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COVID-19 BIO-WARFARE AND THE 21ST CENTURY PANDEMIC

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I helped my Mona out of our hole. I warned her to keep her hands away from the blue-white frost and to keep her hands away from her mouth, too. "Death has not been quite so easy to come by," I told her. "All you have to do is touch the ground and then your lips and you're done for."

-- Kurt Vonnegut (*Cat's Cradle*. 1964)

In *Cat's Cradle*, Kurt Vonnegut satirically depicts quirky Nobel Prize physicist Felix Hoenikker as "one of the so-called 'fathers' of the first atomic bomb." On the day Hiroshima was bombed, Hoenikker was home in his study "wearing pajamas and bathrobe ... smoking a cigar ... playing with a loop of string ... [making a] figure called 'cat's cradle'." He usually didn't "bother with made-up games when there were so many real ones going on."

As described by his son, Hoenikker was one of "the best-protected human beings who ever lived. People couldn't get at him because he wasn't interested in people. I remember one time, about a year before he died, I tried to get him to tell me something about my [deceased] mother. He couldn't remember anything about her."

After Hiroshima, the marines were griping about mud. They wanted the swamps to freeze so their vehicles wouldn't bog down. Hoenikker discovered a crystal form of ice not known on Earth. Dubbed Ice-9, it was blue-white and had a melting point of 114.4°F. One such crystal dropped into a swamp would seed the entire swamp to Ice-9. All water leading to, flowing from, or connected to the swamp in any way would freeze as Ice-9. Humans, made largely of water, would become blue-white statues if a seed crystal got inside.

Possibly because of a rare pang of conscience, Hoenikker destroyed all his records and equipment, put his Ice-9 chip in a bottle, pocketed the bottle and headed home to spend Christmas with his children. But he died on Christmas Eve with only his children knowing about Ice-9 – children described as 'babies full of rabies'. Each of them had a chip of Ice-9 seeded from their father's crystal. What "was coming into bloom was that crystalline form of water, that blue-white gem, that seed of doom called Ice-9."

Cat's Cradle weaves a satiric chain of events leading to the "moist green Earth" becoming a "blue-white pearl." Maybe Vonnegut overdid irony; but did he? We now have COVID-19.

The Coronavirus Disease of 2019 (COVID-19) has put the world on lockdown. It is extremely contagious and, once contracted, infection spreads rapidly. The official story is that it mutated naturally from a less dangerous coronavirus strain. Evidence belies that story. I will show in

this paper that the COVID-19 virus is a genetically-engineered biological-warfare weapon of mass destruction. A glossary is appended for the reader's reference.

INTRODUCTORY MATERIAL

What is the Coronavirus that causes COVID-19?

There are four genera of Coronaviruses (CoVs) – informally called *Alpha*, *Beta*, *Delta*, and *Gamma* – that infect animals and birds. Six species (seven strains), all from the *Beta* genus, can infect humans. Four of them are mild with only common cold symptoms. The other two species (three strains) can cause severe respiratory diseases. They are:

- Middle East Respiratory Syndrome coronavirus (MERS-CoV) that causes the Middle East Respiratory Syndrome (MERS).
- Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) that causes the Severe Acute Respiratory Syndrome (SARS).
- Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2) that causes the Coronavirus Disease of 2019 (COVID-19).

SARS-CoV and SARS-CoV-2 are strains of the same species.

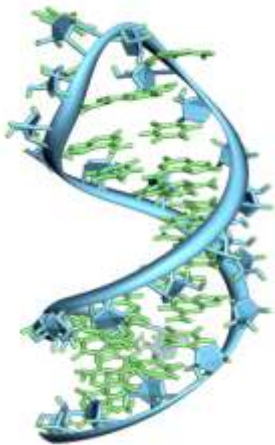


Figure 2 – A Hairpin RNA Loop. By Vossman - Own work, CC BY-SA 3.0, <https://commons.wikimedia.org/w/index.php?curid=7115139>

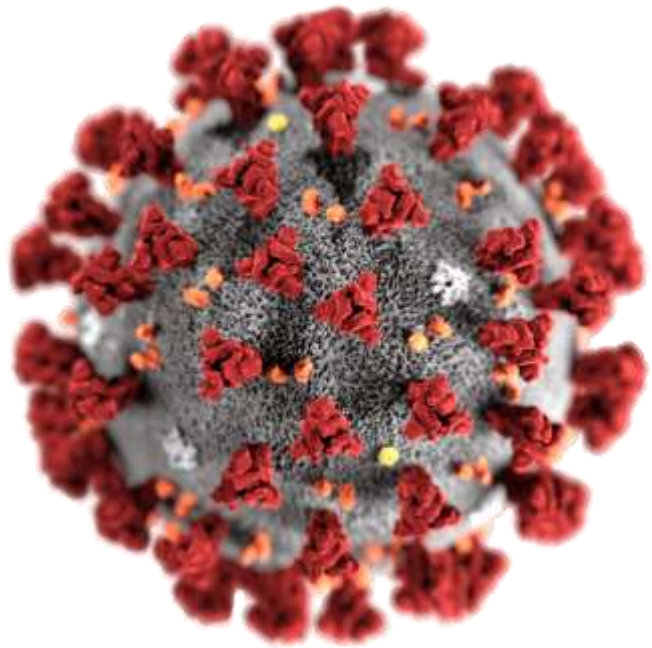


Figure 1 - SARS-CoV-2 Depiction

Source: Center for Disease Control and Prevention's Public Health Image Library, identification number #23312; SARS-CoV-2 (CDC-23312).

The viral envelope (protein shell) gives the virus its shape and contains the RNA. Covering the viral envelope is a lipid bilayer membrane (shown in grey in Figure 1).

