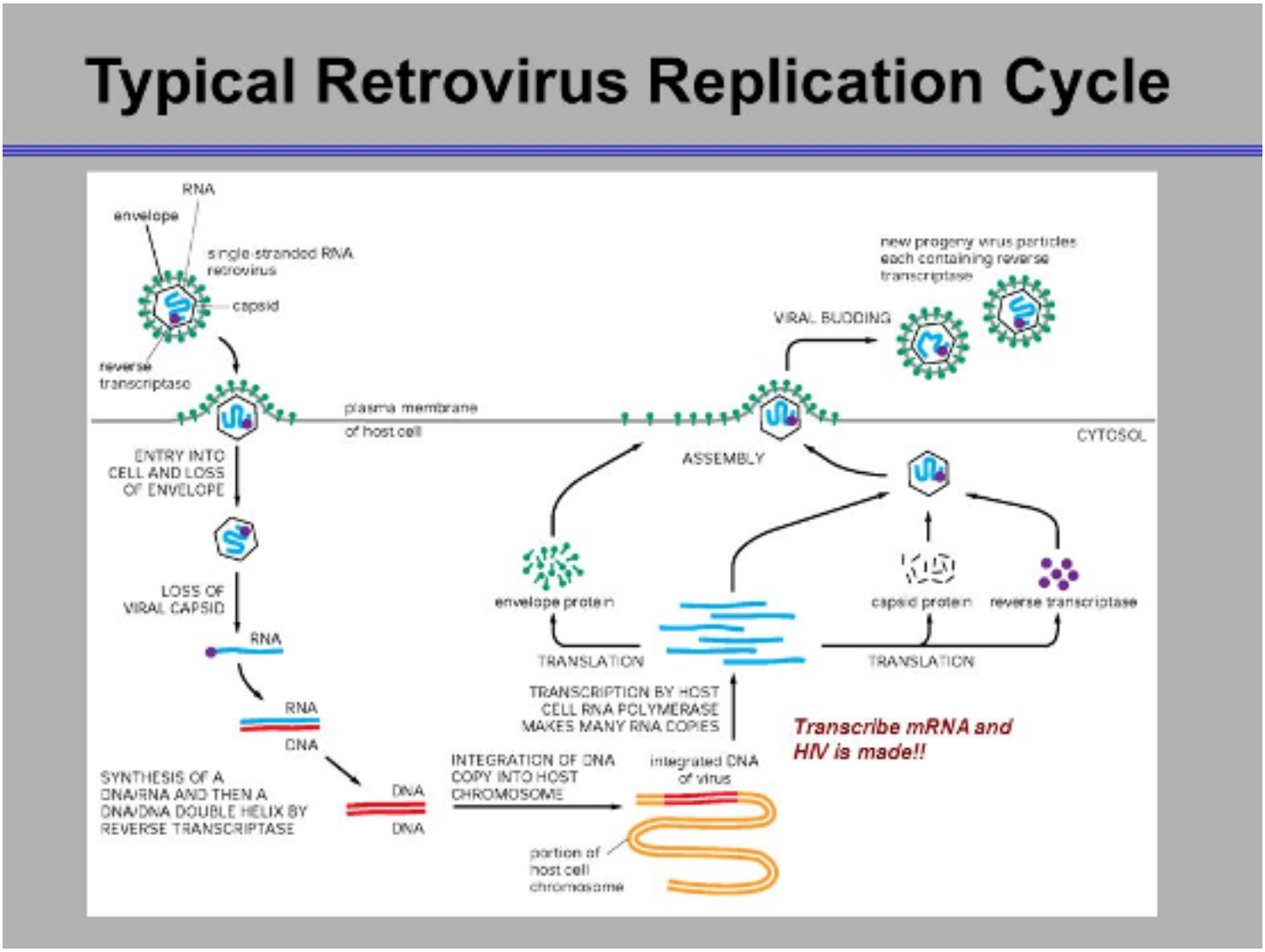


courtesy www.andrew.cmu.edu



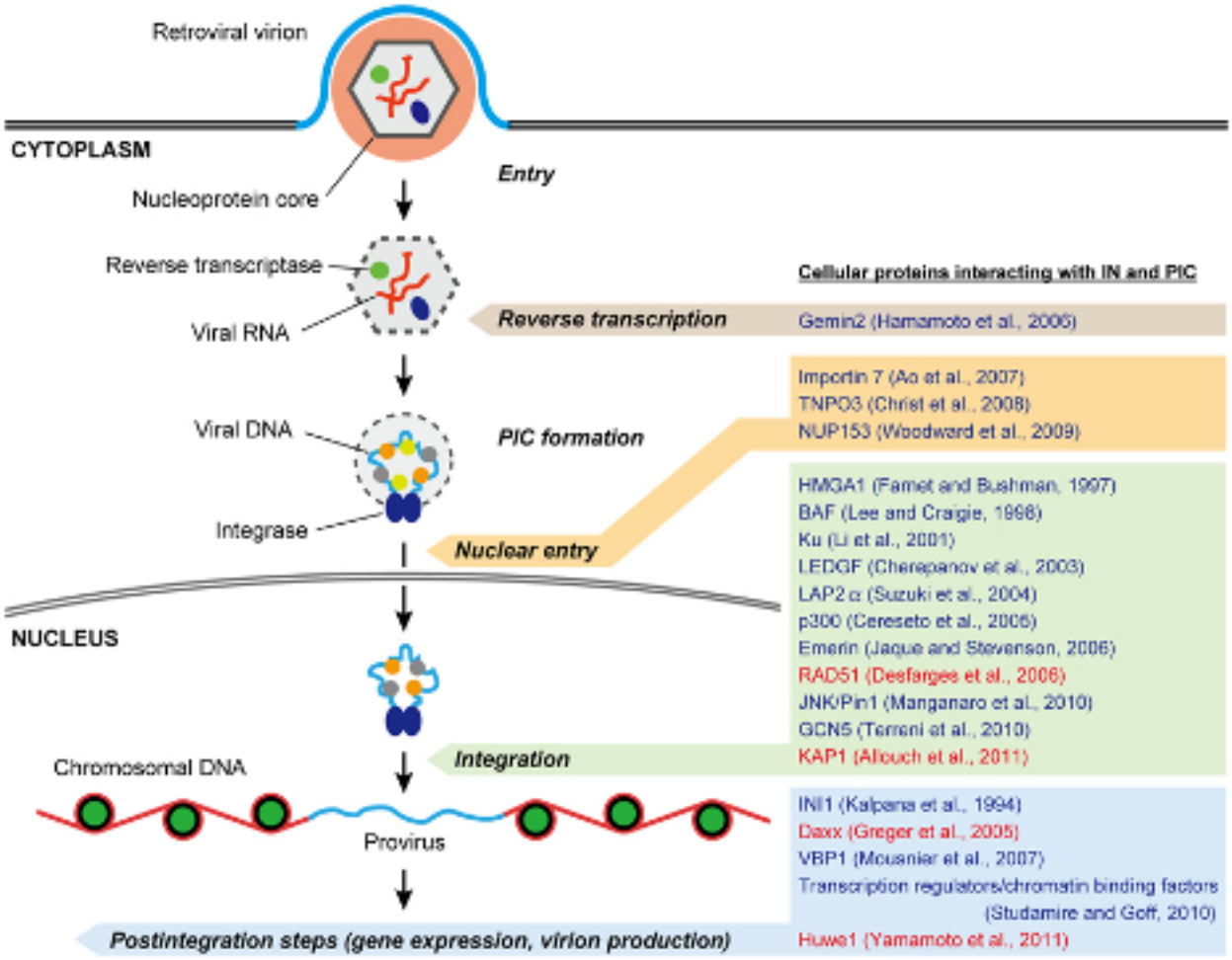
HIV

The National Human Genome Research Institute describes a retrovirus, including HIV-1: *a retrovirus is a virus that uses RNA as its genetic material. When a retrovirus infects a cell, it makes a DNA copy of its genome that is inserted into the DNA of the host cell. There are a variety of different retroviruses that cause human diseases such as some forms of cancer and AIDS.*



In this case, the DNA resides within the nucleus of human cells. Once fused, the DNA copy of HIV-1 and 2019-nCoV/COVID-19 permanently alters the existing DNA of the human host.

This process illustrates how Covid-19 accomplishes two tasks. First, acting as a vector for the entry of HIV-1 fragments into the cytoplasm of a cell. Second, entry of both HIV-1 and the 2019-nCoV/COVID-19 virus into the cell nucleus, thereby gaining access to the host (human) cell's DNA to permanently alter it.



There is a biological symmetry between 2019-nCoV/COVID-19 and HIV-1, with one requiring the natural characteristics of the other. They work in concert with one another, each acting as a vector for the other. A vector is an organism that does not cause disease itself but which spreads infection by conveying pathogens from one host to another.

Within their respective papers, research scientists Prashant Pradhan, et al., and Dr. Montagnier and his co-researcher Jean Claude Perez noted within the complete genomic RNA sequence of 2019-nCoV/COVID-19 the fragments (inserts) of HIV-1. Meaning, the 2019-nCoV/COVID-19 virus itself exists due the presence of HIV-1. The spread, or virality of 2019-nCoV/COVID-19 is dependent upon these fragments of HIV. This is the aforementioned "gain of function".

Once infected, the DNA of the host cell produces a new single strand of RNA. One consisting of both the original DNA of the host, and the new DNA of 2019-nCoV/COVID-19, and HIV-1.

