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Review Article

Covid Cancer Induction: "Stealth Virus" Gain-of-Function Bio Weaponized Genetic Payload and Spike Protein Mutagenesis Prompting Immunopathologies

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Abstract

The incidence of lymphatic system cancers, including multiple myloma ("MM"), lymphoma, and leukemia has increased substantially since 2020, the year "novel" mRNA vaccines and COVID-19 emerged [1]. Causation science attributes this rise in cancer rates to myriad risks other than the virus and/or mRNA vaccines. This paper presumes from published science that increases in lymphatic cancers are largely attributable to the lab engineered viral mutagen and Pfizer and Moderna vaccines derived from genetically modified "gain-of-function" viruses. Stealth virus-like pathogenesis results from the lipid nanoparticle hydrogel ("LNPH") coating of the vaccines, as well as the spike-protein ("S-protein") antigen mutating on the virus, that may cause 'smoldering' hypersensitization best explaining "long COVID" and the rise in immune cell cancers. Therapeutic focus for lyphatic cancers should target these disease vectors, particularly with anti-virals.

Keywords: Covid Cancer; Stealth Virus; Weaponized; Genetic Payload; Protein Mutagenesis

Introduction

According to Huang J, Chan SC, LokV., *et al*. [1]. and scientific concensus, the increased incidence of multiple myeloma globally is attributable to the "higher human development index, gross domestic product, prevalence of physical activity, overweight, obesity, and diabetes." Alternatively, the "fast tracked" COVID mRNA vaccines are generally ignored.

It is now generally-accepted public knowledge that the COVID-19 virus, from which the Pfizer and Moderna vaccines were derived, was bioengineered for "gain-of-function" to evade and burden the immune system. Subsequently, these "novel" genetically-modified mRNA vaccines, designed to prompt DNA production of more COVID-19 S-protein antigens to combat the spreading, unstable, and mutating bioweaponized virus, were distributed worldwide. Overlooked is the likely sensitization and hypersensitization of hosts-those vaccinated or simply environmentally infected-to repeated immune cell challenges, and resulting illnesses including lymphatic cancers following the precise pathogenesis of "stealth viruses" reported by governmental whistleblower, expert vaccine analyst, and former chief of the Bureau of Biologics-forerunner to the FDA- W. John Martin, M.D, Ph.D [2].

Consequently, if this line of reasoning is accurate, the rise in lympatic cancers attributable to latent COVID-19 "stealth virus" infections would best be treated using anti-viral drugs and/or alternative therapies targeting viral and S-protein loads.

Background

Foreshadowing COVID-19's emergence from Anglo-Asian labs under U.S Congressional scrutiny at the time of this writing, more than a quarter century ago, the author warned of dual purpose bioweapons development threatening humanity's extinction [3].

In a previous paper, the author presented his personal case study in his onset and treatment of multiple myeloma ("MM"), with pathogenesis parallelling lymphomas and immune system dysfunction as in HIV/AIDS [4]. Focus there was directed to the lab-engineering of the altered genetic sequences weaponizing the virus and S-protein antigen.

This "gain-of-function" characterizes the antigenic mutagen(s) prompting MM's B-cell memory and plasma cell progeny outputting massive amounts of anti-viral and anti-S-protein antigens called "free light chains" concomitant with amyloid destruction of bones [4]. This MM pathgenesis caused the author's severe osteolysis; bone fractures especially in the spine and ribs; severe musculoskeletal pain, paralysis, and general incapacitation.

The reviewed science [4] considered the altered mRNA COVID lentivirus genetic "payload" that evades the immune system and prompts subclinical COVID or "long COVID" and neurological symptoms such as the loss of smell.

Corroborating studies describe the "hypermutation" [5] of plasma cells by the stealthed virus, and/or LNPH- coated S-protein that would be expected to cause hypersensitization reactions following subsequent or latent infections.

With MM, as with "long COVID," the early stages of this progressive illness is "stealthed." It is distinguished clinically as assymptomic (sub-clinical) "monoclonal gammopathy of undetermined significance," ("MGUS") and "smoldering myeloma." And the progressive illness bears striking resemblance to "stealth virus" pathogenesis [2].

These scientific considerations may best explain the rise in morbidity and mortality from MM and related immune cell cancers following COVID-19's emergence followed by the global mRNA vaccination campaign, repeated infections and antigenic challenges, with increased S-protein transmissions by 'shedding,' all causing mutagenesis of host defenses.