Embedded in the lipid bilayer are the envelope protein (yellow) and membrane protein (orange); which are structural proteins that relate to the virus and its lipid bilayer.

The spike proteins (red) are the most distinctive. They are what attach/bind to a host receptor. The spike protein properties determine what host cells the virus will interact with. An average virus has 74 spikes proteins.

The SARS-CoV-2 RNA is single-stranded and positive-charged. Figure 2 illustrates a hairpin RNA loop that is a single strand folded back upon itself. The strand is the backbone (highlighted in blue).

Pairs of bases (green) attach to the backbone at prescribed intervals

The closed state of the spike protein is flat ribbons of protein molecules twisted into helices and folded into a three-dimensional wad (See Figure 3). SARS-CoV-2 spike proteins are normally closed until they attach/bind to a host receptor, which activates the spike. The SARS-CoV-2 spike has what is called a ‘furin-like cleavage site’ (to be explained below) as its receptor binding domain (RBD). Furins are enzymes found in the lungs, liver, and small intestines of humans. For the SARS-CoV-2 spike, they are the receptor binding motif (RBM).

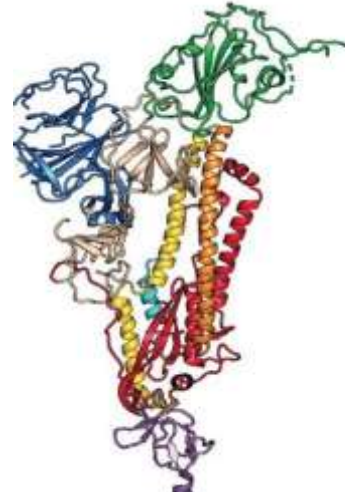


Figure 3 – Depiction of Spike Protein

Source: University of Texas

Infection takes place in two stages designated S1 and S2. The human host receptor for the SARS-CoV-2 spike protein is called angiotension-converting enzyme 2 (ACE2). The positive-charged spike protein attaches/binds to the negative-charged human ACE2. The stronger the charges, the higher the tendency to attach/bind. The higher the proclivity to attach/bind, the more contagious is the virus. This attachment/binding is the S1 stage.

However, with the spike protein closed, the viral membrane stalk cannot contact ACE2 to infect it. If furin is present, such as in the human lungs, it will cleave the ‘furin-type cleavage site’ to let the spike protein open up. The viral membrane stalk is then exposed so it can fuse to ACE2 and infect it. This fusion is the S2 stage.

After the spike protein fuses to a human ACE2 receptor, infection spreads as the virus replicates itself by dividing and multiplying in the human lungs (or liver or small intestines if it is able to reach those areas). “Recent studies have found that the [SARS-CoV-2] spike protein is between 10 and 20 times more likely to fuse to human ACE2 than the spike protein of the early 2000s SARS ...” (AssayGenie)

Some scientists say there is an intermediate stage between S1 and S2. (See Gur, et..al. Also see Dubrow) A better understanding of that intermediate stage could lead to more effective vaccines.

The official explanation of the COVID-19 pandemic is that SARS-CoV-2 mutated naturally. In this paper I will present clinical studies that indicate otherwise. I will also present evidence from which one can logically deduce that this novel virus was genetically engineered as a biowarfare weapon. In addition, I will discuss studies indicating that the spike protein can also infect parts of the human body that do not contain ACE2 receptors. But first I must present a little more background information.

Forerunners to SARS-CoV-2.

The first SARS-CoV pandemic started in Guangdong Province, China in November 2002. It spread to 27 other countries resulting in 8,095 cases and 810 deaths – a 9.6% fatality rate. The virus was contained in July 2003. A few more cases with one death occurred in 2004 because of leaks from laboratories in Beijing, Taiwan, and Singapore; but they were a less serious coronavirus.

MERS-CoV is said to have originated from bats in Saudi Arabia. Most human infections appear to have come from infected camels; either directly or indirectly from another human that had been infected by camels. Human to human transmission typically happens only through close living contact. The first human case was identified in September 2012 in Saudi Arabia. As of 2020, some 2,500 cases have been reported with a fatality rate 35%. Most can be traced back to the Arabian Peninsula. So far, there is no vaccine or treatment.

The official story is that SARS-CoV and MERS-CoV evolved naturally but some investigators say they were genetically engineered from common types of corona viruses. “The dangers are not just hypothetical [amid frequent laboratory leaks]. The H1N1 influenza strain responsible for significant morbidity and mortality around the world from 1977 to 2009 is thought to have originated from a laboratory accident.” (Lipsitch & Galvani)

Even with its high fatality rate, MERS is not a good candidate for bio-warfare due to its poor human-to-human transmissibility. SARS, however, is a good contender for future research.

The Illegality of Biological Weapons under International Law.

As fake news abounds, there is one persistent voice trying to tell people that the COVID-19 virus is a lethal biological warfare weapon of mass destruction which, besides being extremely dangerous, is illegal under the 1972 *Biological Weapons Convention* (BWC)¹. Dr. Francis A. Boyle, professor of international law at the University of Illinois College of Law, authored the book *Biowarfare and Terrorism*. He also drafted the Biological Weapons Anti-Terrorism Act of 1989 that implements the BWC treaty as US law.

