# COVID 19: Mounting Evidence of International Fraud

## COVID 19: Mounting Evidence of International Fraud

by **Iain Davis**, *In This Together*
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**COVID 19, and the subsequent governmental responses, appear to be part of an international conspiracy to commit fraud. It seems there is no evidence that a virus called SARS-CoV-2 causes a disease called COVID 19.**

Sometimes you have to go with your gut. I am not an expert in genetics and, as ever, stand to be corrected. However my attention was drawn to some research published by the Spanish medical journal *D-Salud-Discovery*. Their advisory board of eminently qualified physicians and scientists lends further credibility to their research. Their claim is astounding.

The genetic primers and probes used in RT-PCR tests to identify SARS-CoV-2 do not target anything specific. I followed the search techniques outlined in this English translation of their report and can corroborate the accuracy of their claims about the nucleotide sequences listed in the World Health Organisations protocols. You can do the same.

D-Salud-Discovery state there are no tests capable of identifying SARS-CoV-2. Consequently all claims about the alleged impact of COVID 19 on population health are groundless.

The entire official COVID 19 narrative is a deception. Ostensibly, there is no scientific foundation for any part of it.

If these claims are accurate we can state that there is no evidence of a pandemic, merely the illusion of one. We have suffered incalculable loss for no evident reason, other than the ambitions of unscrupulous despots who wish to transform the global economy and our society to suit their purposes.

In doing so this *"parasite class"* have potentially committed countless crimes. These crimes can and should be investigated and prosecuted in a court of law.

## Identification of What Exactly?

The World Health Organisation (WHO) classified COVID-19 (COronaVIrus Disease 2019). They declared a global COVID 19 pandemic on March 11th 2020.

The WHO's Laboratory testing guidance states:

*"The etiologic agent [causation for the disease] responsible for the cluster of pneumonia cases in Wuhan has been identified as a novel betacoronavirus, (in the same family as SARS-CoV and MERS-CoV) via next generation sequencing (NGS) from cultured virus or directly from samples received from several pneumonia patients."*

The WHO's claim is that the SARS-CoV-2 virus *causes* the *disease* COVID-19. They also allege this virus has been clearly identified by researchers in Wuhan.

In the WHO's Novel Coronavirus 2019-nCov Situation Report 1, they state:

*"The Chinese authorities identified a new type of coronavirus, which was isolated on 7 January 2020……On 12 January 2020, China shared the genetic sequence of the novel coronavirus for countries to use in developing specific diagnostic kits."*

These two statements from the WHO clearly suggest the SARS-CoV-2 virus was isolated (meaning purified for study) and then genetic sequences were *identified* from the isolated sample.

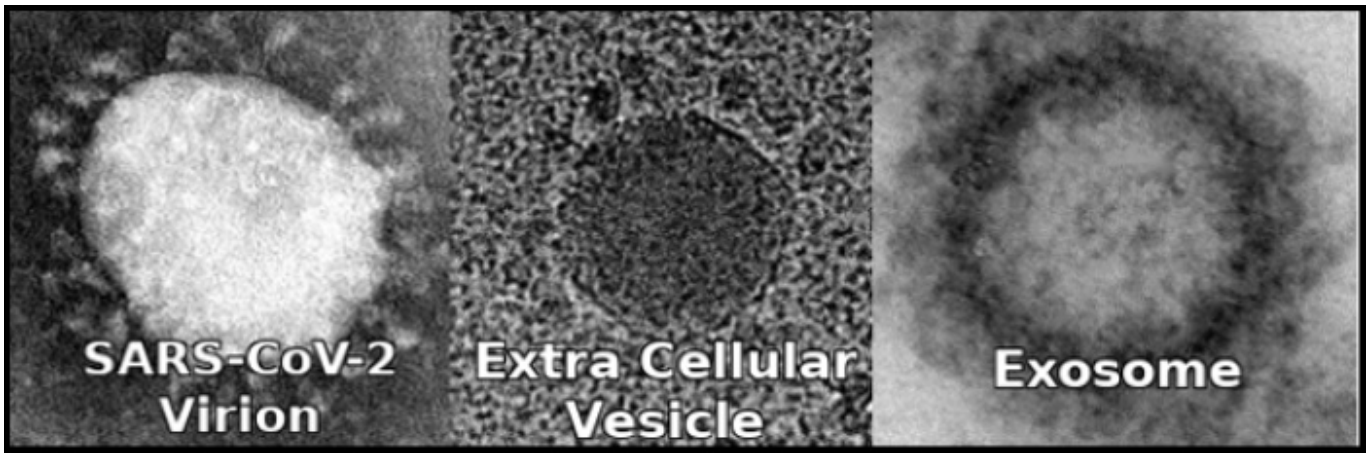
From this, diagnostic kits were developed and distributed globally to test for the virus in towns, cities and communities around the world. According to the WHO and Chinese researchers, these tests will find the virus that *causes* COVID 19.

