

Reflections on Bright Pandemic Prospects

This is what we know about the pandemic causing viruses and universal remedies.



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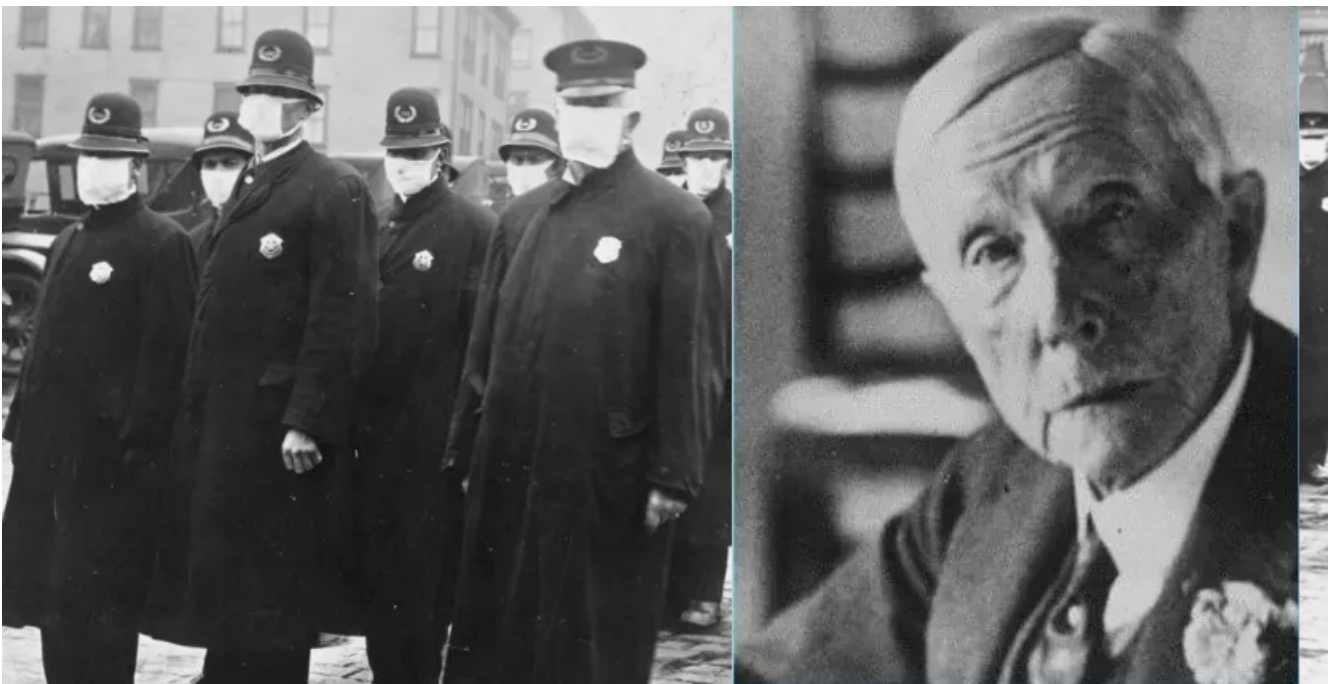


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Let's review the reader responses to my [informal quiz in the previous post!](#)

Quiz Results

Three schools of thought came up on top in response to the question of “**what universal remedy there is to all five prospective pandemic viruses** (Ebola, Marburg, SARS, Nipah, H1N2 a.k.a. swine flu)”:

1. ***There is/are no virus(es)***
2. ***Chlorine dioxide***
3. ***Ivermectin***

As will be explained shortly, all answers have their merits.

Going into the quiz, I had my formed opinions and prepared answers. I must admit that the three groups of answers above forced me to reevaluate my opinions and upgrade my understanding of the issue, and foremost in regard to the “no virus” point of view. Serendipitously, a recent event enticed me to look deeper into the subject matter. [Mike Yeadon has just complained](#) that his presentation at the AfD-staged Covid symposium at the German Parliament building (Nov. 11-12), ignored by the rest of the German political class and by the mainstream German media, has been shamelessly censored by the symposium organizers and expunged from the record, in the best “1984” tradition, to the point that he can’t even get the recording of his own speech. The censored doing their own censoring?

The main reason might be that Mike Yeadon allowed himself to express doubts as to the existence of the SARS-CoV-2 virus, and the AfD leadership seems to have decided that this train of thought takes them a bridge too far in the unelectable direction, all Germans being united by the unflagging faith into the basic scientific dogmas, viruses and vaccines being two cornerstones thereof.