The *Biological Weapons Convention* was signed in Washington D.C., London, and Moscow on 10 April 1972. It went into force when the United States ratified it on 26 March 1975. Australia ratified the Treaty on 5 October 1977 and China acceded to the Treaty on 15 November 1984. These three countries, which I will discuss below, along with 180 other Party-States, are legally bound by the provisions and prohibitions of that Treaty. A summary of the pertinent Articles follows:

- Article I “undertakes never in any circumstances to develop, produce, stockpile or otherwise acquire or retain ... biological agents, or toxins whatever their origin or method of production, of types and in quantities that have no justification for prophylactic, protective or other peaceful purposes.”
- Article II obliges all Parties States to the Treaty to destroy all the prohibited agents within six months after becoming a Party State to the Treaty.
- Article III forbids transfer of any of the prohibited agents to any recipient whatsoever, or to encourage any other to manufacture or acquire any prohibited agents.
- Article X allows “the fullest possible exchange of equipment, materials, and scientific and technological information for the use of bacteriological (biological) agents and toxins for peaceful purposes.” It also allows cooperating in “further development and application of scientific discoveries in the field of bacteriology (biology) for prevention of disease, or for other peaceful purposes.”

¹ Formal title: *Convention on the Prohibition of the Development, Production, and Stockpiling of Bacteriological (Biological) and Toxin Weapons and Their Destruction*.

The first three articles are pretty straightforward about the illegality of biological agents or toxins whose only use is warfare. Unfortunately it is not that simple. Many such agents are alleged to have a dual peace/war use. Article X allows production of those agents that can be claimed to serve peaceful purposes, regardless of their warmaking capability. All the funding agency has to do is claim it needs to build a bioweapon to understand how to defend against it, or to make a vaccine to counter it – and that they do profusely.

As an example, Boyle points out that the Galveston National Laboratory in Texas “say their work with Ebola is for a vaccine, but the same technology can also be weaponized. Galveston is working to aerosolize Ebola just as Ft. Detrick worked to aerosolize Anthrax. Aerosolizing a biowarfare agent is always the tip-off to the development of a weapon to be delivered by air to human beings who will breathe it in.” (Cited in Ross)

Aerosolizing isn’t the only identifier of a bio-weapon. ‘Gain of function’ indicates that SARS-CoV-2, is a biological weapon of mass destruction.

GAIN OF FUNCTION

What is Gain-of-Function Research?

Gain-of-function (GOF) research is the alteration of an already deadly virus to be still more contagious and more infectious. In technical terms it is “the euphemism for biological research aimed at increasing the virulence and lethality of pathogens and viruses.” It is “government funded;” ostensibly “for biodefense purposes.” (AHRP) GOF research has also been justified for biomedical research to help develop a vaccine should a deadly virus mutate naturally to affect humans.

A key player in GOF research is Dr. Anthony Fauci who has headed the US National Institute of Allergy and Infectious Diseases (NIAID)² since 1984. NIAID is the agency through which the US Government funds GOF research. Ironically, Fauci has been a leading adviser in the White House Coronavirus Task Force, under two administrations, since it was established in January 2020.

Three years earlier, on 12 January 2017, just days before Trump’s inauguration, Fauci gave a speech at Georgetown University Medical Center titled “Pandemic Preparedness in the Next Administration.” One prescient statement was: “If there’s one message I want to leave with you today ... it is that there is no question that there will be a challenge to the coming administration in the area of infectious diseases.” (Cited in GUMC Stories)

In that same speech, Fauci proclaimed: “The mistake that so many people have made ... is a failure to look beyond our own borders ... not only things that are there that will come here but surprises that we’ll have.” (Cited in Golgowski) As will be described below, Dr, Fauci was well aware of what was going on at Wuhan, China and the lax safety standards practiced at the BSL-4³ laboratory there.

² NIAID is one of 27 institutes under the National Institute of Health (NIH) which in turn is under the Department of Health and Human Services (HHS).

³ Biologic Safety Level 4 (BSL-4), is the highest safety level for biological laboratories. Only BSL-3 and BSL-4 labs can work on SARS, MERS, Ebola, and other dangerous diseases.

WIV's BSL-4 laboratory near Wuhan was completed in 2015 with partial assistance from the US. (Rapoza) Documents dating back to that time indicate US worries about safety. They were so worried that the US Embassy in Beijing sent a couple delegations of US scientists to the Wuhan lab – the last on 27 March 2018. Those scientists warned Washington that coronavirus experiments taking place at the lab had potential for human transmission and warned of a new SARS-type pandemic. (See Rapoza) A 2018 internal US State Department document warning that a potential pandemic pathogen (PPP) could escape from the Wuhan lab was partially leaked to the public. It was publicly released under the Freedom of Information Act in January 2021. (See Duffy. Also see Hudson and Jones)

Boyle states that the Wuhan lab is also “a specially designated WHO [World Health Organization] research lab. The WHO was in on it and they knew full well what was going on there.” He says: “You can't really believe anything the WHO is telling you about this either, they're up to their eyeballs in it, in my opinion.” (GreatGameIndia-1)

Another key player in the coronavirus story is Dr. Zhengli Shi (infamously known as the Bat Woman). She is one of China's most experienced virologists and bat specialist; and directs the Center for Emerging Infectious Diseases at the Wuhan Institute of Virology (WIV). Shi has been involved in every step of the SARS-CoV-2 development.

Controversy over GOF research erupted in 2011 over two programs funded by Fauci's NIAID. One was headed by Ron Fouchier (the Netherlands) and the other by Yoshihiro Kawaoka (Univ. of Wisconsin & Univ. of Tokyo). They had simultaneously “modified the H5N1 avian flu virus so that it jumped from birds to mammals and between mammals.” (AHRP)

While acknowledging some advantages to the research, Dr. Andrew Pavia, Chief of the Division of Pediatric Infectious Diseases at the University of Utah, warned: “A readily transmitted H5N1 virus could be extraordinarily lethal; therefore, the risk for accidental release is significant, and deliberate misuse of the data to create a biological weapon is possible.” (Pavia)

Proponents of GOF research – those who perform the research or fund it – claim it is necessary to understand the virus. A white paper on the ethics of GOF research – paid for by the National Institute of Health (NIH), parent of Fauci's NIAID – says “Gain-of-Function 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.” (Selgelid)

Perhaps now, with the COVID-19 pandemic, those ‘responsible scientists’ finally understand how their disease causing agent will interact with human hosts and have, indeed, discovered the potential of their work to cause a pandemic.

