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Case Study

Medical Armageddon: A Case Study in S-Protein Bioweapon "Gain-of-Function" Cancer Induction for Depopulation Encouraging Targeted Remedies

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Abstract

Armageddon, by definition, characterizes the war between good and evil. This is evidenced in this report and case study relaying the author's diagnosis of "multiple myeloma" ("MM")—an increasingly common immune system cancer that compounding evidence reviewed in this case study largely attributes to the lab-engineered COVID-19 virus and "Spike-protein" ("S-protein") "gain-of-function" bioweapon, largely sourced from research and developments in the field of HIV/AIDS molecular genetics and immunopathogenesis [1].

In MM, transfected bone marrow B-cell memory impacts plasma cell differentiation and related antibody over-production of damaging free light chain antibodies and also amyloid fibril bone destruction. Intertwined with the mRNA COVID lentivirus "payload", the S-protein antigen prompts immune-pathology and threatens death following osseous invasion, demineralization, amyloid infiltration, bone fractures, and damaging sequella to organ systems.

Corroborating studies describe "hypermutation" [2] of the S-protein damaged plasma cells. This intelligence may best explain the rise in morbidity and mortality from MM related immune cell cancers, such as lymphomas, following COVID vaccinations and S-protein shedding substantially neglected and censored by a 'captured' scientific media [3].

Finally, this study reviews promising remedies and proposes complementary therapies [4] that target plasm cell pathology, [5]. S-protein detoxification or neutralization, and overall inflammation reduction for bone healing.

Keywords: S-protein; United Nations' ("UN"); Virology

Introduction and Background

More than sixty (60) years ago, science scholars in virology and vaccinology warned of the existential threat to civilization posed by lab engineered microbes [1] Between 1967 and 1972, debate raged over whether America's chemical-and-biological warfare ("CBW") industry should be scrubbed or bolstered. Dr. Joshua Lederberg relayed the concensus of protestors in a 1971 Science article [6]. Germ warfare, he wrote, "has been universally condemned as a vile perversion of scientific insight. . . . Strategic and political instabilities would follow worldwide spread of infectious disease. In the interest of world order . . . biological weaponsry must be controlled by international agreement. . . . In a word, the intentional release of an infectious particle, be it a virus or bacterium, from the confines of the laboratory must be condemned as an irresponsible threat against the whole human community" [6].

That "international agreement" was subsequently crafted by the United Nations' ("UN") World Health Organizstion ("WHO") following debate in which Professor Lederberg served the WHO's Advisory Committee on Medical Research [1].

The UN, financed in 1946 by the Rockefeller family as an "extra-territorial" globalist authority by treaty with the U.S. Government, was built in 1952—the same year John D. Rockefeller III founded the Population Council [of the City of New York] following Rockefeller's "Conference on Population Problems". Key among those problems was unionization of workers challenging commerce and the oligarchy's autonomy. Population control and depopulation became central concerns, as evidenced by verbatim transcripts of the Conference featuring Columbia University historian Matthew Connelly. Summarized by Susan Yoshihara, Ph.D., the clandestine 1952 "modern population control establishment" largely consisted of "the heads of the United States Atomic Energy Commission, National Academy of Sciences, and top scientists "from embryology to economics," including past and present Nobel Prize winners [7].

Assembled and financed by the Rockefeller commercial and governmental (public and private) enterprise, the Population Council was justified by the oligarchy's interests in preventing "inferior populations" from degrading "the genetic quality of the human race". Quoting Yoshihara, "They decided radical measures to reduce birthrates were justified in order to save 'Western Civilization' from being dragged down by the growing humanitarian demands of Third World countries. Thus was born the Population Council, which would in turn become the nexus of the entire population control movement, going on to coordinate the work of the United Nations, the Ford and Rockefeller foundations, and International Planned Parenthood Federation (IPPF), that was founded three weeks later, intertwined with major pharmaceutical firms [8].

