

This text refers to an article in the German magazine Multipolar – <https://multipolar-magazin.de/artikel/corona-biowaffe> – in which Paul Schreyer engages with a work by Dirk Gerhardt. The interview prompted me to analyze the whole issue as 'neutrally' as possible. This is how I see it:

Is the whole construct really a biological weapon?

1. Gain of function research
2. Modifications to SARS viruses according to the cited studies
3. When can a modification be declared a 'bioweapon'
4. Is there evidence for the use of such a defined bioweapon
5. What really made people sick?
6. The virus/microbe dogma and the 'vaccine'
7. Are viruses and microbes really a primary threat to us?
8. Viruses and the mod-mRNA vaccine

1. Gain of function research

In gain-of-function (GoF) research, targeted genetic modifications are made to organisms—usually microorganisms such as viruses or bacteria—to create new or enhanced traits. The goal is usually to better understand how these organisms function, spread, or cause disease. This can include, among other things, increasing the infectivity, pathogenicity, or transmissibility of a pathogen.

The main goals of gain-of-function research are

- Understanding disease mechanisms: Researchers want to understand how mutations affect a virus's ability to infect cells or evade the immune system.
- Predicting potential pandemics: Simulating potential natural mutations helps estimate which variants of a pathogen could potentially arise and whether this poses a pandemic threat.
- Drug and vaccine development (see also 6.): Research can contribute to the targeted development of drugs or vaccines before dangerous variants arise in nature.
- Investigating host switches: This involves analyzing how and why a virus transmits from an animal to humans (zoonoses), e.g., through targeted mutation of the binding sites for cell receptors, and clarifying why this happens in nature.

This inevitably leads to controversies and risks:

- Biosafety risk: The organisms created could escape from the laboratory or be misused.
- Dual-use issue: Research results could be used for both medical purposes and biological weapons.
- Ethical debates: Critics call for stricter regulation or a ban on particularly risky GoF experiments.

Gain of Function research should be distinguished from:

- Loss-of-function research: Opposite – a gene or function is switched off to understand its role.
- Directed evolution or mutagenesis: Related concepts in which mutations are deliberately introduced, but not necessarily with the goal of gaining function.

There are no effective national or international control mechanisms for biological high-risk research. One should not believe that such research only takes place in a few 'secret' locations around the world. Corresponding laboratories exist everywhere, even in the heart of Europe,

including Germany. Moreover, such laboratories are increasingly being established, some supported by private funders and NGOs. Even the WHO promotes such laboratories. Without effective control mechanisms from states and multilateral treaties from individual nations on this issue, people are exposed to an increasing risk regarding biosafety and also to the risk of abusive military use of these research areas.

2. Modifications to SARS viruses according to the cited studies

Based on over 94 cited studies, Dirk Gerhardt points to specific characteristics of SARS viruses and SARS-CoV-2 and their effects. Some of these characteristics may have occurred naturally. However, it is likely that several traits were deliberately modified and inserted into the virus's genome. Such work is indeed constantly being carried out as part of gain-of-function research. The most important studies on this topic are listed under 'References.'

It is highly likely that the so-called furin cleavage site (FCS), which distinguishes SARS-CoV-2 from many other sarbecoviruses, is not of natural origin in SARS-CoV-2. This cleavage site is already present in the bat strain RaTG13, but in SARS-CoV-2, it additionally displays an insertion of four contiguous PRRA (proline-arginine-arginine-alanine) amino acids in the middle of the spike protein. This cleavage site increases the infectivity of the virus by facilitating the cleavage of the spike protein by cellular enzymes (furin), thus facilitating viral entry into cells.

A 2022 article in *Frontiers in Virology* reports 100% sequence homology between the SARS-CoV-2 FCS and the negative strand of a sequence patented in 2017.¹ A commentary on this article argues that the sequence match could have been purely coincidental, while the authors calculate a low probability of chance. Theoretically, a convergence of under-appreciated laboratory experiments and technologies could also have led to the SARS-CoV-2 FCS insert.² Another risk of the GoF that should be considered.

