Covid-19 Is A Retrovirus

The important point of this article to remember is that this is a **"Bioweapon".** For those of you that do not understand what a "bioweapon" is, it is a pathogenic element that has been jacked-up to increase its damage, harm, or death. The Cambridge Dictionary defines it as:

a living substance, such as bacteria, used to intentionally cause damage or death to people, animals, or crops:

•The highly infectious plague bacterium has been seen as a possible bioweapon.

• A future bioweapon attack could involve antibiotic-resistant strains of anthrax.

What has been called Covid-19 is not a virus, it is a Retrovirus, and became a bioweapon, by what was added to and it was copied into the human genome as RNA.

This article will contain all the essential information, along with all the scientific information that may not be essential for the reader. It was a challenge for me to decide what to leave out for ease of reading. It is important that you know this is the truth about the "Gain-of-Function" issue of which Senator Rand Paul of KY was trying to get Dr. Anthony Fauci to admit to in his Senate hearings on Covid-19. Dr. Fauci is plain and simple a liar, a fraud, a criminal, and a murderer.

Nobody to this point in the media has addressed this as Dr. David Martin states, call it for what it really is: A "Bioweapon", there is no better or accurate way to describe it. When you read the content, you can skim past the technical data and focus on the non-technical data. I've included technical material to corroborate the truth of what this really is about: making people ill, and degrading their immune system over time with the poison vaxxes. The perpetrators of this insidious scheme reveal their skill and even from the type of lab this "Gain-of-Function" was performed.

This proof puts to rest the initial lie we were told that Covid-19 was a "novel rogue virus from nature", it was not any of that!

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.

The RNA-based vaccine 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 nano-materials such as gold and diamond (functioning as bio-sensors inside the human body). Working in tandem 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 fragment s 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 morbidity, without an increase in mortality.

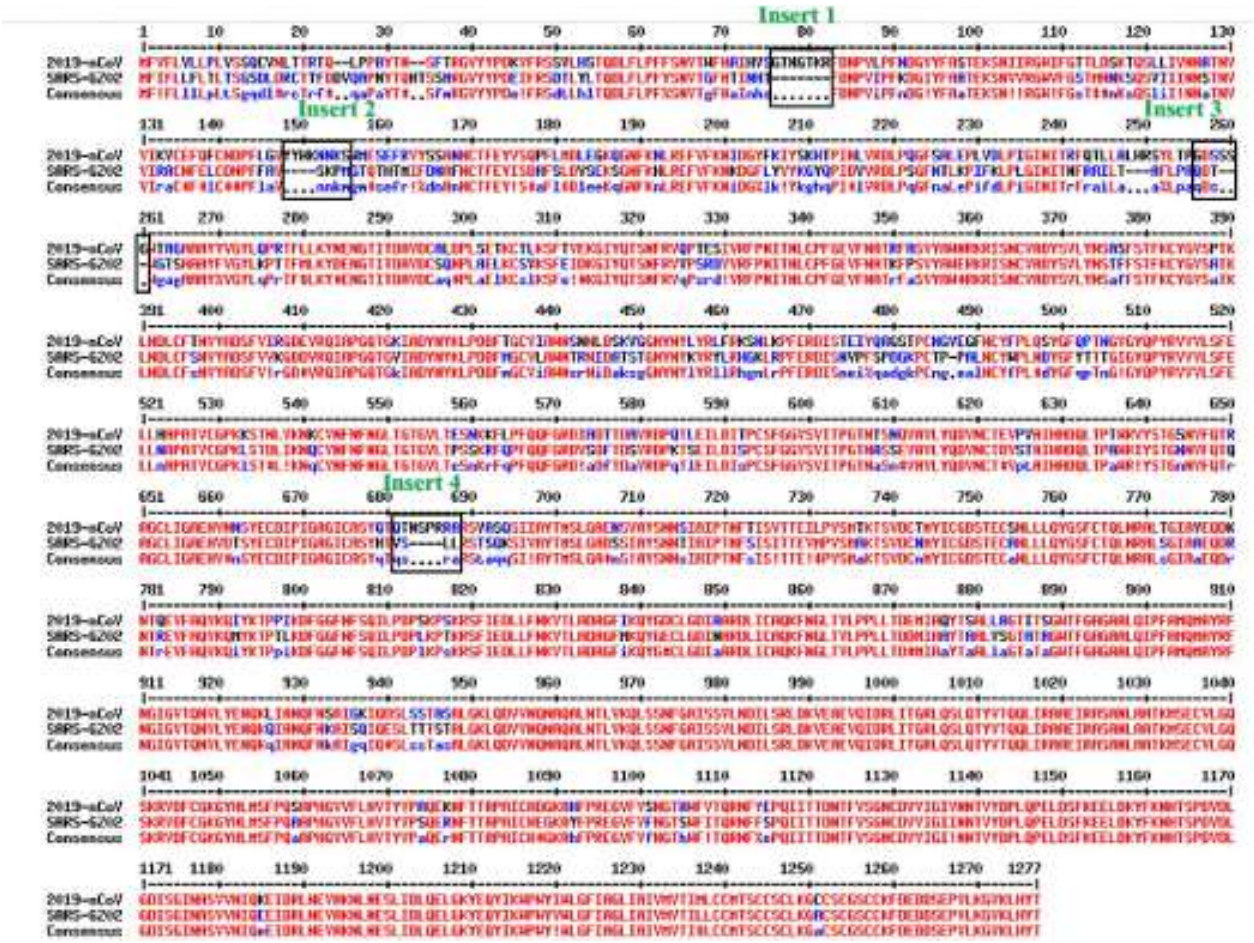
The grand delusion of 2019-nCoV/COVID-19 and its attendant mainstream narrative proclaiming the virus being of natural origin, has obfuscated verified scientific evidence to the contrary. Specifically, not 4, or 6, but 18 genomic fragment s (inserts) of HIV-1 (Human Immunodeficiency Virus) have deliberately and artificially been placed within the overall genome of Covid-19, a single-stranded RNA (Ribonucleic acid) virus, or 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 fragment is to promote viral entry into a host cell. Not only entry of HIV-1, but the 2019-nCoV/COVID-19 virus itself. The 18 fragments of the HIV1 genome contained 92% of what constitutes HIV1 pathogen. In the genome printout on the next page the four inserts are identified by a group of Indian scientists.