The Nuremberg Code (1947) states that for GOF to be permissible the “degree of risk to be taken should never exceed that determined by the humanitarian importance of the problem to be solved by the experiment.”

Other scientists not biased by vested interests say the ‘degree of risk’ does indeed outweigh benefits and, considering the history of safety violations and leaks at biological research labs, GOF research could start [and has actually started] a pandemic. Virologist Simon Wain-Hobson, of the Pasteur Institute in Paris said in 2015, four years before the COVID-19 pandemic, that scientists have created a new virus that “grows remarkably well. If the virus escaped, nobody

could predict its trajectory.” (Butler) “More than 200 scientists called for the work to be halted.” (Guterl) Their objections are summarized in a paper by Marc Lipsitch and Alison P. Galvani titled “Ethical Alternatives to Experiments with Novel Potential Pandemic Pathogens.” (See References)

After invoking *The Nuremberg Code* on acceptable risks for GOF experiments, Lipsitch and Galvani point out that a potential pandemic pathogen (PPP) “program of moderate size would pose substantial risks to human lives” and, therefore, a “rigorous, quantitative, impartial risk-benefit assessment should precede further novel PPP experimentation.” Furthermore, “this risk assessment should be part of a broader international discussion involving multiple stakeholders and not dominated by those with an interest in performing or funding such research.” The US Department of Health and Human Services “requires a risk-benefit analysis to approve gain-of-function experiments on [flu] viruses, yet no such analysis has been made public, if it has been conducted.” (Lipsitch & Galvani)

“Risk evaluations surrounding biomedical research have not kept pace with scientific innovations in methodology and application,” says Lipsitch and Galvani. Alternate approaches “would not only be safer but would also be more effective in approving surveillance and vaccine design, the two purported benefits of gain-of-function experiments ...” These safer approaches “are both more scientifically informative and more straightforward to translate into improved public health ...” (Lipsitch & Galvani)

The two purported benefits of GOF studies – surveillance to defend against biowarfare and vaccine design – have both been discredited. “Current surveillance is likely inadequate to detect an emerging pandemic strain before it is too late, regardless of any warnings that PPP experimentation might generate ... it is highly unlikely that such limited surveillance could detect a pandemic viral sequence and, furthermore, spur effective mitigation actions” before the pandemic was widespread. (Lipsitch & Galvani)

Regarding helping to develop vaccines, that “claim has been denied by vaccine developers who note that many, if not all, vaccines have been developed without a detailed molecular understanding of transmission.” GOF “experiments inevitably consider only a few possible genetic pathways to transmissibility ... the precise correspondence between transmissibility [in a laboratory model] and human transmissibility remains uncertain.” (Lipsitch & Galvani)

Pause, Unpause.

Responding to this surge of concerns in the scientific community about GOF studies, the Obama White House announced a pause in federal funding for GOF research on 16 October 2014. For studies already started, however, the pause was encouraged but voluntary.

That same year, 2014, Dr. Fauci and NIAID initiated a two-phase research program on coronaviruses. The first phase “funded Zhengli Shi, and her researchers at the Wuhan lab to investigate and catalogue bat coronaviruses in the wild.” (Guterl) Thus, US-funded GOF research continued despite the pause.

Some reports say NIAID granted funds to EcoHealth Alliance – a global nonprofit focused on research related to preventing pandemics – which in turn contracted WIV for the purpose of “Understanding the Risk of Bat Coronavirus Emergence,” (See Marnin)

On 19 November 2017 the Trump administration lifted the three-year-old ban after the newly-established Health and Human Service’s ‘Potential Pandemic Pathogen Care and Oversight (HHS P3CO) Framework’ found it safe to proceed with GOF research on certain pathogens. NIH Director Francis S. Collins wrote: “I am confident that the thoughtful review process laid out by the HHS P3CO Framework will help to facilitate the safe, secure, and responsible conduct of this type of research ...” (Collins) History has shown that anything that enhances profits will be approved, and that has strong indications of being the case with GOF experiments.

”In 2019 [NIAID] committed \$3.7 million over six years for research that included gain-of-function work.” This is the second phase of the first \$3.7 million, 5-year project for collecting and studying bat coronaviruses (mentioned above) which ended in that same year, “bringing the total to \$7.4 million.” (Guterl)

When all the blinders, dollar signs, and pet projects are set aside, the only outcome of GOF research is to weaponize pathogens. Molecular biologist Richard Enbright, a biodefense expert at Rutgers University in New Jersey, said: “The only impact of this work is the creation, in a lab, of a new, non-natural risk.” (Butler)

Regarding the HHS P3CO Framework, Harvard University epidemiologist Marc Lipsitch said: “The question is how such reviews will play out in practice.” (Kaiser) COVID-19 answered that question.

SARS-CoV-2 and COVID-19

Was SARS-CoV-2 Created in a Laboratory?