In 2020, Luc Montagnier and Jean-Claude Perez published a paper showing how 16 fragments (Env, Pol, and integrase genes) from various, both diversified and very recent strains of HIV-1, HIV-2, and SIV retroviruses show high homology to parts of the SARS-CoV-2 genome.³ These fragments are 18 to 30 nucleotides long and can therefore alter SARS-CoV-2 gene expression. The authors referred to these fragments as exogenous informative elements (EIEs), a large portion of which already existed in the first SARS genomes in 2003. These EIEs are not randomly scattered but concentrated in a small part of the SARS-CoV-2 genome, suggesting a non-natural origin. They also point to a new region with four exogenous informative elements (HIV1 and HIV2) that fundamentally distinguishes all SARS-CoV-2 strains from all SARS and bat strains, with the exception of bat RaTG13. This part contains a 225-nucleotide region that is unique to SARS-CoV-2 and bat RaTG13. The authors hypothesized that the modifications to SARS viruses arose during attempts to develop an HIV vaccine using SARS viruses as the vector.

¹ Ambati, B. K. et al. (2022). Msh3 homology and potential recombination link to sars-cov-2 furin cleavage site. *Front. Virology* 10, 834808. doi:10.3389/fviro.2022.834808

² Mueller S (2023), Recombination between coronaviruses and synthetic RNAs and biorisk implications motivated by a SARS-CoV-2 FCS origin controversy. *Front. Bioeng. Biotechnol.* 11:1209054. doi: 10.3389/fbioe.2023.1209054

³ Perez, J. C. Montagnier, L.. (2020). COVID-19, SARS AND BATS CORONAVIRUSES GENOMES PECULIAR HOMOLOGOUS RNA SEQUENCES. *International Journal of Research -GRANTHAALAYAH*, 8(7), 217-263. <https://doi.org/10.29121/granthaalayah.v8.i7.2020.678>

A preprint from an Indian research group from December 2021⁴ described that the omicron variant contains a short, 6-8 amino acid-coding HIV-equivalent sequence that matches a sequence in the human genome (more precisely, the genome of an endogenous retrovirus) and also a small sequence in the HIV-1 virus. However, these sequence motifs can also occur purely randomly in many organisms, including viruses and bacteria. There is currently no evidence that these sequences are functionally significant.

Luc Montagnier's group also pointed to a prion region in the various spike proteins of the original SARS-CoV-2 and all its subsequent variants⁵, which is also present in all 'vaccines' based on the sequence of the SARS-CoV-2 spike from Wuhan. The authors described 26 cases of Creutzfeldt-Jakob disease in this context. SARS-CoV-2 appears to be the only coronavirus with a prion-like domain in the receptor-binding domain of the S1 region of the spike protein.⁶

The cited studies raise the suspicion that various properties of this virus were artificially manipulated or are relics of previous GoF experiments. However, no functional retrovirus gene, nor any functional SIV or HIV gene segment, was detected in the mRNA of the COVID-19 vaccine. Based on local reports, it is suspected that the first cases of illness in Wuhan were the result of a laboratory accident.

3. When can a modification be declared a 'bioweapon'?

What is a bioweapon? A bioweapon is a biological weapon that uses living organisms or their products to deliberately harm or kill humans, animals, or plants. It falls under the category of weapons of mass destruction, similar to chemical or nuclear weapons. It can consist of bacteria, viruses, fungi, or parasites that can cause disease, but also of toxins and additional delivery systems.

Biological weapons are used to:

- Spread fear and chaos
- Incapacitate or kill people and/or animals
- Destruct crops or livestock
- Destabilize societies and infrastructure

Because their effects often occur gradually or with a delay, biological weapons are difficult to control and detect.

The interpretation of the diverse modifications evident in SARS-CoV-2 is challenging and can range from harmless research to deadly destructive potential.