Infected with a viral payload of 92% of the HIV1 may not give a person AIDS, but that said, unbeknownst to the infected person, a degraded immune system has been found by scientists in several countries to date, and this degradation process reduces natural immunity between 2% and 8% a month. In the past few weeks of November, three or four sites have asked the question; *"Does the vaxx give a person HIV?"* Possibly that happened when the person was tested with the nasal swab inserted far up the nasal cavity near the blood-brain barrier. Recent findings have shown the nasal swabs were found to have contained aluminum, graphene oxide, and other impurities.

The picture below is the virus genome marked off with 4 specific areas of “inserted” genetic material. This is a string of the RNA containing the 18 fragments of HIV1 and 4 fragments of the SARS2. This is the definitive proof of what was done to the ordinary cold 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 SARSCoV (GZ02, Accession AY390556) were aligned using MultiAlin software. The sites of difference are highlighted in boxes.

The Abstract of the eleven Indian scientists states as follows:

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 ot her 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 amino acid residues in key structural proteins of HIV-1 is unlikely to be fortuious 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. 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 Balakr ishnan Menon, James Gomes, Perumal Vivekanandan, Bishwajit Kundu. (doi:https://doi.org/10.1101/2020.01.30.927871)

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.

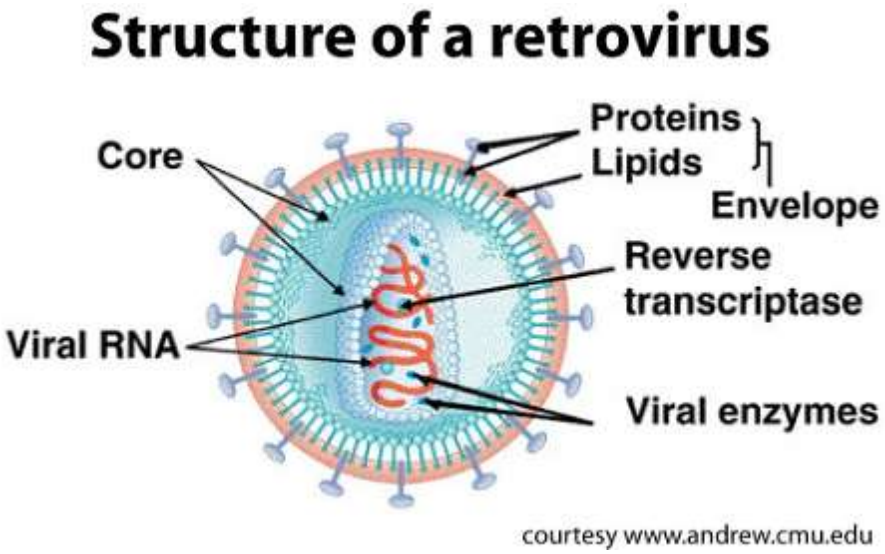
In this case, the DNA resides within the nucleus of human cells. Once fused, the DNA copy of HIV-1 and 2019-nCoV/COVID-19 permanently alters the existing DNA of the human host. The National Human Genome Research Institute describes a retrovirus, including HIV-1: a retrovirus is a virus that uses RNA 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.

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.

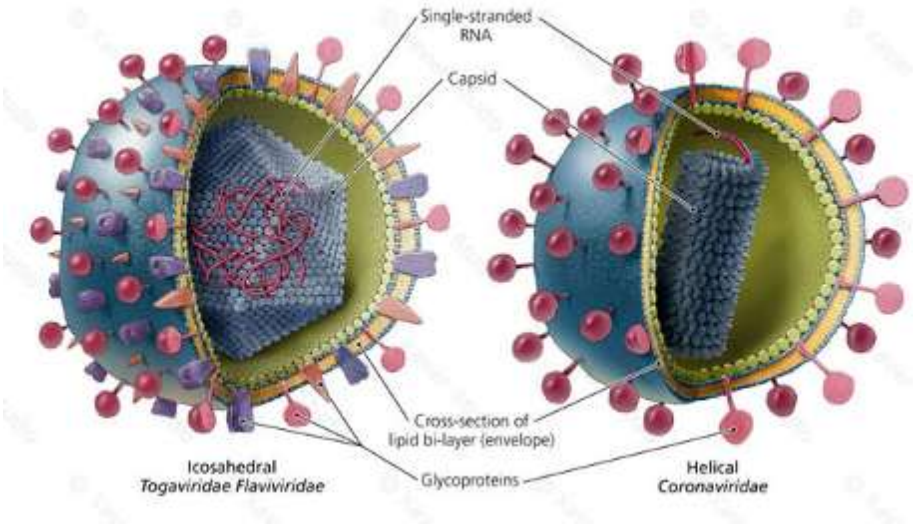
Within their respective papers, research scientists Prashant Pradhan, et al., and Dr. Montagnier and his co-researcher Jean Claude Perez noted within the complete genomic RNA sequence of 2019-nCoV/COVID-19 the fragments (inserts) of HIV-1. Meaning, the 2019-nCoV/COVID-19 virus itself exists due the presence 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.

