Review

Why It Remains Statistically Probable That SARS-CoV-2 Was Isolated and Then Accidentally Lab-Leaked before the First COVID-19 Outbreak

Carp Theodor-Nicolae *

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Review

Why it Remains Statistically Probable that SARS-CoV-2 Was Isolated and Then Accidentally Lab-Leaked, before the First COVID-19 Outbreak

Carp Theodor-Nicolae

Independent Researcher, Freelance; theodore.nicholas100@gmail.com

Abstract: The SARS-CoV-2-induced acute COVID-19 pandemic disorder seems to have begun all of the sudden in 2020, with very little data available regarding prior times in which people experienced mysterious flu-like illness symptoms characteristic of the pandemic disease. The scientific community seems to be divided into a few parts with regards to the belief of the kind of viral origins. A significant number of scientists believe that the virus solely has natural origins and that it underwent a thorough process of zoonosis, independent of laboratory research-based research that would only catalyse zoonosis due to helping the virus gain additional function of transmission and virulence. Many other scientists believe that the virus has wide origins characteristic of "gain-of-function" laboratory research, whilst many other scientists believe that most of the viral genome has natural origins, with the zoonotic process having been artificially catalysed only in its latter part of transmission to humans. Considerable extent of scientific evidence suggests that the virus underwent a restricted, but considerable extent of "gain-of-function" research, prior to having been accidentally leaked into the nearby environment, whilst its process of zoonotic spillover into humans was influenced by such events, given for example the multidimensional pathogenetic process displayed by the virus and its main antigen of action, the spike glycoprotein, causing all kinds of immune pathophysiology - including transient immunosuppression. Investigations into the origins of the novel coronavirus have been lasting for years, seemingly with no concrete end in sight, and the available molecular testing methods to detect SARS-CoV-2 infection displaying less than perfect results have not significantly helped the process. Evidence even started pointing toward the existence of artificial, laboratory research-based viral origins, exposing a probable accidentally-induced artificial process of "accelerated viral evolution", which could be particularly dangerous because of the nature of the SARS-CoV-2 pathogenic agent. Likewise, it is possible that the prevention of distribution of scientific data regarding scenarios as such in fact constitutes censorship, rather than regulation of data that may be considered not to be significantly evidence based. Simultaneously, it is important not to regard all hypotheses and preliminary reports of scientific research as evidence-based, but to ensure that due diligence is performed in all cases. The integrity of scientific research and ultimately of the innovation process of medical solutions depends on the integrity of democracy and the rule of law, as well as on regulating partnerships with scientific companies from world nations where autocracy rules their society.

Keywords: SARS-CoV-2; polymorphic virus; variant; species; environment; positive-sense; single-stranded RNA; zoonosis; bats; pangolins; minks; viral isolation; outbreak; epidemic; pandemic; RT-PCR; innate immunity; first-line; second-line; adaptive immunity; third-line; democracy; autocracy; ideology; natural selection; artificial selection; gain-of-function; cloud seeding; scientific integrity

Introduction

In order to investigate the data supporting an alleged "gain-of-function" research of SARS-CoV-2, prior to its accidental leak into the nearby environment, the definition of zoonosis needs to be explained and thoroughly understood. An overall zoonotic spillover of a virus into humans would

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cover several steps of isolated and local transmission events into people, and before an actual outbreak occurs, years of isolation and in the end, local zoonotic events would have to first occur. SARS-CoV-2 all of a sudden began infecting hundreds of millions of people, with extremely restricted moments of human infection having occurred in the several years beforehand, and many by relative viruses, like the circulating coronaviruses causing the common flu. Previous exposure of humans to previous relatives to the novel coronavirus, such as SARS-CoV-1 and MERS-CoV, is not included in the zoonotic process of SARS-CoV-2, as it is an individual species of the beta-coronavirus genus. Despite the fact that local populations in Vietnam and China underwent respiratory illnesses with new variants of coronaviruses, there may be significantly insufficient data to suggest that SARS-CoV-2 underwent a thoroughly natural process of zoonosis, without an event of laboratory research-based catalysis of zoonotic spillover into humans. Likewise, a statistical probability that events contrary to such a scenario occurred remains rather visibly existent. It is possible that a gain-of-function laboratory research process not only made the virus more virulent, but actually more capable of infecting humans and causing severe disease in the process. Only a gain-of-function research process would have helped the virus jump all the steps of zoonotic spillover into humans, making it directly capable of impairing the health state of millions of people, from all distinct areas of the world, and in a relatively indiscriminate manner. Likewise, the statistical probability that the virus fully underwent natural zoonosis now looks to be considerably lower than the statistical probability that, whilst the virus has most of its origins natural and that it underwent multiple cross-species transmission events, it underwent an extent of gain-of-function laboratory research and then it was leaked from the laboratory, probably gaining a much higher ability to infect neighbouring human organisms, making clinicians probably even unable to contain it in the laboratory environment.