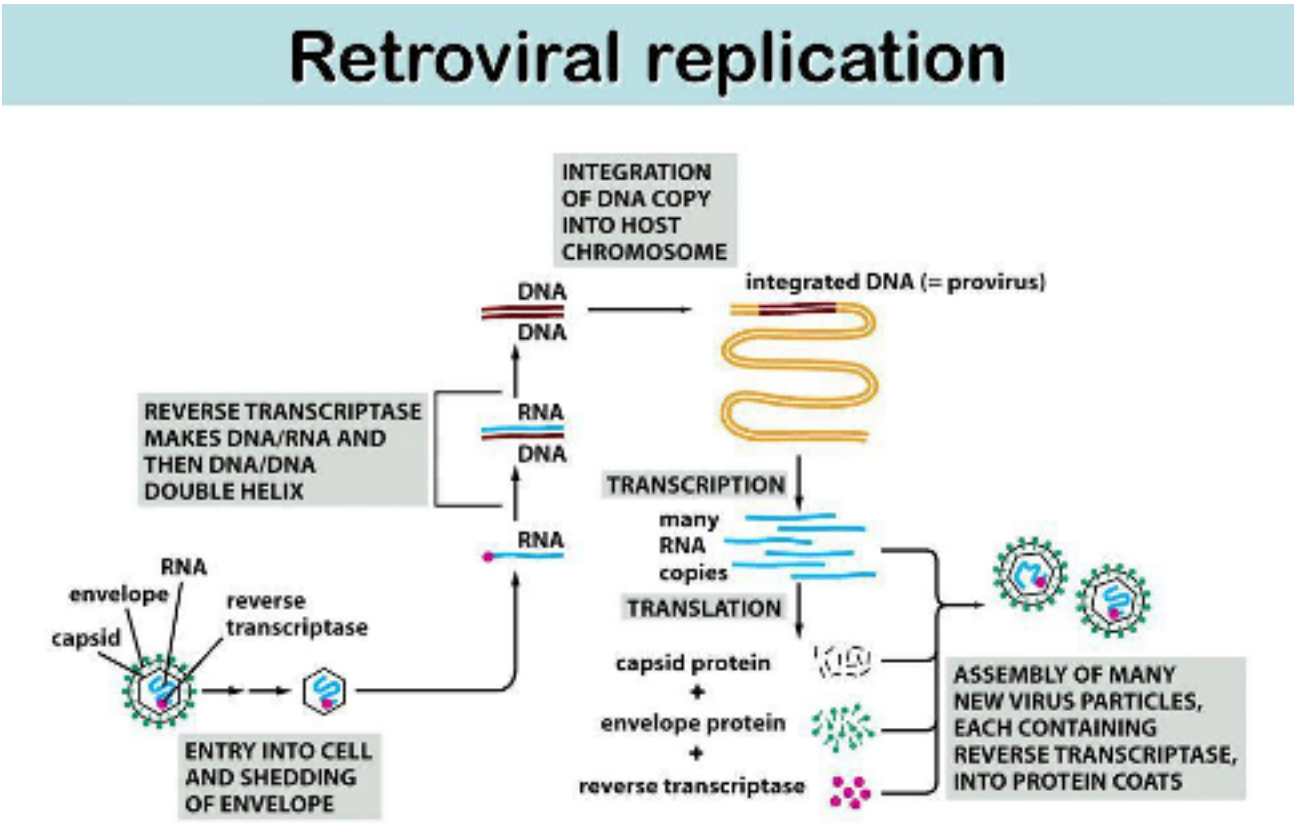
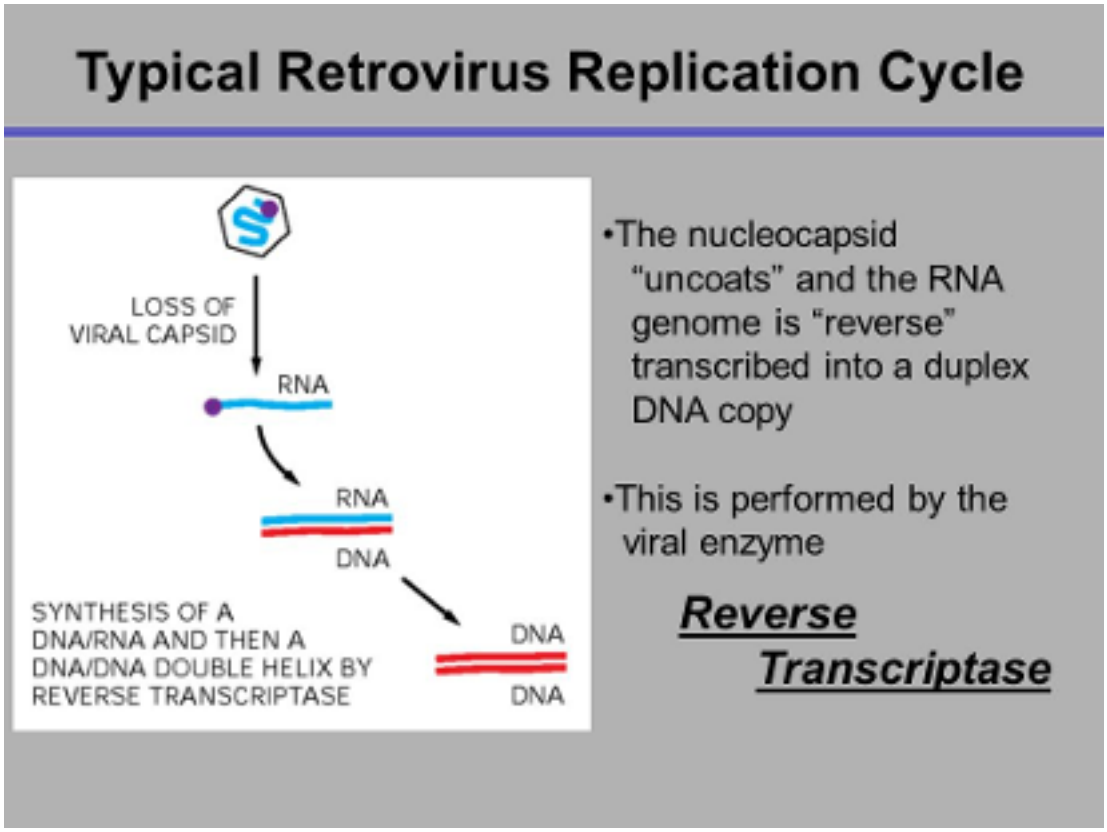
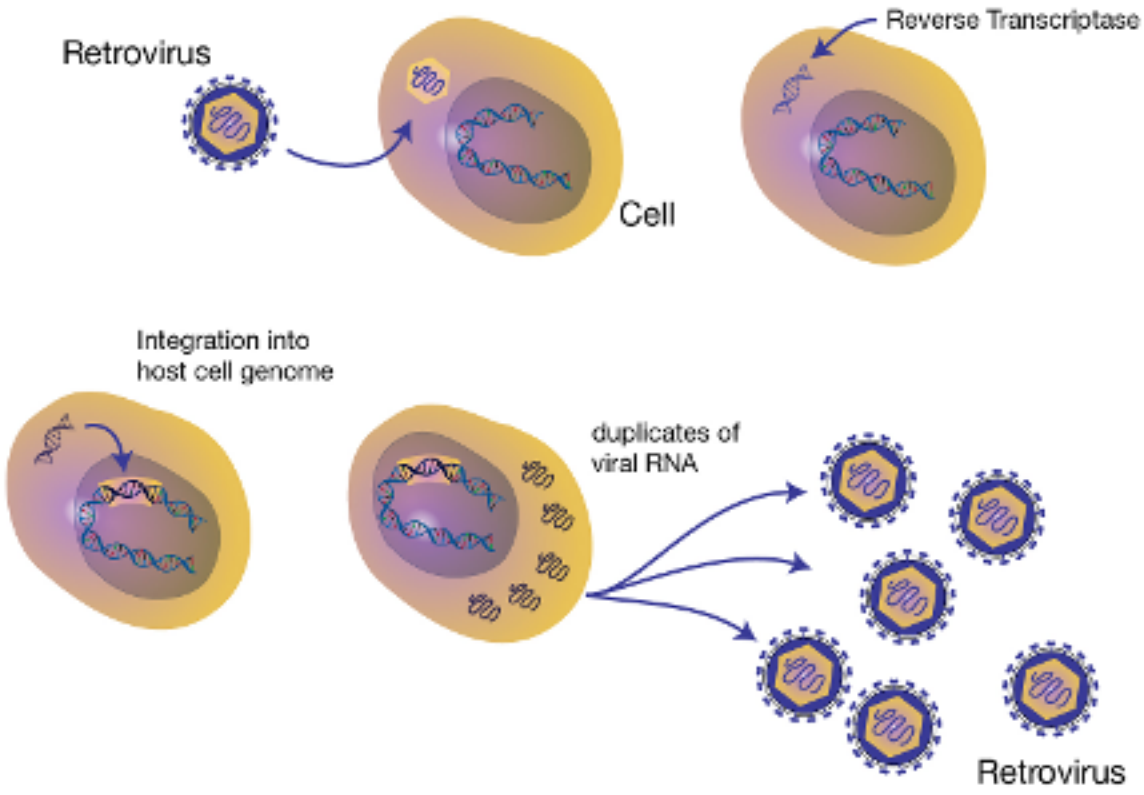


Figure 3.17 *The Biology of Cancer* (© Garland Science 2007)

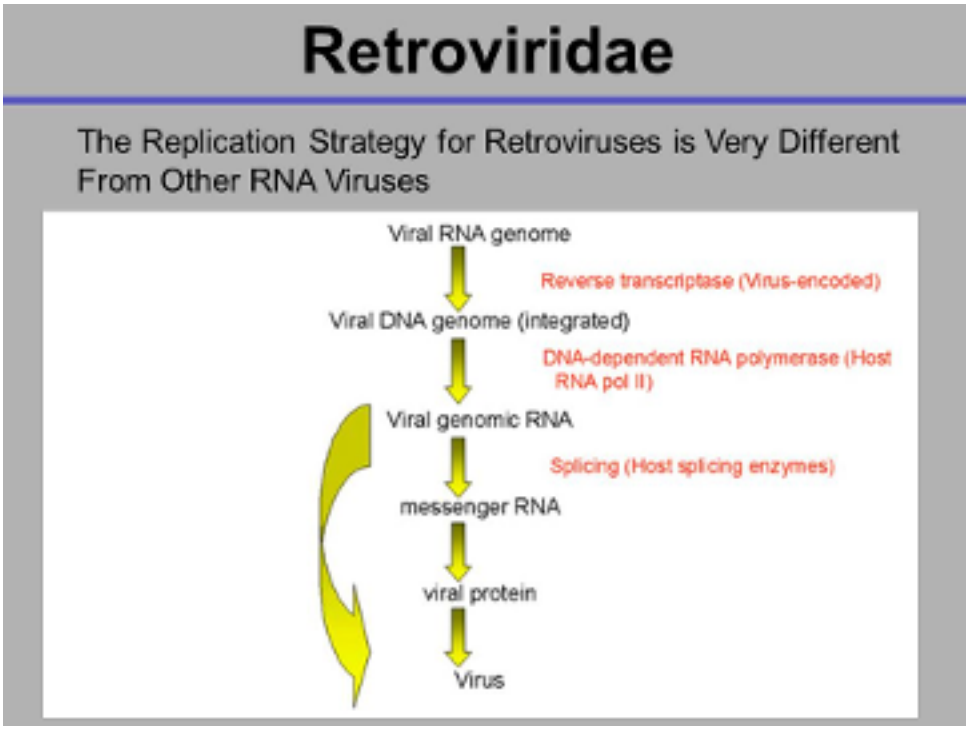
Initially, as a single RNA strand, 2019-nCoV/COVID-19 and HIV-1 move into the fluid of a cell, the cytoplasm. The RNA then produces a copy, a complimentary single strand of itself, referred to as cDNA. It is a single strand of DNA. Next, a second complimentary strand is produced, matching the first. The two intertwine into the familiar double helix of common DNA. This is still referred to as cDNA, or dscDNA (double stranded complimentary DNA). This cDNA consists of the combined genome of 2019-nCoV/COVID-19 and HIV-1.



The new cDNA (as a familiar double helix) enters the nucleus of the cell and binds to the existing DNA of the host (human) cell. This permanently changes the host DNA of this specific cell into a retrovirus: 2019-nCoV/COVID-19 and HIV-1.



The virus, like all viruses, wants to reproduce. It wants to "go viral". It does so by producing a single strand of messenger RNA (mRNA), itself a copy of the viral cDNA (the newly formed, altered host DNA). This single strand mRNA exits the nucleus, then the cell itself, moving on to the next cell, thus "going viral".