If I attach a modification to a vehicle, let's say a pickup truck, to which various devices can be attached, hardly anyone will view it critically, even if, for example, a machine gun could be mounted on this mount. However, the moment this happens, the pickup truck clearly becomes a weapon. However, the additional question then arises: is this weapon being used or is it merely serving demonstrative purposes, for example, to demonstrate that a pickup truck can be turned into

⁴ P. Pradhan et al. (2021) Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag, <https://doi.org/10.1101/2020.01.30.927871>, Work was withdrawn

⁵ Jean Claude Perez et al. 2022, Towards the emergence of a new form of the neurodegenerative Creutzfeldt-Jakob disease: Twenty six cases of CJD declared a few days after a COVID-19 "vaccine" Jab, <https://www.researchgate.net/publication/358661859>

⁶ G. und V. Tetz, 2022, Prion-like Domains in Spike Protein of SARS-CoV-2 Differ across Its Variants and Enable Changes in Affinity to ACE2, <https://doi.org/10.3390/microorganisms10020280>

a weapon (or to prevent this from happening). The situation with GOF is similar. The core problem of gain-of-function research is the blurring of the distinction between technical neutrality and potential danger.

4. Is there evidence for the use of such a defined bioweapon?

The following questions now arise for the modified SARS-CoV-2:

1. Were the various modifications deliberately carried out to turn the virus into a weapon?
2. Were the modifications carried out to better understand how this virus operates?
3. Can this virus actually be used as a weapon, and how harmful would the consequences be?

Regarding 1), it must be said that it is conceivable, but there is no evidence, for example, a 'military' document or information from a whistleblower from which such a procedure could be directly deduced. Research on viruses and microbes is often conducted progressively, meaning that modifications made once are left in place and new modifications are added. This could explain the accumulation of artificial changes. Something is done because it is feasible. Effects are only determined later, but targeted work cannot be ruled out. The problem remains the human factor.

Regarding point 2), it's a common and ongoing research approach. What entry points into the cell does a virus use? What happens when such interfaces are altered? It can never be ruled out that malicious intent may occasionally be behind it. Here too applies: Some of this research can be viewed as playful, meaning that something is done simply because it's possible and then attempts are made to understand the consequences.

To discuss point 3), it makes sense to delve a little deeper into epidemiology, virology, and evolutionary biology.

First, it is necessary to clarify whether a pandemic actually occurred. A pandemic is a worldwide spread of an infectious disease that spreads across national borders and continents, typically affecting a large number of people. The term says nothing about the severity of a disease, nor about mortality—only about its spatial and numerical spread. The term 'pandemic' has been modified several times recently. According to the WHO's current definition, COVID would have been a pandemic, but it was primarily characterized by the fact that it was based on positive PCR tests rather than disease progression. According to our interpretation of the term 'disease,' there was no pandemic.

What would have been expected if SARS-CoV-2 had triggered this so-called pandemic as a biological weapon?

The term 'weapon' implies that it would cause severe damage and many deaths. However, COVID course showed that there was little difference from recurring waves of infection with other respiratory viruses such as influenza, including overall mortality from the disease. The fact that predominantly polymorbid or very old people died also applies to other respiratory viral diseases. Some of the 'severe' cases and deaths can also be attributed to the special measures taken to combat the pandemic or are iatrogenic, such as incorrect medication due to overdoses of hydroxychloroquine, benzodiazepines such as midazolam in very old people, excessively high doses of oxygen, early intubation and positive pressure ventilation, nosocomial infections, and

neglect of antibiotics in secondary bacterial infections. For the majority of people, COVID was a harmless cold or even asymptomatic.

But what did occur was a huge number of registered COVID diagnoses as a result of excessive testing measures with PCR C_t (cycle threshold) values that were far too high, including in hospitals, which in Germany were able to claim a care surcharge of up to €9,508 per treatment case and thus had an incentive to make a 'positive' diagnosis.⁷ It should be noted that neither PCR tests nor rapid COVID tests provide evidence of the presence of the original, modified virus or variants derived from it. Virus cultivation in cell cultures and precise genome sequencing were performed only in very rare cases. In contrast, the positive Corman-Drosten PCR test was commonly considered the gold standard for COVID-19.

