The Origin of the #CoronaVirus #COVID19
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What is clear is that the #COVID19 was bio-engineered. The Science [and I am not a scientist] is irrefutable and in the public domain for those with a modicum of intellectual interest. This information is being deliberately suppressed.

This took me to Thomas Pynchon

“If they can get you asking the wrong questions, they don’t have to worry about answers.”
— Thomas Pynchon, Gravity’s Rainbow
And Don Delillo

“There’s always more to it. This is what history consists of. It is the sum total of the things they aren’t telling us.”
— Don DeLillo, Libra

Now Why are we being led away from this irrefutable Truth.

It seems to me that Everyone not just China, but the US, Canada and others have been exploring this “bio-engineering” space and in many cases there is evidently funding and deeply intertwined ties between these Institutions.
“A paranoid is someone who knows a little of what’s going on.”
— William S. Burroughs

Want to go down a (strictly fact-based) rabbit hole? I’ve put together a timeline of facts to help understand the controversial links between COVID-19 and HIV, and COVID-19 and Wuhan Institute of Virology. Thread @scottburke777
https://twitter.com/scottburke777/status/1233907363041742848?s=20

I do think however that information is being downplayed and suppressed by some scientists and media outlets and it’s our duty to find out the facts about this virus, do what we can to mitigate the outbreak, and prevent it from happening again. Ready?
So there’s original SARS, which is a type of coronavirus. SARS infects cells through the ACE2 receptor in hosts. @scottburke777
https://twitter.com/scottburke777/status/1233907368527826945?s=20

The S spike protein plays a key role in how the virus infects cells. Each of the little spikes that surround the coronavirus is a spike protein (or S protein). @scottburke777
https://twitter.com/scottburke777/status/1233907369568088067?s=20

The S spike protein plays a key role in how the virus infects cells. Each of the little spikes that surround the coronavirus is a spike protein (or S protein). That’s what gives the coronavirus it’s name - it’s “crown” of these spikes.

The S protein binds to the targeted cell through the ACE2 receptor, and boom, your cell is infected and becomes a virus replication factory. @scottburke777
https://twitter.com/scottburke777/status/1233907371069657088?s=20
After the first SARS outbreak, there was a “land rush” to find other coronaviruses. A collection of SARS-like coronaviruses was isolated in several horseshoe bat species over 10 years ago, called SARS-like CoVs, or SL-CoVs. Not SARS exactly, but coronaviruses similar to SARS.

in 2007, a team of researchers based in Wuhan, in conjunction with an Australian laboratory, conducted a study with SARS, a SARS-like coronavirus, and HIV-1. @scottburke777
https://twitter.com/scottburke777/status/1233907373829500928?s=20

The researchers noted that if small changes were made to the S protein, it broke how SARS-CoV worked - it could no longer go in via ACE2. So they inferred the S protein was critical to the SARS attack vector. @scottburke777
https://twitter.com/scottburke777/status/1233907375238717440?s=20

They also predicted based on the S-ACE2 binding structure, that SARS-like CoVs were not able to use this same attack method (ACE2 mediation).

They decided to create a pseudovirus where they essentially put a SARS-like CoV in a HIV envelope.

It worked. Using an HIV envelope, they replaced the RBD (receptor binding domain) of SL-CoV with that of SARS-CoV, and used it to successfully infect bats through ACE2 mediation. 12 years goes by.

A SARS-like CoV begins sweeping the globe that is far more infectious than previous outbreaks.
Ground Zero for this outbreak (not first human patient, but first spreading event) is considered to be Wuhan Seafood Market.