Material to this case study and history, at the time of this writing, U.S. Congressional investigators are scrutinizing the S-protein 'gain-of-function' bioweapon. Investigators learned from National Institutes of Health (NIH) principal deputy director, Lawrence Tabak, that U.S. taxpayers funded the gain-of-function research at the Wuhan Institute of Virology in China, and was complicit in the pandemic and cover-up. This admission followed four years of denials by federal public health officials—including Tabak and former National Institute of Allergy and Infectious Diseases (NIAID) director Dr. Anthony Fauci. All denied and concealed the risky research making the SARS-CoV2 mutagen more transmissible with the goal of supposedly improving vaccines and cancer treatments [9]. Investigators learned that NIH funded gain-of-function research at the Wuhan Institute of Virology was administered through the EcoHealth Alliance. This occurred under the direction of Dr. Peter Daszak, who lied to Congress by testifying his organization "never has and did not do gain-of-function research, by definition".

Daszak's claim was additionally contradicted by private correspondence and sworn testimony from other experts, such as Dr. Ralph Baric, who presumably sourced the Wuhan lab gain-of-function bat virus research first conducted at the University of North Carolina, Chapel Hill. These disclosures prompted the Department of Health and Human Services (HHS) to suspend grants to EcoHealth Alliance and block future funding. "The controversy deepened further with revelations" about the alleged organized cover-up involving Dr. David Morens, a senior advisor to Dr. Fauci at the NIH. Testimony revealed that Morens, a 'mentor' to EcoHealth Alliance's Daszak, had purportedly learned 'how to make emails disappear' after receiving public records requests" [10].

Accordingly, given officials' and the scientific community's propensity to repeatedly conceal hidden agendas and scientific facts to protect rogue actors, bio-weapons programs, depopulation agendas, and the profitable cancer vaccination industry, closer scrutiny is indicated considering the S-protein antigen within this case study and context of medical malfeasance and depopulation politics.

This closer scrutiny best begins with reconsideration of the highly censored research of Prashant Pradhan., *et al*. still awaiting revisions after four years of censorship and obfuscation [11]. In fact, Dr. Fauci's most disturbing and incriminating concerns and illegal actions immediately followed Pradhan group's disturbing and revealing publication. Prior to its highly suspicious "temporary" "withdrawal", Pradhan., *et al*. concluded: "The finding of 4 unique inserts in the 2019-nCoV, all of which have identity/similarity to amino acid residues in key structural proteins of HIV-1 is unlikely to be fortuitous in nature". Pradhan's highly reputable group reported on the protein crystal spike genetics in the SARS-COV2 mutant with respect to apparently spliced HIV genes inserted into the bioweapon central to viral infectivity, 'gain-of-function,' host-viral membrane attachment, and "payload" delivery to alter host cell genetic expression. They wrote in relavent part: "Surprisingly, each of the four inserts aligned with short segments of the Human immunodeficiency Virus-1 (HIV-1) proteins. The amino acid positions of the inserts in 2019-nCoV and the corresponding residues in HIV-1 gp120 and HIV-1 Gag are shown in Table. The first 3 inserts (insert 1,2 and 3) aligned to short segments of amino acid residues in HIV-1 gp120. The insert 4 aligned to HIV-1 Gag. [I] it is unlikely that all 4 inserts in the 2019-nCoV spike glycoprotein fortuitously match with 2 key structural proteins of an unrelated virus (HIV-1). . . . This is startling as it is quite unlikely for a virus to have acquired such unique insertions naturally in a short duration of time. . . . Unexpectedly, all the insertions got aligned with Human immunodeficiency Virus-1 (HIV-1). Further analysis revealed that aligned sequences of HIV-1 with 2019-nCoV were derived from surface glycoprotein gp120 (amino acid sequence positions: 404-409, 462-467, 136-150) and from Gag protein (366-384 amino acid) (Table). Gag protein of HIV is involved in host membrane binding, packaging of the virus and for the formation of virus-like particles. Gp120 plays crucial role in recognizing the host cell by binding to the primary receptor CD4.This binding induces structural rearrangements in GP120, creating a high affinity binding site for a chemokine co-receptor like CXCR4 and/or CCR5. . . . To our surprise, these sequence insertions were not only absent in S protein of SARS but were also not observed in any other member of the *Coronaviridae* family (Supplementary figure). . . . . Unexpectedly, all the insertions got aligned with Human immunodeficiency Virus-1 (HIV-1). Further analysis revealed that aligned sequences of HIV-1 with 2019-nCoV were derived from surface glycoprotein gp120 (amino acid sequence positions: 404-409, 462-467, 136-150) and from Gag protein (366-384 amino acid) (Table). . . . .This is startling

as it is quite unlikely for a virus to have acquired such unique insertions naturally in a short duration of time [N]one of these 4 inserts are present in any other coronavirus, the genomic region encoding these inserts represent ideal candidates for designing primers that can distinguish 2019-nCoV from other coronaviruses" [11].