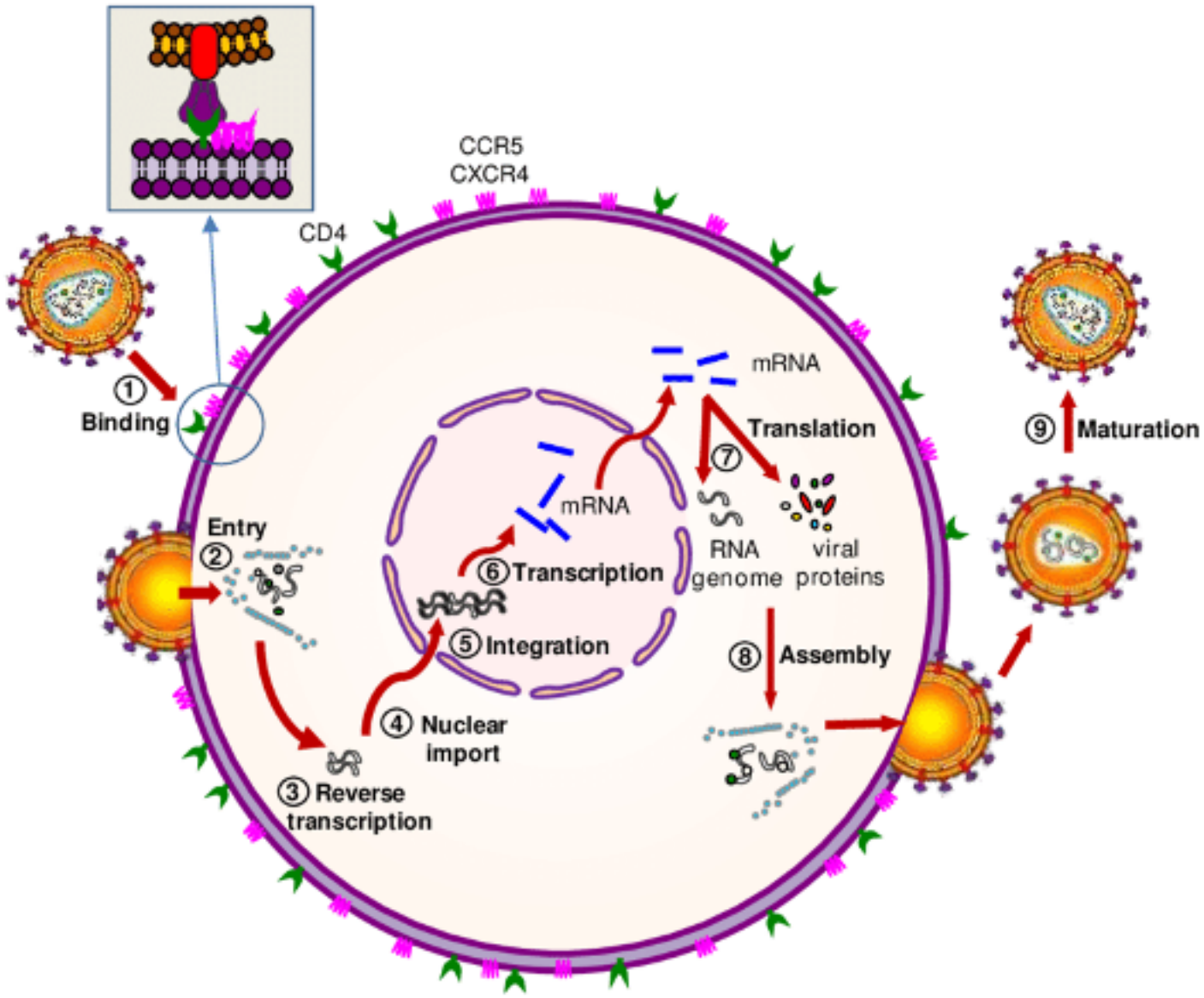
In the following, we are presenting published research from well known and respected scientists, including that of Dr. Luc Antoine Montagnier, the 2008 Nobel Laureate in Physiology or Medicine for his discovery of the human immunodeficiency virus (HIV).

In previous editions of this magazine we have cited the paper entitled; *Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag*, authored by Prashant Pradhan, Ashutosh Kumar Pandey, Akhilesh Mishra, Parul Gupta, Praveen Kumar Tripathi, Manoj Balakrishnan Menon, James Gomes, Perumal Vivekanandan, Bishwajit Kundu. Included was their statement; *"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."*

We now offer as a follow-on to the above, the latest research from that of Dr. Montagnier and his co-researcher Jean Claude Perez, beginning with; *COVID-19, SARS AND BATS CORONAVIRUSES GENOMES PECULIAR HOMOLOGOUS RNA SEQUENCES.*

Excerpts:

> ***"18 RNA fragments of homology equal or more than 80% with human or simian retroviruses have been found in the COVID_19 genome."***
>
> ***"HIV1 EIE with a crucial Spike mutation."***

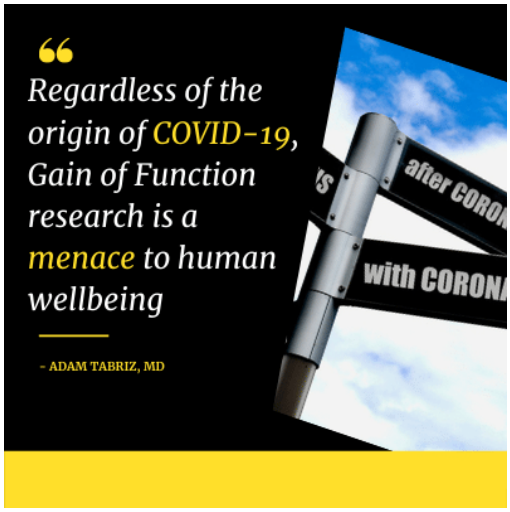


HIV-1 Replication Cycle

Excerpts continued:

> ***"Through the 14 facts relating to each of the 14 paragraphs of this article, everything converges towards possible laboratory manipulations (End Note below) which contributed to modifications of the genome of COVID_19, but also, very probably much older SARS, with perhaps this double objective of vaccine design and of "gain of function" in terms of penetration of this virus into the cell."***

The conclusions of these scientists and others cited herein are; the genome of 2019-nCoV/COVID-19 was man-made in a laboratory and contains not simply 4 inserts as cited by Prashant, et al. but 18 of human or simian retroviruses (HIV-1).



With respect to the *"gain of function"* objective, this is for the purpose of increasing the rate of infection, the pathogenic transmissibility (mobidity) of a virus within a host population. Not necessarily leading to an increased number of mortalities. This is leveraging the natural processes of a virus in increasing the quantity of infected hosts, without killing them off.

This is accomplished by enhancing the ability of a virus to penetrate into a host cell. The presence of HIV-1 genetic material, the 18 RNA fragments, indicates the targeting of host cell DNA. The natural process of all retroviruses like HIV-1 is to fuse its genetic material to that of the host DNA, thus permanently changing it. From there, this modified DNA naturally produces a single strand of RNA containing the virus and moves on to infect the next host cell. It "goes viral".

Dr. Luc Antoine Montagnier, the 2008 Nobel Laureate in Physiology or Medicine for his discovery of the human immunodeficiency virus (HIV).

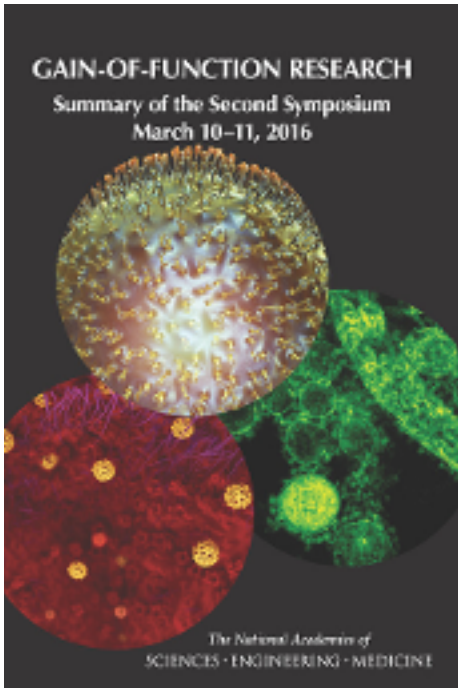
Gain-of-Function Research: Ethical Analysis

Sci Eng Ethics. 2016; 22(4): 923–964.

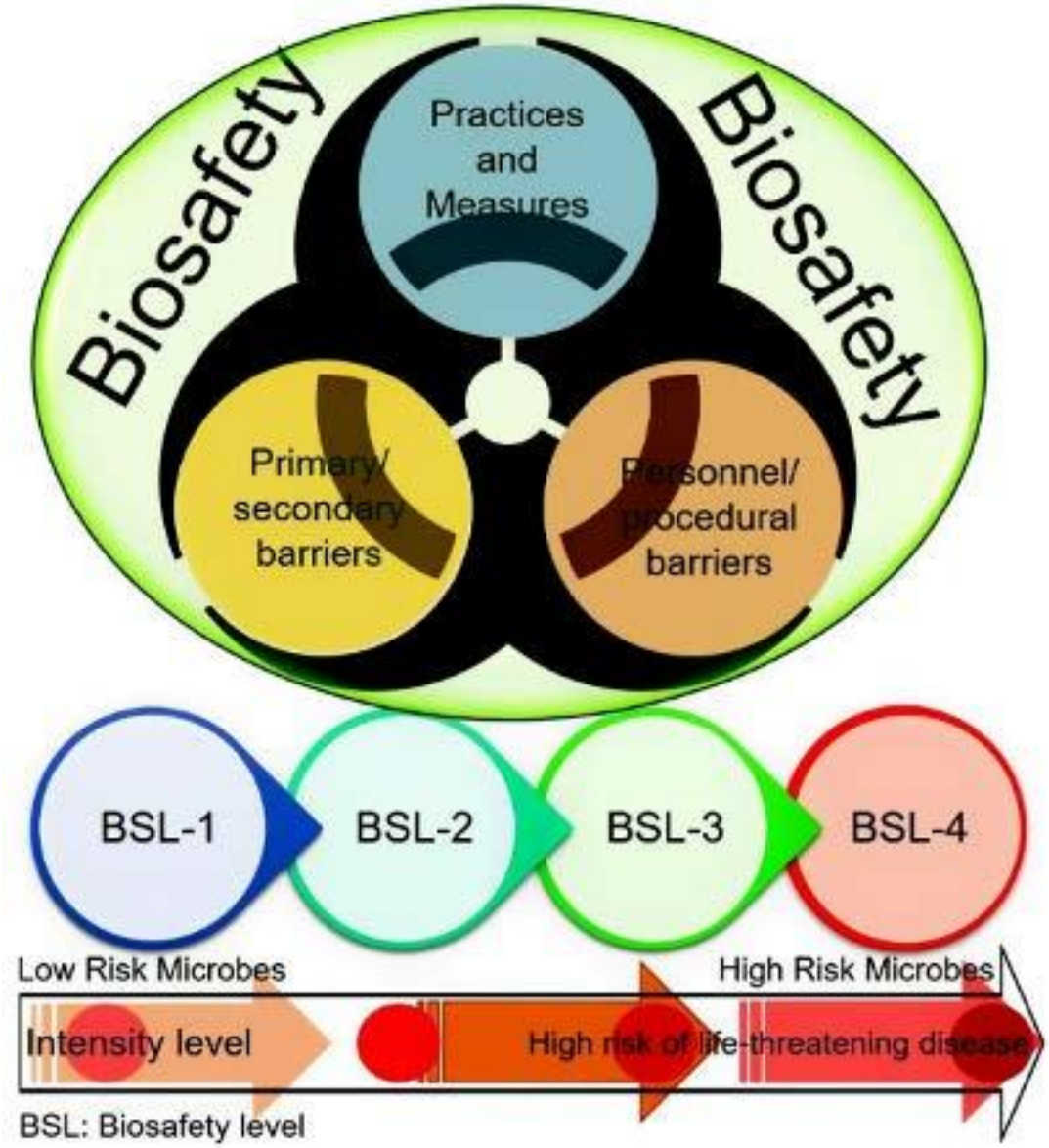
Published online 2016 Aug 8.doi:10.1007/s11948-016-9810-1

Executive Summary

Gain-of-function (GOF) research involves experimentation that aims or is expected to (and/or, perhaps, actually does) increase the transmissibility and/or virulence of pathogens. Such research, when conducted by responsible scientists, usually aims to improve understanding of disease causing agents, their interaction with human hosts, and/or their potential to cause pandemics. The ultimate objective of such research is to better inform public health and preparedness efforts and/or development of medical countermeasures. Despite these important potential benefits, GOF research (GOFR) can pose risks regarding biosecurity and biosafety. GOFR is a subset of "dual-use research"—i.e., research that can be used for both beneficial and malevolent purposes.