The imperfect state of world democracies, accompanied by existing forms of authoritarianism and totalitarianism, as well as existing monopolisation of financially-influential scientific corporations, may have brought a major contribution to the significant delay with regards to a thorough international investigation of the SARS-CoV-2 origins. Such a delay risks having been camouflaged into a form of pseudo-security that the virus had completely natural origins and that artificial interventions against natural processes of viral evolution and zoonosis in undemocratic areas of the world could not have possibly occurred without the knowledge of the general public. Artificial efforts aimed to improve the stability and quality of the environmental phenomena have become part of reality during the third industrial revolution, which took place from the twentieth century, when research regarding extreme weather management, as well as the synthesis of genetically-modified organisms started taking place in countries like the United States of America (USA), the United Socialist Soviet Republics and later on, in China People's Republic. Likewise, the concept of viral "gain-of-function" laboratory research would not be depicted from a science-fiction scenario, but from a realistic potential of scientific research covering the environment with her living human and animal inhabitants. The intent behind such efforts is certainly to make the environment an accessible place to live for all people; nevertheless, an artificial implication of inducing environmental changes, in the attempt of reversing effects of climate change, could bring colossal risks to the integrity of the entire environment, with her inhabitants. However, negative "side effects" of such processes could prove to be enormous. For example, "seeding clouds in the atmosphere", "influencing the growth of various types of clouds" and "influencing air flow currents", and plans to "physically or chemically inhibit or even completely block solar ultraviolet radiation in the atmosphere" in remote or local areas of the world could eventually result in the sudden development of unprecedented weather hazards, which in the worst case scenario could destroy large parts of the ecosystem. Such attempts of artificial natural phenomenon-management constitute risky practices, given their unintentional companionship with the increased rates of artificially-induced damages of wide areas of the natural environment, such as forests and land under which valuable natural resources are located. Not to mention that "gain-of-function" research of viruses could result in their accidental spillover into animal species or even into humans, causing the development of biological hazards that would claim numerous human lives. As a result, scientific committees decided to rule artificial practices of environmental interventions, such as "seeding the atmosphere to improve

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weather phenomena", "the creation and artificial selection of genetically-modified organisms", as well as "gain-of-function laboratory research of microbes" unethical, and multiple governments around the world passed laws prohibiting or seriously restricting such practices, except for designated laboratories and if accompanied by severe protective measures around such experiments, in spite of the evident existence of good intention behind them. The rationale behind stringent regulations and prohibitions could be well understood by a wide body of the populations of democratic countries, given that direct interventions against processes of natural selection could severely disturb the process of human and animal evolution, with existent risks of even causing a transiently reverse process of the evolutionary pathway, at least in local situations. Ultimately, the most important, yet paradoxically still seemingly neglected message of medicine in several areas of the world, is to cause no harm in the process of developing life-saving solutions to dilemmas of complicated diseases. Whilst it remains essential to consider all sides of the debate valid, it is important to note that, if SARS-CoV-2 underwent laboratory "gain-of-function" research even in the slightest and most subtle fashion prior to the first COVID-19 outbreak, the evolutionary battle between human immunity and viral immune evasion "intelligence" may have become much harder to be held, requiring more intellectual and clinical efforts, as well as time, by the world-class scientific communities.

