'Leaky Vaccines': Misdirection or Fraud?

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The paradoxical resurgence of COVID-19 in the most highly COVID-vaccinated countries is being blamed on "leakiness" of vaccines. A vaccine is said to be "leaky" when it no longer suppresses mutation of the virus, allowing some "variants" to escape and become the dominant viruses in circulation. Reviewing basic scientific logic, looking at the actual construction of the lab-manipulated spike protein, and reviewing the decades-long bench science concerning coronavirus (and coronavirus vaccine development) casts serious doubt on this explanation for the COVID-19 upsurge.

The development of bacterial antibiotic resistance is well understood. In a mixed population of bacteria, those most sensitive to the effects of a given antibiotic will be preferentially killed, leaving behind the most antibiotic-resistant subspecies. Metaphorically, the toughest boxer makes it to the final round, and the toughest bacteria live to fight on in the primary host, then may spread as a more deadly (antibiotic-resistant) strain to others.

Viruses, however, are not bacteria, and vaccines are not antibiotics. There is also a fundamental scientific logic that is being ignored. Nature is efficient: The simplest explanation for any biologic process is usually the correct one. The primary fact we need to explain is how, after months of declining COVID-19 cases, hospitalizations, and deaths, countries with the highest vaccination rates against SARS-CoV2 are experiencing the biggest increase in all categories—during an "off season" for viral illness.

Simply put, ***increased COVID vaccination*** is associated with ***increased COVID morbidity and mortality***. How this occurs can be debated, but *the simplest explanation is that the vaccine itself is toxic, making people ill and killing people*. Everything else—including the idea of "variants"—is a more complicated and circuitous explanation.

Looking at "variants" as the explanation, we have several pieces of information that make this unconvincing.

Reasons to Question COVID-19 Variants

First, variability is mathematically calculated by reported gene sequences, which are themselves manufactured by computer analysis. As Stefan Lanka has said in his refutation of the entire virus paradigm: "The basic insight is that these manipulations, called 'alignments,' simply do not correspond to any 'complete' or known genetic material of a virus."[1] Recently, mainstream COVID-19 researchers, regarding the reliability of banked sequences for calculation of variability, have stated: "Among the 129 sequence variations reported, many were generated randomly by the algorithms during the alignment of the multiple sequences, therefore these should be removed or adjusted."[2] In other words, the degree of modeling error is unknown, and results are highly subject to technique and interpretation.

Second, although the vast majority of RNA viruses mutate rapidly, especially the single-strand RNA viruses (of which coronavirus is an example), coronavirus is a notable exception. This positive-strand RNA virus has a type of proofreader in the form of nsp 14-Exon.[3] In fact, during more than a decade of development of vaccines against coronavirus, it was noticed that coronavirus genetic "variable" and "hypervariable" regions change (mutate) 30–60 percent more slowly than many other viruses.[4-6]

Third, SARS-CoV-1, the cause of severe adult respiratory syndrome, is 97.7 percent similar to SARS CoV-2 at the spike domain, but only 52.5 percent similar at the N terminus and 85.5 percent at the nucleocapsid, and yet human monoclonal antibody to the S glycoprotein of SARS-CoV-1 neutralizes SARS-CoV-2,[7] suggesting that variability outside the spike protein isn't that important.

During the development of COVID-19 vaccines, researchers purposely chose to target "highly conserved" regions of the spike protein. "Highly conserved" is geneticist patois meaning "they don't vary." *The researchers state specifically that they sought out "highly conserved" vaccine target areas to avoid the problem of variant escape*.[8]

Was the "spike protein" lab-created or altered? The seminal paper by Pradhan et al. looked at all the various genetic sequences of pathologic specimens reported to the gene data bank.[9] They discovered four "inserts" that were in every sample collected from COVID victims. Notably, these four inserts were not present in SARS-CoV-1 from 2002, and were never present in any other members of the extensive family Coronaviridae. Furthermore, the insert sequences, when analyzed, were a match to areas from the human immunodeficiency virus (HIV). Most importantly for this discussion, the four inserts were 100 percent conserved throughout all the pathological SARS-CoV-2 specimens, i.e., they presented with 0 percent variability. Given the ability of vaccine developers to target the most invariant areas for vaccine antibody binding, it seems unlikely that one or more of these areas would not be the target. Put another way, if the developers didn't take advantage of these invariable regions, then they purposely created vaccine escape.