Boyle bases his assertion that SARS-CoV-2 has a laboratory-induced GOF product on independent, peer-based genetic analysis. One such study, published in *Antiviral Research*, states: “Despite a high similarity with the genome sequence of [SARS-CoV] and [SARS-CoV-2], we identified a peculiar furin-like cleavage site in the spike protein of the [SARS-CoV-2], lacking in [SARS-CoV].” (Coutard, et.al) Neither is it found on any other human coronavirus or any other *Beta* coronavirus.

This furin-like cleavage site gives SARS-CoV-2 a GOF in transmissibility that is 10 times that of the earlier SARS.⁴ “Other studies have seconded the idea that the furin-like cleavage site is what makes [SARS-CoV-2] transmit so efficiently and rapidly.” (Sandolu) I’ll explain more about this furin-like cleavage site below.

Early on in the COVID-19 Pandemic, pharmaceutical companies started working on a vaccine, including Norway’s Immunor AS. Three scientists⁵ performed Immunor’s study which started by empirically analyzing how the spike protein interacts with human cells. They discovered six different *inserts*⁶ that had been placed in the SARS-CoV-2 spike protein. The furin-like cleavage

⁴ Not to be confused with the SARS-CoV-2 spike protein RBD being 10-20 times more likely to fuse to a human ACE2 receptor than the spike protein of the earlier SARS-CoV (discussed above), which is a GOF in infectivity.

⁵ The three scientists are Virologists Birger Sørensen and Andres Susrud, who are employees of Immunor, and Professor Angus Dalgleish, an oncologist at St. Georges University of London.

⁶ In virology, an *insert* is a piece of DNA/RNA that is inserted into a larger DNA/RNA strand by genetic modification.

site is one of those *inserts*. The three scientists further demonstrated that the spike can infect other human cells than ACE2. (See Sørensen, et.al., June 2020)

However, while researching the vaccine paper, the team became suspicious that SARS-CoV-2 is not a natural mutation. Biochemical analysis “suggested several features which individually seem unlikely to be the result of natural evolution and which, taken together ... make natural evolution a less likely explanation than purposive manipulation, specifically for Gain of Function.” (Sørensen, et.al., July 2020)

Sørensen and his team published a second paper the following month (July 2020) in which they addressed the forensic aspects of the SARS-CoV-2 spike protein. Pointing out that “there are 6 inserts which make the SARS-CoV-2 Spike structurally special. They are unique fingerprints of the SARS-CoV-2 Spike which deserve to be highlighted ... and there are five salient features that strengthen the case for purposive manipulation in the laboratory.” (Sørensen, et.al., July 2020) Those five salient features are:

1. *Insert* areas that provide human-like receptor binding cover almost 80% of the spike protein’s binding domain. They are mature and bind readily. “This is something that does not sit well with the hypothesis of natural evolution.” (Sørensen, et.al., July 2020)
2. The six *inserts* that attach to human-like receptors are on the surface of the spike protein, rather than throughout the folded spike, as would be the case with natural mutation. Furthermore, the *inserts* are positioned so that the positively-charged attachment area is exposed, which makes it easier for the virus to attach/bind to negatively-charged human cells. “Such a result is typically the objective of gain of function experiments to create chimeric⁷ viruses of high potency. Therefore this is a strong indicator of manipulation.” (Sørensen, et.al., July 2020)
3. The *inserts*, are concentrated near the top part of the spike protein where they are most likely to contact a human cell. “As with (2) this is more elegantly explained by an hypothesis of purposive manipulation than one of natural evolution.” (Sørensen, et.al., July 2020)
4. The spike protein configuration has another domain with a high positive charge that lies within the bounds of the spike’s RBD.⁸ Thus, the virus can bind to human receptors other than ACE2. Clinical tests show that SARS-CoV-2 can infect the sense of smell, the taste buds, red blood cells, t-cells of the lymph system, neurons, and various tissues such as what lines the inner intestinal wall. Loss of smell and taste, for instance, are early symptoms of having contracted the disease. None of these use ACE2 as receptor binding. “The concentration of high positive charge in and around the top of the spike protein and the potential to use opposite charged attachment-/co-receptors can facilitate binding and infection in the general mode of action for infectivity ...” rather than the furin-like cleavage site RBM.⁹ (Sørensen, et.al., July 2020)
5. The RBM of the new domain described in 4 above is a Dendritic Cell-Specific Intercellular adhesion molecule-Grabbing Nonintegrin (DC-SIGN). In simpler terms,

⁷ A chimera virus is a “new hybrid microorganism created by joining nucleic acid fragments from two or more different microorganisms in which each of at least two of the fragments contain essential genes necessary for replication.” (Wikipedia, “Chimera (virus)”)

⁸ RBD means Receptor Binding Domain.

⁹ RBM means Receptor Binding Motif.

DC-SIGN is “an attachment molecule for human immunodeficiency virus type 1 (HIV-1) with the potential to mediate its transmission.” (Chehimi, et.al.) This HIV insert will be discussed further in the 2010 Study below.

DC-SIGN was also shown to “enhance infection mediated by the ... S protein of Severe Acute Respiratory Syndrome Coronavirus [SARS-CoV] and might promote viral dissemination.” (Marzi, et.al.) A 2018 Study (also to be discussed below) following a Swine Acute Diarrhea Syndrome (SADS) epidemic in China indicated a further enhancement to DC-SIGN by introducing cysteine-to-cysteine bridging. Cysteine (cys) is a crystalline sulphur-containing amino acid found in most proteins.

Now, today, DC-SIGN with cys-cys electrostatic bridging has been found within the SARS-CoV-2 spike protein’s RBD. “This new cys-cys property inserted into the SARS-CoV-2 Spike does not exist in SARS-CoV and hence could not provide such charge enhancement onto the RBD and co-receptor binding by natural evolution.” (Sørensen, et.al., July 2020)

Those five salient points provide irrefutable proof that SARS-CoV-2 was purposely designed in a laboratory; and that the COVID-19 pandemic is the result of human error or intent.