Accordingly, this paper extends consideration into: (1) the detailed molecular biology and genetic alterations causing COVID-19 vaccination risks as reviewed by Hilscher N, McCullough PA and Marotta DE [6]; and (2) the report by Martin pursuant to "stealth virus" bioengineering and pandemic distribution via vaccinations, environmental transmissions, or lab "leaks." [7]. Finally, this study reviews promising emerging anti-viral epigenetic remedies and their basis in scence [8].

COVID mRNA Vaccine Complexity and Mutagenicity

Throughout this discussion, it must be kept in mind that in order to develop targeted vaccines against specific pathogens, you must first isolate or create the germs in a lab. This isolation or bioweaponization process is technically challenging, as is mRNA vaccine production.

Moreover, if manufactured viruses' and mRNA vaccines' genetic sequences are spliced together, they are known to be unstable and more likely to recombine with genetic material in neighboring (transfected) viruses, bacteria, or host cells. This can cause untoward events, downstream 'crossovers,' and genetic mutations causing pathogenesis such as seen in MM with the production of excess antibodies and bone destroying amyloid [9].

Purportedly, the drug industry has surmounted these obstacles, including the "limited stability and transient nature" of mRNA vaccines, by incorporating modified nucleosides and LNPH coatings to protect against immunogenicity and presumably pathogenesis [10].

Pursuant to the COVID-19 virus and the mRNA vaccines, Hilscher's group [6] provided a comprehensive understanding of the synthetic mRNA in the virus and the lipid nanoparticle ("LNP") hydrogel surrounding the vaccine 'payload' important to pharmacokinetics. Circumventing traditional FDA regulations, "Operation Warp Speed" 'fast-tracked Moderna's and Pfizer's BNT162b2 and mRNA-1273 vaccines, respectively. These vaccines incorporate the "SARS-Cov-2" prefusion full-length S-protein, and include "stabilizing *substitutions* at the K986 and V987 positions," according to the often fallable scientific consensus [6]. [Emphasis added.]

According to Pradhan., *et al*. [11] similar gene sequence 'substitutions' were found within a substantial part of the S-protein antigen weaponizing the COVID-19 virus, largely responsible for immune resistance. In other words, beneath the stealthing LNPH coating of the vaccine mRNA, the S-protein attachment device of the virus derives from "4 unique inserts, . . . all of which have identity/similarity to amino acid residues in key structural proteins of HIV-1." [11]. Accordingly, good cause exists for identifying the pathogen as "SARS-Cov-2-HIV-1."

This, gain-of-function substitution/mutation genetically-sequenced by Pradhan et. al. was "unlikely to be fortuitous in nature," their highly reputable team reported [11]. This S-protein crystal genetic mutation is central to host-viral membrane attachment, and "payload" delivery. And this mutagen alters host cell defenses and genetic expression of more than S-protein antigens. In this author's suffering with MM, the B-cell line and progeny plasma cells were altered producing the symptoms of the immune dysfunction, much like HIV-1 causes lymphomas, leukemias and sarcomas. Pradhan., *et al*. findings are important, if not urgent, despite being generally neglected, disparaged, and unconscionably censored.

Relatedly, BNT162b2 and mRNA-1273 vaccines transmit to lymph cells genetic substitutions for each uridine amino acid in the viral genome. N1-methyl-pseudouridine is substituted to enhance mRNA secondary structure stability and decrease inherent mRNA immunogenicity, according to Hilsher., *et al*. [1]. Additionally, notwithstanding the stealthing function of the S-protein and LNPH coating, this group reviewed studies that showed modified uridines induced "global changes in the mRNA secondary structure which may explain the reduced recognition of modified mRNA by RNA-binding proteins involved in innate immunity." [6] Accordingly, this uridine genetic modification of the mRNA vaccines contributes substantially to "stealthing" to evade immune cell recognition and neutralization much like the bioweaponzed virus operates. These mutagenic dynamics are presumably responsible for the increasing numbers of COVID-19 clads, justifying calls for booster shots.

Furthermore, Hilscher et. al. [6]. pondered the introduction of N1-methyl-pseudouridine that ostensibly increases the melting point of mRNA and, therefore, could enhance mRNA stability in the mRNA-1273 and BNT162b2 vaccines. It is widely known that overheating these vaccines is contraindicated due to the risk of mutagenesis and causing genetic damage to recipients without benefit.

Overall, Hilscher., *et al.* [6]. considered five primary modifications to the mRNA genetic sequence that lend credence to the likely mutagenic impact of Pfizer and Moderna vaccinations on lympatic cells. Specifically, lymphatic cancer cell induction must be presumed based on the bulk of scientific determinations and genetic mutagens delivered by the weaponized virus and the suspected vaccinations.