The Corman-Drosten test uses primer probes that amplify sections of the SARS-CoV-2 genome. It typically targets conserved regions of the virus, particularly the E gene (envelope protein), which can also be found in other beta-coronaviruses, and the RdRp gene (RNA-dependent RNA polymerase), which is more specific for SARS-CoV-2. The RdRp is a functional enzyme required by all RNA viruses (with few exceptions) to replicate or transcribe their RNA genome. Human cells do not have a classical RdRp for genome replication – which is why it is a typical viral signature enzyme. Other variants of the test target the N gene (nucleocapsid protein) or the S gene (spike protein). The N gene is not specific to SARS-CoV-2, but only to its exact sequence variant, which is not addressed. The spike gene is also not specific to SARS-CoV-2. However, there is a specific sequence variant of the SARS-CoV-2 spike gene. What is specific are the polybasic furin cleavage site (PRRAR) and specific RBD conformations (ACE2 affinity) along with mutation patterns (e.g., D614G, Omicron cluster). These specific spike elements are not specifically or functionally detected in the Corman-Drosten test. SARS-CoV-1 spike and MERS-CoV spike are very similar to SARS-CoV-2 spike.

Combining the target sequences slightly increases specificity for SARS-CoV-2 but does not provide evidence of a modified form of the virus. In the early stages of the pandemic, a multiplex approach with several genes was commonly used to maximize specificity and robustness.

With supposedly increasing experience and variant certainty, detection of the E gene was eventually considered sufficient to 'reliably' detect SARS-CoV-2. However, the E gene is not specific to SARS-CoV-2, but, as mentioned, also occurs in other coronaviruses, particularly some sarbecoviruses (e.g., SARS-CoV-1). This increased the risk of false-positive results due to cross-reactions, especially with SARS-like viruses. This was accepted because it allowed the positive numbers to be artificially inflated.

The so-called rapid tests usually focus only on the N-protein (nucleocapsid), which is also relatively conserved and does not provide specificity for a 'laboratory variant' or specific mutations, but rather detects generally SARS-like viral proteins - although with significantly lower sensitivity than PCR.

Overall, it remains unclear whether the presumably genetically manipulated so-called COVID-19 original variant actually spread worldwide or whether the test predominantly detected other susceptible variants that had long been present. The latter is much more likely.

It cannot be ruled out that peaks of excess mortality that occurred in some cities around the world in 2020 (e.g., Bergamo, New York) were caused by a local release of the virus. The logistics for such an undertaking would be relatively complicated but not impossible: refrigerated transport

⁷ German: <https://www.schwaebische.de/politik/milliarden-deal-so-kassierten-die-kliniken-in-der-corona-pandemie-ab-3676086>

from an appropriate lab, primarily administered to a specific age group, followed by the destruction of all possible evidence, etc. This would require sophisticated logistics for which there is currently no evidence. Additionally, the virus would have had to spread differently from these points – assuming it remains stable. I would have expected 'small waves.' However, from a global perspective, we had a nearly homogeneous spread of SARS-CoV-2 as a result of the testing.

The result of this analysis does not, of course, rule out the possibility of a biological weapon, but it does make it improbable. The purely speculative statement that 'something else could come along' can at best be viewed as a scare tactic to keep people compliant and, for example, encourage them to get vaccinated. The virus bioweapon hypothesis is intended to keep people's fear and anxiety levels high.

Despite globalization and worldwide travel, the coordinated use of a virus as a biological weapon would be associated with many imponderables and uncertainties regarding the desired 'negative outcome.' Viral infections, especially fatal ones, limit their spread because the deceased hosts can no longer transmit the virus. Some regions would be completely inaccessible to such a virus due to climatic conditions. The isolated peaks in excess mortality that occurred primarily regionally and in the short term in 2020 speak against the logical spread of a 'deadly' virus. Due to cross-immunity, there will always be people who would not be harmed at all by such a virus. After all, there is a risk that the virus could sooner or later also affect its 'designers.'

5. What really made people sick?

Coronaviruses are respiratory viruses and usually cause flu-like illnesses, although the individual symptoms are not specific. However, through media propaganda, individual symptoms were highlighted as specific, such as loss of smell. This is clearly wrong. Loss of smell can occur not only with coronaviruses but also with rhinoviruses, RSV, influenza and parainfluenza viruses, various enteroviruses, and also adenoviruses. Such illnesses are usually uncomplicated, but occasionally, particularly in very elderly and polymorbid individuals, severe courses and even death can occur. Secondary bacterial infections can cause additional serious problems.