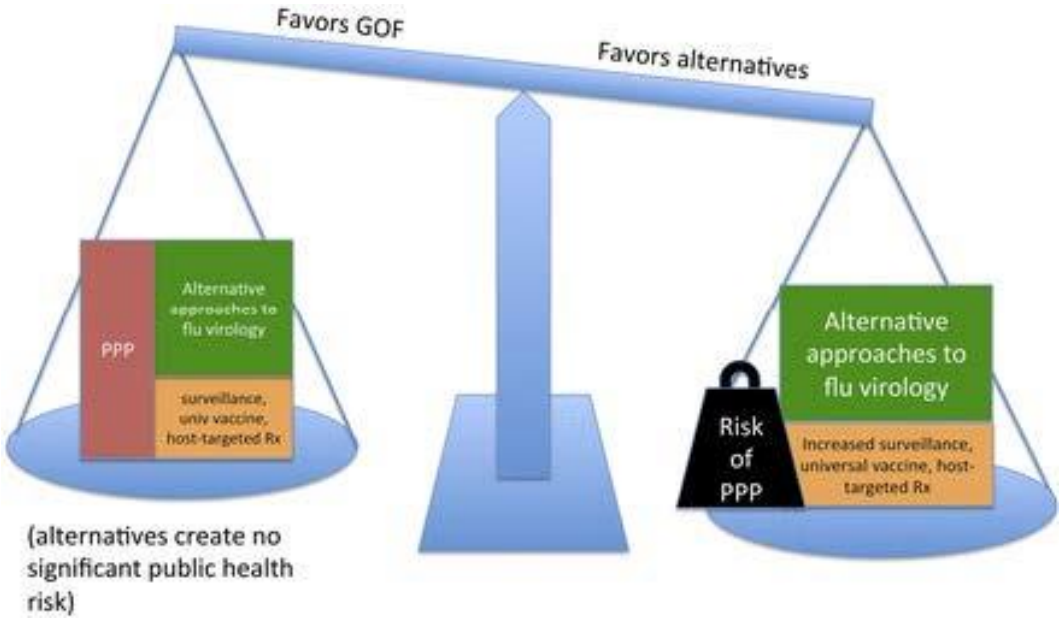


Whereas the dual-use life science research debate has largely focused on biosecurity dangers associated with potential malevolent use of research, the GOFR debate has more explicitly focused on risks involving both biosecurity and biosafety—the point being that creation of especially dangerous pathogens might pose highly significant biosafety risks that are independent of, and perhaps more feasible to measure/assess than, risks associated with malevolent use.



Executive Summary continued

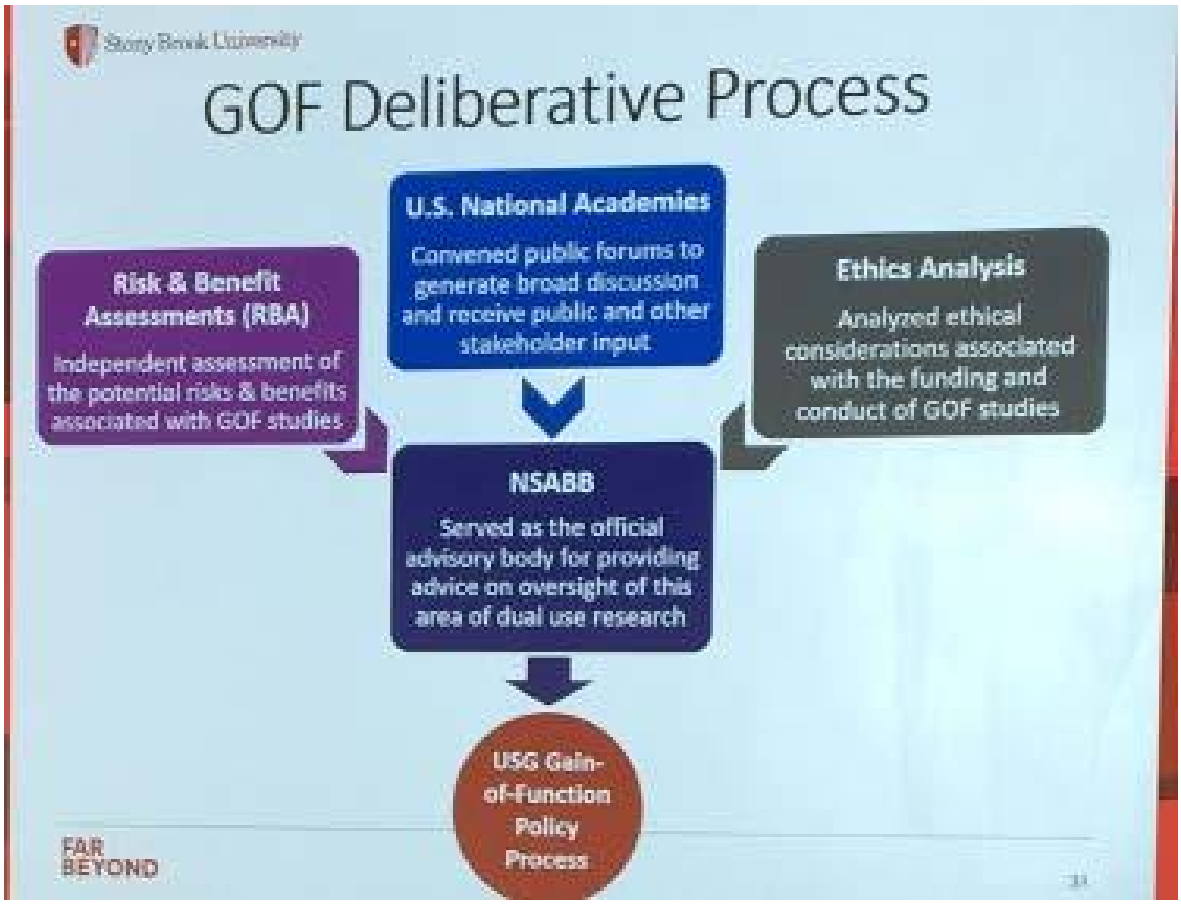
Following controversy surrounding research, published in 2012, that led to the creation of highly pathogenic H5N1 (avian) influenza virus strains that were airborne transmissible between ferrets—and more recent reports of biosafety mishaps involving anthrax, smallpox, and H5N1 in government laboratories—in 2014 the administration of US President Barack Obama called for a "pause" on funding (and relevant research with existing US Government funding) of GOF experiments involving influenza, SARS, and MERS viruses in particular.



Potential Pandemic Pathogens (PPP)

This pause applies specifically to experiments that "may be reasonably anticipated to confer attributes … such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route" (White House 2014). With announcement of this pause, the US Government launched a "deliberative process … to address key questions about the risks and benefits of gain-of-function studies" (White House 2014) to inform future funding decisions—and the National Science Advisory Board for Biosecurity (NSABB) was tasked with making recommendations to the US Government on this matter.

(End of Executive Summary - Gain-of-Function Research: Ethical Analysis)

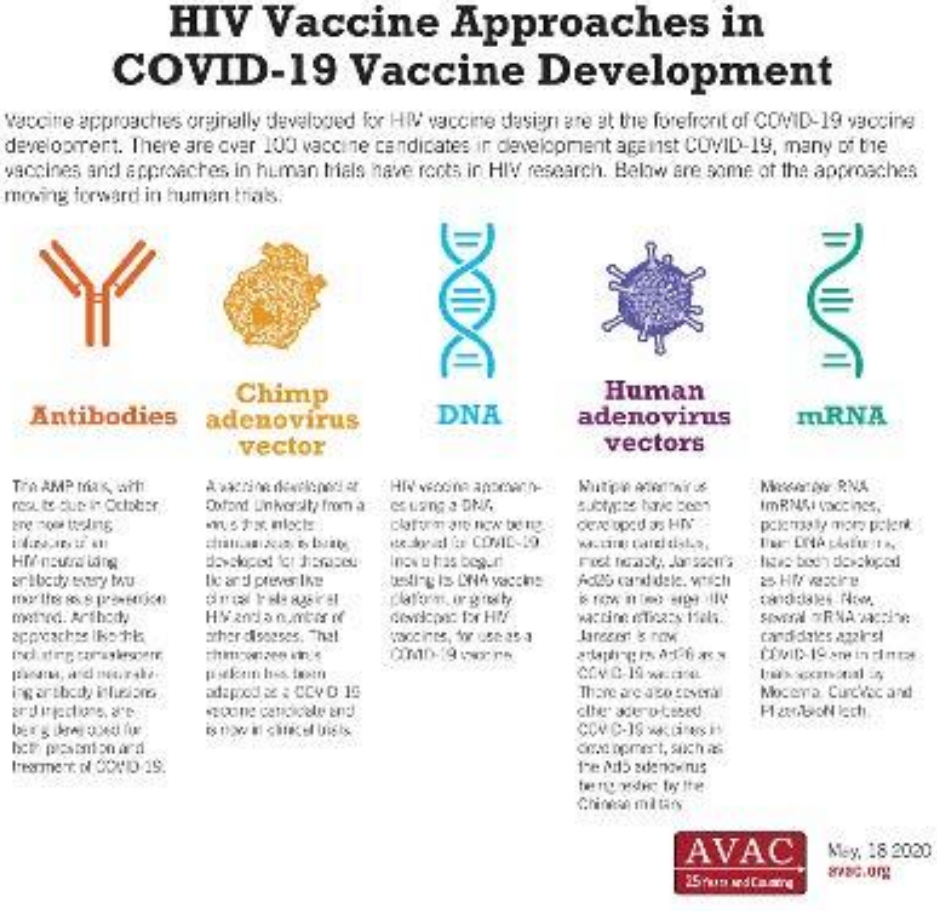


Commentary

The question arises regarding ongoing research into the development of one or more vaccines for COVID-19, as to why the deliberate actions towards an increase in "gain of function", when the stated purpose of a vaccine is to reduce the cases of morbidity and mortality.

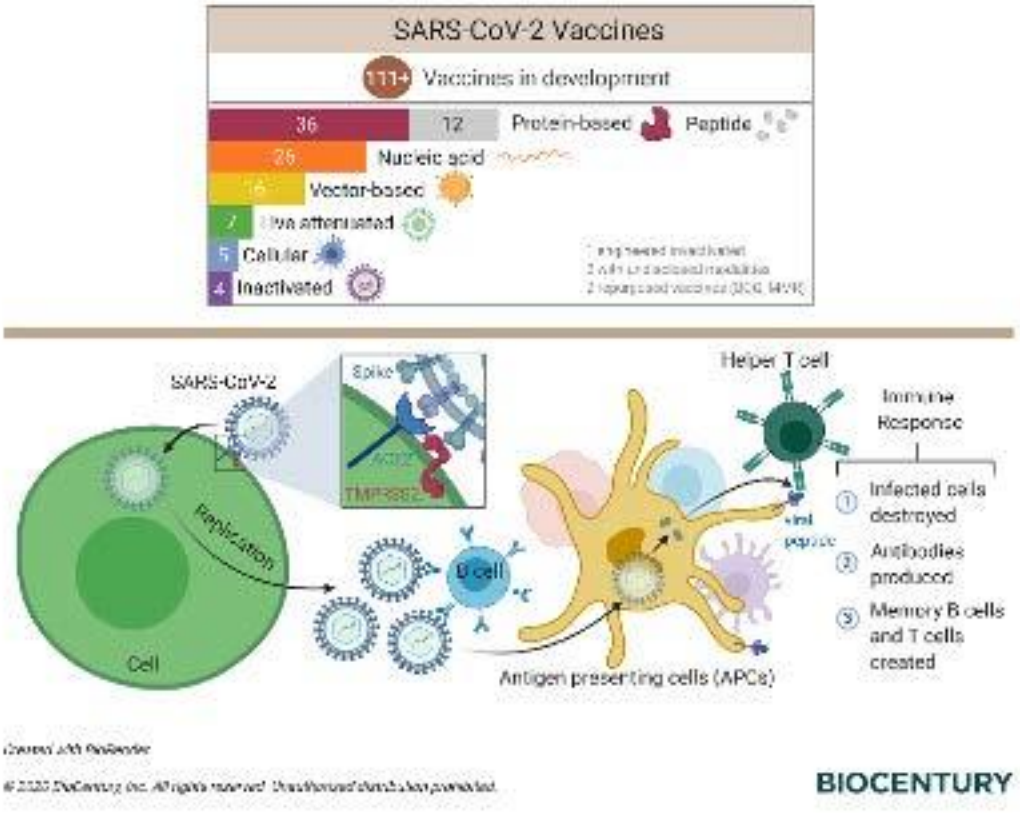
Our summation, following examination of this and further research papers, is not simply to spread 2019-nCoV/COVID-19, but to target and permanently change the DNA of every person. This is accomplished through a global vaccination mandate. Please reference our extensive published evidence within previous editions of this magazine.

For it must be kept in mind, a vaccine by its very nature is derived from and designed to function in a manner coinciding with that of the virus itself. Current research and developement specific to 2019-nCoV/COVID-19 is primarily based upon the DNA and RNA of this virus.



The stated intent of pharmaceutical companies involved in the production of these vaccines is to elicit a low level response by the human immune system. In past vaccines, weakened (attenuated) forms of a virus served this purpose, with recipients experiencing milder signs and symptoms of the disease.