Quoting liberally from their highly technical expertise, [6] "the 5' cap, 5' untranslated region (UTR), open reading frame (ORF), 3' UTR and poly (A) tail constitute the five primary elements of mature eukaryotic mRNA. These elements were incorporated into the BNT162b2 and mRNA-1273 vaccines to optimize mRNA design and to enhance mRNA translation efficiency. Moderna inserted the 110-nt 3'-UTR of human α-globin gene between the terminal stop codon and a poly (A) tail while . . . [in the] Pfizer-BioNTech mRNA vaccine [a] . . . modified 136-nt AES segment was inserted downstream from the second stop codon with the 139-nt human mitochondrial 12S rRNA inserted directly after. However, the inclusion of N1-methyl-pseudouridine introduces greater base pair wobble as it can pair with 8 A, G, C and U. This substitution can result in misreads by near-cognate tRNA. Moreover, since all U nucleotides were substituted in the BNT162b2 and mRNA-1273 mRNA vaccines to avoid mRNA degradation, the stop codons use the more promiscuous N1-methyl-pseudouridine. Such substitutions increase the chance of readthrough and the generation of longer proteins of unknown fate. Furthermore, synthesized mRNA must be purified. Impurities such as double-stranded RNA and DNA-RNA hybrid molecules have been shown to elicit an innate immune response. Additionally, purification of mRNA has been shown to reduce the expression of type 1 interferon and increase protein translation while substantially impacting mRNA vaccine safety."

Compromising vaccine safety, Martin similarly cautioned that "[a] potential mechanism of stealth viral DNA replication is through the bridging of viral fragments with long RNA molecules" as manufactured by BNT162b2 and mRNA-1273 engineers [7].

Lympathic cancers and stealth virus pathogenesis

According to Martin, [7] and consistent with the aforenetioned detailed mutagenic pathways reviewed by Hilsher., *et al*. [6],

cytopathic "stealth-adapted" bioweaponized viruses "bypass the cellular immune defense mechanisms because of molecular deletion or mutation of critical antigen coding genes." [7] The substitution of N1-methyl-pseudouridine for the uridine amino acid in the Pfizer mRNA vaccine genome may be one such risk factor.

As established with long COVID, [12] bioweaponized stealth viruses "do not provoke the inflammatory reaction typical of infections with the conventional viruses from which stealth adapted viruses are derived," Martin explained more than ten years ago [7]. "Stealth adapted viruses establish persistent, systemic virus infections. Like long COVID and the SARS-CoV-2/HIV-1 mutant, [11] according to Buonsenso and Tantisira [12], samples from 225 patients who had recovered from mild COVID-19 showed that the viral RNA was "distributed across ten distinct solid tissues, plasma, and blood cells up to 4 months after infection. Importantly, detection of viral RNA, and higher virus copy numbers, were significantly associated" with the post-COVID-19 long COVID condition [12].

Pursuant to MM and the other lymphatic cancers, as in the author's personal case study, [4] such infectious pathogenesis and disease persistence might result in long COVID-like symptoms through "direct host-cell changes, immune activation, latent virus reactivation, or combinations of the three," Buonsenso and Tantisira noted [12]. From an immune activation perspective, as in MM, other lymphatic cancers, and HIV/AIDS, patients with long COVID have complement dysregulation with signs of thromboinflammation, higher concentrations of circulating non-conventional monocytes associated with various chronic inflammatory conditions, and a T-cell phenotype consistent with T-helper-2-cell-skewed $CD4^+$ T-cell activation." [12,13].

Martin detailed the cognitive and behavioral impacts of stealth virus infections on brain function, commonly causing major mood swings, mental disorders, chronic fatigue, seizures, and various manifestations of autonomic nervous system impairment [7]. In the author's in-depth investigation of HIV/AIDS and Ebola's origins from labs financed during the Special Virus Cancer Program, [3] America's most advanced biological weapons developments and containment facilities were administered under the acronym "MKNAOMI" that was determined to be a subordinate enterprise under the CIA's infamous "MKULTRA" program that sought to develop similar biological and chemical weapons triggering brain and nervous system dysfunctions [3]. Martin later listed stealth virus symptoms resulting from such laboratory creations, including: "1) induced autoimmunity, 2) antibody formation against virus antigens, 3) virus-induced cellular damage to non-brain tissues and 4) induced heightened overall immune reactivity such that normally unrecognized components of the virus begin to become targeted by the cellular immune system." Such hypersensitization, an important pathogenic mechanism, "is relevant to the reported neurological and psychiatric adverse effects of vaccination in certain individuals," Martin cautioned. It is seen in autistic spectrum disorders and chronic fatigue immune dysfunction syndrome. Martin reported that it is appropriate to consider transmissibility of the infectious component of stealth adapted viruses threatening family members, and others at risk of becoming infected, sensitized, hypersensitized, reinfected, and/or suffering resurgent infections. Chronic ailments, such as long COVID and MM appear to be similarly susceptible to hibernating or stealth viruses, and/or even shed S-protein exposures causing immune system reactivations.