Due to mass media censorship and officials' malfeasance, few people realize that S-protein structures are present on both HIV and the SARS-COV2-HIV mutagen. Albeit, they are structurally different, but functionally similar, and crucial in the pathogeneis of all three viruses and pandemics.

Reflecting on this sobering science, massive sequestered evidence now presumes that HIV/AIDS was also lab engineered between 1968 and 1972, as this author previously detailed [12]. Massive irrefutable scientific records move investigators to conclude that COVID-19 follows a pattern-and-practice of covert engineering immune suppressive bioweapons, developed for depopulation, with HIV/AIDS especially recombined to induce the never-before-seen leukemia, lymphoma, sarcoma immune suppression cancer complex following infections and/or tainted vaccinations.

The Case

Repeat COVID/S-protein exposures

The author subject ("Patient") is a 72-year-old male who was initially exposed to SARS-COVID-19-HIV and its S-protein antigen in September, 2020, then became symptomatic. His respiratory and immune system illness gradually resolved within 6 weeks.

Subsequently, in early August 2021, the Patient suffered a second exposure to the suspect S-protein. His car was struck by a truck causing spinal vertebral dislocations injuring his lower back requiring medical care and many weeks of physical therapy. During that therapy, the unvaccinated Patient was again presumably exposed to the S-protein antigen shed from COVID-19 vaccinated attending healthcare personnel. (It is public knowledge that vaccine-induced 'shedding' of the unstable lab-engineered S-protein mutagen occurs, and immunopathogenesis may be exacerbated by genetic expression following mRNA-to-DNA messaging induced by the lentivirus infection [13].

First Hospitalization data

In the Patient's traumatized, distressed, immune-compromised, and repeatedly S-protein/virus exposed state, he suffered chills, weakness, fever, shortness of breath, chest tightness, and wheezing. He accessed Lee County Hospital in Cape Coral, Florida for emergency care, and was diagnosed by attending personnel on August 6, 2021, with "SARS CORONAVIRUS 2, RNA "Positive". Patient's First Filed Vitals the day of admission and Complete Blood Count (CBC") and Comprehensive Metabolic Panel on August 6, 2021, the day of admission, showed anemia and several metabolic irregularities.

Following four days of chemotherapy with Remdesivir and Decadron IV; Vitamins, and Lovenox, inter alia, the Patient's Complete Blood Count (CBC") on August 10, 2021, showed notably high Glucose, BUN, Creatinine, Protein, AST (SGOT), and Prothrombin Time; and low Sodium, Anion Gap, A/G Ratio, and GFR. Atypical lymphocytes were elevated from < 1 to 2%.

Known side effects of Remdesivir

It is public knowledge that "very common" hematologic side effects of Remdesivir include [d]ecreased hemoglobin (up to 15%), decreased lymphocytes (up to 11%), [and] prolonged prothrombin time" [14] Additionally known side effects include prolonged activated thromboplastin time, and decreased white blood cells.[14] Accordingly, the bone marrow immune cells negatively impacted by the Patient's IV treatment with Remdesivir are evidenced including the Megakaryocytes (MKs) [15,16] MKs regulate the bone marrow niche, supporting the development and function of plasma cells and hematopoietic stem cells, including S-protein antigen memorizing B-cells [15].

Accordingly, on the morning of August 11, 2021, the Patient's certified advocate appeared and demanded Remdesivir's removal from the treatment regimen. Contrary to the hospital record that erroneously claims the Patient then began self-administering hydroxychloroquine, that is contraindicated during Remdesivir therapy, the advocate provided the Patient with "OxySilver™ with 528" (Healthy World, LLC), Zinc, and Vitamin D supplements that the Patient began taking that afternoon.

Following steady decline in SpO2 levels during Remdesivir administration, and subsequent improvement to 87% the morning of August 14, 2021, the Patient was discharged with CBC and Metabolic Panel data recorded.

The complete discharge recorded included the patient's social history and erroneously recorded self-medication record in which hydroxychloroquine was falsely cited and substituted for the patient's use of OxySilver™.

