

New Study Published by Top British Biomedical Scientist Proves the COVID-19 Fraud Is a Crime Against Humanity

Virology's Voodoo Scientism Is Not Real Science

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Global Research, December 07, 2021

[The Expose](#) 3 December 2021

Region: [Europe](#)

Theme: [Science and Medicine](#)

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The purported novel coronavirus called SARS-CoV-2, has not been proven to exist in nature and has not been established as the cause of "COVID-19", the pandemic disease concocted by the World Health Organisation (WHO). Likewise, there are no variants of the "virus", which also only exist hypothetically in computers, and in online gene banks.

This COVID-19 fraud has enabled the widespread use of highly experimental and dangerous injections that contain a computer-generated spike protein mRNA sequence that instructs the body to poison itself. These injections also contain undeclared non-biological substances for unknown purposes and are killing many thousands of people worldwide and seriously harming many more.

Virological fraud enables these crimes against humanity because SARS-CoV-2 has never been physically isolated or shown to be the causal agent of COVID-19.

The genome of a "virus" that hadn't been isolated and purified, was published in early January 2020, named SARS-CoV-2 by the International Committee on Taxonomy of Viruses on 11 February, the same day the WHO's Director-General, **Tedros Adhanom Ghebreyesus**, announced its supposed resultant disease (COVID-19) with symptoms that are indistinguishable from other respiratory diseases.

The vast majority of the public and the medical profession are unaware that modern virology uses anti-scientific methods to claim the existence of the SARS-CoV-2 virus as well as other viruses. Most people would be surprised to learn that the "virus" has never been found inside a human or shown to be the cause of any disease.

The COVID-19 fraud requires the absence of this virus so there is no material reference against which the computer-generated genome can be cross-checked.

Virology's double deception is as follows:

- 1) The substitution of the dictionary and scientific meaning of the noun isolate for the opposite meaning. Isolate (real definition): Chemistry, Bacteriology. to obtain (a substance or microorganism) in an uncombined or pure state.
- 2) The substitution of the proxy of inducing cytopathic effects (CPEs) by inoculating abnormal cell lines in vitro for the established proxy of infecting a non-diseased host in vivo to determine causality between the proposed pathogen and the disease.

Even using "normal" healthy cell lines would not establish causality by Koch's postulates or any other scientific postulates used to establish causality, because they are only in vitro observations involving alleged viruses.

The production of CPEs is central to modern virology's fraudulent claims of isolation and pathogenicity: a sample (e.g. a nasal swab) is taken from a person and added to some cells in a test tube, if the cells die, it is falsely declared that a virus has been "isolated".

By definition, a virus is an infectious particle that can cause a disease in a living host. None of these defining properties have been demonstrated in any of the virological experiments describing supposed isolation and pathogenesis.

Virologists spent several decades attempting this unsuccessfully but instead of admitting to a problem with the whole virus theory, they just changed the meaning of the word isolate in the 1950s. Virologists do not actually isolate viruses, they just falsely claim that they do.

The process virologists use to claim "isolation" can be summarised as follows:

From the mixed biological "soup" taken from a patient's lungs or nose swabs containing all sorts of material including human cells, innumerable commensal microbes, and potential contaminants (bacteria, fungi), de novo assembly platforms search for short genetic fragments.

After finding millions of unique fragments in the soup, the software programmes then piece together one long piece (a "genome") based on parameters set in the programme. There is some cutting-and-pasting of sequences and if pieces are "missing" other ready-made templates can be added to fill the gaps. The man-made algorithms, probability models and arbitrary selections cannot determine its physical existence in nature, because any coronavirus "genome" used as a template in its production will also be hypothetical.

This methodology provides no confirmable connection with the material or physical world, which makes the newest member of the Coronavirus genus just another product of virology's self-referential processes. This is how virologists keep inventing viruses to stay in business, providing pharmaceutical companies with the justification for producing lucrative vaccines.

The anti-science of virology and the perversion of the word "isolation" is delusional, dishonest and highly misleading. It is not a sound basis for the health and well-being of individuals or whole populations.

Fan Wu et al. were the first inventors of the SARS-CoV-2 genome and used a patient's lung fluid sample for de novo sequencing assembly platform analysis to search for short genetic

fragments or “reads”. It is important to understand that the samples sequenced were not physically isolated viruses but crude samples containing millions of genetic fragments from the patient himself, and the numerous different microbes (bacteria, fungi) that make up the microbiome, as well as potential environmental contaminants.

It’s not clear how Fan Wu et al. knew which “genome” to choose when all of the options were hypothetical computer constructs, but they chose the longest (30,474 nucleotides), because it had a nucleotide identity of 89.1% with the in silico (computer-generated) bat coronavirus genome (SL-CoVZC45) that was invented in 2018. It was subsequently reduced to 29,875 nucleotides in the next version on GenBank perhaps to make it look more like the 29,802 nucleotides of the bat model genome. The final model was redrawn with a completely different terminal sequence featuring 23 consecutive adenine bases, thereby making it look more like the bat model which featured 26 consecutive adenine bases on its tail.