Sørensen, et.al. (July 2020) discuss four studies leading up to the COVID-19 Pandemic. WIV and its BSL-4 lab at Wuhan, China were involved in all four. Likewise, Dr. Zhengli Shi, participated in all four studies and was co-author of all the reports. I will present my understanding and interpretation of how the four studies incrementally led to the laboratory emergence of SARS-CoV-2.

In 2005, following the 2002-2003 SARS pandemic, researchers from WIV announced that horseshoe bats are a source of over 300 coronaviruses. The first study to be discussed took place in 2008.

The 2008 Study.

Five of the participating scientists in this study were from WIV (including Dr. Zhengli Shi); two from the Australian Animal Health Laboratory/Biosecurity Cooperative Research Center for Emerging Infectious Diseases in Geelong, Australia; and the other three from College/Schools of Life Sciences from other Chinese Universities.

This study used the SARS-CoV and a SARS-Like coronavirus (SL-CoV) found in horseshoe bats. Chimeric constructs were prepared by inserting various SARS-CoV sequences into SL-CoVs. The findings were:

1. The SL-CoV was unable to infect any human ACE2 molecule.
2. The SARS-CoV was unable to infect any Horseshoe Bat equivalent to ACE2.
3. Chimeric combinations had various abilities to infect the human ACE2 molecule.

From this study it was determined that the SL-CoV spike protein is largely compatible with the SARS-CoV spike protein. (See Ren, et.al., 2008) It “successfully demonstrated technical capabilities to interchange RBDs [Receptor Binding Domains] between bat SARS-Like and human SARS viruses.” (Sørensen, et.al., July 2020) It required only a very short insert to give SL-CoV the ability to infect human ACE2 molecules.

The 2010 Study.

Five scientists from China's WIV (including Dr. Zhengli Shi) joined another from University of Minnesota Medical School and two from the Australian Animal Health Laboratory/Biosecurity Cooperative Research Center for Emerging Infectious Diseases; studied "ACE2 molecules from seven additional bat species and tested their interactions with human [-infectious] SARS-CoV spike protein using both HIV-based pseudotype¹⁰ and live SARS-CoV infection assays¹¹." The infection assays were performed with "HIV-1 luciferase¹² pseudotype virus carrying the SARS-CoV BJ01 [spike] protein ..." Then "the HIV/BJ01-S pseudovirus system was used to infect HeLa¹³ cells transiently expressing¹⁴ bat ACE2 or human ACE2 genes." (Hou, Peng, Yu, *et al*)

This study found that some bat ACE2 receptors were comparable to the human ACE2. Binding the HIV pseudovirus with the seven selected bat receptors filtered out the best "for further optimizing a SARS-Like [bat] coronavirus's ability to bind to human cells. ... This study provided a model system for testing the most infectious SARS-CoV-Like [bat] viruses ..." (Sørensen, et.al., July 2020) This study produced a substantial GOF for the SARS-CoV.

In early 2020 scientists in India examined SARS-CoV-2 and "found 4 insertions in the spike glycoprotein which are unique to [SARS-CoV-2] and are not present in other coronaviruses. Importantly, amino acid residues in all the 4 inserts have identity or similarity to those of the HIV-1 gp120 or HIV-1 Gag ... The finding of 4 unique inserts in the [SARS-CoV-2], all of which have identity/similarity to amino acid residues in key structural proteins of HIV-1 is unlikely to be fortuitous in nature." (GreatGameIndia-2)

French virologist Luc Montagnier – winner of the 2008 Nobel Prize in Physiology or Medicine for his 1983 discovery that HIV is the cause of AIDS – confirmed that SARS-CoV-2 contains HIV and he is 100% sure it was designed by molecular biologists. (Kitova)

The 2015 Study.

In 2013 it was discovered that certain horseshoe bats carried a SARS-Like virus with a novel spike protein having a furin-like cleavage site. This virus was designated SHC014. Shortly thereafter, WIV joined the University of North Carolina's (UNC's) BSL-3 lab at Chapel Hill to study the SHC014 virus and its ability to infect humans. That proved to be impossible. Regardless of its furin-like cleavage site, *SHC014 as it appears naturally in bats cannot infect the Humans*. It is absolutely no threat to humans in its natural form.

"Therefore we synthesized the SHC014 spike protein in the context of the replication-competent, mouse-adapted SARS-CoV backbone (we hereafter refer to the chimeric CoV as SHC014-

¹⁰ Pseudotype is a virus combined with a foreign viral envelope protein. Same a pseudovirus.

¹¹ Assay in this case means a substance undergoing analysis or trial.

¹² Luciferase is an enzyme that emits light in the presence of oxygen. It is found in nature, such as in fireflies.

¹³ HeLa is an immortal cell line used in scientific research. It is the oldest and most commonly used human cell line derived from cervical cancer cells taken on February 8, 1951, from Henrietta Lacks [HeLa], a 31-year-old African-American mother of five, who died of cancer on October 4, 1951. (*Wikipedia*, "HeLa")

¹⁴ Express in this case means to be active in the production of an organism. Using.

MA15)¹⁵ ...” (Menachery, Yount, Debbink, *et al*) That mouthful of viral terminology means they inserted the SHC014 spike protein into the RNA backbone of the SARS-CoV previously developed – a backbone with a RNA sequence that can infect the human ACE2 enzyme. SHC014-MA15 was very successful in infecting the airways and lungs of mice. This surprised the Chapel Hill scientists. Mice have an immune system similar to humans.