In the instances of DNA and RNA-based vaccines, the goal is the expression of protein(s) from within the cytoplasm of a host cell. These are then recognized by the human immune system, which responds by producing antibodies specific to them.



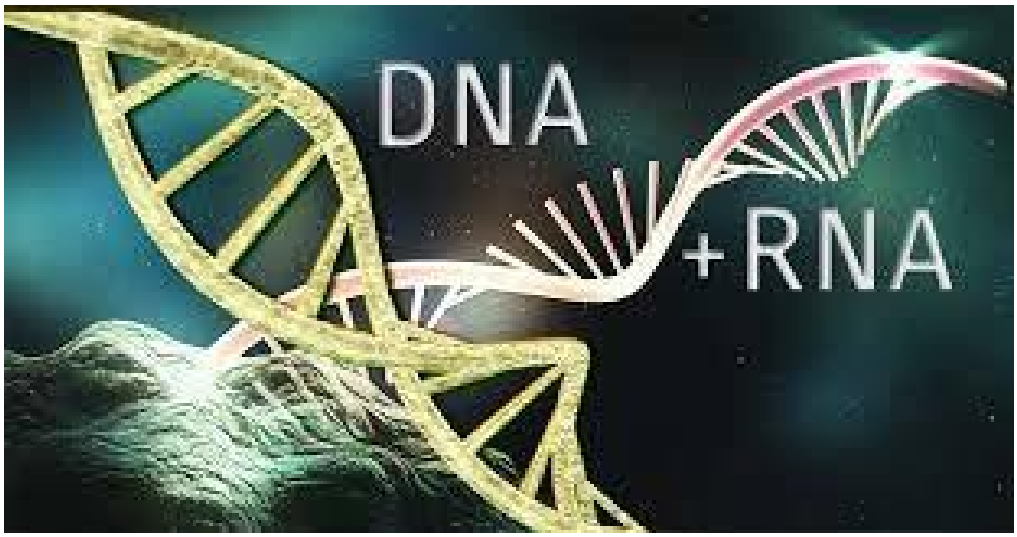
What has not been made transparent is the deliberate inclusion of:

"18 RNA fragments of homology equal or more than 80% with human or simian retroviruses have been found in the COVID_19 genome."

- Montagnier/Perez

This means, the vaccine(s), as with such treatments derived from an original virus, likewise contain 18 RNA fragments having the same structural features and pattern of genes (homologous) found in human or simian (apes/monkeys) retroviruses *(any of a group of RNA viruses which insert a DNA copy of their genome into the host cell in order to replcate, e.g. HIV.)* - Definitions from Oxford Languages

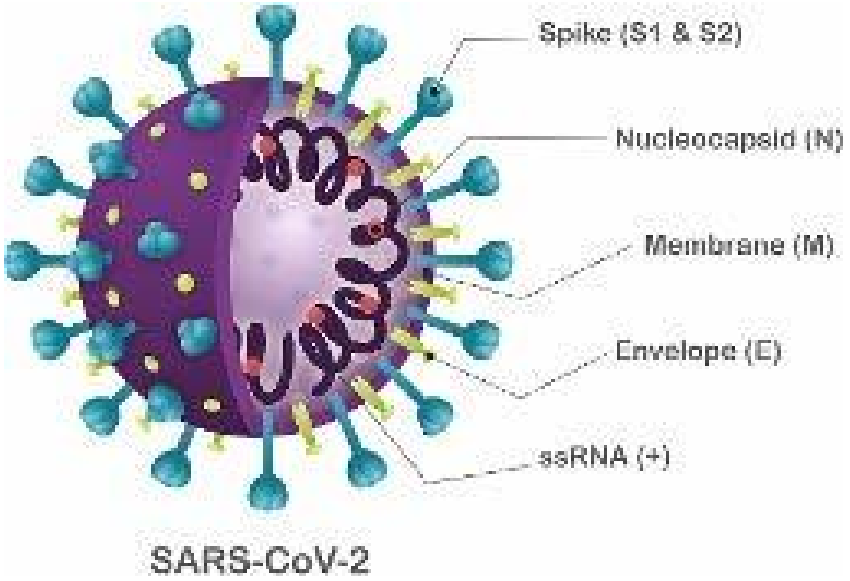
Does this necessarily result in a person contracting HIV from such a vaccine? No, for the entire RNA genomic sequence is not included, only fragments according to the research findings of Dr. Montagnier and his co-researcher Jean Claude Perez. And the inverse is true with respect to those previously infected with HIV and retroviral alteration of their DNA. Their DNA has not undergone the same changes as those to be initiated by the upcoming vaccines.



It seems reasonable to expect these and other researchers with similar findings to be unsure as to what extent these changes to host DNA will manifest. However, it is their opinion, based upon the scientific evidence obtained, 2019-nCoV/COVID-19 is indeed a man-made virus:

"Through the 14 facts relating to each of the 14 paragraphs of this article, everything converges towards possible laboratory manipulations (End Note below) which contributed to modifications of the genome of COVID_19, but also, very probably much older SARS, with perhaps this double objective of vaccine design and of "gain of function" in terms of penetration of this virus into the cell."

- Montagnier/Perez



SARS-CoV-2

It is our expectation, further research discoveries by Montagnier, Perez and others will yield conclusive evidence of significantly greater changes to human DNA through the administration of 2019-nCoV/COVID-19-based vaccines, than simply the expression of proteins and enhancements of transmissability.

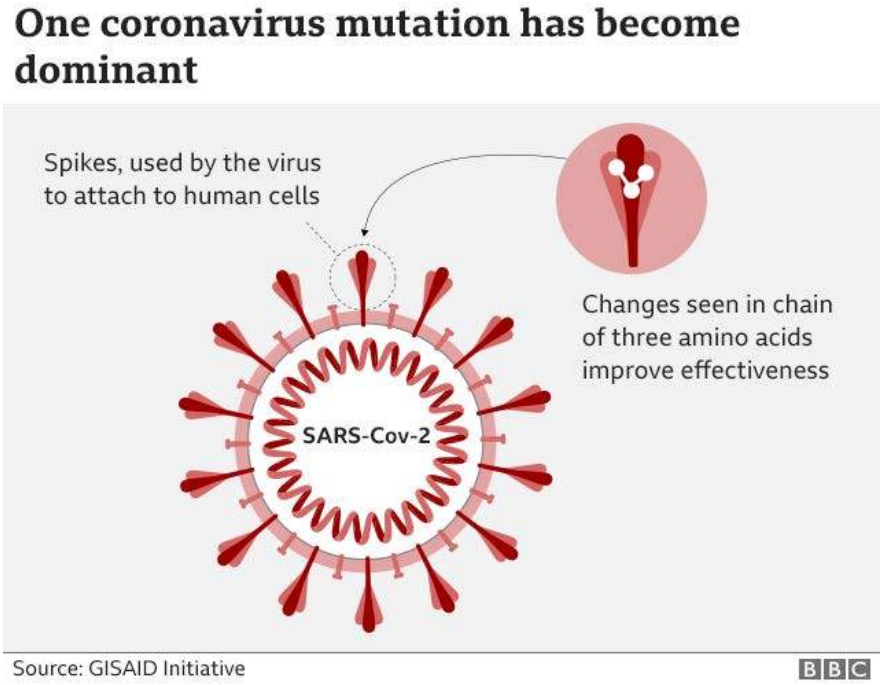
The question arises with respect to enhanced virulence and infectivity: is the goal to increase lethality, or simply to vaccinate the global population? We anticipate further scientific discovery of the latter will be the case.

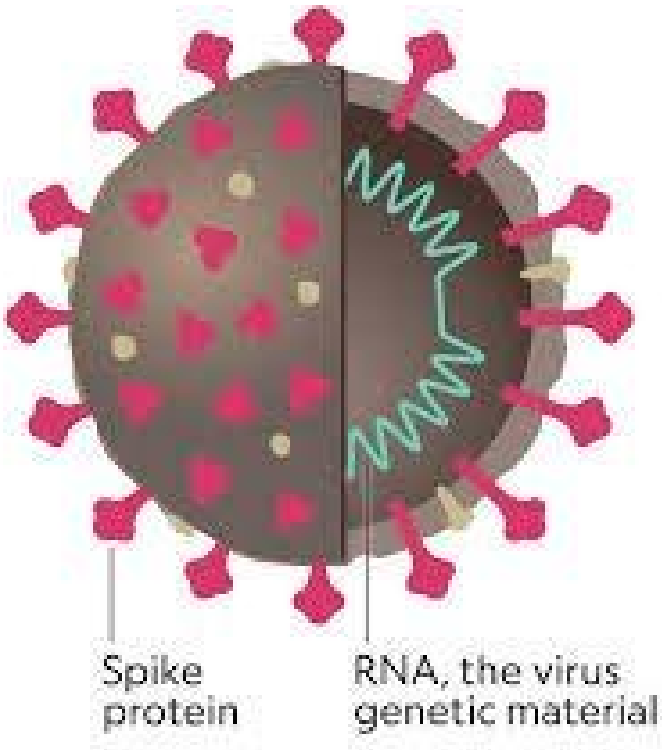
If only to vaccinate, then to what end? Recall, *a retrovirus is any group of RNA viruses (including HIV) which inserts a DNA copy of their genome into the host cell in order to replicate.* - Definitions from Oxford Languages

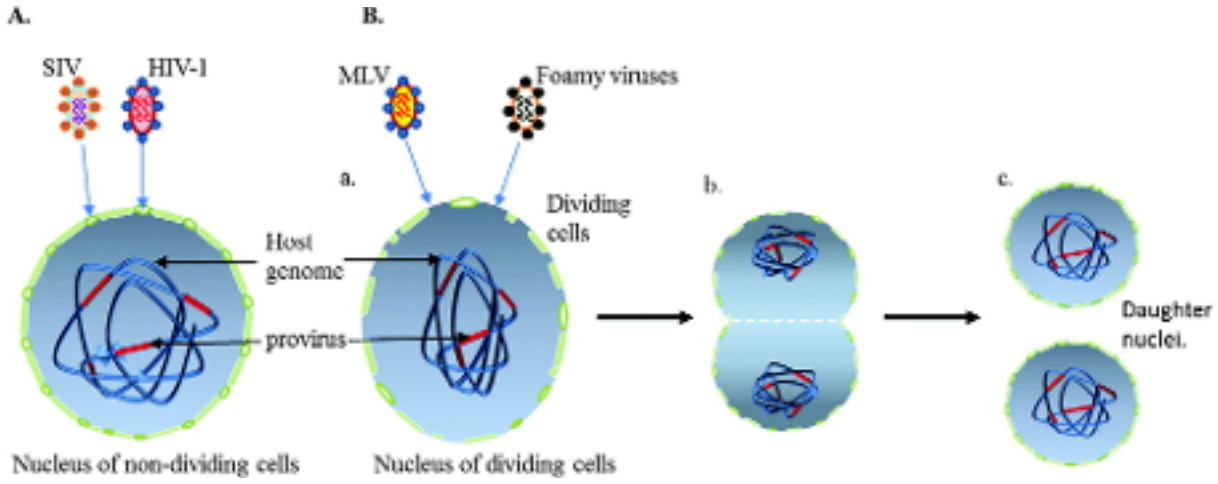
Probable answer: To permanently alter everyone's DNA. This is a logical conclusion based upon the global scientific, academic, corporate, media, political, sociological, economic, even theological movements coalescing upon this fine needle-point focus.

The tip-of-the-spear vaccine research and development is not DNA based, rather, RNA. Specifically, messenger RNA (mRNA). This is concurrent with discoveries of inclusions as presented by Dr. Montagnier and Jean Claude Perez:

> ***"18 RNA fragments of homology equal or more than 80% with human or simian retroviruses have been found in the COVID_19 genome."***
>
> ***"HIV1 EIE with a crucial Spike mutation."***







Beginnig at the end, we present the following corroberating evidence the 2019-nCoV/COVID-19 virus was created by man in one or more laboratories.