Second Hospitalization data

The Patient presented to Cleveland Clinic in Port St. Lucie, FL, on April 29, 2024, following a series of traumatic injuries to the spine, lower back, and diaphragm, coupled with stressors from 'fast-pace-living' and chronically-neglected self-care including prudent dietary observances. A Complete Metabolic Panel was obtained upon emergency hospitalization.

The Complete Blood Count for the Patient showed anemia and plasma cell myeloma with severely elevated free kappa cell light chain antibodies at 80%. Plasma cell chromosomal mutations were also recorded.

Discussion

Defective science or intentional depopulation

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 presumption is established by common sense, scientific evidenced presented in this paper, and the current psychosocial, economic, and geopolitical condition that permits global commerce that is most accurately characterized as 'genocide' or 'iatrogenocide'—a term coined by the late Dr. Robert Mendelsohn specifically referencing vaccine induced morbidity and mortality.

The "Medical Armageddon" presumption is evidenced by the facts aforementioned, establishing the thesis that increasing MM and lymphoma cancers are being diagnosed following COVID-19's emergence from the Wuhan lab. This elevated carcinogenesis may be attributed to initial or 'booster' S-protein antigen exposures occurring during infections or mRNA vaccinations, all intoxications involving the S-protein SARS-COV2-HIV DNA-targeting "gain-of-function" mutagen [11].

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 [17].

In this context of socio-political, economic, and public health exploitation, further evidenced by mass media bias and censorship, white blood cell disorders have been mounting, including lymphomas and MM. In the US, MM now accounts for almost 2% of cancers diagnosed, and over 2% of cancer deaths (more than double the global proportion) [18]. 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 [19]. The official record on February 1, 2021, evidences this striking increase in cancer deaths one year after the "Indian paper" S-protein warning was published by Pradhan., *et al*. [11] then censored by Dr. Fauci and fellow NIH/NIAID officials.

Meanwhile, little-to-no attention has been given to these S-protein-related illnesses and intoxication threats. This defective discernment is heavily damaging, because it 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 S-protein antigen intertwined with man-made genetic assaults is the root disorder. And without proper diagnosis, treatments cannot be curative, only palliative.

Such is the case with MM, as evidenced by the current, standard, most promising, palliative, albeit costly and life-extending treatments [20].

Similar cases evidencing S-protein-related pathogenesis

Similar cases evidencing S-protein-related pathogenesis are mounting. Risk factors generally cited for MM include age (average age of diagnosis is 69), race (African Americans are over double as likely to be diagnosed), sex (men are at a 1.5× risk), and family history. But recklessly missing from this epidemiological data is the "gain-of-function" S-protein bioweapon itself, central to COVID immunogenicity, structurally characterized in the sections below.

Pursuant to mounting cases, Cavanna L and Grassi SO., *et al*. [21] reported on a number of individuals suffering post-vaccination B-cell pathology, beginning with a 66-year-old man who developed B-cell lymphoma shortly after receiving his third dose of the S-protein laden BNT162b2 vaccine. The S-protein antigen is the primary immunogen genetically manufactured en-masse following COVID vaccination. Their review revealed eight additional cases of non-Hodgkin lymphoma ("NHL") that developed shortly after COVID vaccination. There were four cases of diffuse large-B-cell lymphoma ("DLBCL"); one case of extranodal NK/T-cell lymphoma; one patient with subcutaneous panniculitis-like T-cell lymphoma; one case of marginal zone B-cell lymphoma and one primary cutaneous anaplastic large-cell lymphoma (PC-ALCL). In five cases, the lymphoma developed after BNT162b2 mRNA vaccination, including one case after ChAdOx1 nCOV-19; one case after the adenovirus type 26 (Ad26) vaccine; and one after mRNA-1273/Spikevax (ModernaTX).

In addition, Sekizawa A and Hashimoto K., *et al*. [22] reported on an 80-year-old Japanese woman who developed a B-cell lymphoma following mRNA COVID-19 vaccination. The cancer appeared the morning after she was administered her first mRNA COVID-19 'immunization' (BNT162b2). The mass gradually decreased in size but persisted over 6 weeks after her first vaccination (i.e., 3 weeks after her second vaccination). Their findings suggested lymph node inflammation was exacerbated by the woman's booster shot.