Wuhan Seafood Market is 20 miles from the National Biosafety Laboratory at Wuhan Institute of Virology.  
@scottburke777  
https://twitter.com/scottburke777/status/1233907383199502338?s=20

Amidst the outbreak, a team of Indian bioinformatics specialists at Delhi University released a paper pre-print.  
http://j.mp/2VKrfDt  

COVID-19 has a unique sequence about 1,378 nucleotide base pairs long that is not found in related coronaviruses. They claimed to identify genetic similarities in this unique material between COVID-19 and HIV-1.  
@scottburke777  
https://twitter.com/scottburke777/status/1233907387272179714?s=20

Specifically, they isolated 4 short genetic sequences in key protein structures (the receptor binding domain, or RBD).  
@scottburke777  
https://twitter.com/scottburke777/status/1233907388442435584?s=20
Two of the sequences were perfect matches (albeit, short), and two of the sequences were matched but each with an additional string of non-matching material appearing in the middle of the sequence. @@scottburke777
https://twitter.com/scottburke777/status/1233907391055454211?s=20

<table>
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<th>Motifs</th>
<th>Virus Glycoprotein</th>
<th>Motif Alignment</th>
<th>HIV protein and Variable region</th>
<th>HIV Genome Source Country/subtype</th>
<th>Number of Polar Residues</th>
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<td>India*/C</td>
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<td>2 1</td>
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<tr>
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<td>2 4</td>
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The paper was criticized and numerous attempts have been made to debunk it. After the criticism, the authors voluntarily withdrew it, intending to revise it based on comments made about their technical approach and conclusions.
https://twitter.com/scottburke777/status/1233907393832128520?s=20

One key debunking attempt claims this: The same sequences are found in a variant called BetaCoV/bat/Yunnan/RaTG13/2013, which had been found “in the wild” in bats. @scottburke777
https://twitter.com/scottburke777/status/1233907394956185600?s=20

This is an attempt to prove that it was not engineered, but mutated naturally in the wild. But there’s a problem-

This strain was only known by and studied at the Wuhan Virology Institute, and although they claim it was discovered in 2013, it wasn’t published or shared with the scientific community until immediately after the Indian paper, on January 27, 2020.
http://j.mp/2TqsQvg

The RatG13 strain publication and the HIV research paper from 2008 share an author. I discovered this on my own by comparing the two papers and then quickly realized this scientist’s contact information was the information that ZeroHedge was suspended from Twitter for sharing. Their article (which I will not link to) identifies this author in question including some contact information from the Wuhan Virology Institute web site.
There is a line of inquiry about how the sequences are remarkably stable in between the “bat” CoV and the nCoV, where in nature they would likely have mutated in between their shared evolution. Also a call for greater scientific evidence that the strain was collected in the wild.
https://twitter.com/scottburke777/status/1233908492047704064?s=20

Here is the only point in this thread where I will offer my opinion rather than a list of facts: In light of all the previous facts, the efforts to debunk the paper are not yet convincing in my view.

The RaTG13 paper makes the claim that, oh, that HIV-related material you identified that happens to protein fold to become a perfect attack vector for nCoV to attack ACE2? It’s a relative of this other secret virus which came from the wild...
...which we forgot to tell the scientific community about until now for no reason. Here’s the secret virus - it came from bats - and here’s the new virus, see, they have the same HIV-related sequences... so... bats! Totally not secret pathogen research which escaped the lab.

#coronavirus far more likely than Sars to bond to human cells due to HIV-like mutation, scientists say @SCMPNews #COVID19
http://j.mp/2w60OgG
Scientists say the new coronavirus may be significantly different from Sars. The new coronavirus has an HIV-like mutation that means its ability to bind with human cells could be up to 1,000 times as strong as the Sars virus, according to new research by scientists in China and Europe.

Scientists showed that Sars (severe acute respiratory syndrome) entered the human body by binding with a receptor protein called ACE2 on a cell membrane.

And some early studies suggested that the new coronavirus, which shares about 80 per cent of the genetic structure of Sars, might follow a similar path.

But the ACE2 protein does not exist in large quantities in healthy people, and this partly helped to limit the scale of the Sars outbreak of 2002-03, in which infected about 8,000 people around the world.

Other highly contagious viruses, including HIV and Ebola, target an enzyme called furin, which works as a protein activator in the human body.

Many proteins are inactive or dormant when they are produced and have to be “cut” at specific points to activate their various functions.

When looking at the genome sequence of the new coronavirus, Professor Ruan Jishou and his team at Nankai University in Tianjin found a section of mutated genes that did not exist in Sars, but were similar to those found in HIV and Ebola.