Am I too? Yes, I have been. I thought that Mike Yeadon became carried away and slightly unscientific in [denying the existence of respiratory viruses](#). As I did have my run-in with Covid back in the fall of 2021, and I know what a loss of smell and a week-long wicked cough feels like — like nothing I have ever experienced before! *Must be the novel SARS-CoV-2 virus!* My mind has been made up. Wouldn’t it be silly of me to deny the evidence of my own experience?

And yet, it wouldn’t. By trying to learn where Mike Yeadon is coming from, I searched, read, watched and listened, and I want to share with you what I have come to understand just now, in the most simple and brief terms. I will have to drop a lot of context and material for brevity, but I hope to spike your interest.

To start with, you can watch this rumble video clip with Dr. JJ Couey where he comments on the Netflix “documentary” “[EXPLAINED: The Next Pandemic](#)”, released in November of 2019, right before Covid “hit” - what a “coincidence”!



Although JJ has no doubts that viruses exist (and what I admit to believe), the problem is with RNA flu viruses not being very good at replicating themselves, like not at all ([45:30-48:40](#))! SARS just fizzled on its own in no time. Where [JJ speaks of infectious clones](#), he means the lab-created and then cDNA replicated exact copies of the SARS virus (the “original” Covid virus, the first iteration thereof, and the first mass experiment of the concerted clone release).

This goes beyond mere observations. Watch this fragment of JJ’s video conference with Mike Yeadon and Paul Alexander, “Yeadon, Alexander, Couey: COVID at 50000 foot level; clone theory; multiple release - Part 1” ([27:20-30:13](#))

<https://genome.cshlp.org/content/29/9/1545.full.pdf>

Genome Analysis | High Resolution

GB
HRLN
IB

Method

Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis

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Sequence analysis of RNA virus genomes remains challenging owing to the exceptional genetic plasticity of these viruses. Because of high mutation and recombination rates, genome replication for viral RNA-dependent RNA polymerases leads to populations of closely related viruses, so-called “quasispecies.” Standard short-read sequencing technologies are ill-suited to reconstruct large numbers of full-length haplotypes of RNA virus genomes, and long-read sequencing (LRS) approaches based on nanopore or characteric viral RNAs produced by cells infected with a human coronavirus. By using DRIS, we were able to map the temporal (t-SM) consensus read in the viral reference genome. By combining Oxford Nanopore sequencing, we reconstructed a highly accurate consensus sequence of the human coronavirus (HCoV-229E) genome (27,303). Furthermore, by using long reads that did not require an assembly step, we were able to identify, in infected cells, diverse and novel HCoV-229E RNAs that remain to be characterized. Also, the DRIS approach, which circumvents reverse transcription and amplification of RNA, allowed us to detect modifications such as 5mC RNA. Our work opens the way for haplotype-based analyses of viral quasispecies by showing the feasibility of virus-variant haplotype separation. Even though several technical challenges remain to be addressed to realize the potential of the consensus sequencing fully, our work illustrates that DRIS may significantly advance genomic studies of complex virus populations, including applications in long-range transmission in individual full-length RNA haplotypes.

(Supplemental material is available for this article.)



To recap, in a study from Sep. 2019, “[Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis](#)” (Genome Research), the scientists cultured coronavirus strains in vitro and then analysed the results:

*...full-length genomic RNAs of HCoV-229E, HCoV-229E_SL2-SARS-CoV, and HCoV-229E_SL2-BCoV, respectively, were transcribed in vitro using purified *Cla*I-digested genomic DNA of the corresponding recombinant vaccinia virus as a template; 1.5 µg of full-length viral genome RNA, along with 0.75 µg of in vitro transcribed HCoV-229E nucleocapsid protein mRNA, was used to transfect 1 × 10⁶ Huh7 cells using the TransIT-mRNA transfection kit according to the manufacturer's instructions (Mirus Bio). At 72 h post transfection (p.t.), cell culture supernatants were collected and serially passaged in Huh7 cells for 21 (WT) or 12 times (HCoV-229E_SL2-SARS-CoV and HCoV-229E_SL2-BCoV), respectively.*