Especially in the initial phase of the COVID waves, autopsies of the lungs revealed distinctive, apparently characteristic histological changes related to COVID-19, which were deemed to be the cause of death in most patients. Histologically, sequential alveolar damage was observed due to focal capillary micro-thrombosis. This leads to the death of patients either before or after the induction of fibrosis in the lung parenchyma. Diffuse lung damage was only detectable in patients who were invasively ventilated.⁸ This histology is not in conflict with other severe viral pneumonias and therefore cannot be regarded as reliably specific, especially since the described atypical enlarged multinucleated and syncytial pneumocytes, which are often seen in the lungs of COVID-19 patients, have also been described previously in SARS, MERS, and other pulmonary viral infections.⁹

Hardly had the general fear of dramatic disease progression among the population subsided somewhat at the end of 2020 when Long-COVID was 'launched' in Germany. The main symptoms are non-specific symptoms such as exhaustion, fatigue, reduced performance, and chronic fatigue

⁸ German: Kommos, Felix K.F. et al. (2020) Pathologie der schweren COVID-19-bedingten Lungenschädigung, Deutsches Ärzteblatt | Jg. 117 | Heft 29–30 | 20. Juli 2020

⁹ Caramaschi, S., et al. (2021) Histopathological findings and clinicopathologic correlation in COVID-19: a systematic review. *Mod Pathol* **34**, 1614–1633 (2021). <https://doi.org/10.1038/s41379-021-00814-w>

syndrome. Late effects, such as cardiac arrhythmias following endocarditis or myocarditis or pericarditis in the context of severe COVID-19, have also been included.

However, corresponding late symptoms are just as frequently found after other viral infections such as Epstein-Barr virus infections (mononucleosis) or severe influenza courses, e.g., influenza-related cardiomyopathy. Overall, such infection-related late effects are rather rare - clearly less frequent than the late effects after the mRNA vaccination. Long COVID primarily serves to incite panic but does not justify vaccination!

Since the majority of people are now COVID-vaccinated, and COVID infections occur particularly in vaccinated individuals after the mod-mRNA injection – due to the altered balance of the immune response (TH1-TH2 shift: cellular immunity, antiviral ↓, humoral immunity, antibodies, IgE ↑), the so-called 'Post-VAC Syndrome' has been incorporated into 'Long-COVID' or 'Post-COVID.' With this, the German government has cleverly escaped responsibility after it accepted contracts with the 'vaccine manufacturers' that included liability waivers in advance. Long-COVID and Post-COVID are thus classified as fateful events, for which no one has to take responsibility.

In fact, the majority of Long-COVID or Post-COVID patients are 'vaccinated,' and their symptoms can be traced primarily to the mod-mRNA injections. This can now be proven by laboratory tests. In terms of cognitive dissonance, these relationships are ignored by health authorities, many doctors, and partly even by the affected individuals.

6. The virus/microbe dogma and the 'vaccine'

Many doctors and scientists struggle with the realization that viruses and microbes are far more than mere pathogens and 'enemies.' They dogmatically cling to the traditional 'war' against what they see as the primary pathogens, especially since significant profits can be generated from it. The entire COVID story can be viewed from this perspective.

What Dirk Gerhardt clearly highlighted are the negative effects of the mod-mRNA vaccination.

The so-called vaccination against SARS-CoV-2 is not carried out with conventional antigens. Rather, nucleic acids are introduced into human cells using lipid nanoparticles or transgenic vectors. The mod-mRNA particles (modified mRNA)¹⁰, which contain N1-methyl-pseudouridine instead of uracil, do not trigger an immune response themselves. They contain only the nucleic acid blueprint for a protein, but not the antigenically active spike proteins. Therefore, these particles are absorbed by our body's cells regardless of existing immunity. They are virtually invisible to our immune system. They induce protein production in the cells, and only after the spike has been produced does the immune system react in its usual way, classifying the entire cell as foreign and beginning to destroy it.