Initially, as a single RNA strand, 2019-nCoV/COVID-19 and the inserted 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 inter twine into the familiar double helix

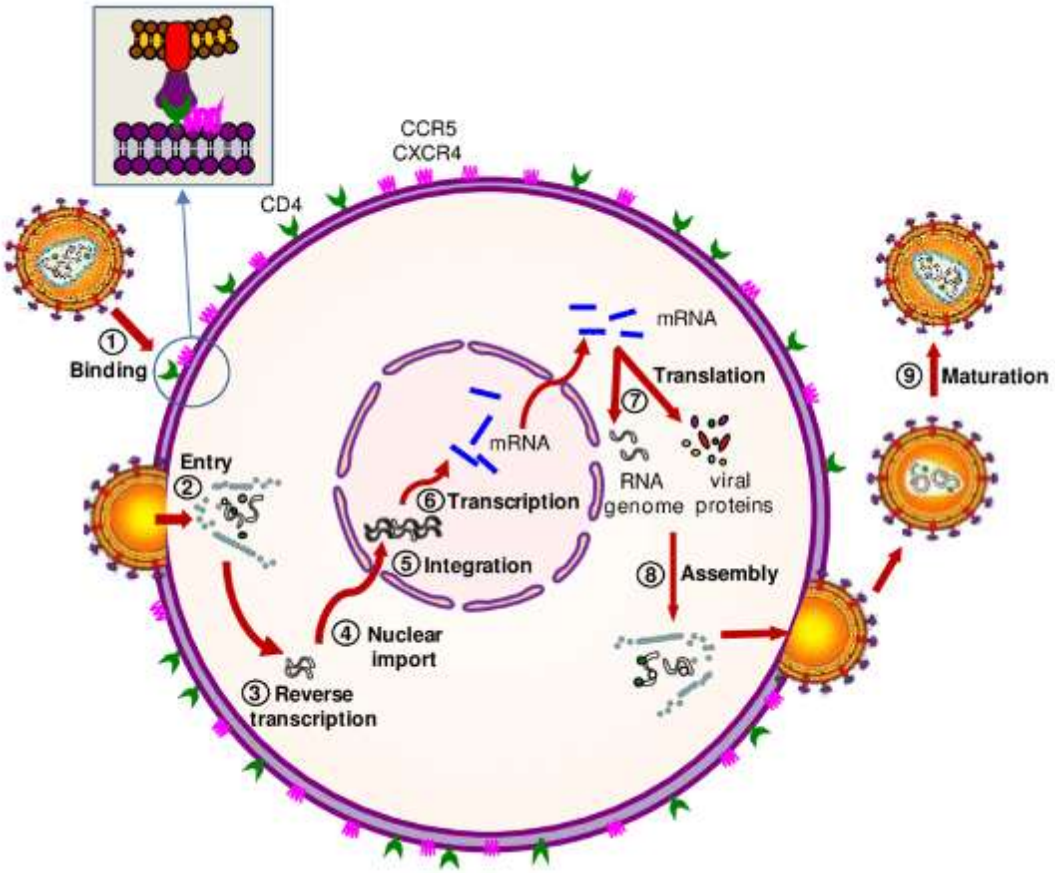


of common DNA. This is still referred to as cDNA, or dscDNA (double stranded complimentary DNA). This cDNA consists of the combined genome of 2019-nCoV/COVID-19 and HIV-1. The new cDNA (as a familiar double helix) enters the nucleus of the cell and binds to the existing DNA of the host (human) cell. This permanently changes the host DNA of this specific cell into a retrovirus: 2019-nCoV/COVID-19 and HIV-1.



HIV

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".



HIV Replication Cycle

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

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 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. 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. 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 replicate, 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

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, event of the logical 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."

Beginning at the end, we present the following corroborating evidence the 2019-nCoV/COVID-19 virus was created by man in one or more laboratories.
Rule of Law Society & Rule of Law Foundation, New York, NY, USA.
Li-Meng Yan (MD, PhD), Shu Kang (PhD), Jie Guan (PhD), Shanchang Hu (PhD)
Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route.

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

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.

3. Final remarks continued
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 noted 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 et c ..). ==> 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 Anthony Patch has gone on to state, "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 one's DNA, condemn 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 refer red 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.

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

Building upon the evidence, we further postulate a synthetic route for SARS-CoV-2, demonst rating 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 laborat or ies. 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 pivot al importance in the fundament al 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 or in 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.

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. 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 plat forms. Nonetheless, analyses of these reports have repeatedly pointed to severe problems and a probable fraud associated with the reporting of RaTG13.

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 the creation of novel coronaviruses possessing unique proper ties. 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.
(End of Li-Meng Yan (MD, PhD), et al.)