Results

Following a thorough process of scientific literature review, it was deduced that the virus has increased abilities to camouflage its' genetic material against Pattern Recognition Receptors, leading to an unprecedented extent of Interferon-Stimulated Gene suppression of activation and of restricted signalling to the third line of immunity, and such a process led to serious delays of adaptive immune cell recruitment, which would be proportional with the lengthy asymptomatic stage of the disease. It was deduced that the main element of virulence, the spike glycoprotein, caused clinical impairment in nearly all organ systems, thereby the viral infection displaying multi-lateral effects of pathophysiology, despite the nomenclature of the disease pointing only specifically to the respiratory system. It was deduced that the ability of the spike protein to particularly target the circulatory system would facilitate the induction of multi-systemic illness following the spread of the SARS-CoV-2 copies of the viral load. Furthermore, it was deduced that the receptor binding domain of the spike glycoprotein is highly interactive with the ACE2 receptor of human host cells, that the high level of homology between the spike protein and human host proteins is responsible for the unprecedented incidences of developed autoimmune reactions, both to the viral disease and to the vaccine spike protein. It was deduced that such generalised human health problems caused by SARS-CoV-2 and its main byproduct of the spike glycoprotein likely reflects the existence of an artificially-induced catalysis of the viral zoonotic spillover process into humans, as a result of a successful laboratory isolation moment, followed by the unethical performance of a process known as "gain-of-function" research, even if intended to be brief in extent and implicate an insignificant extent of antigenic additions to the virus. Despite the fact that remote cases of SARS-CoV-2 transmission occurred from minks to humans after the spread of the virus worldwide (Tan Z. et al., 2024), there is no conclusive evidence to state that the virus came from minks, through a completely natural process, given also the fact that the virus was capable of spillback from humans into minks by the time the pandemic started (Hayashi T. et al. 2023). Following the performance of the scientific literature review-based research, the author deems the risks of existence of "gain-of-function" laboratory research as part of viral genesis to be higher than the threshold level established by the competent health authorities, and likewise, the author encourages further investigations into the origins of the virus, accompanied by transparent scientific debates in order for scientists from all sides of the debate to receive the viable opportunity to present their collected pieces of evidence. Currently, there is no conclusive evidence to state that the virus has completely natural origins, despite claims made so by scientists who utilised a rather informal language of personal attacks against scientists who brought inconclusive, yet simultaneously valid research data, regarding a probable artificially-induced catalysis of the viral zoonotic process of spillover into humans.

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Discussion

The recent events regarding zoonotic spillover of the avian H5N1 strain of the Influenza A Virus (IAV) represent a major example of how the entire process of zoonotic spillover into humans is lengthy, and highly unlikely if it involves sudden steps. The case of SARS-CoV-2 zoonotic spillover into the human host may have been catalysed by an alleged gain-of-function research, claims that have also been moderately supported by U.S. government sources. It is evident that zoonosis occurred, and that much of the viral genome has natural origins, with a few intermediate species of transmission having been implicated in the process. Nevertheless, the virus might have been given considerable new powers of infection and virulence during the restricted extent of the alleged "gain-of-function" research, thereby scientists risking to slightly and evidently unintentionally have played "Mother Nature" if they actually performed such viral research, just as existent processes of "cloud seeding" and "cloud growth management" that evidently have occurred in a restricted manner, still present similar risks. The principal question that the scientific community has been asking herself is how direct and wide human interventions may need to be in the effort to improve the living conditions of the Earth's environment, and where the narrow space of equilibrium is, given the colossal risks that any extent of exaggeration presents. Data suggests that the process of viral laboratory research implicated testing on bats captured by scientists for such purposes of clinical testing. An eventual leak from the laboratory environment may have been caused by the given additional powers of infection and virulence by the virus, as well as by gaps of imperfect measures of protection taken in and around the laboratory where it was being researched. The nature of novel coronaviruses, like SARS-CoV-1, MERS-CoV and their direct phylogenetic relatives, would likewise implicate major risks, even in the performance of slight "gain-of-function" viral research, given the fact that the disease they cause display increased rates of morbidity and lethality. Data supporting claims of a lab-leak event of the novel coronavirus include an increased concentration of the local population, specifically nearby the Wuhan Institute of Virology, rather than the Huanan Seafood Market, utilising the local internet search engines in order to look for flu-like symptoms, and many becoming ill with mysterious respiratory illness-specific symptoms, toward the end of 2019 and at the beginning of 2020, before the initial outbreaks in the People's Republic of China and then Italy were officially announced. The Senate of the U.S. ruled the scenario of laboratory origins of SARS-CoV-2 as most likely and, in June 2023, the U.S. Government considered laboratory origins of the virus to a moderate extent, offering data to the general public regarding employees of the P4 Wuhan Institute of Virology who became ill with respiratory flu-like symptoms at the end of 2019. Furthermore, the partially transparent regime ruling the population of Wuhan did not allow hospital doctors to freely discuss about a novel, mysterious respiratory illness that affected many hospital doctors and nurses before the outbreak was officially announced, and allegations of regime persecution upon the doctors discussing events as such as they directly witnessed were distributed internationally. Because of such lack of transparency, the virus was allowed to be freely transmitted locally, nationwide and even internationally, with high-speed train stations and airports remaining restriction-free during the times when the virus was likely spreading heavily by people with relatively mild symptoms of the disease. Once the outbreaks occurred internationally, immediate measures of viral spread containment took place, but such measures played a role in delaying the process of analysis of the viral genetic and protein-related origins, as clinical scientists were required to work from home. A more general conversation within the scientific community occurred after the disease became endemic in nature, and it was when the academic and clinical voices started to gather when substantial questions regarding the origins of the virus were finally raised, despite the unusual extent of virulence observed during the clinical development of the infectious disease. It is not the severity of the disease per se that concerned many scientists, but the largely multi-dimensional extent of disease morbidity that the virus and its spike glycoprotein caused in the host human and animal organisms.