“**This finding suggests that 2019-nCoV [the new coronavirus] may be significantly different from the Sars coronavirus in the infection pathway,**” the scientists said in a paper published this month on Chinaxiv.org, a platform used by the Chinese Academy of Sciences to release scientific research papers before they have been peer-reviewed. “**This virus may use the packing mechanisms of other viruses such as HIV.**”

According to the study, the mutation can generate a structure known as a cleavage site in the new coronavirus’ spike protein.

The virus uses the outreaching spike protein to hook on to the host cell, but normally this protein is inactive.

The cleavage site structure’s job is to trick the human furin protein, so it will cut and activate the spike protein and cause a “direct fusion” of the viral and cellular membranes. **Compared to the Sars’ way of entry, this binding method is “100 to 1,000 times” as efficient, according to the study.**

Just two weeks after its release, the paper is already the most viewed ever on Chinaxiv. In a follow-up study, a research team led by Professor Li Hua from Huazhong University of Science and Technology in Wuhan, Hubei province, confirmed Ruan’s findings.
The mutation could not be found in Sars, Mers or Bat-CoVRaTG13, a bat coronavirus that was considered the original source of the new coronavirus with 96 per cent similarity in genes, it said.

This could be “the reason why SARS-CoV-2 is more infectious than other coronaviruses”, Li wrote in a paper released on Chinaxrivar on Sunday.

**Meanwhile, a study by French scientist Etienne Decroly at Aix-Marseille University, which was published in the scientific journal Antiviral Research on February 10, also found a “furin-like cleavage site” that is absent in similar coronaviruses.**

A researcher with the Beijing Institute of Microbiology, Chinese Academy of Sciences in Beijing, said the studies were all based on genetic sequencing.

“Whether [the virus] behaves as predicted will need other evidence including experiments,” said the researcher who asked not to be named.

“The answer will tell how the virus makes us ill,” he said. Scientists’ understanding of the new coronavirus has changed dramatically over the past few months.

At first the virus was not considered a major threat, with the Chinese Centres for Disease Control and Prevention saying there was no evidence off human-to-human transmission. But that assumption was soon invalidated, and as of Wednesday, there had been more than 81,000 confirmed infections around the world.

Chinese researchers said drugs targeting the furin enzyme could have the potential to hinder the virus’ replication in the human body.

These include “a series of HIV-1 therapeutic drugs such as Indinavir, Tenofovir Alafenamide, Tenofovir Disoproxil and Dolutegravir and hepatitis C therapeutic drugs including Boceprevir and Telaprevir”, according to Li’s study.

This suggestion is in line with reports by some Chinese doctors who self-administered HIV drugs after testing positive for the new coronavirus, but there is as yet no clinical evidence to support the theory.

There is also hope that the link to the furin enzyme could shed light on the virus’ evolutionary history before it made the jump to humans.

**The mutation, which Ruan’s team described as an “unexpected insertion”, could come from many possible sources such as a coronavirus found in rats or even a species of avian flu.**

Scientists found a section of mutated genes in the new coronavirus that were similar to those found in HIV and Ebola. Photo: AP @SCMPNews
http://j.mp/2w60QgG
So who had ‘mutated bat-snake flu’ as their top market risk for 2020? tweeted @tracyalloway.

The Precise origins of the Corona virus are yet to be established with Wiley’s Journal of Medical Virology saying it may be may be snake- to-human transmission and some even pointing the Finger at the Wuhan Institute of Virology and the Wuhan bio-safety level four (BSL-4) laboratory and surmising that the only explanation left is artificial DNA modification, possibly by the Wuhan Institute of Virology, which since 2007 has collected samples from thousands of bats across the country and done genetic experiments with them.
Looking at the phylogenetic tree recently published derived using all the full genome sequence, we see the 2019-nCoV virus does not have clear monophyletic support given the bootstrap value of 75 (Fig 1).