In fact, as early as 2000, [14] Durie, Collins and Martin determined that all 20 patients with MM screened positively for the presence of stealth-adapted viruses. They concluded as this author corroborates with the aforementioned science:

Since stealth virus replication can lead to varying recombinations of mutated viral and cellular genetic sequences, virus assimilation and over-expression of genes coding myeloma growth factors could enable a stealth-adapted virus to promote the development of myeloma.

Pathogenesis of COVID-19 and S-Protein induced MM and lymphomas

According to generally-accepted science, the COVID S-protein antigen on the virus and suspected vaccines leads to the activation, proliferation, and differentiation of B cells into plasma cells. Activated plasma cells generally produce a diverse (polyclonal) array of antibodies. Each of these antibodies are believed to target a different part of the S-protein, collectively contributing to a robust immune defense. This is considered a 'normal' and 'desired' outcome of vaccination, supposedly enhancing the body's ability to protect against infection.

When the S-protein serves as an antigen, it is recognized by multiple B cells. Each of these B cells has a unique B cell receptor ("BCR") that binds to a specific part (epitope) of the S-protein. Since the S-protein has multiple epitopes, different B cells will recognize and bind to different parts of the protein. This triggers *polyclonal* antibody production. The term polyclonal refers to antibodies that originate from multiple B cell clones, each producing an antibody targeting a different epitope. This contrasts with *monoclonal* antibodies, which are produced by identical immune cells (clones) and are identical to each other, targeting the same epitope of an antigen. This B-cell dynamic and specificity of epitope attack is therapeutically important in the threatment of MM as further detailed below.

Once activated B cells memorize the antigenic epitope, proliferate, and genetically "up-regulate" to differentiate into plasma cells, each plasma cell is thus genetically-programmed to produce antibodies specific to the epitope the B-cell recognized and memorized. In this context of genetic expression, a normal balance of kappa and lambda free light chain antibodies are produced.

Thus, the anticipated immune response to COVID-19 and mRNA vaccinations injecting S-proteins is polyclonal. It involves the equal or balanced production of multiple types of antibodies (polyclonal proteins) by plasma cells, including two main types: heavy chains and light chains. And there are two types of "light chains"- *kappa* and *lambda*. Each antibody consists of two light chains that can be either kappa or lambda, but not both. A single antibody will have two identical light chains of one type [15]. These proteins target different parts of the same S-protein, and each light chain gets expressed by specific genes upregulating this gene(tic) expression.

This diversity is claimed to be immunologically crucial as it enhances the immune system's ability to effectively neutralize the virus and S-protein, providing broader protection. But, in a hypothetical scenario, and in this author's clinical case, where a mutation or another genetic anomaly occurs in a single B cell during proliferation and differentiation, it could lead to the abnormal cloning and cell line expansion of just one defective oncogenic B cell line, or subsequently plasma cell progeny expressing MM oncogenesis.

Further considering this pathogenesis, in this patient's MM, the ratio of kappa to lambda light chain antibodies varies greatly (~80% kappa). In a healthy individual, the kappa to lambda ratio is approximately 2:1. The resulting MM diagnosis was established based on findings that approximately 80% of the free kappa light chains produced by the chronically ill plasma cell line induced the patient's painful bone fractures.

In clinical practice, levels of "free kappa" and "free lambda" light chains in the blood are measured to help diagnose and monitor diseases like MM. In the context of vaccination, the production of kappa and lambda light chains is part of the 'normal immune response,' and not supposedly altered [16]. But in this author's case study, [4], the patient was not vaccinated against COVID-19, but had been infected by the virus and S-protein at least once, probably twice.

Accordingly, ideal treatment based on this discerning diagnosis must target and neutralize: 1) the latent virus stealthed within cells that Martin explains may combine with intracellular bacteria to co-infect host cells and corrupt normal genetic expression as seen within the B-cell and plasma cell lines of MM patients; [17]; and 2) the S-protein antigens repeatedly challenging and hyper weaponizing the immune system, prompting the plasma cell antibody discrasias [18].