In 2022, Ishimitsu A and Tojo A., *et al*. reported on a 70-year-old woman who died from primary AL amyloidosis and secondary AL amyloidosis associated with myeloma. The authors wrote these two ailments, "are considered to be similar entities associated with plasma cell dyscrasia, but their clinical prognosis appears to be different". (Ishimitsu A, Tojo A, Hirao J, Yokoyama S, Ohira T, Murayama Y, Ishimitsu T, Kang D, Honda K, Ehara T, Ishida K, Ueda Y. AL-Kappa Primary Amyloidosis with Apolipoprotein A-IV Deposition. Intern Med. 2022;61(6):871-876. doi: 10.2169/internalmedicine.7955-21. Epub 2022 Mar 15. PMID: 35296622; PMCID: PMC8987257.) This case is material to the theory that S-protein pathogenesis with viral mRNA gene shuffling or by "frameshifted proteins" within the B-cell/plasma cell axis, generates amyloidosis with fibrils and bone lysis damaged by free light chain antibody over-production.

In 2023 Tsaftaridis N, Potoupni V and Koraka., *et al*. published a case report of a 75-year-old female patient hospitalized two weeks after she received the second dose of the S-protein laden Moderna COVID-19 vaccine (mRNA-1273). Serum protein immunofixation showed monoclonal kappa [light chain] zones, and a bone marrow biopsy revealed 5% plasma cell infiltration.

Suffice it to say, substantial medical scientific evidence has mounted, supplemented by case reports, pointing to the S-protein antigen as the most likely trigger of MM and lymphoma pathogenesis, and not idiopathic genetically-altered B-cells or plasma cells, per se.

Pathogenesis of S-Protein induced MM and lymphomas

According to generally-accepted science, the S-protein antigen in 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 spike 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 treatment 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 thrusted 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 [23]. These 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 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.

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 [24]. But in this case study, the Patient was not vaccinated against COVID-19, but had been infected by the virus and S-protein at least once, probably twice. The resulting MM diagnosis was established based on the findings that approximately 80% of the free kappa light chains produced by the Patient's chronically ill plasma cell line induced the Patient's painful bone fractures.

Accordingly, ideal treatment based on this discerning diagnosis must target and neutralize: 1) the genetic alteration within the B-

cell and plasma cell lines; and 2) the S-protein antigens repeatedly challenging the immune system, prompting the plasma cell antibody dycrasias.

This understanding also helps demystify the progressive pathological process distinguished clinically from assymptomic (subclinical) "monoclonal gammopathy of undetermined significance," ("MGUS") then subsequently "smoldering myeloma" [17]. During the Patient'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. The international staging system considers beta 2 microglobulin and albumin levels, while the revised system contemplates prognostic factors such as lactate dehydrogenase levels and chromosomal abnormalities [17].

S-Protein structural or conformational considerations

The structure of the S-protein is well detailed by Magazine N, Zhang T., *et al*. [25].

The primary mechanism of SARS-CoV-2 initial infection is viral entry mediated by the S-protein (on the virus) and ACE2 (on host cells) interacting in humans (See: Figure 1a) as well as in model organisms such as nonhuman primates [28].

The SARS-CoV-2 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, and cellular entry by SARS-CoV-2-HIV, with S1 and S2 playing distinct roles during this process. The S1 bioengineered subunit is responsible for target recognition and enhanced binding (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). 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 [28]. 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 components manufactured to enable mRNA COVID vaccinations to dock at the RBD, as detailed further below.

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 immune escape [28].

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 Rojas 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" [26].

Vaccine hydrogels confounding 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 unable or elicit neutralizing responses following a "prime-boost immunization" [27]. In 2021, Gale EC and Powell AE., *et al*. 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" [32].

In 2023, Zhong R and Talebian S.., *et al*. [28] reported on two non-viral lipid hydrogel nano-particals ("NPs") incorporated into two mRNA vaccines (BNT162b2 by Pfizer/BioNTech and mRNA-1273 by Moderna) in clinical use. 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.

"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, as aforementioned, 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 [29].

Contemporaneously, aware of these trials and predicted plague (i.e., "plandemic"), the CEO of Pfizer's parent company, Glaxo-SmithKlein, 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 the aforementioned 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 administers the aforementioned genocidal depopulation in which this case study unfolds. 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.