On the basis that RNA of unknown origin was part of the culture in which many cells died (perhaps due to induced starvation and stress with cytotoxic substances), Fan Wu et al claimed that they had successfully isolated the 2019-nCoV BetaCov virus.

This fraud was rewarded with grants in 2020 totalling US\$900,000 from the Bill and Melinda Gates Foundation made to the two institutions with which 14 of the 19 co-authors of the fraudulent paper were affiliated.

Peng Zhou et al. then made their contribution to the fraud by publishing a paper that fulfilled none of the postulates to identify a virus or confirm it as being causative of any disease. The supposed virus was not physically isolated and purified for biochemical characterisation and so remains entirely theoretical.

The Chinese Academy of Sciences, with which 24 of the 27 co-authors were affiliated, were rewarded with a 2020 COVID-19-related grant totalling US\$359,820 from the Bill and Melinda Gates Foundation.

Na Zhu et al. also claimed isolation of the virus, but it is clear that the authors do not mean “isolation” in the dictionary scientifically postulated sense but virology’s substituted antonymic meaning and the substitution of diseased for non-diseased host cells to establish causality between a purported virus and the patient’s symptoms.

Unlike Fan Wu et al. and Peng Zhou et al., Na Zhu et al. did produce images of what they called “2019-nCoV particles” but without any verification of their biochemical composition from a purified specimen. It is not possible to establish from their images that the particles are infectious disease-causing viruses or that they contain the alleged SARS-CoV-2 genome.

“Although our study does not fulfil Koch’s postulates, our analyses provide evidence of implicating 2019-nCoV in the Wuhan outbreak.” Na Zhu *et al*

This claim is based on pictures of extracellular vesicles of unknown composition and origin which the authors have named “2019-nCoV”.

The National Institute for Viral Disease Control and Prevention, with which 13 of the 18 co-authors of the Na Zhu *et al* paper were affiliated were rewarded with US\$71,700 in 2020 from the Bill and Melinda Gates Foundation for this fraudulent research.

Caly *et al.* claimed that Vero cells (monkey kidney cells) “showed cytoplasmic membrane-bound vesicles containing coronavirus particles”, but were not able to see typical “virions” with the spike protein. They added more protein-digesting trypsin to the cell cultures which digested the outer protein layer of a 100 nm spherical “virion” to manufacture “the characteristic crown-like fringe of spike proteins”, thereby they “immediately improved virion morphology.” In other words, when the vesicles (possibly exosomes) did not look like their expectations of a coronavirus, they artificially engineered it with an extra-large dose of the enzyme trypsin.

These supposed virions were not purified so their biochemical composition could not be confirmed. The “genome” was in fact put together after generating “approximately 30,000,000 reads” from the tissue culture mix. As with all other papers of this nature, no explanation was provided as to how these particles are known to cause disease or whether these same particles exist inside humans. Scientifically speaking they can only be called extracellular vesicles of unknown significance, produced by stressed abnormal monkey kidney cells in vitro.

Despite the deceptions permeating virology, virologists still adhere to their non-scientific beliefs. This is scientism not science.

Scientism is the uncritical application of technical methods which becomes a secularised belief system relying for its authority on its own presupposition and performativity. Assumptions, hypotheses and abstractions are considered to be conclusive and real.

In contrast, the scientific method includes the following:

- 1) Objective observation: Measurement and data.
- 2) Evidence.
- 3) Experiment and/or observation as benchmarks for testing hypotheses.
- 4) Induction: reasoning to establish general rules or conclusions drawn from facts or examples.
- 5) Repetition.
- 6) Critical analysis.
- 7) Verification and testing: critical exposure to scrutiny, peer review and assessment.

Virologists claim that they have elucidated the entire genomes of viruses such as “SARS-CoV-2” and they upload this onto databanks. They claim that they have an “isolate” of the virus but this is declared after they have constructed the genome from their mixed brew containing genetic fragments of unknown origin using computer algorithms.

Virologists do not work with a complete genome because they do not work with a complete virus. They work with random bits of biological material and then claim that it constitutes evidence of a virus. When their experiments are examined carefully there is no material proof of a virus.

No virus called SARS-CoV-2 has ever been properly isolated and purified as a

whole unique structure. What happens is the shotgun sequencing of crude samples that contain numerous mixed genetic fragments of unknown origin. Shotgun sequencing is a method used for sequencing random DNA strands which is named by analogy with the semi-random shot grouping of a shotgun. There is no evidence whatsoever that the resulting in silico “genome” actually exists in nature or has anything to do with a “virus”. The invention of the “virus” is presented as a discovery, its faux status is secured through the act of naming it into existence.

The PCR (Polymerase Chain Reaction) can only amplify selected nucleotide sequences but cannot determine their provenance or significance. The Virology PCR fraud relies on the attribution of meaning to the amplified sequences:

1) Reference to the imaginary in silico genome but not to a proven physical entity called SARS-CoV-2.