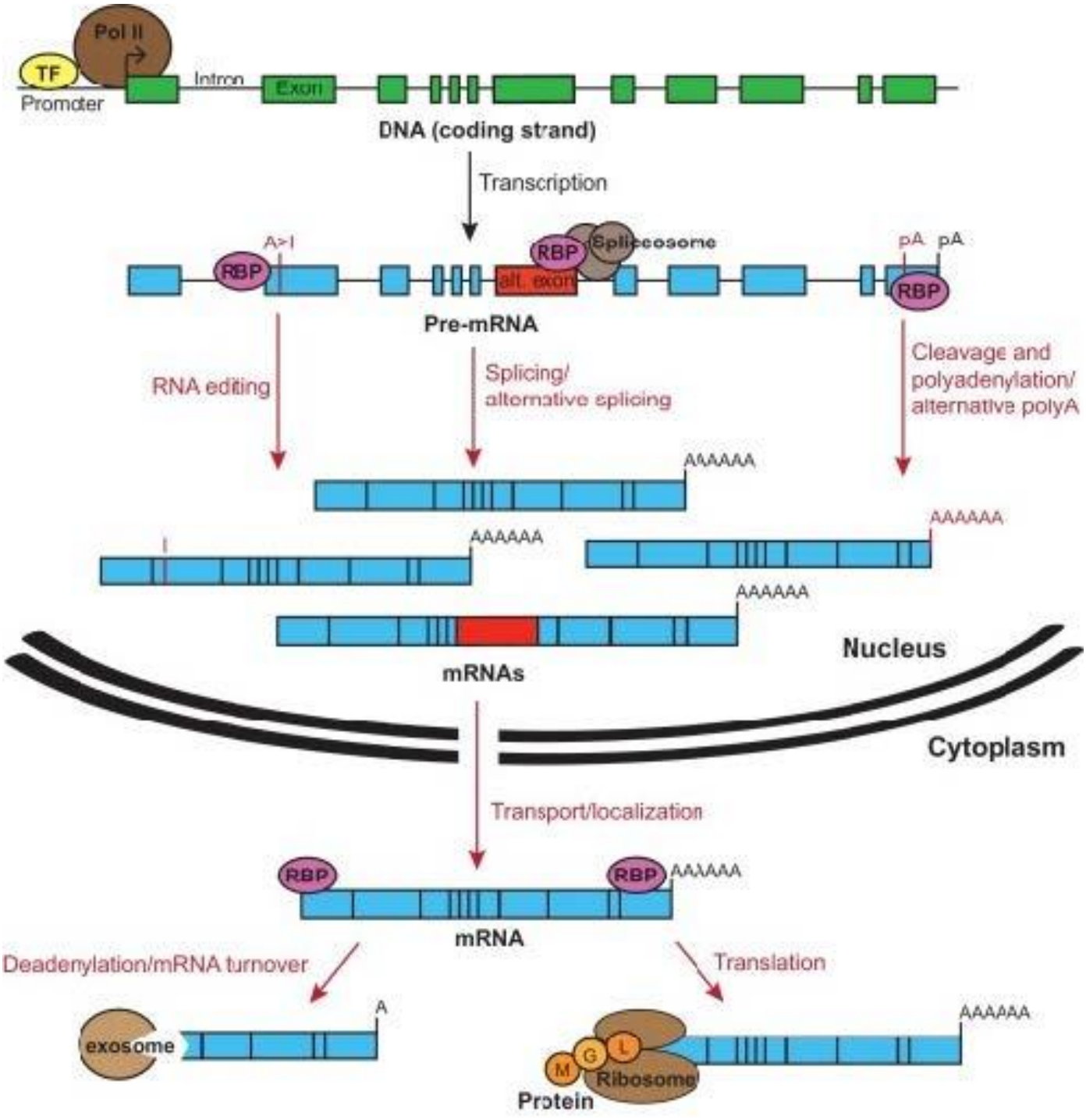
Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route

Li-Meng Yan (MD, PhD), Shu Kang (PhD), Jie Guan (PhD), Shanchang Hu (PhD)

Rule of Law Society & Rule of Law Foundation, New York, NY, USA.

3. Final remarks

Many questions remain unanswered about the origin of SARS-CoV-2. Prominent virologists have implicated in a Nature Medicine letter that laboratory escape, while not being entirely ruled out, was unlikely and that no sign of genetic manipulation is present in the SARS-CoV-2 genome. However, here we show that genetic evidence within the spike gene of SARS-CoV-2 genome (restriction sites flanking the RBM (Ed. note: RNA binding motif proteins, also RBP, RNA binding protein): tandem rare codons used at the inserted furin-cleavage site) does exist and suggests that the SARS-CoV-2 genome should be a product of genetic manipulation. Furthermore, the proven concepts, well-established techniques, and knowledge and expertise are all in place for the convenient creation of this novel coronavirus in a short period of time.



RBP, RNA Binding Protein

3. Final remarks continued

Motives aside, the following facts about SARS-CoV-2 are well-supported:

1. If it was a laboratory product, the most critical element in its creation, the backbone/template virus (ZC45/ZXC21), is owned by military research laboratories.

2. The genome sequence of SARS-CoV-2 has likely undergone genetic engineering, through which the virus has gained the ability to target humans with enhanced virulence and infectivity.

3. The characteristics and pathogenic effects of SARS-CoV-2 are unprecedented. The virus is highly transmissible, onset-hidden, multi-organ targeting, sequelae-unclear, lethal, and associated with various symptoms and complications.

4. SARS-CoV-2 caused a world-wide pandemic, taking hundreds of thousands of lives and shutting down the global economy. It has a destructive power like no other.

Judging from the evidence that we and others have gathered, we believe that finding the origin of SARS-CoV-2 should involve an independent audit of the WIV P4 laboratories and the laboratories of their close collaborators. Such an investigation should have taken place long ago and should not be delayed any further.

We also note that in the publication of the chimeric virus SHC015-MA15 in 2015, the attribution of funding of Zhengli Shi by the NIAID was initially left out. It was reinstated in the publication in 2016 in a corrigendum, perhaps after the meeting in January 2016 to reinstate NIH funding for gain-of-function research on viruses. This is an unusual scientific behavior, which needs an explanation for.

What is not thoroughly described in this report is the various evidence indicating that several coronaviruses recently published (RaTG1318, RmYN0230, and several pangolin coronaviruses 27-29,31) are highly suspicious and likely fraudulent. These fabrications would serve no purpose other than to deceive the scientific community and the general public so that the true identity of SARS-CoV-2 is hidden.

Although exclusion of details of such evidence does not alter the conclusion of the current report, we do believe that these details would provide additional support for our contention that SARS-CoV-2 is a laboratory-enhanced virus and a product of gain-of-function research. A follow-up report focusing on such additional evidence is now being prepared and will be submitted shortly.

(End of 3. Final remarks)

As noted in the Final remarks above:

Although exclusion of details of such evidence does not alter the conclusion of the current report, we do believe that these details would provide additional support for our contention that SARS-CoV-2 is a laboratory-enhanced virus and a product of gain-of-function research.

The research findings of Dr. Montagnier and Jean Claude Perez provide details of such evidence, thus supporting Li-Meng Yan (MD, PhD), et al.:

> **Why could COVID-19 come from Laboratory manipulations? The following 4 proofs concern differences with respect to SARS either common to COVID-19 and bat RaTG13, or facts radically differentiating these 2 sequences of which it is claimed that the first (COVID-19) comes from a natural evolution of the second (bat RaTG13).**
>
> **We have ranked these 4 proofs in ascending order of importance according to our point of view.**
>
> **1) Four EIE formally distinguishes COVID-19 and bat RaTG13 genomes from all other SARS or bats genomes. However, their level of HIV/SIV homologies appears much more affirmed for COVID-19 than for bat RaTG13, as if these EIE fragments had recently been "re-injected" into the COVID-19 genome. ==> see & 7, (figures 4 and 5).**

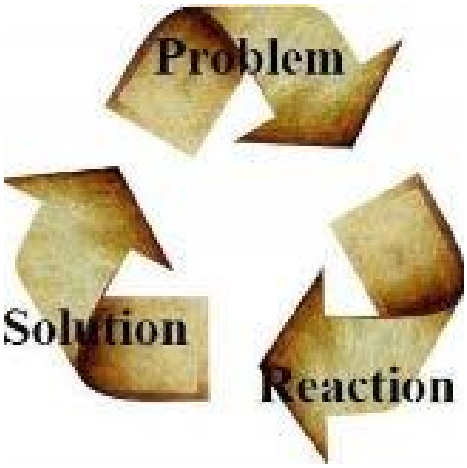
2) natural deletions (USA WA Seattle state) apply in priority to EIE inserts (HIV Kenya etc ..). ==> see full Part III and Figure 12 in §13.

3) Synonymous codons mutations within the 1770 bases region of the Spike, which simulate a natural evolution of bat RaTG13 towards COVID-19 while maintaining the optimality obtained in amino acid values, probably from "gain of function" Laboratory experiments (optimality common to both RNA sequences COVID-19 and bat RaTG13) ==> see Figure 10 in & 11 and Figure 11 in §12.

4) "PRRA" amino acids was inserted exactly on the Spike location already theoretically optimal on both COVID-19 and RATG13 (of which it constitutes the main difference). ==> see Figure 13 in & 14.

As we correlate the findings within these two respective papers, it should be emphasized the coronavirus bat RaTG13/RaTG1318 (same) and 2019-nCoV/COVID-19 are formally distinguished from all other coronaviruses. With the additional findings of Li-Meng Yan (MD, PhD), et al. specific to the origin of bat RaTG13/RaTG1318 as *"highly suspicious and likely fraudulent.*" Of which, it is claimed 2019-nCoV/COVID-19 comes from a natural evolution of bat RaTG13/RaTG1318.

Li-Meng Yan (MD, PhD), et al. debunk the 2019-nCoV/COVID-19 natural origin theory, comprising the broader narrative delivered by the mainstream media. Itself, accepted by those choosing either deliberately to deceive or, in furtherance of their own hidden, typically financial, agenda.



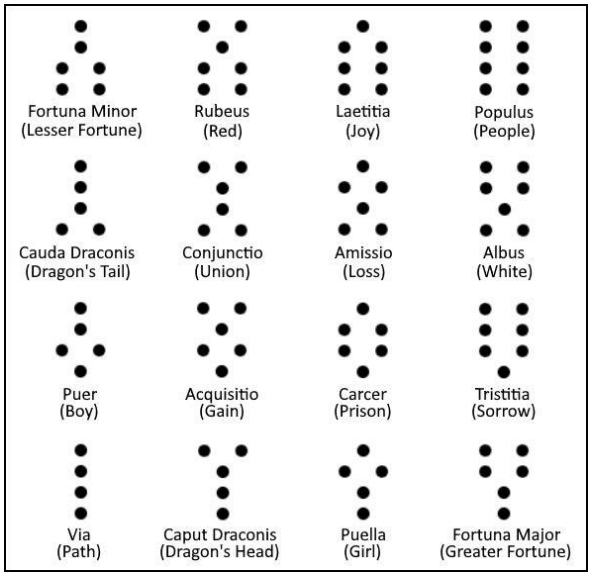
Through the *modus operandi* of problem, reaction, solution, those formulating this narrative seek first to imprison and control. Then, ultimately through permanent modification of DNA, condem a person's soul for all eternity to perdition. Masses of the human population are and will continue to believe the lie. It being the vaccine as their final solution to the artificially created problem of 2019-nCoV/COVID-19 they've been duped into reacting to.