There is no doubt that there is a novel sequence in 2019-nCoV; we confirmed this via sequence alignment. Here’s the DOT plot:

Option 4. A recombined virus made in a laboratory for the purpose of creating a vaccine. The disease progression in of 2019-nCoV is consistent with those seen in animals and humans vaccinated against SARS and then challenged with re-infection. Thus, the hypothesis that 2019- nCoV is an experimental vaccine type must be seriously considered.
Evidence for: Sequence homology between INS1378 to pShuttle Coronavirus vaccine; presence of a SARS-like Spike protein in bat coronavirus, otherwise most similar to bat coronaviruses; low bootstrap value.

Evidence against: Low sequence homology (but highly significant). NB these viruses are RNA viruses and they can evolve quickly, even under laboratory conditions. Status: Most likely.

16-FEB-2020 :: #COVID19 #coronavirus #2019nCoV
http://bit.ly/37vP1Fn

The section in the box has never been seen before in any #coronavirus and is comprised of several bat species. Bc this didn’t occur naturally, it’s thought to be made in a lab.
@davegreenidge57
https://twitter.com/davegreenidge57/status/1228267306310131713?s=20
An article published on The Lancet reported that 41 people in Wuhan were found to have the acute respiratory syndrome and 27 of them had contact with Huanan Seafood Market. The 2019-nCoV was found in 33 out of 585 samples collected in the market after the outbreak.

The market was suspicious to be the origin of the epidemic, and was shut down according to the rule of quarantine the source during an epidemic. **The bats carrying CoV ZC45 were originally found in Yunnan or Zhejiang province, both of which were more than 900 kilometers away from the seafood market. Bats were normally found to live in caves and trees.**

But the seafood market is in a densely-populated district of Wuhan, a metropolitan of ~15 million people. The probability was very low for the bats to fly to the market. According to municipal reports and the testimonies of 31 residents and 28 visitors, the bat was never a food source in the city, and no bat was traded in the market. **There was possible natural recombination or intermediate host of the coronavirus, yet little proof has been reported. Was there any other possible pathway?**

We screened the area around the seafood market and identified two laboratories conducting research on bat coronavirus. Within ~280 meters from the market, there was the Wuhan Center for Disease Control & Prevention (WHCDC) (Figure 1, from Baidu and Google maps). **WHCDC hosted animals in laboratories for research purpose, one of which was specialized in pathogens collection and identification.**

In one of their studies, 155 bats including Rhinolophus affinis were captured in Hubei province, and other 450 bats were captured in Zhejiang province. The expert in collection was noted in the Author Contributions (JHT). Moreover, he was broadcasted for collecting viruses on nation-wide newspapers and websites in 2017 and 2019. He described that he was once by attacked by bats and the blood of a bat shot on his skin. He knew the extreme danger of the infection so he quarantined himself for 14 days. In another accident, he quarantined himself again because bats peed on him. He was once thrilled for capturing a bat carrying a live tick. **Surgery was performed on the caged animals and the tissue samples were collected for DNA and RNA extraction and sequencing.**

The tissue samples and contaminated trashes were source of pathogens. They were only ~280 meters from the seafood market. The WHCDC was also adjacent to the Union Hospital where the first group of doctors were infected during this epidemic. **It is plausible that the virus leaked around and some of them contaminated the initial patients in this epidemic, though solid proofs are needed in future study.**

The second laboratory was ~12 kilometers from the seafood market and belonged to Wuhan Institute of Virology, Chinese Academy of Sciences. This laboratory reported that the Chinese horseshoe bats were natural reservoirs for the severe acute respiratory syndrome coronavirus (SARS-CoV) which caused the 2002-3 pandemic. **The principle investigator participated in a project which generated a chimeric virus using the SARS-CoV reverse genetics system, and reported the potential for human emergence.**
A direct speculation was that SARS-CoV or its derivative might leak from the laboratory. **In summary, somebody was entangled with the evolution of 2019-nCoV coronavirus. In addition to origins of natural recombination and intermediate host, the killer coronavirus probably originated from a laboratory in Wuhan.**

Safety level may need to be reinforced in high risk biohazardous laboratories. Regulations may be taken to relocate these laboratories far away from city center and other densely populated places.