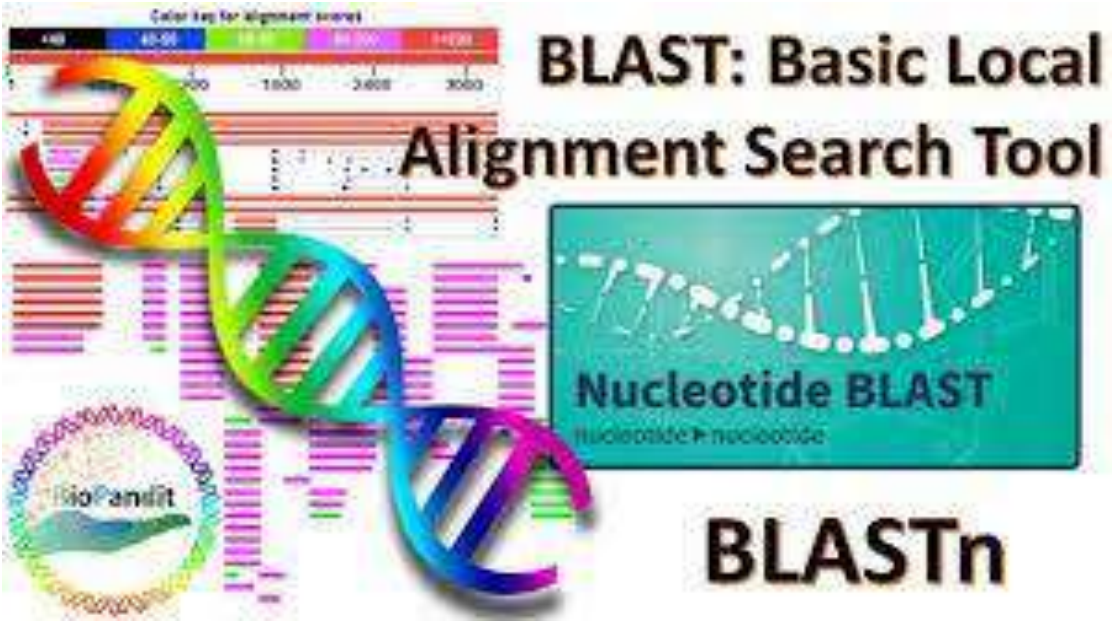
Importantly, part 2 should be viewed as a demonstration of how SARS-CoV-2 could be conveniently created in a laboratory in a short period of time using available materials and well-documented techniques. This report is produced by a team of experienced scientists using our combined expertise in virology,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

We must recall here that the BLASTn analysis on April 10, 2020 option "SARScoronaviruses" 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.

COVID-19, SARSAND BATSCORONAVIRUSESGENOMESPECULIAR HOMOLOGOUSRNA SEQUENCES
Jean Claude Perez, Luc Montagnier

DOI: https://doi.org/10.29121/grant haalayah.v8.i7.2020.678
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 globe, not simply the original singular RNA genomic sequence from China.

We recommend following the arrow link to the original document. 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 Apr il 2020, pathogenic.