In this case study, the Patient's amyloid fibril accumulation and osseous destruction was not detected on staining. The Patient had not been vaccinated, but had been exposed to the virus and S-protein antigen 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 antigen intoxications and amyloid fibril formations following suspected vaccinations have been reported by Castelletto V and Hamley IW [30] Although amyloid staining was un-detected in the instant case, the author/Patient'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 the author/Patient. In Castelletto and Hamley's experiments, roughly 8% of the proteins produced from their experimental mRNAs were pathologically frameshifted [30].

This science may best explain the Patient'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 the Patient's second hospitalization following gene regulated frameshifting, plasma cell mutation(s), and kappa light chain osteolysis., Understanding this pathogenesis is crucial for administering effective treatments.

Standard care

The standard of care for newly diagnosed multiple myeloma is called induction therapy, or front-line therapy. It is aimed at controlling or destroying MM cells, rather than neutralizing the genetic damage tainting immune cell lines, or directly addressing the S-protein bioweapon intoxication (s).

Standard "front-line management" generally includes an "induction regimen," maintenance therapy, and hematopoietic cell transplantation for eligible patients. Bisphosphonates or bone-stimulating agents for the prevention of skeletal events are often added.

Customary treatment for relapsed disease includes monoclonal antibody administration targeting the CD38 receptor on the offending plasma cells using Daratumumab, proteasome inhibitors, immunomodulating agents, and investigational therapies such as B cell maturation antigen chimeric antigen receptor T cells [21].

While incidence of MM has risen by 126% globally, and over 40% in the US since 1990, mortality has reportedly fallen by 18% in the U.S. due to Daratumumab targeted therapy and bone marrow transplant techniques [18].

Induction therapy typically consists of a three-drug or four-drug combination regimen given over three to four cycles, each of which typically lasts 3 or 4 weeks. This is followed by an autologous stem cell transplant (if eligible) and maintenance therapy. Collectively, these are considered one line of therapy.

The three-drug regimen (triplet therapy) generally includes an immunomodulatory drug (Revlimid [Lenalidomideor] or Pomalyst), a proteasome inhibitor (Velcade, Kyprolis, or Ninlaro), and a steroid (dexamethasone or, less commonly, prednisone). Four-drug regimens (quadruplet therapy) are similar to three-drug regimens but also include the anti-CD38 monoclonal antibody (Darzalex [Daratumumob] or Sarclisa).

Although the S-protein has been chosen as the target antigen in most vaccine applications, this approach to immunogenicity is now being widely questioned. Analysis of SARS-CoV-2-derived HLA class I and class II T cell epitopes demonstrate that other structural, non-structural, and accessory proteins are important, and may become the target in infected individuals. (Antonopoulou T, Athanassakis I. SARS-CoV-2 immunogenicity: Is S protein the best target for vaccination? Vaccine. 2022 May 20;40(23):3093-3095. doi: 10.1016/j.

vaccine.2022.04.061. Epub 2022 Apr 22. PMID: 35484041; PMCID: PMC9023356.).

Accordingly, alternative and complementary therapies targeting genetic damage and/or lesser known S-protein susceptibilities are summarized below.

Alternative and complementary therapies

Antonucci N, Pacini S and Ruggiero M. reviewed the array of 'alternative therapies' and nutritional regimens associated with dramatic decreases in serum free Kappa light chains and normalization of the Kappa/Lambda ratios in multiple myeloma [31].

In addition, Das S and Juliana N., *et al*. [32] reviewed "multiple myeloma and its treatment, drug resistance, the molecular basis of epigenetic regulation, the role of natural products in epigenetic regulators, diet, physical activity, addiction, and environmental pollutants, . . . ". They noted that that MM is "one of the most expensive cancers in terms of monetary costs. Because multiple myeloma is so heterogeneous and complex, treating people with the same drug is often difficult. . . .Initially, the patients become responsive to treatment, but at later stages they become resistant. This is the main challenge encountered with MM treatment.

"One of the processes underlying medication resistance is alteration in the myeloma cells' adhesive abilities to the extracellular matrix or stromal cells in the bone marrow. Researchers showed that genetic abnormalities and epigenetic aberrations that affect the patterns of DNA methylation and histone modifications of genes, mainly tumor suppressors, play a vital role in drug resistance in MM resistance".