Furthermore, the process of molecular diagnostics of SARS-CoV-2 infection was imperfect, despite detecting a form of illness and media-related claims that the process was accurate. The inventor of the RT-PCR molecular testing procedure of single-stranded RNA molecules, Dr. Kary

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Mullis stated that his testing procedure was not intended for clinically ill patients, and that the procedure may detect any viral agent consisting of a single-stranded RNA molecule whilst returning a positive result. Likewise, the RT-PCR testing method was not sufficient to bring concrete results regarding SARS-CoV-2 infection, in spite of successfully detecting infectious disease of the upper and lower respiratory tract much of the time. Furthermore, the testing procedure was often found to return positive results solely after detecting RNA molecules of inactive particles of viruses that were not always even copies of the SARS-CoV-2 species, but oftentimes, it was suggested that dead copies of flu-like RNA viruses were found in the lining of upper respiratory tract, meaning that the rate of false positive results was higher than expected. At the same time, there were generally no unusual rates of false negative test results detected and shared in the medical and scientific communities. Moreover, the antigen-specific tests, designed to detect COVID-19 through the detection of IgM and IgG antibodies on the upper respiratory tract's wall, also were not sufficient in specifically detecting copies of SARS-CoV-2, as they were created based on the model of RT-PCR tests, but in a manner that clinical disease caused by RNA viruses would be detected faster, with lower requirements of financial expenditure. The entire aspect makes the situation regarding a thorough analysis of the viral origins more difficult, and likewise, it could be that the flawed available processes of molecular testing did not bring a considerable catalysis to the process of international investigations, which has shown to be a rather lengthy one.