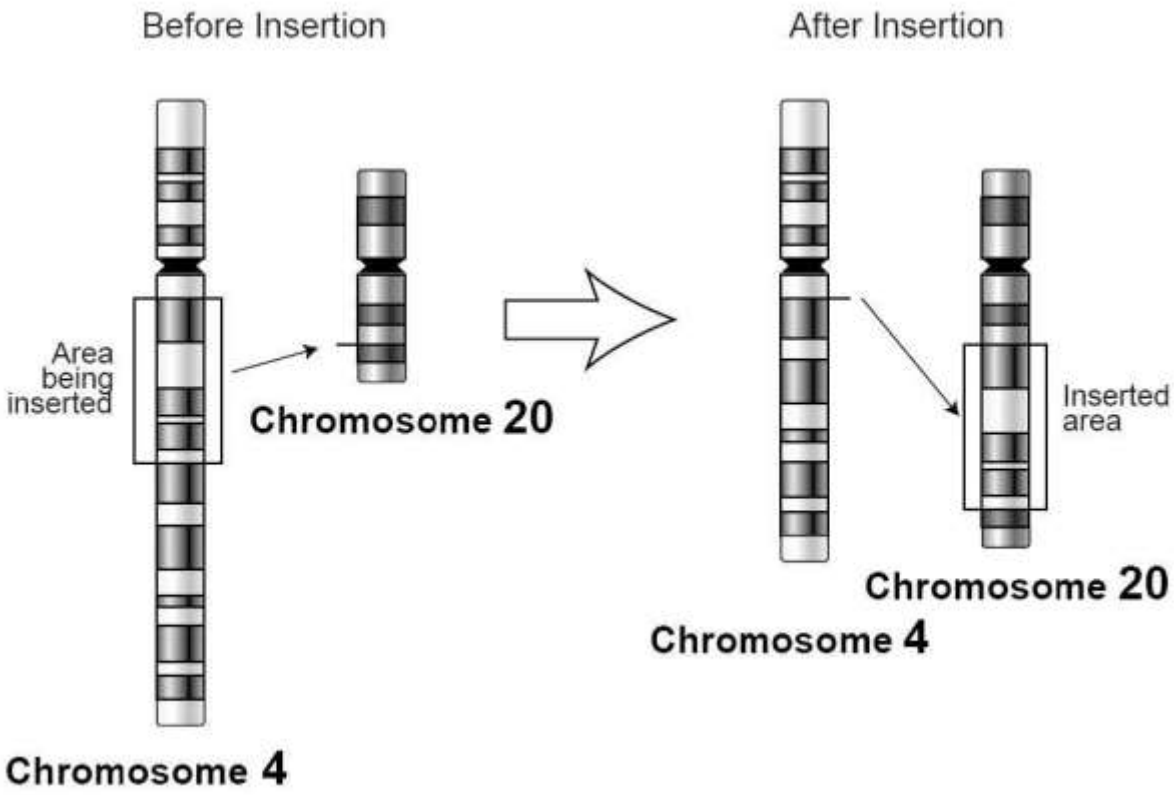


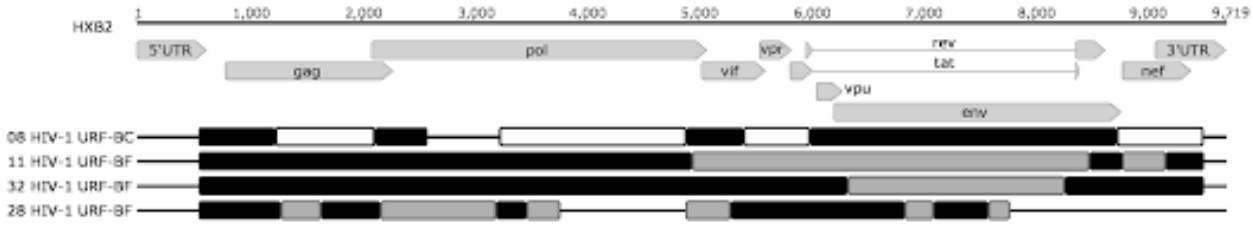
A BLASTn analysis dated April 11, 2020 produces the following results: 386 sequences in total, whose: 351 strains with full 100% homology with 225 bases area. 17 strains with mutations in 225 bases area. 18 strains bat. Now let's look at these 17 cases of mutations in the 220 bases region.

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.





Characterization of HIV-1 Near Full-Length Proviral Genome

Below are the reported variants of Covid-19 as of Thanksgiving, 2021. The scientists would have us believe that these are all the result of mutations around the world. That may or may not be true. In the news just before Thanksgiving it was reported that the African continent had few problems from Covid-19 and they were largely unvaxxed.

Part of the issue that has the public in fear comes from the fact that this virus was created on a computer and through “synthetic biology”. The spread of Covid-19 around the world in the spring of 2020 may or may not have occurred through air travel of affected travelers in tight quarters of jet commercial airliners. I suggest the spread and

dissipation of this pathogen was from the exhaust portals on commercial, military, and contract aircraft spraying these pathogens through chemtrail spraying.

This is not about a virus and public health, but rather it is about "Depopulation" agenda to remove millions if not billions off the planet. The evidence worldwide is about the escalating death rate among those fully vaxxed. The spike Protein is degrading the human immune system, and now the evidence is confirming this to be the case. Several sources in November, 2021 have been posted to the effect that people are now dying of HIV1:AIDS, and cancers along with the various blood clotting and related respiratory issues. They are reporting human immune systems degrading between 2% and 8% a month. At that rate of degradation, those having taken the 2-vaxx "gene" therapy will be dead in 18-months! Clif High and other well-known and respected physicians are predicting deaths globally to be as many as a billion people.

Having read Dr. Judy Mikovits books *'Ending Plague'* and *'Plague of Corruption'* and her knowledge of the (XMRV) gene carried unknowingly by people that received through the

blood supply and other vaccinations, Dr. Judy Mikovits estimates 55-million Americans will die after they receive the vaxxes with the spike Protein (PEG). It has to do with all those people for one reason or another that inherited the (XMRV) gene going back to the days of Chronic fatigue syndrome (CFS) a debilitating disorder characterized by extreme fatigue or tiredness that doesn't go away with rest and can't be explained by an underlying medical condition. Dr. Judy Mikovits co-discovered the (XMRV) gene of xenotropic murine leukemia virus-related virus (XMRV) in 2007. (CFS) is what Dr. Robert Gallo and Dr. Anthony Fauci colluded together later and diagnosed it to be HIV:AIDS, hoping to earn huge profits in medicines that would be required to stay alive with HIV:AIDS.

It was the French virologist Dr. Luc Montagnier, quoted in this article that first discovered HIV and was awarded the 2008 Nobel Peace Prize in Medicine for his discovery of the virus that caused acquired immune deficiency syndrome, AIDS in 1983, a year before Dr. Robert Gallo.