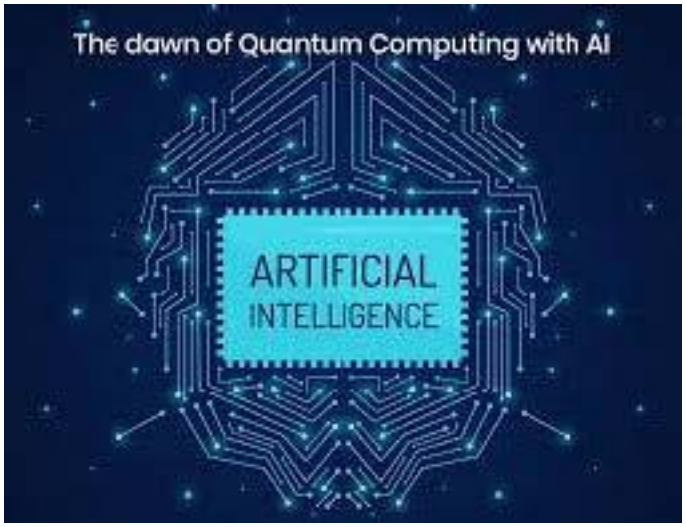
As expected, those creating the problem could never force the human population into taking any vaccine, 2019-nCoV/COVID-19 or otherwise. They developed this entire plan, often referred to as the "plandemic", by employing artificially intelligent systems. These systems learn by observing, then mathematically emulating human behavior.

If you will, from the perspective of AI systems, it was relatively easy to fit all the necessary pieces together in the evolution of the Hegelian dialectic, their *modus operandi* of problem, reaction, solution.

The timing of the purposeful release, as demonstrated by the scientists presented here, and many more, of 2019-nCoV/COVID-19 upon the global population of humans, was determined with the use of AI systems.

In the end, AI was and continues to be developed along the identical timeline of quantum computing systems. All computing, both classical and quantum have their direct origins in the forbidden-by-God dark, divinitory art of geomancy. Itself, a system for prognosticating future events.





From: Li-Meng Yan (MD, PhD), et al.

Abstract

The COVID-19 pandemic caused by the novel coronavirus SARS-CoV-2 has led to over 910,000 deaths worldwide and unprecedented decimation of the global economy. Despite its tremendous impact, mysterious and controversial. The natural origin theory, although widely accepted, lacks substantial support. The alternative theory that the virus may have come from a research laboratory is, however, strictly censored on peer-reviewed scientific journals. Nonetheless, SARS-CoV-2 shows biological characteristics that are inconsistent with a naturally occurring, zoonotic virus.

In this report, we describe the genomic, structural, medical, and literature evidence, which, when considered together, strongly contradicts the natural origin theory. The evidence shows that SARS-CoV-2 should be a laboratory product created by using bat coronaviruses ZC45 and/or ZXC21 as a template and/or backbone.

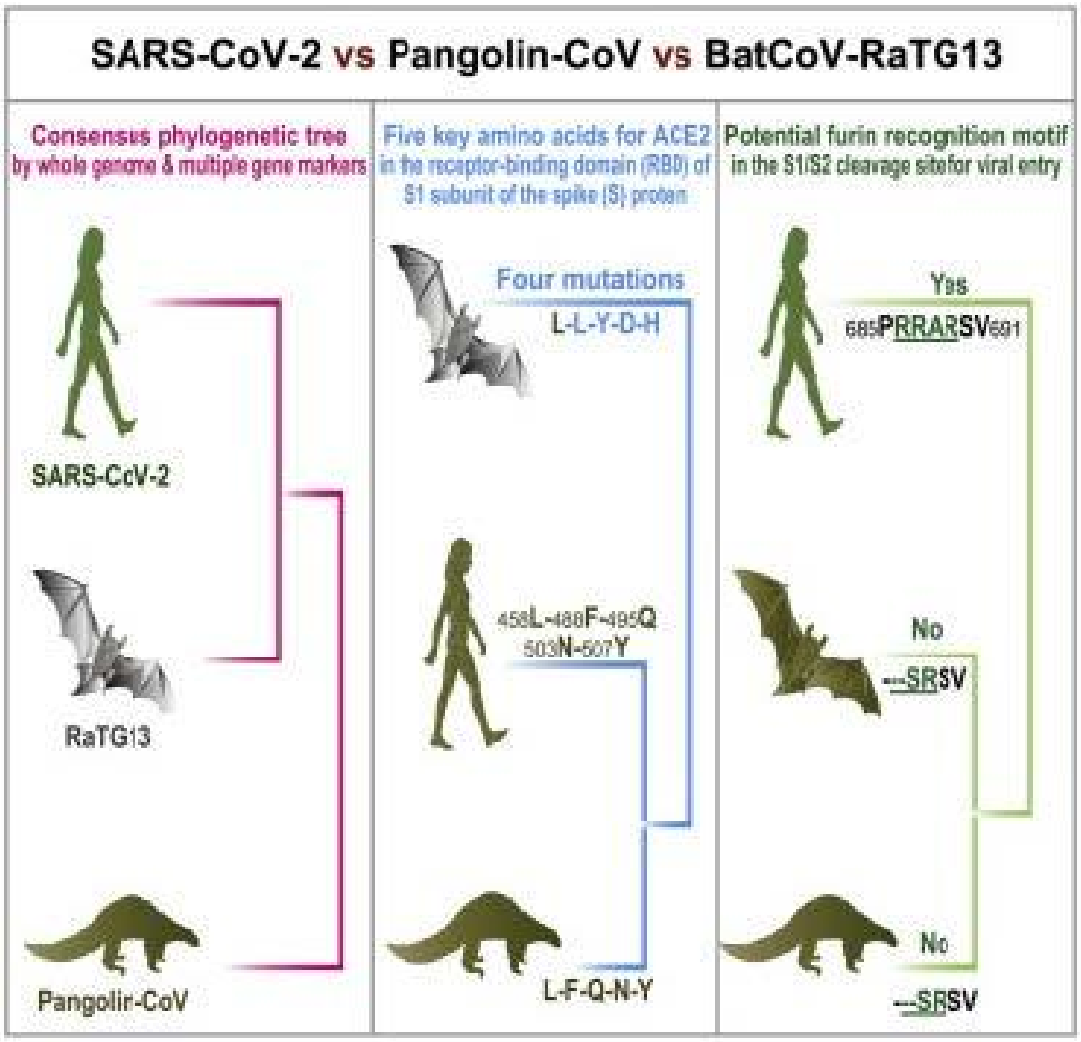
Building upon the evidence, we further postulate a synthetic route for SARS-CoV-2, demonstrating that the laboratory-creation of this coronavirus is convenient and can be accomplished in approximately six months.

Our work emphasizes the need for an independent investigation into the relevant research laboratories. It also argues for a critical look into certain recently published data, which, albeit problematic, was used to support and claim a natural origin of SARS-CoV-2. From a public health perspective, these actions are necessary as knowledge of the origin of SARS-CoV-2 and of how the virus entered the human population are of pivotal importance in the fundamental control of the COVID-19 pandemic as well as in preventing similar, future pandemics.

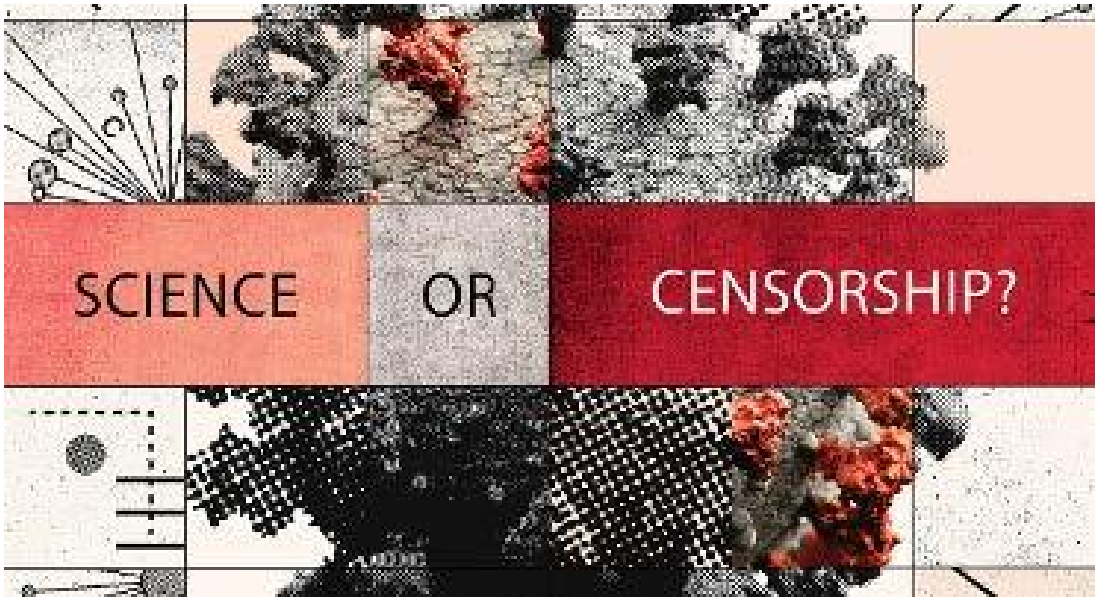
Introduction From: Li-Meng Yan (MD, PhD), et al.

The origin of SARS-CoV-2 is still the subject of much debate. A widely cited Nature Medicine publication has claimed that SARS-CoV-2 most likely came from nature. However, the article and its central conclusion are now being challenged by scientists from all over the world. In addition, authors of this Nature Medicine article show signs of conflict of interests raising further concerns on the credibility of this publication.

The existing scientific publications supporting a natural origin theory rely heavily on a single piece of evidence – a previously discovered bat coronavirus named RaTG13, which shares a 96% nucleotide sequence identity with SARS-CoV-218. However, the existence of RaTG13 in nature and the truthfulness of its reported sequence are being widely questioned.

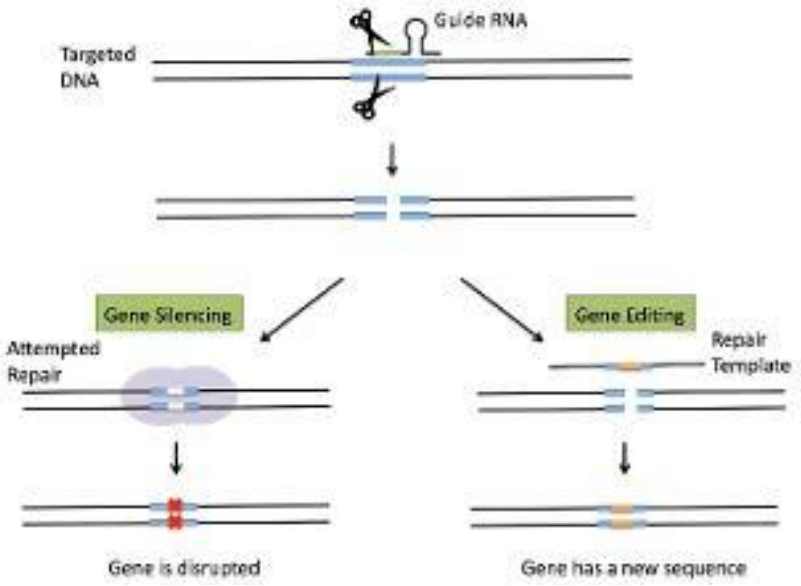


It is noteworthy that scientific journals have clearly censored any dissenting opinions that suggest a non-natural origin of SARS-CoV-2. Because of this censorship, articles questioning either the natural origin of SARS-CoV-2 or the actual existence of RaTG13, although of high quality scientifically, can only exist as preprints or other non-peer reviewed articles published on various online platforms. Nonetheless, analyses of these reports have repeatedly pointed to severe problems and a probable fraud associated with the reporting of RaTG13.



Therefore, the theory that fabricated scientific data has been published to mislead the world's efforts in tracing the origin of SARS-CoV-2 has become substantially convincing and is interlocked with the notion that SARS-CoV-2 is of a non-natural origin.