The pathological nature of the spike glycoprotein antigen raises considerable concerns with regards to some of the viral origins. Namely, it was discovered that the level and extent of morbidity caused by the spike glycoprotein are similar to the ones of a superbug, causing pathogenesis in multiple, distinct kinds of host tissues. Some research data regards the spike glycoprotein as a "superantigen" due to its generalised effects of pathophysiology in human and animal organisms. In the worst cases, the spike glycoprotein caused systemic organ damage and inflammation. Furthermore, scientists discovered that its receptor binding domain has a particularly high binding affinity to the ACE2 endothelial cell receptor, with approximately 79% of its structure having displayed homology with human proteins. As a result, the spike glycoprotein is substantially capable of causing the development of autoimmune responses. Moreover, the spike glycoprotein was recorded to contain an unusual furin cleavage region in its amino acid chain, and it is known that a furin cleavage assists the process of viral receptor-mediated endocytosis. Furthermore, the biophysical makeup of the amino acid chain constituting the spike protein is highly unusual, with existing groups of four consequent amino acids having their side chain positively charged, and both the data regarding the high degree of human homology and the data regarding the unusually high degree of electric charge duplicity of consequent amino acid building blocks of the spike protein indicates there is a high degree of viral adaptability to the human host organism, particularly via the human ACE2 receptor, potentially raising a statistical probability that the virus once encountered laboratory-based catalysis during its evolutionary pathway that implicated a zoonotic spillover process into the human organism. Moreover, following the commencement of the COVID-19 mass vaccination campaigns, a few clinical trials occurred, and evidence-based data regarding the existence of a highly unusual molecular phenomenon was collected and distributed. Namely, it was indicated, via in-vitro cellular studies, that during a biodistribution of the spike glycoprotein-encoding vaccine mRNA, shelled into the lipid nanoparticle (LNP) layer, into hepatic cells, LINE-1 Reverse Transcriptase enzymes became activated and transformed approximately 1% of the mRNA into double-stranded DNA, which was then inserted into the genome of the cell. Such an event is highly, if not extremely unusual for a non-retroviral, positive-sense, single-stranded RNA molecule, and it may only raise substantial scientific enquiries, calling for a thorough investigation of the genetic nature and origins of each particular viral region. Additionally, other receptors were recorded to undergo activation, locally including even the CCR5 and CXCR4 co-receptors, during the entry of SARS-CoV-2 viral copies into host cells. Some research projects have exposed an existing ability of SARS-CoV-2 with the spike glycoprotein to suppress the quality of future immune responses, and it was recorded that the virus even caused transient symptoms characteristic of the acute immunodeficiency syndrome (AIDS) thereby sharing a few molecular behaviours with the HIV

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retrovirus. It would be rational to state that such transient immunosuppression may only be responsible for the onset of secondary respiratory infection with certain pathogenic bacteria or yeasts, raising risks for the development of microbial pneumonias, particularly in people with one or more comorbidities. The visible characteristics of multidimensional pathogenesis displayed by SARS-CoV-2 represents a viable concern with regards to a possible existence of an artificially-induced catalytic process during the viral zoonotic spillover into humans. Furthermore, the unprecedented frequency and even diversity of vaccine-induced adverse reactions developed during the SARS-CoV-2 mass vaccination campaigns further support the argument of existing peculiar origins of the virus. The particularly high biodistribution rates displayed by the spike glycoprotein, which could be proportional with the high ability of SARS-CoV-2 transmission from infected individuals, may also be in accordance with concerns of artificial origins of the virus, given that data collected during the initial phase of the mass COVID-19 vaccination campaigns displayed a proportion of 100% of vaccinated, uninfected patients with anti-spike glycoprotein IgA immunoglobulins present in their saliva.