2) Reference to a “disease” that with absurd circular reasoning has been defined by the PCR result itself.

The faudsters disingenuously refer to the PCR as the “gold standard” test but in reality, at best it is merely a surrogate test for a whole virion and at worse, it is a false positive artifact generating test.

When PCR is performed badly and/or at high cycle numbers (as has been common) the target sequence may not even be present in the sample and a “positive” result is simply an artefact of the PCR process. The PCR cannot diagnose the infectious status of a person in any proven way and no consistent link has ever been found between a disease state and the PCR results.

The misapplication of a completely inaccurate PCR means that COVID-19 is a scientifically meaningless construct that is nothing more than a self-referential illusion.

Christian Drosten *et al.* published non-peer reviewed PCR assay sequences designed to detect the purported virus “without having virus material available” in January 2020.

The Drosten paper was published in Eurosurveillance on 23 January which was only two days after submitting the manuscript. Drosten who is facing charges for holding a fraudulent doctoral title did not declare that he was a member of the Eurosurveillance editorial board.

Chantal Reusken a co-author, also failed to declare that she was on the Eurosurveillance editorial board. Olfert Landt another of Drosten’s co-authors who is CEO of TIB the maker of a lucrative PCR kit based on the published assay sequences didnt declare his conflict of interest until 29 July 2020.

Mass PCR testing using the Drosten protocol quickly resulted not in a viral pandemic but a PCR pandemic. The university hospital of Charité Berlin where many of the Drosten PCR authors were based subsequently received a 2020 “covid” grant totalling US\$249,550.70.

The PCR has been designed to detect genetic sequences of a “virus” that has not been proven to exist in nature but instead is detecting sequences of unknown origin and generates high numbers of false positive results.

As a result of PCR testing, medical tyranny has been imposed on most of the world, based

on scientism disconnected from the real world and so absurd that detecting a few genetic fragments of something in one person can be used as the excuse to lock up an entire country.

The completely useless PCR test generated astronomical case numbers which then formed the basis of “COVID-19” outbreak computer models. Outbreak modelling is notorious for its inaccurate predictions and produced “COVID-19” numbers that were preposterous and all based on worthless numbers.

Lockdown flouting **Neil Ferguson** of Imperial College London (ICL) has a long history of producing doom mongering wildly inaccurate speculative nonsense with his computer modelling.

In 2001, the ICL team did the modelling on foot and mouth disease which led to a cull of six million sheep, pigs and cattle costing the UK approximately £10 billion. The ICL work on this has been described as ‘severely flawed’ by real experts.

In 2002, Ferguson predicted that up to 50,000 people would die from mad cow disease which he claimed could rise to 150,000 if sheep were involved. In the UK, the total number of deaths was 177.

In 2005, Ferguson claimed that up to 200 million people could be killed by bird flu. The total number of deaths was 282 worldwide.

In 2009, Ferguson and the ICL team claimed that swine flu would kill 65,000 people in the UK. In reality, swine flu killed 457 people in the UK.

Ferguson was the lead author of an ICL Report, published without peer review on 16 March 2021, predicting that 550,000 people in the UK and 2.2 million people in the US would die from COVID-19 within approximately three months.

When the Ferguson reports programming was eventually released for public scrutiny it was ridiculed by academic experts. It relied on 13-year-old computer coding intended to model flu which was a “buggy mess that looks more like a bowl of angel hair pasta than a finely tuned piece of programming” according to one expert. Scientists at the University of Edinburgh reported that it failed “the basic scientific test of producing the same results given the same initial set of parameters”.

The ICL was rewarded with Gates Foundation grants for 2020 totalling US\$91,494,791. Since 2002 the Bill and Melinda Gates Foundation have provided ICL with grants totalling US\$302,164,640, which is US\$16,000,000 per year for the last 19 years.

Inaccurate computer models based on false case numbers have resulted in fear and confusion leading to heated debates about why the “virus” behaves so differently in different places, whether or not there is excess mortality, and whether or not the “vaccines” are effective.

The aggressively marketed remedy for this alleged deadly virus is a spike protein produced by a genetic sequence that is not found in nature but in a US patent from 2007. The “vaccines” based on this sequence have killed many thousands of people around the world and injured millions more.

If these anti-science methods continue to be believed and accepted, we are likely to see even more pseudo pandemics requiring more “vaccines”, continuing indefinitely as part of the “new normal”. We are already seeing this with a steady stream of “variants of concern.”

There is nothing normal about the pharmaceutical industry and globalist organisations creating demand for unnecessary gene therapies through fear and the creation of pseudo-pandemics. There is nothing normal about the unprecedented censorship of scientific debate and the prevention of medical practitioners providing real advice and informed consent.

The virus isolation fraud, the artificial viral genome fraud (including new variants), the pathogenicity fraud, the PCR fraud, and the experimental gene therapy “vaccine” fraud are crimes against humanity enabled by virology’s unscientific self-referential scientism.

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Sources

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