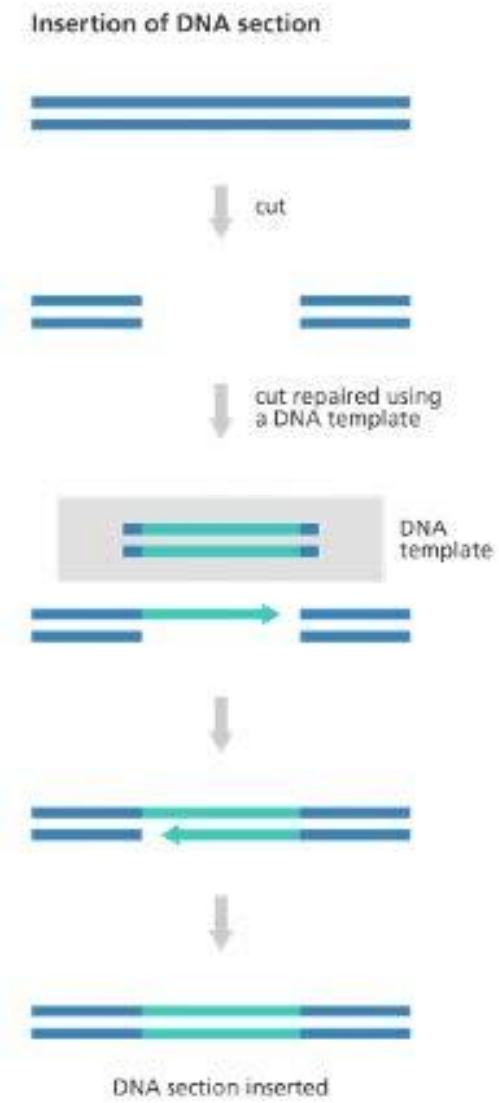
Consistent with this notion, genomic, structural, and literature evidence also suggest a non-natural origin of SARS-CoV-2. In addition, abundant literature indicates that gain-of-function research has long advanced to the stage where viral genomes can be precisely engineered and manipulated to enable thecreation of novel coronaviruses possessing unique properties. In this report, we present such evidence and the associated analyses.



Part 1 of the report describes the genomic and structural features of SARS-CoV-2, the presence of which could be consistent with the theory that the virus is a product of laboratory modification beyond what could be afforded by simple serial viral passage. Part 2 of the report describes a highly probable pathway for the laboratory creation of SARS-CoV-2, key steps of which are supported by evidence present in the viral genome.

Importantly, part 2 should be viewed as a demonstration of how SARS-CoV-2 could be conveniently created in a laboratory in a short period of time using available materials and well-documented techniques. This report is produced by a team of experienced scientists using our combined expertise in virology, molecular biology, structural biology, computational biology, vaccine development, and medicine.

(End of Li-Meng Yan (MD, PhD), et al.)



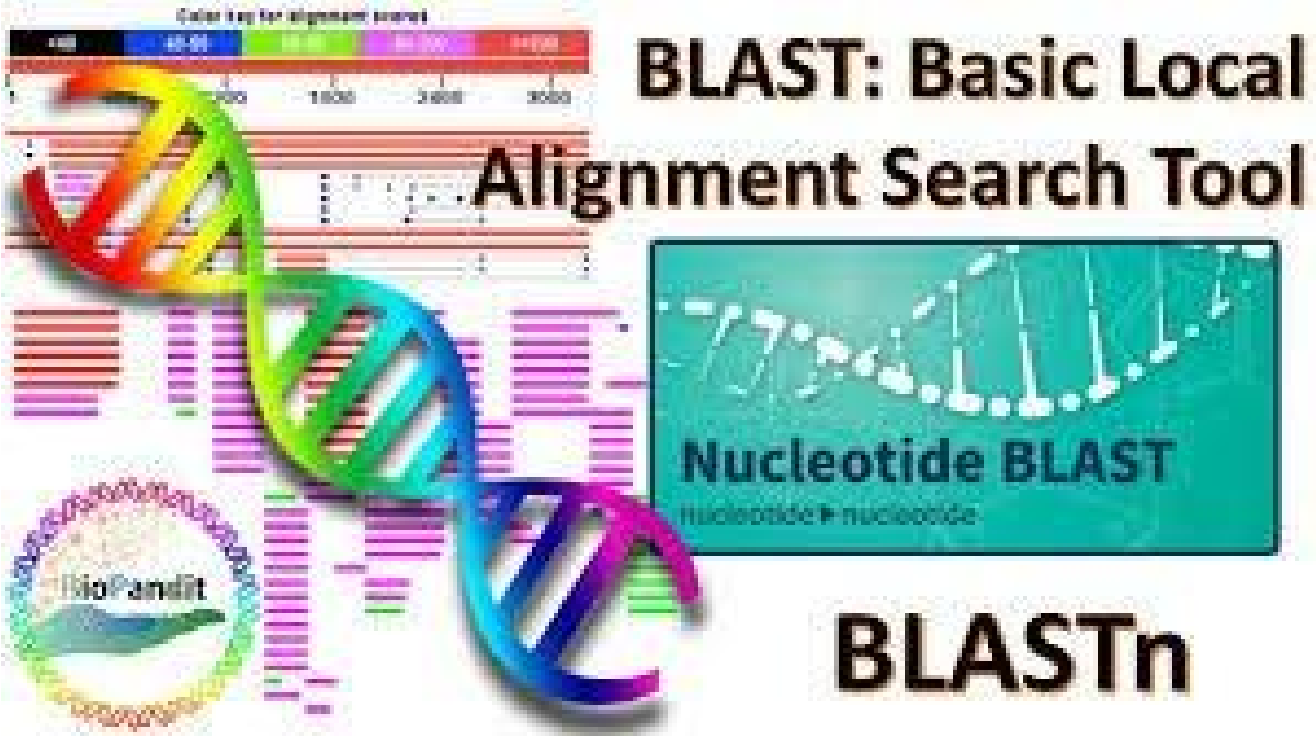
Excerpts taken from the following paper serve as introduction to the extensive and complex data of sample strains of 2019-nCoV/COVID-19. The author's findings are derived from numerous sample sites around the globle, not simply the original singular RNA genomic sequence from China. We recommend following the arrow link to the orginal document.

COVID-19, SARS AND BATS CORONAVIRUSES GENOMES PECULIAR HOMOLOGOUS RNA SEQUENCES

Jean Claude Perez, Luc Montagnier

DOI: https://doi.org/10.29121/granthaalayah.v8.i7.2020.678

We must recall here that the BLASTn analysis on April 10, 2020 option "SARS coronaviruses" reports 386 occurrences including 16 bats, 2 Rhinolophus, and 368 COVID_19. The same research running on 16 april 2020 reveals 523 strains sequences. The number of COVID_19 sequences available is therefore constantly changing principally due to USA new sequences deposits.



We were interested in the first cases of significant COVID_19 mutations in this key region of 225 bases (homologies of the order of 96%). we find 5 of them located in the BLASTn just in front of and near RaTG13, all come from the USA, taken and sequenced in April 2020, pathogenic.

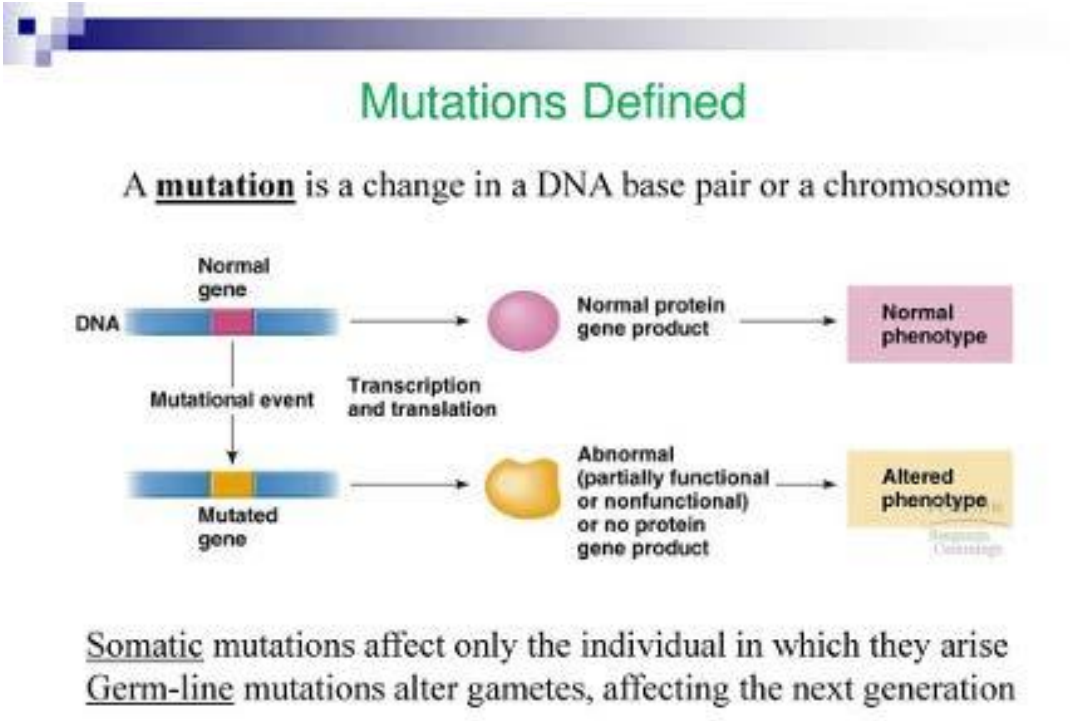
A BLASTn analysis dated April 11, 2020 produces the following results: 386 sequences in total, whose:

351 strains with full 100% homology with 225 bases area.

17 strains with mutations in 225 bases area.

18 strains bat.

Now let's look at these 17 cases of mutations in the 220 bases region.



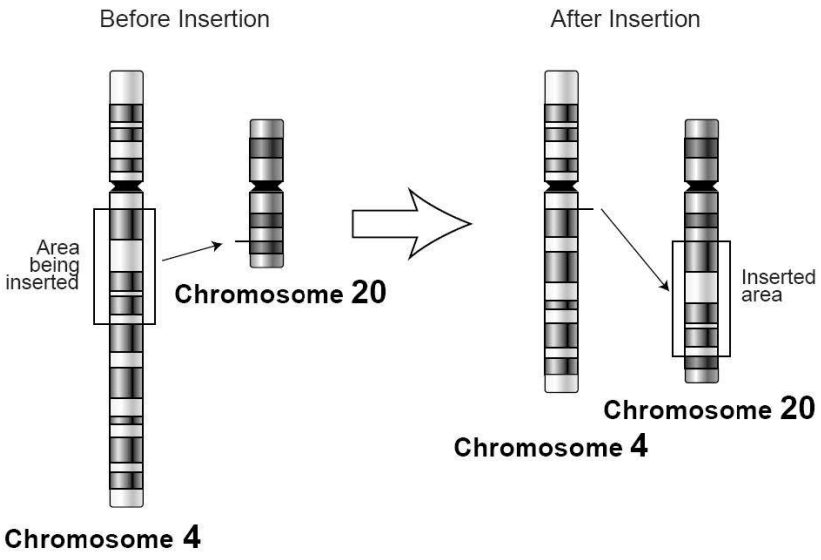
We observe that out of these 17 cases of mutations, the majority of them (13/17) concern the USA with dates posterior to the Chinese origin of the pandemic. Only 3 relate to China and one to Finland. There is probably the beginning of a mutation strategy of the genome to balance and integrate exogenous HIV EIE.

9 of these 17 mutations directly affect an HIV / SIV region. The others affect the intermediate region separating the 2 and 2 HIV / SIV pools.

It will also be noted that the majority of these strains come from recent samples (12/17 have dates of collection posterior or equal to March 2020). These dates would therefore correspond to a "mature" period of the COVID_19 genomes, which have now entered a phase of diversified mutations.

Finally, we observe the repetition of several mutations, proof of a robust mutation strategy which eliminates the hypothesis of sequencing errors.

We note that 5 different HIV/SIV EIE and 5 mutations regions are matching within the 17 different COVID_19 strains.



Revelation 13

16 And the second beast required all people small and great, rich and poor,free and slave, to receive a mark on their right hand or on their forehead, 17 so that no one could buy or sell unless he had the mark—the name of the beast or the number of its name. 18 Here is a call for wisdom: Let the one who has insight calculate the number of the beast,for it is the number of a man,and that number is 666.

"18 RNA fragments of homology equal or more than 80% with human or simian retroviruses have been found in the COVID_19 genome." **- Dr. Montagnier and Jean Claude Perez:**

"If not now, then when?" **- Anthony and Kathleen Patch**