This intelligence also helps demystify the progressive pathological process distinguished clinically from assymptomic (sub-clinical) "monoclonal gammopathy of undetermined significance," ("MGUS") then subsequently "smoldering myeloma," before the illness progresses to the later stages of MM.

During this author's first hospitalization, MGUS was not apparent or diagnosed. MGUS is suggested when the level of M-protein (monoclonal light chains) is high (>3 g/dL) coupled with signs and symptoms of end-organ damage. This is called "CRAB," and includes hypercalcemia, renal failure, anemia, and bone pain.

S-Protein structural or conformational considerations

The structure of the S-protein is well detailed by Magazine N, Zhang T et. al [18].

The primary mechanism of SARS-CoV-2-HIV initial infection is viral entry mediated by the S-protein (on the virus) and ACE2 on host cells in humans as well as in model organisms such as nonhuman primates.

The SARS-CoV-2-HIV S-protein comprises two subunits, S1 and S2, which can be subdivided into two and five primary subdomains, respectively. Pradhan., *et al*. identified four HIV gene inserts in this S1 attachment conformation [11].

The S-protein, as a whole, is responsible for target recognition, binding, viral stealthing, and cellular entry by SARS-CoV-2-HIV, with S1 and S2 playing distinct roles during this process [19]. The S1 bioengineered subunit is responsible for target recognition and enhanced binding and stealthing (i.e., "gain-of-function"), while S2 is involved in membrane fusion and endosomal escape.

The S1 subunit contains an N-terminal domain (NTD) and a C-terminal receptor-binding domain (RBD) [28]. The RBD (~21 kDa) is responsible for the recognition of the angiotensin-converting enzyme 2 (ACE2) which acts as the receptor for SARS-CoV-2-HIV viral entry [20]. This mimics the GP120 RBD in HIV infections.

The RBD recognizes a number of other structurally related targets, though the RBD's role in recognition of these receptors is not yet well-understood in the context of disease progression, symptoms, and severity.

The complexity of this pathogenic pathway and therapeutic challenge is compounded by S-protein hydrogel stealthing components manufactured to additionally enable mRNA COVID vaccinations to dock at the RBD [21].

In contrast to the RBD, the NTD of S1 is underinvestigated and therefore less well-characterized. The NTD plays a critical role in overall S protein structural conformation, and mutations occurring in the NTD are linked to SARS-CoV-2-HIV immune escape [22].

The NTDs of related coronaviruses are capable of facilitating infection via the recognition of sugar-containing molecules such as glycoproteins, although the exact role of this potential binding is debated in the context of SARS-CoV-2.

Uniquely, Arbeitman CR and Roas P., *et al*. showed "with the help of atomistic simulations, that external electric fields of easily achievable and moderate strengths can dramatically destabilise the S-protein, inducing long-lasting structural damage." [23].

Vaccine hydrogel stealthing confounds pathogenesis with amyloidosis

Compounding S-protein complexity and targeted treatment viability, mRNA vaccine hydrogels pose additional risks of pathogenesis and impediments to cures. Most mRNA vaccines are formulated with adjuvants to enhance their immunogenicity. These include Alum, AddaVax, and CpG/Alum, added to neutralize responses following a "prime-boost immunization." [24].

In 2021, Gale EC and Powell AE., *et al*. [24]. showed that "sustained delivery of an RBD subunit vaccine comprising CpG/Alum adjuvant in an injectable polymer-nanoparticle (PNP) hydrogel elicited potent anti-RBD and anti-spike antibody titers, providing broader protection against SARS-CoV-2 variants of concern compared to bolus administration of the same vaccine and vaccines comprising other clinically-relevant adjuvant systems." Notably, their SARS-CoV-2 spike-pseudotyped lentivirus neutralization assay revealed that hydrogel-based vaccines elicited potent neutralizing responses when bolus vaccines did not." [24].

In 2023, Zhong R and Talebian S., *et al.* [25]. reported on the two non-viral lipid hydrogel nano-particles ("NPs") incorporated into the two mRNA vaccines (BNT162b2 by Pfizer/BioNTech and mRNA-1273 by Moderna). Injectable hydrogels had already been tested for local delivery of SARS-CoV-2 polymeric nano-vaccines (containing the SARS-CoV-2 S-protein with/without adjuvant) in animal models [26].