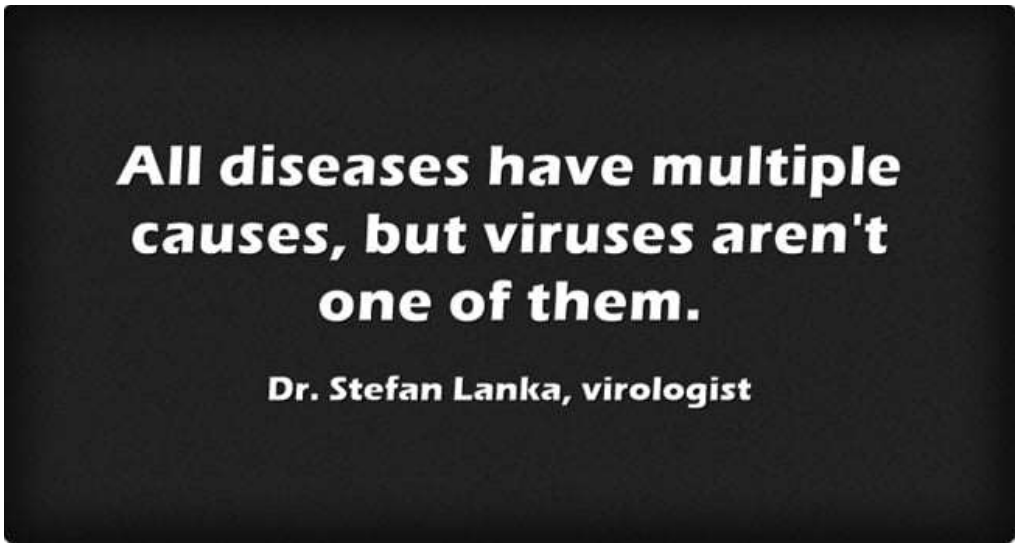
Dr. Judy Mikovits is a fighter for truth and integrity and so has fought back against those who destroyed her career and reputation. In her books, co-authored with Kent Heckenlively, JD and Dr. Francis W. Ruscetti, she sets the record straight with what is posted on the internet at the NIH site under the title of "Fake Science: XMRV, COVID-19, and the Toxic Legacy of Dr. Judy Mikovits". The PubMed piece debunks the XMRV finding by Dr. Mikovits and reveals how they set out to destroy Dr. Judy Mikovits career and reputation. With the "good old boys, including liar and criminal in chief, Dr. Anthony Fauci the major names at the NIH destroyed her career and reputation. Anyone wanting to know about Dr. Judy Mikovits should read Mikki Willis, producer of the video "VAXXED", and author of *'Plandemic: Fear is the Virus, Truth is the Cure!'*

If Dr. Judy Mikovits is correct, that 55-million Americans will die as a result of the Covid-19 vaxx "Gene" therapy shots, justice may be realized against the pharmaceutical industry which has killed millions, and done so under full impunity from legal claims. As I have pointed out in other articles, Big Pharma has a long criminal record of poisoning and killing people with impunity! The original big one was the Polio vaccine laced with SV-40 that killed millions with cancer; then there is the enzyme Nagalase found in the blood stream of children with autism. Nagalase inhibits Vitamin D synthesis in the human body and facilitates the growth of cancers. Jonas Salk creator of the Polio vaccine was involved in the Eugenics movement with Margaret Sanger and others. Polio was not a virus but caused by the spraying of DDT, and polio disappeared once spraying DDT ceased in the 1960s. It was removed from the military's use in 1965 and ultimately the chemical was banned in 1972.

According to Tucker Carlson, Christianity is dying and being replaced by a cult of coronavirus and Joe Biden is the chief apostle of the new creed. Carlson argues that America has not lost its religion. It's just replaced its religion. What's dying is the faith that created Western civilization – Christianity. In its place is a new creed, and like all religions, it has its own sacraments, its own sacred texts. It's the cult of coronavirus.

Tragically, there is an element of truth in Tucker Carlson's rant, especially now that you know Covid-19 is a **"Bioweapon"** designed to harm, disable you, weaken your natural God-given immune system with pathogens that ultimately succumb to the Jesuit poison needle of Dr. Anthony Fauci. Vaccines are the creation of the Jesuits!

As Dr. Stefan Lanka has said in court, and the evidence is on his side. The German courts decided in a legal case that he is correct. Certainly, as this article has shown the evidence that Covid-19 is not a virus but rather a **"Bioweapon".**



The world is kept in fear by those with disingenuous purposes, to fatten their bank accounts, to kill off "useless eaters" as stated by Dr. Henry Kissinger, and to reduce the world's population by 15% as stated by Bill Gates of Microsoft fame, or as Dr. Peter Daszak stated his famous quote, *"We must create 'hype' to get the public to buy off on what now is a gene therapy being illegally marketed as a vaccine so that the human race becomes dependent forever on the modified genetics created by a vaccine industry out of control."* Then there is the Herland Report: Covid Fascism: *"Man is born free but everywhere is in chains."*—Jean-Jacques Rousseau

The Herland Report is more likely closer to the Agatha Christie fan today. *"We are moving fast down the road to fascism. This COVID-19 pandemic has shifted us into high gear.*

The heavy-handed collusion between the Techno-Corporate State and the U.S. government over vaccine mandates is merely the latest manifestation of the extent to which fascist forces are working to overthrow our constitutional republic and nullify the rights of the individual, writes John Whitehead."

We know with total certainty that Covid-19 is a **"Bioweapon"**, now all we need do is to have someone come forth with the real reason why it was released upon the public. It resembles the film *"Murder on the Orient Express"* when Inspector Hercule Poirot said *"there are too many clues!"* Agatha Christie would have a field day with this! The military-industrial-pharmaceutical complex wants us dead if we refuse to be their guinea pig lab rats. If not, then why would the Australian army have begun forcibly removing residents in the Northern Territories to the Howard Springs quarantine camp located in Darwin?

Northern Territory government is force vaccinating the people in the community, *"using military, using foreign military, foreign police officers, local military and local police officers to pressure our people into taking this "bioweapon"* he says. *"They are not informing the people, they are lining them up."*

An anonymous poster has detailed their experiences in an Australian quarantine camp. The poster claims he was confined after flying into Australia from Singapore.

Despite being vaccinated and having taken 3 tests on his trip, which were all negative, he was forced to attend the camp.

In the post, the writer says that he was forced onto a bus with blacked-out windows by armed guards for a two-hour ride to the quarantine camp. Inmates are allegedly forced to take the vaccine, but also tested regularly and watched by cameras and armed guards. Detainees are charged $2,500 for their two-week involuntary stay.