Yet the WHO also state:

*"Working directly from sequence information, the team developed a series of genetic amplification (PCR) assays used by laboratories."*

The Wuhan scientists developed their genetic amplification assays from *"sequence information"* because there was no isolated, purified sample of the so called SARS-CoV-2 virus. They also showed electron microscope images of the newly discovered virions (the spiky protein ball containing the viral RNA.)

However, such protein structures are not unique. They look just like other round vesicles, such as endocytic vesicles and exosomes.




Virologists claim that it is not possible to *"isolate"* a virus because they only replicate inside host cells. They add that Koch's postulates do not apply because they relate to bacteria (which are living organisms). Instead, virologists observe the virus' cytopathogenic effects (CPE), causing cell mutation and degradation, in cell cultures.

When Chinese researchers first sequenced the full SARS-CoV-2 genome they observed CPE in Vero E6 and Huh7 cells. Vero E6 are an immortalised monkey cell line and Huh7 are immortalised cancer (tumorigenic) cells. Meaning they have been maintained in vitro (in petri dish cultures) for many years.

Central to the official SARS-CoV-2 story is the idea that it is a zoonotic virus, capable of bridging the species gap from animals to humans. When scientists from the U.S. CDC *"infected"* various cells with the novel virus they noted the following:

*"We examined the capacity of SARS-CoV-2 to infect and replicate in several common primate and human cell lines, including human adenocarcinoma cells (A549) [lung celles], human liver cells (HUH7.0), and human embryonic kidney cells (HEK-293T), in addition to Vero E6 and Vero CCL81 [monkey cells]……No cytopathic effect was observed in any of the cell lines except in Vero cells [monkey cells]…….HUH7.0 and 293T cells showed only modest viral replication and A549 cells [human lung tissue cells] were incompatible with SARS-CoV-2 infection."*

The CDC did not observe any CPE in human cells. They saw no evidence that this alleged virus caused any human illness. Nor did this supposed human virus show any notable replication in human cells, suggesting human to human infection would be impossible.