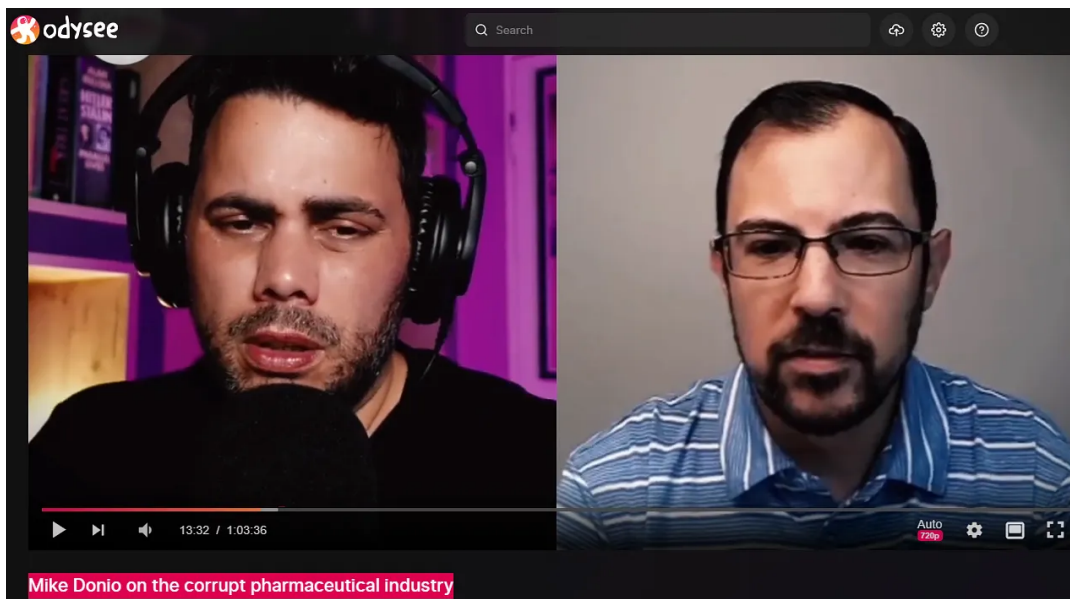
The low fidelity of the viral RNA replication resulted in a soup of short RNA fragments, mostly:

The median read length for the combined set of reads from both samples was 826 nt, with a maximum of 26,210 nt, covering 99.86% of the 27,276-nt-long virus genome, missing only 21 nt at the 5'-end, 15 nt at the 3'-end, and those nucleotides that correspond to the skewed error distribution, with 5.7 percentage points more deletions than insertions (see Table 1). The median read length might sound short; however, most of the viral RNAs (including many DI-RNAs) identified in HCoV-229E-infected cells were <2000 nt in length. Furthermore, this number nearly doubles the longest read length that can be obtained with short-read sequencing methods. We observed an abundance of very short reads, representing the 3' (poly[A]) end of the genome. This could be an artifact of RNA

degradation, although we cannot estimate the exact fraction of affected transcripts. Because sequencing starts at the poly(A) tail, fragmented RNA will not be sequenced beyond any 3' break point. It is thus best to minimize handling time during RNA extraction and library preparation. Innovations in these fields will directly translate into larger median read lengths.

We thereby recovered 99.57% of the reference genome in a single contiguous sequence at 99.90% sequence identity to reference using this approach with the single longest read from the SL2 sample.

Also watch this fragment from “[Mike Donio on the corrupt pharmaceutical industry](#)” (13:32-17:05):