Despite all such alarming data regarding the high degree and multi-dimensionality shown by the SARS-CoV-2 process of virulence induction, as well as the fact that the novel coronavirus was shown to be particularly capable of suppressing the activation of the interferon system, which constitutes the main element of both first-line and second-line host immunity, several clinical trials implicating the administration of a fairly low dosage of human recombinant Type I Interferons prevented the development of COVID-19 in nearly all participants of the experimental groups, thereby displaying rates of efficacy approximate to 99%, with some perfect disease-preventive results of 100%. Paradoxically, the same area that displayed higher vulnerability to the induction of viral immune evasion were the areas that brought the best results of infection combat and clinical disease prevention and effective early treatment, showing thereby the elevated potential that first-line and second-line, innate immunity plays in regulating the spread of viruses, including the ones that are highly polymorphic in nature. The fast discoveries of newer concepts, particularly in innate immunity, perhaps shows the principal “battlefield” of the evolutionary struggle between the human and animal immune systems and polymorphic viruses; the first- and second-line of immunity, which are located in the innate immune system and predominantly in its mucosal department. Research communities centred around vaccine development managed to develop a few vaccines that would more directly implicate the activation of the principal elements that natural immunity include, given the context of higher rates of both innate and adaptive immune evasion caused by modern-day polymorphic viruses. Moreover, the fact that microbial toxicity exists within microbial toxicity, as well as immune protection within immune protection, displays the application of the Theory of Relativity into the Theory of Evolution, via the Germ versus Terrain theories. Namely, two potential facts emerge from such an application of physics into biology; that germs can constitute terrains for other germs and that the ability of the host terrain to be protected from germs can be calibrated by specific factors. An example of immunity existing within immunity is the CD4+ helper T-Lymphocyte containing its own immune system, whose adequate, timely calibration may prevent its infection with the Human Immunodeficiency Virus, which represents a negative-sense, single-stranded RNA (-ssRNA)-based retrovirus. For example, a prior treatment of helper CD4+ T-Lymphocytes with a fairly low dosage of human recombinant Type I and Type III Interferons may help such immune cells to develop stronger protection against the virus, by means of localising and lysing it before it successfully infects the host cell and commences its own procedure of molecular self-camouflaging inside it. As a result of a potentially increased trained immunity of T-lymphocytes, they may slowly undergo a process of transformation into “super-lymphocytes”, whilst not denying the fact that a number of host T-lymphocytes will still undergo apoptosis following infection with HIV. In short, a thorough understanding of the processes of human and microbial evolution would require adjustment through the apprehension of the fact that physics represents the foundational layer of all Earthly sciences, which means that biological phenomena are in fact dependent upon the theories, principles and laws observed in physics (Carp T., 2023). Perhaps through a similar kind of research pattern, scientific data collected from various clinical trials showed not only that the innate immune

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system contains its own "memory", but that it contains "specific memory" (Kurtz J., 2005). Likewise, it was observed that the innate immune system ultimately presents adaptive characteristics. In the same manner, it was discovered that the adaptive immune system presents its own characteristics lacking specificity. Such a bilateral aspect of the immune system perhaps indicates that its innate and adaptive compartments are interdependent (Muraille E., 2016). As a result, it is becoming increasingly probable that certain elements of natural immunity play a role in bringing effects of immunisation, following initial projections that did not lean toward such observations.

Challenges impeding the reach for the best abilities of clinical research have also been present in First-World countries, with current ideologies involving capitalism and bureaucracy having infiltrated scientific research rather considerably. A barrier between science and politics has not been established, with political views and ambitions, as well as local financial interests, having infiltrated major research communities. One major case may implicate the fact that influential U.S. corporations invested a voluminous amount of money into "gain-of-function" viral research at the Wuhan's Institute of Virology a few years before the SARS-CoV-2 outbreak occurred in the city. Despite the fact that China is ruled by a regime with imperfect transparency and limited freedom of speech and informational flow, the U.S. government allowed for such a level of investment into "gain-of-function" research. Even if there is no association between the investments and the SARS-CoV-2 outbreak, the fact that they occurred decreased the credibility of influential U.S. corporations of Science, not just nationwide, but internationally. There may be an excessive level of financial interest from world-class corporations, which could eclipse scientific progress and even prevent necessary scientific research from occurring. Such imperfections in Western democracies have caused delays in the process of scientific research of innate immune evasion by polymorphic viruses, as well as of potential methods of wider natural immune inclusion in the domain of vaccinology. The dilemma centred around brief and subtle "gain-of-function" laboratory research involving novel viruses with diverse mechanisms of pathogenesis and virulence induction is the fact that the researched viruses may gain a higher evolutionary advantage over the presented weaknesses in the natural immune system. As a result, scientists will become required to bring about a general change of course with regards to clinical research into vaccine development. Namely, it is probable that, if novel viruses of potential public health concern that are undergoing even the most subtle "gain-of-function" research by means of foreign antigen addition, vaccine-based research may be needed to cover much larger areas of natural immunity, and much smaller areas of adaptive immunity, as rates of innate immune evasion would begin to skyrocket, leading to a widespread induction of immune evasion, despite the creation of effective vaccines. Such vaccines would be effective only for the present viral variants, and future mutations could help the virus evade antibodies against the previous variants and induce significant disease, despite the valid innovative efforts to create life-saving vaccines. It has already become increasingly difficult to create pathogen or antigen-derived vaccines against polymorphic viruses, as they have displayed increasing rates of immune evasion following new rounds of mutation.