In this author's case study, [4] amyloid fibril accumulation and osseous destruction was not detected on staining; the patient had not been vaccinated, but had been exposed to the S-protein antigen at least twice prior to his MM diagnosis. Exposure from S-protein 'shedding' by attending healthcare workers is suspected of having caused the patient's second or 'booster' exposure to the S-protein antigen and subsequent B-cell/plasma cell MM.

mRNA-hydrogel enhanced S-protein stealthing, antigen intoxications, and amyloid fibril formations, following infections and injections with suspected vaccinations have been reported by Castelletto V and Hamley IW [1]. Although amyloid staining was un-detected in the instant case, the author's bone fractures were reported associated with amyloid fibril osteolysis. Castelletto and Hamley recorded amyloid fibril formation by a coronavirus spike

relevant to the stability of the spike protein conformation (or its destabilization via pH change). They concluded that hydrogels formed by coronavirus peptides may be of future interest in the development of therapies. However, their optimistic prognosis for mRNA biotechnology used in the suspect COVID vaccines is challenged by the finding that genetic sequence alterations induces pathogenesis by "frameshifted proteins" secreted by plasma cells. This may be responsible for the amyloid fibril and free kappa light chain osteolysis suffered by this author. In Castelletto and Hamley's experiments, roughly 8% of the proteins produced from their experimental mRNAs were pathologically frameshifted [28].

This science may best explain the author's MM pathogenesis following repeat exposure(s) to the COVID-19 lentivirus and/or shed S-protein antigen. Infectious viral mRNA may have subsequently recombined with S-protein complexes during exposure(s) leading to gene regulated *frameshifting*, plasma cell mutation(s), and kappa light chain amyloid osteolysis [29]. Understanding this pathogenesis is crucial for administering effective treatments.

Specious science or intentional depopulation?

"Operation Warp Speed," to hastily develop a vaccine against COVID-19, began suspiciously and auspiciously April 29, 2020, and the program was officially announced on May 15, 2020. More than three years earlier, on January 12, 2017, Dr. Fauci alerted the incoming Trump administration that a new pandemic was expected. At that time, the BNT162b2 vaccine by Pfizer/BioNTech and mRNA-1273 by Moderna had already undergone preliminary trials. On July 27, 2020, Moderna began mRNA-1273's Phase 3 randomized trials [30].

Contemporaneously, aware of these trials and predicted plague (i.e., "plandemic"), the CEO of Pfizer's parent company, Glaxo-SmithKlein ("GSK"), Moncef Slaoui, retired from GSK on June 30, 2017, and moved to lead Moderna's Board of Directors at that time. These facts, in light of governmental officials' lies and media censorship, gives probable cause to presume one's worst suspicions. That a racketeering enterprise comprised of public and private agents and entities orchestrated COVID-19's emergence. Genocidal depopulation is reasonably suspected given the aforementioned rise in cancer rates. This also best explains the timeliness of emergence of the hydrogel coated S1-protein "gain-of-function" bioweapon integral to the fast-tracked "novel" mRNA vaccines.

Oncologists are among the deceived masses in our collective exploitation by globalists leveraging "novel" lab-created bioweapons for profitable cancer induction and depopulation. This controversial conclusion and presumption is established by the scientific evidenced presented above, common sense analysis, and the current psychosocial, economic, and geopolitical conditions that permit global commerce that is most accurately characterized as 'genocidal.'

Alternatively, had COVID-19 emerged naturally, or accidentally, rather than intentionally, as many investigators and officials have speculated, complicit parties, such as Dr. Anthony Fauci, could not have accurately predicted in 2017 that the Trump administration would face a "surprise infectious disease outbreak." Nor would there have been good cause to conjure "natural origin" theories, mass media denials, diversions, and fraudulent concealments, that enabled the "emergency response" and "fast-tracked" vaccinations that caused millions of predictable and predicted deaths and economic collapse [31,32].

In this context of socio-political, economic, and public health exploitation, mass media bias and censorship compounds suspicions [33].

Moreover, the United States has the highest cancer rate of any nation, according to the NIH that substantially financed the development of the SARS-COV2-HIV mutagen [34]. The adjacent chart (published by OurWorldinData.org) shows the record on February 1, 2021, one year after Pradhan., *et al*, [11]. published their revealing "Indian paper" evidencing COVID's S-protein lab mutations obfuscated by Dr. Fauci and fellow NIH/NIAID officials.

Accordingly, little-to-no attention has been given to the aforementioned science and concerns regarding carcinogenic risks linked to the COVID-19 bioweaponized lentivirus, its S-protein antigen, and the related illnesses and intoxication threats increasing from this apparent imposition.