Although the inmates have internet, which is presumably monitored, GPS is blocked, making them unable to determine exactly where they are. However, other posters suggested that he was imprisoned at the Howard Springs 'National Resilience Center'.

"They asked me about if I was vaccinated, I declined to answer, they threatened me and told me to come with them and called for backup, I was questioned, told to follow them and I boarded a bus with others and we had to sit rows apart and we were brought here. Windows were blacked out."

"I don't know how long I can post here but I came to let you know it is worse than you know."

"There was a girl here who fought a guard and we haven't seen her for six days since then."

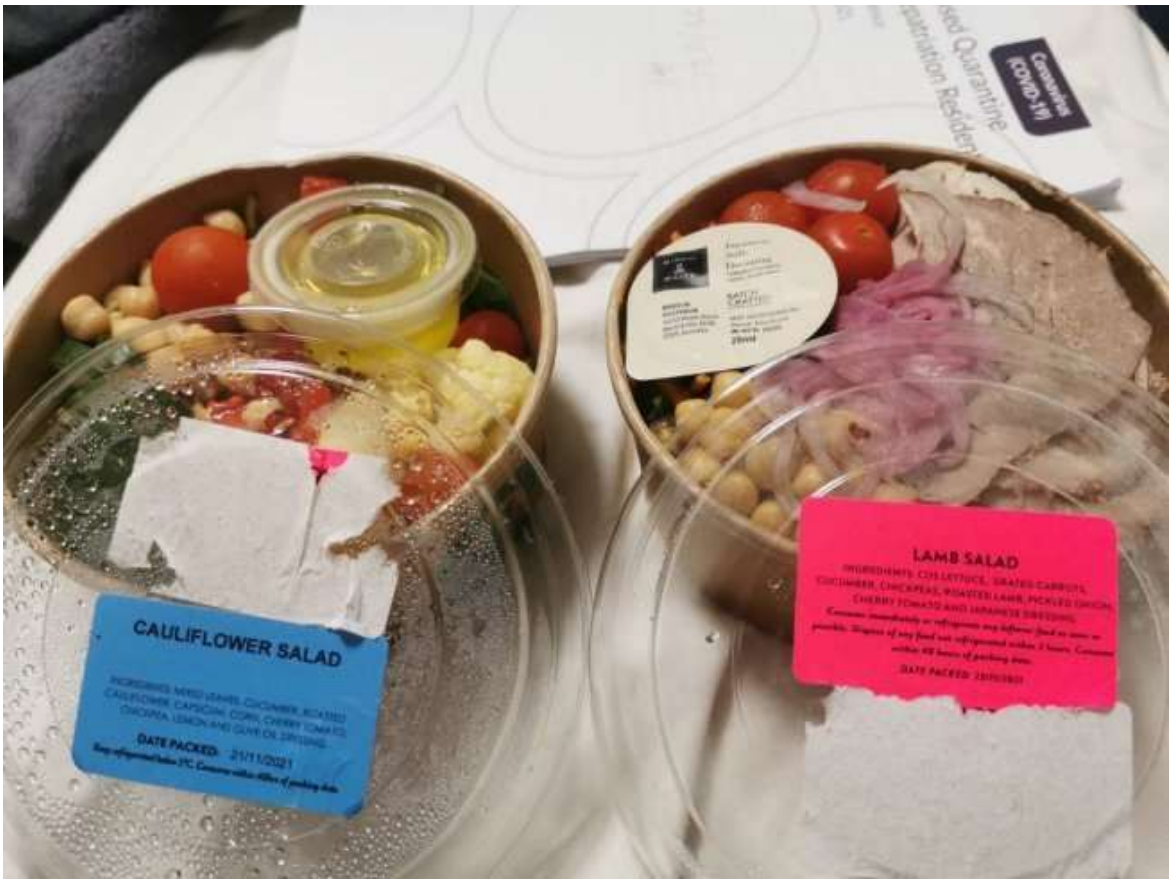
"Another anonymous poster claimed he was next door to a 77-year-old man who had recently drunk himself to death after being repatriated. He further claimed that detainees could only leave their rooms once every 3 days to do laundry, that there were armed police 'everywhere', and that you would be yelled at if you stopped or walked too slow."

"The poster does however report that the food is 'pretty good' and dropped off to inmates once a day at 6 pm. They get one hot and two cold meals."