Following the initial COVID-19 outbreaks in the People's Republic of China and then Europe, scientists quickly sequenced the viral genome and developed a plan to develop a vaccine against the viral disease. The scientific community was situated in a race to combat the rapid effects of pathological destruction caused by unprecedented levels of innate immune evasion, as well as multi-systemic pathological damages caused by the highly interactive receptor binding domain of the spike protein with the ACE2 receptors of vital endothelial cells, causing both respiratory and circulatory illness. The initial plan of vaccine development implicated the usage of the viral genomic regions directly responsible with the induction of pathophysiology - in this case, the spike protein-encoding positive sense, single-stranded RNA molecule, as it would encode the principal effectors for the induction of virulence. Nonetheless, numerous scientists - mostly the ones unaffiliated with major health corporations - abandoned the plan as soon as they observed that more than three quarters of the spike glycoprotein was homologous to human host proteins, raising unprecedented risks of inducing autoimmune reactions to such vaccines. And this projection turned out to be in major concordance with the high frequency of autoimmune responses against the viral disease during the

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critical stages of the pandemic. Furthermore, the superbug-like molecular behaviour, as well as the existing capability of the spike glycoprotein to temporarily inhibit the quality of immune activation further reduced the level of public trust in the spike protein-based prophylactic vaccines, made available through the procedure of emergency medical authorization (EMA). In spite of the genuine intellectual and clinical efforts of world-renowned scientists and researchers to develop life-saving vaccines against COVID-19, the medical and public health context, implicating the highly polymorphic nature of the virus, as well as the uncertainty with regards to its origins and full pathological potentials, resulted in the very low possibility of the scientific community to develop a vaccine with long-term effects of protection and that would be safe for all patients. Much of the data even displayed better results with regards to long-term protection, of unvaccinated young people with no comorbidities that were exposed to the virus, compared to people who received the vaccine. Specifically, whilst many unvaccinated people did not experience the disease more than once or twice, vaccinated people became ill with considerable clinical symptoms repeatedly following multiple rounds of re-exposure to the virus. As a result, trained immunity displayed results more promising than projected beforehand, despite the important roles that vaccines played during past epidemic outbreaks of various kinds, that perhaps would not involve viruses displaying substantial rates of genetic polymorphism. It seems that prophylactic and early therapeutic approaches centred around trained immunity could represent the sole viable medical solutions in case of infectious diseases like COVID-19, as there is a substantial risk that significantly polymorphic viruses will evade the recognition of antibodies against their previous variants following pathogen-derived immunisation efforts. For example, even pathogen-derived vaccines developed against the regular flu have shown flaws in their results, with numerous people experiencing the development of significant clinical symptoms of flu following reinfection. Hence, the existing probability that the virus underwent "accelerated evolution" during its zoonotic spillover process into humans would constitute a major cause of the flaws of the mass COVID-19 vaccination campaigns, and perhaps an acceleration of viral evolution as such made the virus highly polymorphic, and consequently, not usable for the development of pathogen-derived vaccines. A process as such may have accelerated the shift of scientific researchers toward the principal elements of first-line and second-line, natural immunity, in their efforts to develop life-saving therapies and vaccines. Moreover, it was recently shown that, in the case of the recent zoonotic spillover events of the avian H5N1 Influenza A Virus (H5N1 IAV) - which represents a polymorphic, positive-sense, single-stranded RNA (+ssRNA)-based virus - into a few animal species, such as dolphins and poultry, with a few remote cases of human transmission that occurred in the recent months, pathogen-derived vaccines developed and designed against the viral infection in poultry in fact accelerated the evolution of the novel viral strain, increasing the rates of transmission, zoonosis and virulence (Li B. et al., 2023). As a result, such vaccines against H5N1 IAV helped the virus become more infectious and virulent, thereby also stimulating a more abundant production rate of its non-structural protein 1 (NS1), which is known for its effect of camouflaging the virus during its cellular entry, replication and distribution of its load to neighbouring cells and tissues in the upper and then lower respiratory tract. Given that the novel H5N1 strain of IAV is scientifically known to have natural origins, as well as its zoonotic process unaffected by factors specific of artificial selection, it is becoming increasingly probable that the infective and virulence-inductive processes performed by polymorphic viruses can no longer be counteracted by rapidly-developed, pathogen-derived vaccine candidates. As a result, it may be that the matter of a wider inclusion of natural immune elements into vaccine-based research has now become urgent, given the context of advanced viral evolution against points of weakness found in the first-line and second-line immune systems, which constitute the bridge to the adequate activation of the adaptive immune system.