This discernment is distressing and heavily damaging, because it generally precludes proper diagnosis and treatment. Accurate *diagnosis* identifies the 'root cause of the disorder' in order to effectively treat, even prevent, the causitive initiating factor(s). In this case, the virus and its S-protein antigen are intertwined as man-made mutagens assaulting the genetic code of humanity. And without proper diagnosis, treatments cannot be curative, only profitably palliative.

Such is the case with MM, as evidenced by the current, standard, most promising, palliative, albeit costly and life-extending treatments [35].

Antiviral therapies

Given the aforementioned science explaining COVID-19 pathogeness and S-protein mutagenesis underlying MM and other lymphatic cancers, the imporance of anti-virals in "first line" therapy is encouraged [36]. This includes novel, complementary, and 'alternative' therapies, [37] particularly frequency-based interventions that target viral protein crystal conformational susceptabilities.

Viruses and S-protein antigens are primarily protein crystals. They are conformationally arranged following specific geometrical patterns as reviewed by Sevvana, Klose and Rossmann [38]. Accordingly, X-ray crystallography has been the most successful technique for determining the structure of individual viruses since the 1970s [38].

Sidharthan C. reported on a study that "investigated the use of different ultrasound frequencies to disrupt the SARS-CoV-2 spike protein structure and neutralize the virus. Viral replication tested in Vero E6 cells revealed that replication of the Wuhan-Hu-1 strain was inhibited by 3-12 MHz and 5-10 MHz ultrasound frequency ranges, but the cell cultures inoculated with SARS-CoV-2 Gamma and Delta variants showed low viral titers only when the viruses were exposed to 5-10 MHz ultrasound frequencies." [39].

Chandler DL at MIT [40] published that "differences in vibrational characteristics correlate strongly with the different rates of infectivity and lethality of different kinds of coronaviruses." Protein spikes are not static. "They're vibrating and continuously changing their shape slightly." This susceptibility may be useful in developing therapies based on resonance energy of certain frequencies.

In related research, Chandlert reported that environmental engineers Markus Buehler and Yiwen Hu reported that, "Potentially, these findings could also provide a new avenue for research on possible treatments for Covid-19 and other coronavirus diseases. Buehler speculated that it might be possible to find a molecule that would bind to the spike proteins in a way that would stiffen them and limit their vibrations. Subsequent sound or light frequency irradiation might fracture the stiffened structure. Another approach might be to induce opposite vibrations to cancel out the natural ones in the spikes, similar to the way noise-canceling headphones suppress unwanted sounds. Buehler's results indicated that ultrasound frequencies produced by medical devices in everyday use could be used to inactivate SARS-CoV-2. Ultrasound inactivation could be used with other antivirals to reduce viral titers of SARS-CoV-2." [40].

Similarly, Malasian engineer, A.B.H. Kueh [40]. considered "sonication treatment methods," based on encouraging outcomes in disinfection and medical therapies. "Such treatments incapacitate microbes or diseased cells by selectively invoking large deformation at the resonant frequency that initiates structural failure." He reviewed "the deformation state of crystallites embedded in the polycrystalline matrix," published by Reimers W [42]. Kueh's interest included the study of residual stress states in viral conformations. Kueh considered the need to determine "the precise range of resonant frequencies for different biological bodies." [41]. Using a computational approach he concluded that the numerical determination of the resonant frequency of the coronavirus employing the tensegrity method, determined "the operative sonication frequencies range for the resonant state of the virus" and the "structurally destructive" deformation parameters of the coronavirus. He then mapped coronavirus sonication frequencies alongside healthy human cells to provide an "alternative technological avenue in combating the COVID-19 progressive threat." [41].

Bastidas OH and Sevarac Z [43]. Observed the spike protein favored certain frequencies more than others. They reported spike protein conformational changes that reflected "dihedral angle oscillations" of the antigen that favored frequencies of dihedral

angle rotations. They determined the "wild type" spike exhibited a discrete vibration "in the 23-63 MH range with 42.969 MHx being the most prevalent frequency sampled by the oscillations." The oscillations may be a function of position in the primary structure of the composite amino acids amenable to therapeutic initiatives.

Hammerschlag, Levin and McCraty., *et al*. [44] reviewed the emerging discipline of "biofield physiology" and concluded electrical and magnetic fields, and ultraweak coherent photon emissions crucial to genetic expression, provide viable options for advancing therapies.