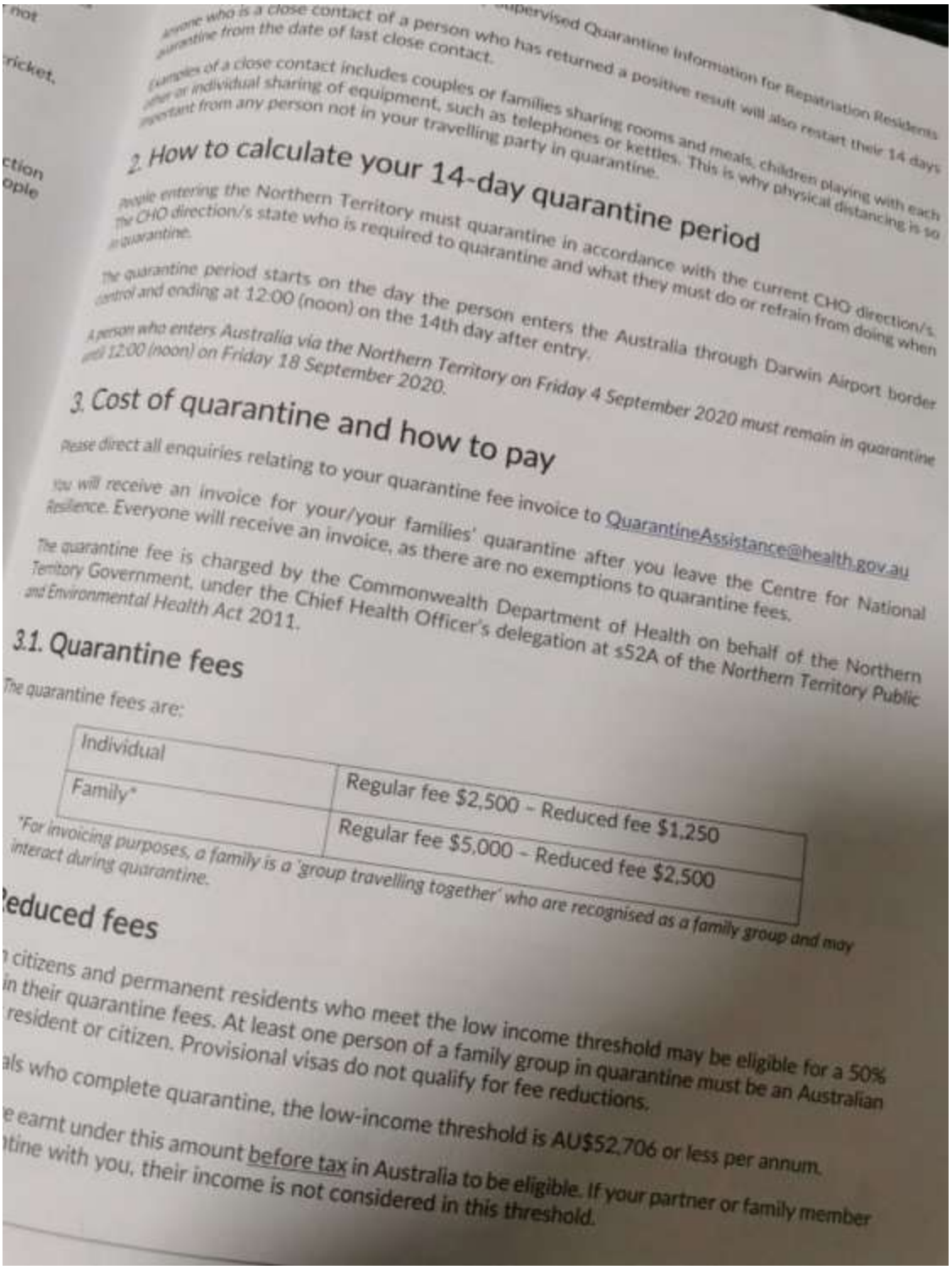
"The anonymous poster claimed he did not have the $2,500 to pay for his 'stay', and wondered what would happen if he didn't pay. He also said he would comply with whatever the guards ordered 'within reason'."

The Howard Springs facility has been in the news recently due to the decision of the Northern Territory government to begin forcibly shipping 38 aboriginal people from Binjari to the camp. The facility has the capacity to house 3,000 people; 2,000

international and 1,000 domestic travelers. It is unknown how many people are currently detained at the camp.



An example of food served to inmates at the camp



Supervised Quarantine Information for Repatriation Residents

Anyone who is a close contact of a person who has returned a positive result will also restart their 14 days quarantine from the date of last close contact.

Examples of a close contact includes couples or families sharing rooms and meals, children playing with each other or individual sharing of equipment, such as telephones or kettles. This is why physical distancing is so important from any person not in your travelling party in quarantine.

2. How to calculate your 14-day quarantine period

People entering the Northern Territory must quarantine in accordance with the current CHO direction/s. The CHO direction/s state who is required to quarantine and what they must do or refrain from doing when in quarantine.

The quarantine period starts on the day the person enters the Australia through Darwin Airport border control and ending at 12:00 (noon) on the 14th day after entry.

A person who enters Australia via the Northern Territory on Friday 4 September 2020 must remain in quarantine until 12:00 (noon) on Friday 18 September 2020.

3. Cost of quarantine and how to pay

Please direct all enquiries relating to your quarantine fee invoice to QuarantineAssistance@health.gov.au

You will receive an invoice for your/your families' quarantine after you leave the Centre for National Resilience. Everyone will receive an invoice, as there are no exemptions to quarantine fees.

The quarantine fee is charged by the Commonwealth Department of Health on behalf of the Northern Territory Government, under the Chief Health Officer's delegation at s52A of the Northern Territory Public and Environmental Health Act 2011.

3.1. Quarantine fees

The quarantine fees are:

Individual	Regular fee $2,500 – Reduced fee $1,250
Family*	Regular fee $5,000 – Reduced fee $2,500

*For invoicing purposes, a family is a 'group travelling together' who are recognised as a family group and may interact during quarantine.

Reduced fees

n citizens and permanent residents who meet the low income threshold may be eligible for a 50% in their quarantine fees. At least one person of a family group in quarantine must be an Australian resident or citizen. Provisional visas do not qualify for fee reductions.

als who complete quarantine, the low-income threshold is AU$52,706 or less per annum.

e earnt under this amount before tax in Australia to be eligible. If your partner or family member ntine with you, their income is not considered in this threshold.

Page from information booklet given to inmates

Blessings, God Help Us All!

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www.pastorbobreid.com
http://jesusisthewaythetruththelife.com/node/22