Curcumin

Turmeric has long been recognized for its medicinal properties. As reviewed by Hawlings SJ and Kalman DS, [33]. "It aids in the management of oxidative and inflammatory conditions, metabolic syndrome, arthritis, anxiety, and hyperlipidemia. It may also help in the management of exercise-induced inflammation and muscle soreness, thus enhancing recovery and performance in active people". Piperine is the major active component of black pepper and, when combined in a complex with curcumin, has been shown to increase bioavailability by 2000%.

Nattokinase

Findings by Tanikawa., *et al*. [34] determined that nattokinase exhibits potential for the inhibition of SARS-CoV-2 infection via S protein degradation. Further, according to Chen and McGowan., *et al*. [35]. Nattokinase is currently being evaluated for its potential as an amyloid plaque-degrading agent. Low doses of nattokinase have been shown to increase expression of the ADAM10 gene, which belongs to a family of proteinases that degrade the amyloid precursor protein [36] "When cell lysates transfected with S protein were incubated with nattokinase, the S protein was degraded in a dose- and time-dependent manner [37].

Hsu RL, Lee KT and Wang JH., *et al*. explored the amyloid-degrading ability of nattokinase, a fibrinolytic subtilisin-like serine protease, and determined the optimal conditions for amyloid hydrolysis [38].

Frequency therapeutics

Scientific evidence is mounting supporting the use of sound and/or electromagnetic frequencies to reverse oncogenetic defects and remedy pathologies.

In 2018, Kumeta M and 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 [39]. "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 the most target 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.

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/Patient's frequency research determinations and publications, discouraging the use of 440Hz in frequency therapeutics and alternatively encouraging A = 444Hz that resets the C-pitch and musical scale base octave at C = 528Hz [40].

Kumeta M and Yoshimura SH's Figure reprinted below charts relative mRNA level depletion in response to sine wave sound vibrations measured over 4 hours [39]. These researchers found " [a] t least two mechanisms likely to be involved in this sound response: transcriptional control and RNA degradation" [39].

In the author/Patient's case, COVID and COVID vaccine RNA degradation would be remedial in purging the B-cell and plasma

cell genetic pathology. Secondarily, transcriptional control using sound may limit: (a) mRNA production from specific oncogenes in these damaging cell lines; (b) post-transcriptional events that regulate mRNA translation into S-protein antigens; and (c) plasma cell antibody transcription yielding overproduction of the Kappa free light chains prompting the diagnosed MM pathology.

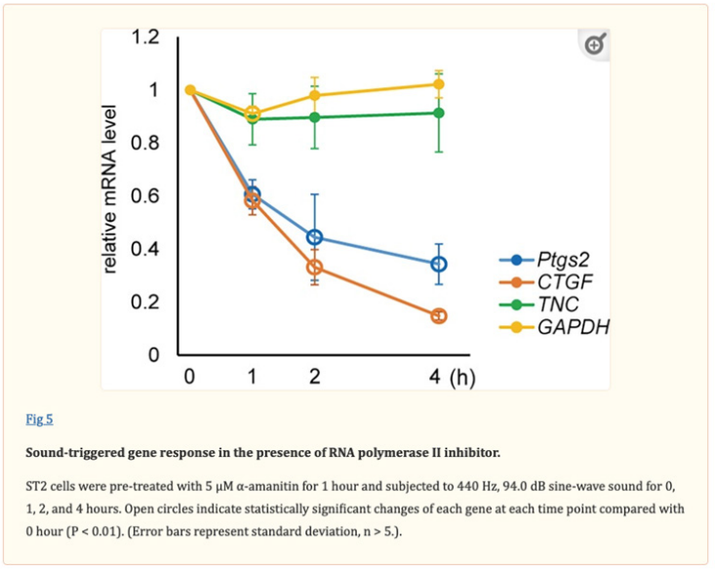

Fig 5

Sound-triggered gene response in the presence of RNA polymerase II inhibitor.

ST2 cells were pre-treated with 5 μM α-amanitin for 1 hour and subjected to 440 Hz, 94.0 dB sine-wave sound for 0, 1, 2, and 4 hours. Open circles indicate statistically significant changes of each gene at each time point compared with 0 hour ($P < 0.01$). (Error bars represent standard deviation, $n > 5$.).