In 2018, Kumeta M an Yoshimura SH reported on "novel relationships between life and sound" considering "mechanosensitive genes" in certain cell types that can be suppressed by audible sound stimulation [45]. "Based on research on mechanotransduction and ultrasound effects on cells, gene responses to audible sound stimulation were analyzed by varying several sound parameters: frequency, wave form, composition, and exposure time." These investigators recorded RNA reduction using sine waves when cell cutures were resonated. "The cells were exposed to sine-wave sound (440 Hz and 94.0 dB) for only one hour, and then cellular RNA was analyzed at different time points. The results revealed that once suppressed by the sound, the target mRNA level remained low for at least 4 hours (Figure 1). Kumeta and Yoshimura charted relative mRNA level depletion in response to sine wave sound vibrations measured over 4 hours. These researchers found "at least two mechanisms likely to be involved in this sound response: transcriptional control and RNA degradation [45].

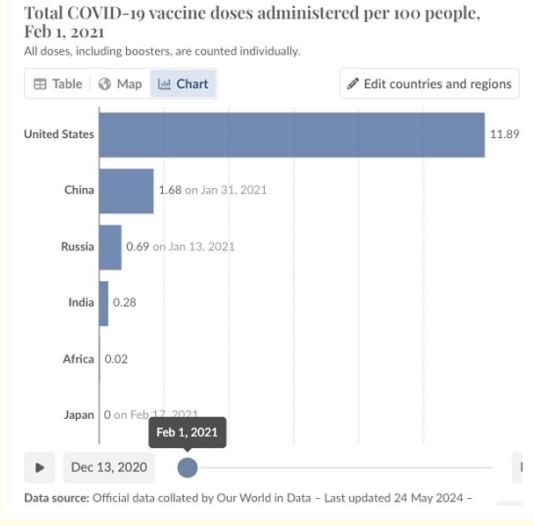

Figure 1

Several random frequencies were not shown to have any significant impact, including the "standard tuning/concert pitch" musical frequency of A = 440Hz. This corroborates the author's frequency research determinations and publications, discouraging the use of 440Hz in frequency therapeutics and alternatively encouraging A = 444Hz that resets the C-pitch base octave at C = 528Hz [46].

Challenging this therapeutic thesis, Gonzalez-Jimenez's group [47] cautioned that body water "is likely to cause phonon modes to be heavily damped and localized." This author largely disagrees and stipulates that attenuation of frequency therapeutics is mooted by water being a superconductor or sound and light energies. Moreover, due to the principles of coherence and quantum physics, the water molecule itself, six-sided hexagonal shaped H_2O, is structurally influenced by, and geometrically coherent with, the strong ambient 528Hz frequency of sound central to nature. That happens to be the "miracle" frequency and "gold" resonance energy of the original Solfeggio musical scale. Knowledge of these facts prompted several independent affirming investigations recording the unique immunological and neurological benefits of 528Hz frequency increasingly used clinically. 528Hz was determined to be a strong anti-oxidant, immune system booster, nerve cell protector, and testosterone generator [48-50].

Conclusion

Increases in lymphatic cancers have followed the emergence of the lab engineered COVID-19 mutagen and the Pfizer and Moderna mutagenuc mRNA vaccines derived from the genetically modified "gain-of-function" virus and HIV-1-laced S-protein. Stealth virus-like pathogenesis results from these mutagens impacting immune cells; compounding the stealthing and immune system risks caused by the lipid nanoparticle hydrogel ("LNPH") coating of the vaccines. These multiple intoxications may cause subclinical impacts, such as 'smoldering-like' hypersensitization reactions, and pathogenesis best explaining "long COVID" and the rise in immune cell cancers. Therapeutic focus for lymphatic cancers should target these disease vectors, particularly with anti-virals and complementary therapeutics.

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Conflicting Interests

The author proudly discloses his conflicting interest in the field of "frequency therapeutics" that he largely pioneered beginning in 1998, subsequently commercializing an array of "electroceuticals" resonating the 528Hz/nm frequencies of sound and light.

Author Biography

Dr. Leonard G. Horowitz, DMD, MA, MPH, DNM (hon), DMM (hon), received his doctorate in dental medicine from Tufts University; trained in periodontology and oral surgery at the University of Rochester; received his master's degree in public health from Harvard University; and subsequently earned multiple awards as an author, filmmaker, energy medicine pioneer, and nutraceutical entrepreneur. He was granted two honorary degrees, one in naturopathic medicine, and the other in missionary medicine, from the World Organization for Natural Medicine, wherein officials named him a "World Leading Intellectual." Dr. Horowitz's official website is: DrLenHorowitz.com.

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