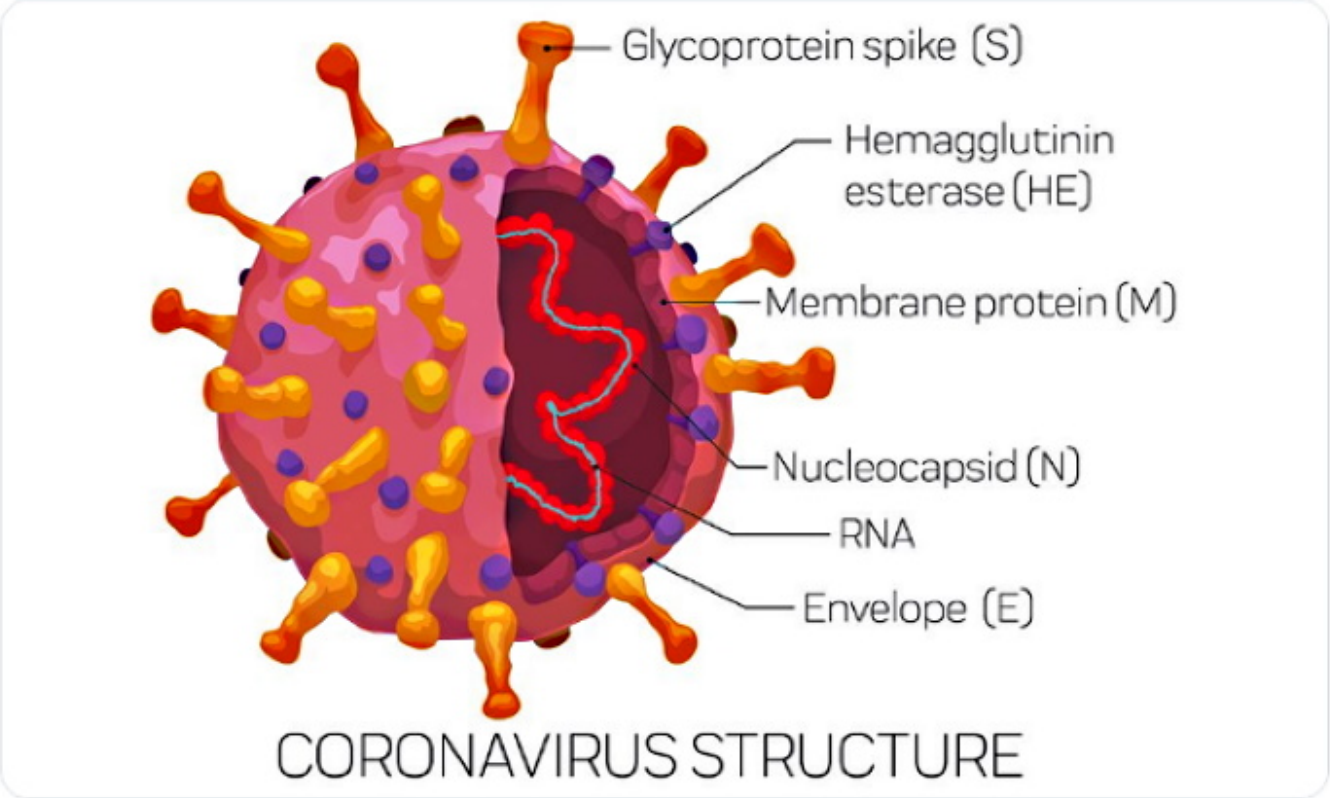
Noting this problem, a team of Polish scientists introduced this sequenced *"virus"* to human epithethelium (airway) cells. They observed the effects on these HAE cultures for 5 days. They noted much greater replication than the CDC scientists but ultimately stated:

*"We did not observe any release of the virus from the basolateral side of the HAE culture."*

Meaning they did not see any evidence of the supposed virions

breaching the cell wall membrane. Again suggesting this so called virus isn't infectious in human beings.

It is not clear that SARS-CoV-2 is a human virus capable of causing illness. It may not even physically exist. Is it nothing more than a concept based upon *predictive* genetic sequences?




## Voyage Of Discovery

The Wuhan Center for Disease Control and Prevention and the Shanghai Public Health Clinical Centre published the first full SARS-CoV-2 genome (MN908947.1 ). This has been updated many times. However, MN908947.1 was the first genetic sequence describing the alleged COVID 19 *etiologic agent* (SARS-CoV-2).

All subsequent claims, tests, treatments, statistics, vaccine development and resultant policies are based upon this sequence. If the tests for this *novel* virus don't identify anything capable of causing illness in human beings, the whole COVID 19 narrative is nothing but a charade.

The WUHAN researchers stated that they had effectively pieced the SARS-CoV-2 genetic sequence together by matching fragments found in samples with other, previously discovered, genetic sequences. From the gathered material they found an 87.1% match with SARS coronavirus (SARS-Cov). They used de novo assembly and targeted PCR and found 29,891-base-pair which shared a 79.6% sequence match to SARS-CoV.

They had to use *de novo assembly* because they had no *priori* knowledge of the correct sequence or order of those fragments. Quite simply, the WHO's statement that Chinese researchers *isolated* the virus on the 7th January is false.

The Wuhan team used 40 rounds of RT-qPCR amplification to match fragments of cDNA (complimentary DNA constructed from sampled RNA fragments) with the published SARS coronavirus genome (SARS-CoV). Unfortunately it isn't clear how accurate the original SARS-CoV genome is either.

In 2003 a team of researchers from from Hong Kong studied 50 patients with severe acute respiratory syndrome (SARS). They took samples from 2 of these patients and developed a culture in fetal monkey liver cells.