Figure 1

Gonzalez-Jimenez, Ramakrishnan G., *et al*. observed coherent delocalized sound packets (i.e., phonons) upregulating DNA under physiological conditions responsible for epigenetic expression and phenotypic results [41]. They explained in detail the fact tiny sound packets produce macroscopic conformational changes in nuceic acid sequences and genetic expressions of DNA prompting related biochemical phenomena. They wrote: "The processes important to the biological function of DNA (replication, transcription, denaturation and molecular intercalation) have in common that they start with the breaking of the hydrogen bonds between the bases of the nucleic acid. Driven by the torsional stress of the molecule, the destablization of the weak bonds leads to the splitting of a section of the double helix of DNA into single strands, forming a gap in the nucleic acid known as a transcriptional bubble".

In this case study, this is precisely what the author/Patient's optimal remedy would provide, to correct the B-cell cell and plasma cell line poisonings by COVID-19's mRNA to the DNA, and/or the S-protein antigen resulting in the MM.

Challenging this therapeutic thesis, Gonzalez-Jimenez's group cautioned that body water "is likely to cause phonon modes to be heavily damped and localized" [49]. This author largely disagrees and stipulates that attenuation of frequency therapeutics is largely mooted by water being a superconductor of 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 of the original Solfeggio musical scale [48]. Knowledge of these facts prompted several independent affirming investigations recording the unique immunological and neurological benefits of 528Hz frequency increasingly used clinically [42-44].

Flavio., *et al*. [45] 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 all the frequencies tested. "The [ultrasound] treatment was able to inhibit the Wuhan strain in all applied frequencies. Interestingly, 3-12 and 6-18MHz did not inhibit SARS-CoV-2 delta and gamma variants infection, on the other hand, 5-10MHz was able to abrogate infection and replication in all experimental conditions" [45].

Contrarywise, the author/Patient theorizes that diminished virus titers had less to do with the variants' resistance than the choice of frequencies, or range of frequencies, applied. Alternatively, Chandler DL at MIT published [46] that "differences in vibrational characteristics correlate strongly with the different rates of infectivity and lethality of different kinds of coronaviruses". S-proteins are not static, "they're vibrating and continuously changing their shape slightly, and that's important" to RBD dynamics and infectivity. Using the metaphore of house locks and keys, Chandler reported that " [k]eys are static, they don't change shape, but what if you had a key that's continuously changing its shape — it's vi-

brating, it's moving, it's morphing slightly? They're going to fit differently depending on how they look at the moment when we put the key in the lock" [46].

In related research Chandler 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 speculates 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. Another approach might be to induce opposite vibrations to cancel out the natural ones in the spikes. This would be similar to the way noise-canceling headphones suppress unwanted sounds. The more the "key" can change, the researchers reasoned, the likelier it is to find a fit [47]. Summarily, ultrasound frequencies produced by medical devices in everyday use could be used to inactivate SARS-CoV-2; and ultrasound inactivation could be used with other antivirals to reduce viral titers of SARS-CoV-2.

Similarly, Malasian engineer A.B.H. Kueh [47] considered "evolving viruses," and "alternatives such as the 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". Kueh discerned that in order to determine "the precise range of resonant frequencies for different biological bodies," a "cost-effective computational simulation approach" might be best. Using this method, Kueh exhibited a large structurally destructive deformation 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" [47].

Kueh referenced the "analysis of the deformation state of crystallites embedded in the polycrystalline matrix" of viruses published by Reimers W [48]. This is of interest to the investigation of crystallite-crystallite viral interactions as a typical physical feature of polycrystalline matter" [48].

Relatedly, Bastidas OH and Sevarac Z observed the spike protein to favor 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 [49]. They determined the "wild type" spike exhibited a discrete vibration "in the 23-63 MHz range with 42.969 MHz being the most prevalent frequency sampled by the oscillations". They thus determined, the spike protein "favored certain frequencies more than others," and that the oscillations may be a function of position in the primary structure" of the composite amino acids amenable to therapeutic initiatives [49].

Thus, these findings indicate that there is a particular frequency domain profile for the S-protein antigen, as well as the oncogenetic COVID-19 cancers, that might provide therapeutic advances for myriad ailments. With this in mind, the author continues to research and test frequency therapeutic and adjunctive protocols consistent with this case study.

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