Conclusion

In order to thoroughly place efforts of research, to prevent the onset of further life-threatening epidemic and pandemic diseases, it is important to protect the values of democracy and freedom of information flow, and not solely to perform the intellectual and clinical efforts to innovate solutions

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as proportionate as possible, given that it is the collection of data regarding the problem with its source that constitutes the most important step in the entire process of problem management and resolution. All the scientific theories, principles and laws are based upon the pattern of Universal free will, and thereby the preservation of freedom is necessary for problem resolution to occur. The prevention of a free flow of information by non-transparent or partially transparent political and ideology-based regimes may cause a wide distribution of false and dangerous types of information, which could even be taken as evidence-based data by renowned scientists, not because they would intend it or have an occult agenda behind, but because the source of the information itself given to such scientists would be subtly corrupt, appearing as factual even to the bright minds of the clinical research communities. As a result, scientists with a clear history of integrity in their practice should not respond to the provocations of unhealthy debate, but unite their genuine efforts of researching the source of the problem and innovating novel clinical solutions, to save human lives in case novel disease outbreaks occur locally and even internationally. And such scientists should simultaneously not be afraid to share and accurately interpret the entire gathered data, even if it exposes certain problems regarding freedom of information flow in specific areas of the world where the first disease outbreak occurred. If such problems of communication in Science are resolved, it is possible that history will not repeat in case of the occurrence of new disease outbreaks in similar geographical areas, or in areas where political problems similar to the ones observed internationally in China have been taking place. According to the current stages of research and investigations, it is accurate to state that it is scientifically probable that the novel coronavirus underwent some extent of artificially-based catalysis in its zoonotic spillover process into humans, just as it is scientifically probable that the novel coronavirus fully underwent the natural process of zoonosis, with subtle, local outbreaks having occurred during several years before the pandemic occurred, given also the incompletely reliable molecular testing methods that are currently available in the world. The next objective should be to learn from mistakes made during the COVID-19 pandemic in order to attenuate the effects of future epidemics and pandemics more efficiently and in a faster manner. Likewise, it is necessary for all the competent scientists to gather all the necessary pieces of evidence and innovate new kinds of solutions, given the fact that viral evolution has used gaps of weakness existent in the innate immune system to facilitate viral replication and spread by means of evading first-line and second-line immune signals. Not only might humanity have assisted to the onset of a pandemic disease caused by a virus that had undergone a considerable form of “accelerated evolution”, in spite of likely being brief with regards to chronology, but the entire response of immunisation against it may have been erroneous and causative of collateral effects, in a large part due to a misunderstanding of the viral evolutionary origins. The present matter indicates that the finest dimension of evolutionary battle between human immunity and pathogenic, polymorphic viruses, implicates the key words of “intelligence” and “counter-intelligence”. The fact that it has been scientifically demonstrated that both the innate and the adaptive domains of the immune system contain their own “memory” reflects the fact that polymorphic viruses use “intelligence” behind their evolutionary processes that involve the hijacking and evasion of key immune elements. The existing probability that “accelerated viral evolution” has occurred in the world should represent a history lesson applicable to all scientific disciplines, and expose the fact that the integrity of democracy, biochemical sciences and history are three interdependent currents that massively impact the progress of human society. Furthermore, above-threshold levels of artificial interventions into environmental patterns, such as weather and climate, could result in the development of further major groups of human and animal casualties, also due to its companionship with the unprecedented levels of artificially-induced harms of deforestation, fertile land displacement and the distribution of other environmental hazards. As a result, the natural environment could undergo a serious period of instability and changes as such may further increase social, national and international tensions, with existing risks for the escalation of current military conflicts. Overall, it is not just probable that the world population will stop increasing, but that a world population pattern of decrease will be observed, and such a scenario would confirm the conspiracy theory that the world will observe a process of depopulation.

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