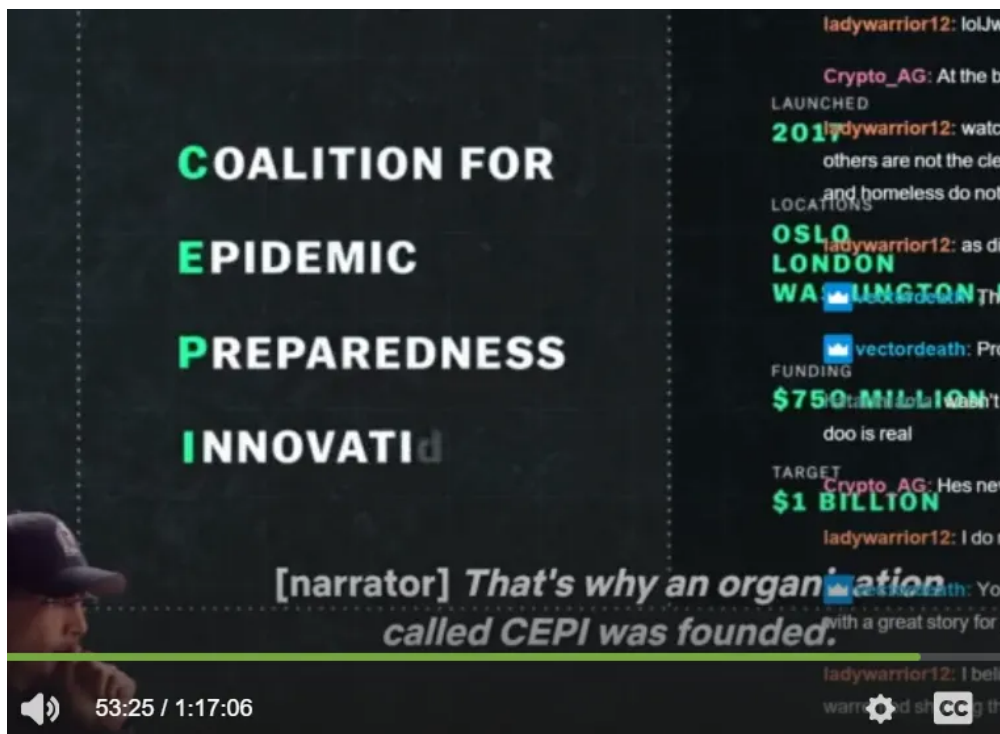
This illustrates the difficulties the scientists are facing in isolating viruses from the samples taken from patients, or even viral cultures, let alone trying later to infect the other humans/animals through the use of such samples. In that sense, “*the respiratory viruses don’t really exist*”. Please provide links to more references on the subject in the comments below.

Taken the above into account, if SARS-CoV-2 were a natural virus spread, even from a Wuhan lab, it should have evolved and fizzled in no time too. JJ thus strongly believes that the simultaneous release (probably repeated) of the SARS-CoV-2 infectious clone

took place around the globe, in order to give justification to the emergency use authorization of the S spike mRNA concoctions from Moderna and Pfizer.

As for my Covid infection, I got it as a result of a nose swab by Canadian Public Health workers at an airport while arriving from overseas in the fall of 2021. And that's how this substack of mine started. Those nose swabs would have been a perfect way to spread the infectious clones all over the globe, with no one asking questions. I was too ignorant and unquestioning back then to know any better.

The “EXPLAINED: The Next Pandemic” says the [CEPI](#) (Coalition for Epidemic Preparedness Innovations) has been created to speed up the vaccine development against “Disease X” (SARS-CoV-2, as we now know), in exactly the way the WARP Speed Covid mRNA jabs have been developed, as proposed by none other than Bill Gates in the movie (53:10-53-57:10):



Strangely enough, the raison d'être for CEPI has been, initially, to develop mRNA jabs against MERS, Lassa fever, Nipah virus, Ebola, Marburg fever and Zika — almost identical to the virus list we are being dangled in front of our faces Nov. 27, 2023:

CEPI was formally launched at the 2017 WEF in Davos, with an initial investment of

US\$460 million by a consortium that included the governments of Norway, Japan, and Germany, The Wellcome Trust, and the Gates Foundation; India joined a short time afterwards. In a launch interview with the Financial Times (FT), Gates said that a key goal was to reduce the time to develop vaccines from 10 years to less than 12 months.

The initial targets were the six EID viruses with known potential to cause major epidemics, being: **MERS, Lassa fever, Nipah virus, Ebola, Marburg fever and Zika.**

The “EXPLAINED: The Next Pandemic” also used the 1918 “flu” pandemic to scare us into believing that zoonotic viruses are the imminent, omnipresent threat to humanity itself (“when a human and a bird met the same pig”, in their parlance, [26:40-33:00](#)), which resulted in 50-100 millions fatalities around the world in 1918-1919:



Except, it was neither “Spanish”, nor “flu”. In all honesty, it was a result of a botched Rockefeller Institute’s crude bacterial meningitis vaccination experiment on US troops at Fort Riley in 1918 (“[The True Story of the 1918 "Spanish Flu"](#)”, Astute News, 2020.11.11). What’s more:

“During WW1, the Rockefeller Institute also sent its experimental anti-meningococcal serum to England, France, Belgium, Italy and other countries, helping spread the epidemic worldwide.”

“The crude anti-bacterial vaccine used in the Fort Riley experiment on soldiers was made in horses.”

“According to a 2008 National Institute of Health paper, bacterial pneumonia was the killer in a minimum of 92.7% of the 1918-19 Pandemic autopsies reviewed.”

When WW1 ended on November 11, 1918, soldiers returned to their home countries and colonial outposts, spreading the killer bacterial pneumonia worldwide.