Compared to previous vaccinations, the genetic immunization experiments for the prevention of COVID-19 largely bypassed necessary tests for efficacy and side effects, utilizing experimental new technologies. However, similar experiments had already led to dangerous side effects in earlier animal studies.

In fact, mod-mRNA injection is not a vaccination, but rather a genetic intervention involving the introduction of artificially modified nucleic acids into human cells. Neither the mode of transmission nor the nature of the antigen contacts bear any resemblance to a natural viral infection. For this reason alone, such interventions are questionable and highly risky.

¹⁰ Karikó, K. et al. (2008) Incorporation of pseudouridine into mRNA yields superior nonimmunogenic vector with increased translational capacity and biological stability. *Mol. Ther.* 16 (2008), 1833–40. pmid: 18797453. doi: 10.1038/mt.2008.200

Conventional vaccines have development times of 8 to 10 years. In contrast, the mod-mRNA-containing injections were developed in a greatly shortened expedited process and marketed under emergency use authorization. In 2020, legislators suspended many of the long-standing laws and regulations regarding drug safety for these substances and, for example, enacted a MedBVS (Medicine Safety and Drug Safety Ordinance)¹¹. In this way, measures for quality assurance, liability rules, labeling obligations, and shelf-life requirements could be bypassed. These processes are unique in Europe.

In sequence analyses of the mod-mRNA vaccines from Pfizer and Moderna in March 2023, *K. McKernan* detected alarming amounts of DNA contamination in the form of plasmids.¹² Other authors confirmed this finding.¹³ These small circular DNA molecules provide the blueprint for the spike protein during the manufacturing process (using *E. coli* bacteria), but sometimes also contain remnants of other plasmid vectors, including their SV40 promoter sequences. SV40 promoters or enhancers are short regulatory DNA sequences that have been used in molecular biology for decades to enable strong gene expression in eukaryotic cells (including human ones). Circular plasmids can, in principle, replicate themselves in bacteria and human cells, enter the nucleus, and, over the long term, induce the cell to produce the SARS-CoV-2 spike protein and other proteins. It is another mechanism for integrating spike-coding gene sequences into the genome, but long-term spike production would also be possible independently of genome integration of the code. It has been found that each vaccine dose contained billions of these plasmids.

The uncertainties of a viral bioweapon are met by a global vaccination campaign that, as it has been shown, could be relatively easily coordinated across various nations and political systems.

A significant contribution to this was the publication of three complete SARS-CoV-2 genome sequences by CDC China on January 10, 2020. The published sequences were precisely the starting point that Moderna, BioNTech/Pfizer, and other developers used for their mod-mRNA vaccines. Based on these digital gene sequences available on the computer, the COVID mod-mRNA development was made possible worldwide without the cumbersome shipping of virus material. According to its own reports, Moderna began vaccine construction (mRNA-1273) within 48 hours of receiving the sequence. They exclusively used the spike protein gene information encoded in the sequence, having no physical access to the pathogen. However, there are indications of a sequence of the SARS-CoV-2 furin cleavage site that was already patented in 2017.^{1,2} As of January 13, 2020, the digital construct was reportedly already available, which was then fed into the mod-mRNA platform. BioNTech (later in collaboration with Pfizer) also started immediately after the publication and already had several mod-mRNA candidates in development by January 27, 2020.

Using a vaccination as a bioweapon under pandemic conditions would be possible in principle. It could be relatively easily adapted to the 'needs' of malicious, ruthless forces. Damage and deaths could be easily concealed and made statistically difficult to access by interspersing the active ingredient among 'harmless' batches. This could also generate long-term effects without attracting much attention from the population and those responsible for politics. The logistical effort for worldwide distribution of a digital matrix or the production of a "vaccine" is relatively low

¹¹ German: <https://www.gesetze-im-internet.de/medbvs/>

¹² McKernan, K., Helbert, Y., Kane, L. T., & McLaughlin, S. (2023, April 10). Sequencing of bivalent Moderna and Pfizer mRNA vaccines reveals nanogram to microgram quantities of expression vector dsDNA per dose. <https://doi.org/10.31219/osf.io/b9t7m>

¹³ U. Kämmerer et al. (2024) Biontech ma-based covid-19 injections contain large amounts of residual dna including an sv40 promoter/enhancer sequence. *science. Public Health Policy and the Law*, 5:2019–24, 2024.

compared to the spread of an active virus. From a warlike perspective, it would be entirely possible for individual nations to produce their own 'ineffective' vaccine and at least pretend to be submitting to a global campaign, coordinated, for example, by the WHO.