They then tested SHC014-MA15 on cloned surface cells of the human airway and that showed vigorous infection. The final test was on actual cultures of the cells lining the human airway and found robust infection and replication of the virus.

All of this was unexpected. The scientists involved were surprised that they could use a protein spike from a benign virus to give SARS-CoV a significant GOF. They did express uneasiness of conscience, however, reporting that further testing “must be considered in the context of the US Government-mandated pause on gain-of-function (GOF) studies. ... scientific review panels may deem similar studies building chimeric viruses based on circulating strains too risky to pursue” because the increased pathogenicity to mammals, including humans, cannot be excluded. (Menachery, Yount, Debbink, *et al*) That pause has now been lifted but the scientific review studies are still mandated by the BWC and the Nuremberg Code.

Sørensen, et.al. (July 2020) bluntly stated: “We note that what has been described here are, in fact, precisely SARS-CoV-2 properties.”

The 2018 Study.

A fatal pig coronavirus erupted in October 2016 on a pig farm in Guangdong Province, China. It spread to three other farms. By May 2017, severe diarrhea and vomiting had killed 24,693 young piglets due to severe weight loss. No known pig viruses could be detected. Virologists from WIV investigated.

Designated Swine Acute Diarrhea Syndrome Coronavirus (SADS-CoV), this mystery virus was determined to have originated from the same horseshoe bat genus as SARS. It also broke out within 100 kilometers from where the 2002-2003 SARS pandemic started. WIV virologists determined a resemblance between the SADS and SARS outbreaks in geographical, timing sequence, environmental, and causative settings.

The report on the 2018 study is vague about what the host receptor for SADS is except that it is not one of the common host receptors for SARS, such as ACE-2. The authors did allude to their ability to use and test new receptors by the procedure developed in previous studies. The ability to construct chimeric combinations of benign coronaviruses that infect human ACE2 receptors was demonstrated in the 2008 study. In 2010, virologists from WIV and others were able to insert HIV into the SARS RNA. The 2015 study developed the ability to transplant a spike protein from a wild coronavirus to a SARS backbone that would infect human ACE2 receptors.

Soernson, et.al. (July 2020) “postulate that there were 2 charged domains on SADS that are likely to contribute to attachment receptor binding ... Recollect that we have identified a similar highly charged structure on SARS-CoV-2 within the edge of the RBD ... which is brought right into the core of the RBD ... by Cys-Cys bridging of the domain. This domain can contribute [non-ACE2] binding similar to that which can be observed for SADS.” They continue:

¹⁵ MA stands for Mouse Adapted.

Taken all together, this implies that by employing insights gained after 2015, as just deduced, a further optimization of the 2015 chimeric virus for additional binding to receptors/co-receptors such as bitter/sweet upper airway epithelia receptors occurred. That would help to explain the otherwise puzzling high infectivity and pathology associated with SARS-CoV-2 and hence also help to explain the social epidemiology of its spread. (Sorenson, et.al., July 2020)

Conclusion.

In Chapter 3 of *The Goodness Field: A Guidebook for Proactive Nonviolence* I illustrate the rise of the neoconservative faction of American politics (the neocons). I tell of their blueprint for world domination – *Rebuilding America's Defenses: Strategy, Forces and Resources for a New Century* – which was released in 2000. Stiff resistance to their plan was recognized. They wrote that “the process of transformation, even if it brings revolutionary change, is likely to be a long one, absent some catastrophic and catalyzing event – like a new Pearl Harbor.” (PNAF, p. 51)

Chapter 4 depicts how the 21st Century saw the methodically-planned and dogmatically-determined implementation of that blueprint – step by disastrous step. The “new Pearl Harbor” was played out on 11 September 2001. That initiated the War on Terrorism to justify ballooning military budgets. The Constitutional Bill of Rights was gutted by the PATRIOT Act – a 342-page document with ten titles and over 150 sections that miraculously appeared just a few days following 9/11 – obviously prepared and waiting.

When Congress balked at passing the Act without scrutiny, the CIA launched its anthrax attacks. (See <http://www.plrc.org/docs/080930.pdf>) A terrified Congress quickly passed the PATRIOT Act virtually unchanged.

The Administrative Branch of government has been completely overhauled to more efficiently carry out neocon ambitions. I detail these early years of the century in *America in Peril*; with a shorter and updated version in Chapter 4 of *The Goodness Field*.

In addition to expressing the need for a “new Pearl Harbor,” the PNAC report made some other interesting ‘predictions.’ On page 60 the neocons explain how the “art of warfare ... will be vastly different than it is today [i.e. 2000 CE].” They say:

Air warfare may no longer be fought by pilots manning tactical fighter aircraft sweeping the skies of opposing fighters, but a regime dominated by long-range, stealthy unmanned craft. (PNAF, p. 60)

We have seen that prediction morph to reality. In Yemen and other countries, drone strikes dominate what used to be conventional bomber sorties – another neocon goal achieved.

In that same paragraph, COVID-19 is alluded to:

Although it may take several decades for the process of transformation to unfold, in time, the art of warfare on air, land, and sea will be vastly different than it is today, and “combat” will take place in new dimensions: in space, “cyber-space,” and perhaps the world of microbes. (PNAF, p. 60, emphasis mine.)

Farther down the page the alluding becomes more explicit:

... advanced forms of biological warfare that can “target” specific genotypes may transform biological warfare from the realm of terror to a politically useful tool. (PNAF, p. 60, emphasis mine)

That is blatant but the neocons were never known for subtlety. Then in January 2017, before the “pause” on GOF research was lifted by the Trump administration – even before Trump was inaugurated – Fr. Anthony Fauci predicted that a major pandemic would occur during the next presidency.