The article by Prashand et al. has been withdrawn by the authors, under protest, with the comment that "they intend to revise it in response to comments received from the research community on their technical approach and their interpretation of the results." Additionally, why would *Zero Hedge*—an on-line economic journal—be de-platformed for simply reporting on this article? It evokes the military pilot dictum that when you are catching big "flak" you are over a big target the enemy does not want you to take out.

Fourthly, bacterial resistance develops only if the

antibiotic actually kills or in other ways prevents spread of the less resistant forms. No study—not even the study by Pfizer that supported the original application for Emergency Use Authorization (EUA)—has demonstrated that these COVID-19 vaccines ever prevented transmission. So how could resistant "variants" arise without selective pressure?

Fifthly, according to a table that compares the case fatality rates of the different "variants," from a June 2021 technical briefing by Public Health England (Table 1),[10] Delta is near the bottom. So, even if it is the emerging circulating virus, it should not be increasing the rate of hospitalization and death but decreasing it. Evolution to decreasing lethality was predicted by researchers and is consistent with historical observations.[11] It is interesting that as of Oct 4, 2021, the U.S. Centers for Disease Control and Prevention (CDC) was not monitoring for the Delta variant.[12] One must logically wonder why not.

And finally, how do variants explain the recent experience of the Belgian contingent at the South Pole? Sixteen of 25 "fully vaccinated" researchers who were thoroughly screened, and presumably isolated prior to leaving for the ice cap, tested positive for Covid seven days into their stint at the facility at Princess Elisabeth Polar Station. A few on this remote outpost are mildly symptomatic according to reports. Based only on supposition (considering the total inability to test for variants there, and most places if truth be known) this "outbreak" has been labelled "Omicron."[13]

The "variant" explanation is not competent scientific reasoning. It is at best "grasping at straws," but is more likely willful obfuscation and misleading the public. Consider possible motives for the promulgation of the "variant" explanation. In law, motive is always considered when assessing truth, but it is rarely considered as a possible reason for scientific data to be skewed. Scientists and bureaucrats paid by the pharmaceutical industry—the people with the most to lose financially—invoked the dreaded "Delta" and now "Omicron" variants. No pharmaceutical producer of these vaccines is going to admit that the vaccines could be directly killing people. Money and truth do not coexist well. Now there is Omicron, next it may be Lambda, and then Sigma. Who knows? An unverifiable "table of variants" and release dates is circulating on the web. Whether true or not, it is certainly consistent with the actions of government so far to confuse and manipulate a scientifically naïve public.

Conclusion

There have been many provable deceptions or errors about COVID-19, but the variant narrative, though scientifically highly improbable, will likely persist. It is too technically difficult for most casual observers to dispute. Plausibility is the most important characteristic of a lie, but lying about pharmaceutical safety can be fatal. Physicians need to educate

Table 1. Comparative Lethality of SARS-CoV-2 Variants of Concern[10]

Variant	Confirmed (sequencing) case number	Probable (genotyping) case number*	Total case number	Case proportion*	Deaths	Case fatality	Cases with 28 day follow up	Deaths among those with 28 day follow up	Case Fatality among those with 28 day follow up
Alpha	219,570	5,515	225,085	70.3%	4,262	1.9% (1.8 - 2.0%)	219,948	4,259	1.9% (1.9 - 2.0%)
Beta	892	54	946	0.3%	13	1.4% (0.7 - 2.3%)	874	13	1.5% (0.8 - 2.5%)
Delta	50,283	41,773	92,056	28.8%	117	0.1% (0.1 - 0.2%)	11,250	32	0.3% (0.2 - 0.4%)
Eta	442	0	442	0.1%	12	2.7% (1.4 - 4.7%)	431	12	2.8% (1.4 - 4.8%)
Gamma	180	45	225	0.1%	0	0.0% (0.0 - 1.6%)	161	0	0.0% (0.0 - 2.3%)
Kappa	439	0	439	0.1%	1	0.2% (0.0 - 1.3%)	420	1	0.2% (0.0 - 1.3%)
Theta	7	0	7	0.0%	0	0.0% (0.0 - 41.0%)	5	0	0.0% (0.0 - 52.2%)
VUI-21APR-03	13	0	13	0.0%	0	0.0% (0.0 - 24.7%)	13	0	0.0% (0.0 - 24.7%)
VUI-21FEB-04	279	0	279	0.1%	1	0.4% (0.0 - 2.0%)	246	1	0.4% (0.0 - 2.2%)
VUI-21MAY-01	177	0	177	0.1%	1	0.6% (0.0 - 3.1%)	135	1	0.7% (0.0 - 4.1%)
VUI-21MAY-02	133	0	133	0.0%	0	0.0% (0.0 - 2.7%)	117	0	0.0% (0.0 - 3.1%)
Zeta	54	0	54	0.0%	1	1.9% (0.0 - 9.9%)	53	1	1.9% (0.0 - 10.1%)

*Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

themselves on the complexities of molecular biology, err on the side of healthy skepticism, and stop taking the word of "experts" on faith.

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REFERENCES

1. Greatreject. Dr. Stefan Lanka: 'All claims about viruses as pathogens are false.' Greatreject; Jun 17, 2021. Available at: https://greatreject.org/dr-stefan-lanka-claims-about-viruses-are-false/. Accessed Jan 29, 2022.
2. Zhao Z, Li H, Wu X, et al. Moderate mutation rate in the SARS coronavirus genome and its implications. *BMC Evol Biol* 2004;4(21). doi:10.1186/1471-2148-4-21. Available at: https://bmcecolevol.biomedcentral.com/articles/10.1186/1471-2148-4-21. Accessed Jan 29, 2022.
3. Sanjuán R, Domingo-Calap P. Mechanisms of viral mutation. *Cell Mol Life Sci*. 2016;73(23):4433-4448. doi:10.1007/s00018-016-2299-6.
4. Kaur N, Singh R, Dar Z, et al. Genetic comparison among various coronavirus strains for the identification of potential vaccine targets of SARS-CoV2. *Infect Genet Evol* 2021;89:104490. doi:10.1016/j.meegid.2020.104490.
5. Rauch J, Capoferri A, Katusiime KG, et al. *PNAS USA* 2020;117(40):24614-24616. Available at: https://doi.org/10.1073/pnas.2017726117. Accessed Jan 29, 2022.
6. Smith EC, Denison MR. Coronaviruses as DNA wannabes: a new model for the regulation of RNA virus replication fidelity. *PLoS Pathog* 2013;9(12):e1003760. Available at: https://doi.org/10.1371/journal.ppat.1003760. Accessed Jan 29, 2022.
7. Pinto D, Park YJ, Beltramello M, et al. Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. *Nature* 2020;583:290–295. Available at: https://doi.org/10.1038/s41586-020-2349-y. Accessed Jan 29, 2022.
8. Yurina V. Coronavirus epitope prediction from highly conserved region of spike protein. *Clin Exp Vaccine Res* 2020;9(2):169-173. doi: 10.7774/cevr.2020.9.2.169.
9. Pradhan P, Pandey AK, Mishra A, et al. Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag. bioRxiv. Published on line Jan 31, 2020. Available at: https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1. Accessed Jan 29, 2022.
10. Public Health England. SARS-CoV-2 variants of concern and variants under investigation in England. Technical Briefing 17; Jun 25, 2021. Available at: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1001354/Variants_of_Concern_VOC_Technical_Briefing_17.pdf. Accessed Nov 30, 2021.
11. Singh J, Pandit P, McArthur AG, Banerjee A, Mossman K. Evolutionary trajectory of SARS-CoV-2 and emerging variants. *Virol J* 2021;18(1):166. doi:10.1186/s12985-021-01633-w.
12. CDC. SARS-CoV-2 Variant Classifications and Definitions; updated Dec 1, 2021. Available at: https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html. Accessed Jan 29, 2022.
13. Ellis R. COVID-19 outbreak hits research station in Antarctica. *WebMD*; Jan 4, 2022. Available at: https://www.webmd.com/lung/news/20220103/covid-19-outbreakohitsoresearchostation-in-antarctica. Accessed Feb 15, 2022.