Using a vaccination campaign as a covert bioweapon is fundamentally possible – and as a strategy, it is significantly more efficient, controllable, and concealable than the open use of a pathogen. That would be asymmetric warfare at the molecular biological level – strategically brilliant, morally catastrophic. This idea is not new, but in public discourse, it has often been dismissed as a "conspiracy theory" without being thoughtfully considered. However, from a security strategy perspective, it should certainly be taken seriously.

While we fundamentally assume that individual actors are malevolent, intent on depopulation and the destruction of humankind, we should not lose sight of alternative options, options that could be more efficient, faster-acting, and more deadly than viral pandemics or vaccination campaigns. One way could be through global wars, poisoning of staple foodstuffs, agrochemicals, environmental toxins, drinking water, and ultimately the air we breathe, to name just a few scenarios. However, given the endless acts of war on the planet and the many environmental toxins in circulation, we cannot be sure whether this isn't already happening covertly.

Dirk Gerhardt clearly describes the so-called vaccine damage or post-vaccine syndrome. This is also discussed in detail in our "[Post-Vac Orientation Guide](#)"¹⁴. Given the fact that much of the damage resulting from mod-mRNA injection is obscured by renaming it to Long or Post-COVID, thoughts of a malicious act cannot simply be dismissed.

*Considering the **whole** thing as a **biological weapon** or a primary depopulation measure is permissible in view of its potential effectiveness, but it is nevertheless far-fetched.*

Nevertheless, it is extremely important to closely monitor all developments of humanity, including the inherent dangers to our own species, as well as the dangers posed by humans to other species and to the environment in general.

So far, humanity has survived on its evolutionary branch for almost 3 million years since the emergence of the genus Homo and has evolved anatomically and culturally into modern humans in the last 50,000 to 70,000 years. Despite all the apocalyptic predictions circulating for decades, it currently does not appear as if our species is seriously endangered.

It is up to each individual whether they unconditionally submit to the narrative of an 'authority', or whether they form their own picture of a situation and are accordingly well-informed and live self-determinedly. Critical articles, like the one by Dirk Gerhardt, are extremely important as long as they are considered in a differentiated manner and not taken as a panic stimulus.

Regardless, people should be aware that uncontrolled gain-of-function research poses enormous risks, that government information sources are not helpful, and that maintaining a state of panic in the population can also be seen as supporting war-preparation propaganda.

7. Are viruses and microbes really a primary threat to us?

Typically, the term 'virus' refers only to the protective capsid, made of proteins that encloses the viral genome information in the extracellular environment. This infectious particle is known as a virion and is generally considered dead. Virions are entities that invade cellular organisms and take

¹⁴ <https://www.hackenberg-hm.de/c-downloads/en/Post-Vac-Orientation-guide.pdf>

control of them to produce more virions. The virion is the extracellular step in a virus's life cycle. It is the dormant and inactive form of the viral genetic information. However, the actual virus is more than its dead shell in the environment. It is part of a living organism once it is inside a host cell.

Most viruses require a specific receptor to bind to a cell, but some can also fuse directly with a cell's membrane. The binding process to the receptor is energy-independent, whereas penetration of the cell wall requires energy. And the cell provides the energy for this. This is actually quite strange. What if this mechanism was intended by evolution?

Regardless of their status, viruses are part of the constantly evolving biosphere and therefore a relevant factor in a wide variety of evolutionary processes. Almost 10% of our genome is known to consist of retroviral genes. Endogenous retroviruses have embedded themselves in our genome since ancient times and have assumed crucial evolutionary functions.