They created 30 clones of the genetic material they found. Unable to find evidence of any other known virus, in just one of these cloned samples they found genetic sequences of *"unkown origin."*

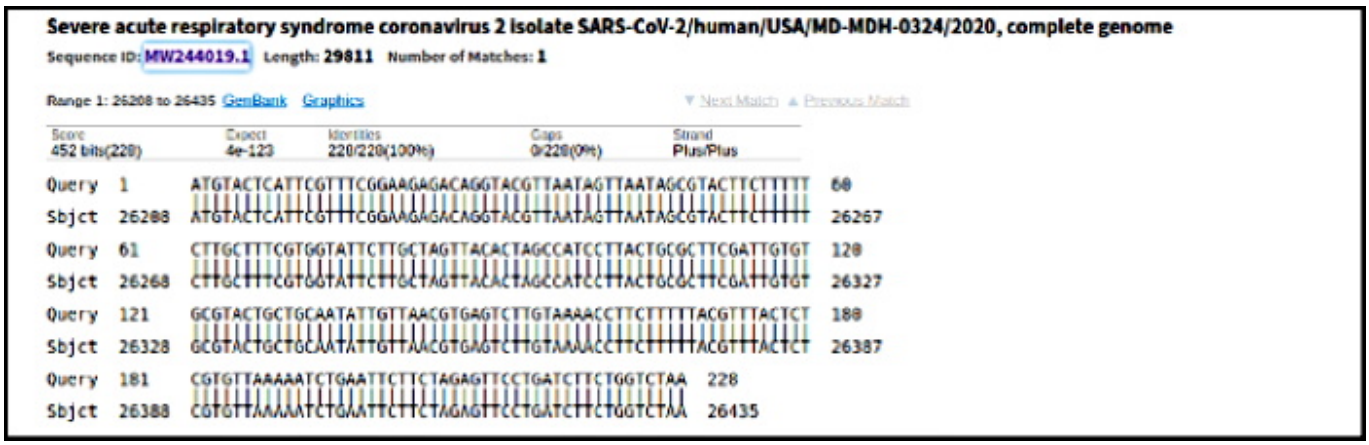



*CHART: E Gene target sequence*

Examining these unknown RNA sequences they found 57% match to bovine coronavirus and murine hepatitis virus and deduced it was of the family **Coronaviridae**. Considering these sequences to suggest a newly discovered SARS-CoV virus (new discoveries being ambrosia for scientists), they designed RT-PCR primers to test for this novel virus. The researchers stated:

*"Primers for detecting the new virus were designed for RT-PCR detection of this human pneumonia-associated coronavirus genome in clinical samples. Of the 44 nasopharyngeal samples available from the 50 SARS patients, 22 had evidence of human pneumonia-associated coronavirus RNA."*

Half of the tested patients, who all had the same symptoms, tested positive for this new alleged virus. No one knows why the other half tested negative for this *novel* SARS-CoV virus. The question wasn't asked.

This supposed virus had just a 57% sequence match to allegedly known coronavirus. The other 43% was just *"there."* Sequenced data was produced and recorded as a new genome as GenBank Accession No. AY274119.

The Wuhan researchers subsequently found an 79.6% sequence match to AY274119 and therefore called it a novel strain of SARS-CoV (2019-nCoV – eventually renamed SARS-CoV-2). No one, at any stage of this process, had produced any isolated, purified sample of any virus. All they had were percentage sequence matches to other percentage sequence matches.

**Isolate Nothing**

Scientists are very annoyed because they keep saying the virus has been isolated but no one believes them. This is because, as yet, no one has provided a single purified sample of the SARS-CoV-2 virus. What we have instead is a completed genome and, as we are about to discover, it isn't particularly convincing.

Investigative journalists Torsten Engelbrecht and Konstantin Demeter asked some of the scientists who said they had images of SARS-C0V-2 virions to confirm these were images of an isolated, purified, virus. None of them could.