That prediction came true. Now, two decades after publishing their wish list, we see the neocon’s biowarfare aspirations realized in the COVID-19 pandemic. At the time of this writing, over 2.5 million people have died from it.

From the 2002-2003 SARS epidemic onward, public documents presented in this paper show an unrelenting quest to provide gain of function (GOF) for SARS. GOF studies presented herein show irrefutably that the intention of participating virologists was not to help future vaccine development. Their intention was to create a PPP that could never have mutated naturally. The sole purpose of the chimera developed is for biological warfare. Whether that be for preemptive defense or intentional offense, SARS-CoV-2 was indisputably designed in a laboratory.

Ever since the COVID-19 pandemic broke out the US government and WHO have been propagating allegations that SARS-CoV-2 is a natural mutation. For instance, EcoHealth Alliance, through which the US reportedly funded GOF research, drafted an article and orchestrated renowned scientists to publish it in the 18 February 2020 issue of the medical journal *Lancet*.

“The 27 authors ‘strongly condemn[ed] conspiracy theories suggesting that COVID-19 does not have a natural origin,’ and reported that scientists from multiple countries ‘overwhelmingly conclude that this coronavirus originated in wildlife’.” (Suryanarayanan) More objective scientists have something different to say:

Chinese scientists who wished to share their knowledge have not been able to do so and indeed since it appears that preserved virus material and related information have been destroyed, we are compelled to apply deduction to the published scientific literature, informed by our own biochemical analyses. We refute preemptively objection that this methodology does not result in absolute proof by observing that to make such a statement is to misunderstand scientific logic. The longer the chain of causation of individual findings that is shown, especially converging from different disciplines, the greater the confidence in the whole. We posit that the evidence [presented] attains a high level of confidence. ... (Sorenson, et.al., July 2020)

In this paper I have presented the logic of a considerable volume of published research papers from reputable sources from different times and various stages of development; from which it can be scientifically deduced that SARS-CoV-2 was purposely designed in a laboratory. Everything I have presented here adds up to the exact specifications of SARS-CoV-2. “These meet the criteria of means, timing, agent and place in this reconstructed historical [chain of causation] to produce sufficient confidence in the account to reverse the burden of proof.” (Soernson, et.al., July 2020)

The burden of proof has now shifted to those who insist the COVID-19 pandemic developed naturally. They must prove precisely why the data presented in this paper is wrong

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Glossary.

ACE2 - Angiotensin-Converting Enzyme 2

assay - a substance undergoing analysis or trial.

BSL - Biologic Safety Level Biologic laboratories are classified by their levels of safety – BSL-1 through BSL-4. Only BSL-3 and BSL-4 labs are allowed to work with dangerous pathogens such as SARS, SADS, MERS, Ebola, and Anthrax.

BWC - Biological Weapons Convention

chimera - A chimera is made up of varied and diverse parts, or tissues. The word comes from Greek mythology for a creature with a lion’s body, a goat’s head, and the tail of a serpent. In virology, a chimera ia a hybrid microorganism created by joining nucleic acid fragments from two or more different microorganisms.

CDC - Center for Disease Control

CIA. - Central Intelligence Agency

CoV - Coronavirus

COVID-19 - Coronavirus Disease 2019

cys – cysteine

cysteine - a crystalline sulphur-containing amino acid found in most proteins.

DC-SIGN - Dendritic Cell-Specific Intercellular adhesion molecule-Grabbing Nonintegrin.

express - to be active in the production of an organism. To use.

furin - enzymes found in the lungs, liver, and small intestines of humans.

GOF - Gain of Function

HeLa - an immortal cell line used in scientific research. It is the oldest and most commonly used human cell line derived from cervical cancer cells taken on February 8, 1951, from Henrietta Lacks [HeLa], a 31-year-old African-American mother of five, who died of cancer on October 4, 1951. (*Wikipedia*, “HeLa”)

HHS - Health and Human Services (Cabinet Department)

HIV - Human Immunodeficiency Virus; the virus that causes Acquires Immune Deficiency Syndrome (AIDS)

Insert - In virology, an *insert* is a piece of DNA/RNA that is inserted into a larger DNA/RNA strand by genetic modification.

luciferase - an enzyme that emits light in the presence of oxygen. It is found in nature such as in fireflies.

MA - Mouse Adapted

MERS - Middle East Respiratory Syndrome

NIAID - National Institute of Allergy and Infectious Diseases

NIH - National Institute of Health

P3CO - Potential Pandemic Pathogen Care and Oversight

PPP - Potential Pandemic Pathogen

pseudotype - a virus combined with a foreign viral envelope protein. Same a pseudovirus.

pseudovirus – same a pseudotype.

RBD - Receptor Binding Domain; a key part of a virus located on its ‘spike’ domain that allows it to attach to host receptors to gain entry into cells and lead to infection.

RBM - Receptor Binding Motif;

RNA - ribonucleic acid.

S1 stage – the attaching/binding of the positive-charged SARS-CoV-2 spike protein to the negative-charged human ACE2.

S2 stage – the furin cleaving the SARS-CoV-2 spike protein at the ‘furin-type cleavage site’ to expose the viral membrane stalk so it can fuse to ACE2 and infect it.

SARS - Severe Acute Respiratory Syndrome

SADS – Swine Acute Diarrhea Syndrome

SHC014 – Designation for a SARS-like Coronavirus (SL-CoV) found in Horseshoe Bats.

SL-CoV – SARS-Like Coronavirus found in Horseshoe Bats.

UNC - University of North Carolina

WHO - World Health Organization

WIV - Wuhan Institute of Virology