A further analysis of our genome quickly reveals that a large portion of what was formerly referred to as junk DNA encodes relics of viral, retroviral, and microbial elements. These relics are the key elements of epigenetic mechanisms. Some, such as the neuronal Arc gene derived from retrotransposons, encode proteins that form virus-like capsids. The Arc protein is essential to our cognitive processes in the brain. The 'virus-like' behavior mediated by exosomes is crucial for brain function.¹⁵

In general, the previous discussion that only retroviruses were capable of embedding themselves in the genome is long outdated. Today, we know that non-reverse transcriptase viruses, both RNA and DNA viruses, can be integrated into our genome and assume long-term functions within our system, and continue to do so continuously. Through non-coding RNAs, miRNAs, viruses influence the regulatory mechanisms of our genetic material and thus promote the organism's phenotypic adaptation to constantly changing environmental conditions.

While viruses contain the information for their reproduction, they lack the necessary cellular prerequisites. Viruses do not have their own metabolism and depend on the metabolism of an intact host cell to reproduce. Viruses possess only one type of nucleic acid: RNA or DNA. In many textbooks, viruses are referred to as parasites. According to recent findings, this is no longer the case. Viruses can also be considered symbionts. And like all life forms, viruses have a purpose in the course of evolution. They can safely be called the USB sticks of evolution, that is, information transmitters that constantly supply us with new genes.

8. Viruses and the mod-mRNA vaccine

If we take the evolutionary biological concept of Luis P. Villarreal and others as a basis¹⁶, namely that all life is based on a original RNA world, which is now responsible for the formation and imaging of the genetically much more stable DNA information (epigenetic mechanisms), the logical consequence arises that as soon as one introduces artificially created or modified mRNA into the body (and, in vaccinations, additionally immune-active adjuvants), diverse complex evolutionarily foreign reactions are triggered. We recognize only a fraction of this because our recognition is always dependent on our search algorithms.

Any intervention in such a highly complex system, which has developed over millions of years and is regulated, among other things, by equilibrium reactions using addiction modules (toxin/

¹⁵ <https://www.cell.com/action/showPdf?pii=S0092-8674%2817%2931504-0#page87>

¹⁶ INFECTIOUS THOUGHTS, Discovering Biology as a Social Science Dialogues, Books, Symposia, Articles
Luis P. Villarreal & Guenther Witzany © Luis P. Villarreal and Guenther Witzany, 2024, DOI: 10.13140/RG.2.2.35183.66725

antitoxin, regulation/restriction, etc.), must bring significant consequences, consequences that we can hardly grasp.¹⁷

Of course, this essentially also applies to any infections with microbes, viruses, or contact with viral remnants, but the circumstances are different here than with the injection of synthetic or modified mRNA. In 'natural' infections there is already an evolutionary connection, which is illustrated in Pathogen-Associated Molecular Patterns (PAMPs) and Pattern-Recognition Receptors (PRRs), recognition patterns anchored in our innate immune system. In early childhood, our immune system is crucially programmed with the help of these evolutionary parameters already stored in the genome, the developing microbiome, the thymus, and the Peyer patches in the small intestine.

A mechanism that repeatedly arises in the assessment of 'vaccine damage' and is always viewed as a weakening of the immune system should perhaps be reconsidered: the reactivation of existing viral and bacterial infections in the body. Is this really to be interpreted as immune weakening in relation to the holobiont status of the body? Could it not instead be a previously insufficiently understood reactive mechanism that serves to restore 'immune balance.' Current statements still support the idea that viruses in our bodies are primarily bad and are only kept in check by the 'power' of our immune system. The cooperative, symbiotic effect is ignored.

Times have changed. Over 200 years of vaccination history now confront findings from evolutionary biology that shed new light on the significance of microbes and viruses. Microbes and viruses are not just pathogenic factors, but also controls of our evolution, indeed of our lives. We live in a virusphere, a 'microbiosphere,' and are directly dependent on it. We should take this into account for all vaccinations, not just for the mod-mRNA platform. It is high time to end the fear mode towards viruses!

Dr. Hans-Michael Hackenberg, June 2025



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