In 1918, “influenza” or flu was a catchall term for disease of unknown origin. It didn’t carry the specific meaning it does today.

To add insult to injury, the doctor responsible for the administration of the infamous jab at Fort Riley was Frederic L. Gates:

*A Report on Anti-meningitis Vaccination and Observations on Agglutinins in the Blood of Chronic Meningococcus Carriers as Recorded by Frederick L. **Gates**, MD in 1918*

*...Between January 21st and June 4th of 1918, **Dr. Gates** reports on an experiment where soldiers were given 3 doses of a bacterial meningitis vaccine. Those conducting the experiment on the soldiers were just spit-balling dosages of a vaccine serum made in horses...*

Of course, there is a helpful Reuters factcheck denying it all: “[A meningitis vaccine trial at a U.S. military camp did not cause the 1918 Spanish Flu](#)” (Reuters Fact Check, 2021.04.13). You be the judge. Except to say, that the “Spanish” “flu” bacterial infection has been successfully battled with [baking soda](#) (***a hat tip to the chlorine dioxide school of thought***). And that is [not the only](#) baking soda testimony from the time of the “Spanish” “flu”. So much for the killer zoonotic respiratory virus. Of course, the medical response to the Spanish flu didn’t have baking soda on its list of *safe and effective* treatments. 50-100 millions died as a result. *Reminiscent of anything?*

As for other killer pandemics in human history, the plagues of 14th-18th centuries were always bacterial epidemics, not viral ones. You know what works best against bacteria? Basic hygiene and disinfection. ***A hat tip to the chlorine dioxide again, and***

also ivermectin, schools of thought. “[Ivermectin: enigmatic multifaceted ‘wonder’ drug continues to surprise and exceed expectations](#)”(The Journal of Antibiotics, 2017.02.15):

*Today, ivermectin is continuing to surprise and excite scientists, offering more and more promise to help improve global public health by treating a diverse range of diseases, with **its unexpected potential as an antibacterial, antiviral and anti-cancer agent being particularly extraordinary.***

Not too shabby for a horse dewormer, eh?

Back to JJ. He stresses that RNA flu viruses never were, are, or will be any threat to humanity. The flu viruses are endemic, omnipresent, opportunistic entities that seasonally infect the frail or people with weakened immune systems (vitamin D3 anyone?), and might be spread from person to person, but we used to call this “life”. The whole scaremongering about the evil scientists’ gain-of-function research, zoonotic origin, and imminent (re)emergence is to scare us shitless (excuse my French) and surrender our human rights to medical authorities in exchange for occasional privileges.

As for the quiz questions, here are my answers:

A. The common denominator of all five viruses is that they are [lipid enveloped RNA viruses](#):

Lipid enveloped viruses, such as SARS-CoV-2, influenza, and HIV, possess a lipid bilayer coat that protects their genome to facilitate entry into the new host cell.

B. [Butylated Hydroxytoluene](#) () dissolves the lipid envelope of all lipid enveloped viruses and prevents their transfection of human cells, as long as there is a built-up concentration of BHT upon exposure. 250mg seems to be an innocuous and sufficient adult dose (70kg) to achieve this end. As a bonus, BHT, being a powerful antioxidant, has some [anti-cancer properties](#) and general wellbeing benefits.

There might be other common, almost free and forgotten nonpharmaceutical substances that also provide wide-spectrum protection against bacteria, colds and

viruses. Castor oil and turpentine jump to mind. Feel free to give your suggestions.

So, what do we conclude? The medical establishment has been highjacked by the dark forces, or the two colluded, to scare us into believing, over the course of many decades and without questioning, into:

1. The imminent pandemic threat to humanity from mutated and/or recombined viruses about to jump on us from every corner of the globe.
2. The saviour “vaccines”, necessarily now the mRNA/genetic “vaccines”, as the only means to save the humanity.
3. Our rights are but a figment of our sick imagination, trumped every time by our debt to the community and our obligation to the society at large to be compliant in the face of whatever orders will come from the WHO and sycophant medical officers of health near you, in response

On top, we have been subjected to censorship, self-censorship, and the psychological warfare methods to confuse and bewilder us, [with the limited hangouts of all possible kinds](#) (this deserves a follow-up post), in order to safeguards these core “beliefs”. The AfD self-censorship is but one of the bright examples.

As it turns out, it’s all just a mirage. Instead of fearing “Disease X”, we should fear the two-legged animals in our midst.

And lead us not into tribulation, but [instead] deliver us from the crafty

For Yours is the kingdom and the power and the glory forever

Amen