In Australia scientists from the Doherty Institute, announced that they had *isolated* the SARS-CoV-2 virus. When asked to clarify the scientists said:

*"We have short (RNA) sequences from the diagnostic test that can be used in the diagnostic tests"*

This explains why the Australian government state:

*"The reliability of COVID-19 tests is uncertain due to the limited evidence base…There is limited evidence available to assess the accuracy and clinical utility of available COVID-19 tests."*

In The UK, in July, a group of concerned academics wrote a letter to the UK Prime Minister Boris Johnson in which they asked him to:

*"Produce independently peer reviewed scientific evidence proving that the Covid-19 virus has been isolated."*

To date they have not received a reply.

Similarly, UK researcher Andrew Johnson made a Freedom of Information Request to Public Health England (PHE). He asked them to provide him with their records describing the isolation of a SARS-COV-2 virus. To which they responded:

*"PHE can confirm it does not hold information in the way suggested by your request."*

Canadian researcher Christine Massey made a similar freedom of information request, asking the Canadian government the same. To which the Canadian government replied:

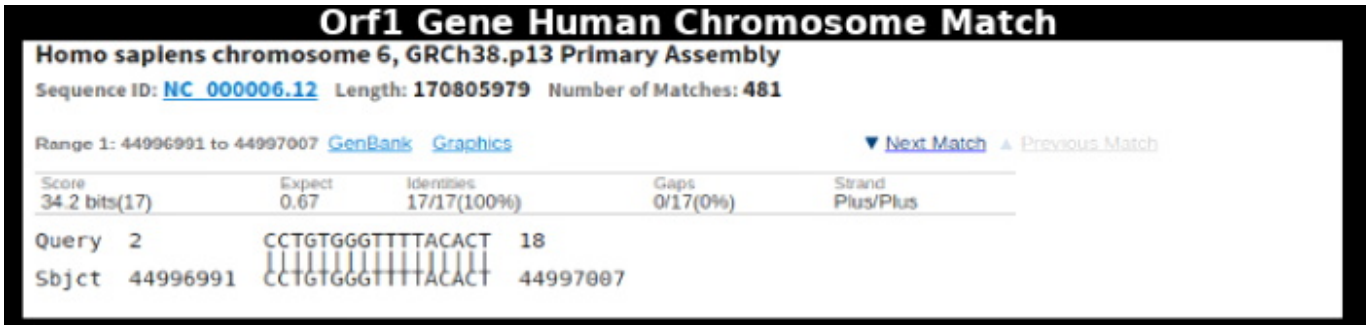
*"Having completed a thorough search, we regret to inform you that we were unable to locate any records responsive to your request."*

In the U.S. the Centre For Disease Control (CDC) RT-PCR Diagnostic Panel state:

*"…No quantified virus isolates of the 2019-nCoV are currently available……..Detection of viral RNA may not indicate the presence of infectious virus or that 2019-nCoV is the causative agent for clinical symptoms."*

Last updated on 13th July 2020, the CDC are yet to obtain any pure viral sample from any patient said to have the disease of COVID-19. They openly admit their tests don't necessarily show if SARS-CoV-2 is either present or causes COVID 19.

We are told that none of this matters. That we are ignorant and just don't understand virology. Therefore, we must except pictures of things we know could be something else and genetic sequences (which could be anything else) as conclusive proof that this virus, and the disease it is supposed to cause, are real.




## Testing For Nothing

The WHO, and every government, think tank, policy steering committee, government scientific advisor, supranational institutions and others who promote the official COVID 19 narrative, assert that SARS-CoV-2 causes COVID 19. While no one has ever produced a sample of this supposed virus, the

alleged SARS-CoV-2 genome has been published. It is in the public domain.

Key genetic sequences, in the SARS-CoV-2 genome, are said to have specific functions. These are the target proteins that scientists test for to *identify* the presence of the *"virus"*. These include:

- RNA-polymerase (Rd-Rp) gene – This enables the SARS-CoV-2 RNA to replicate inside the cytoplasm of COVID 19 diseased epithelial cells.
- S gene (Orf2) – this glycoprotein forms the spike on the SARS-CoV-2 virion surface which supposedly facilitates SARS-CoV-2 binding to the ACE2 receptors on cells, allowing the RNA inside the virion protein shell (capsid) to pass into the now *infected* cell.
- E gene (Orf1ab) – small membrane protein used in viral assembly
- N gene (Orf9a) – the nucleocapsid gene which binds the RNA in capsid formation

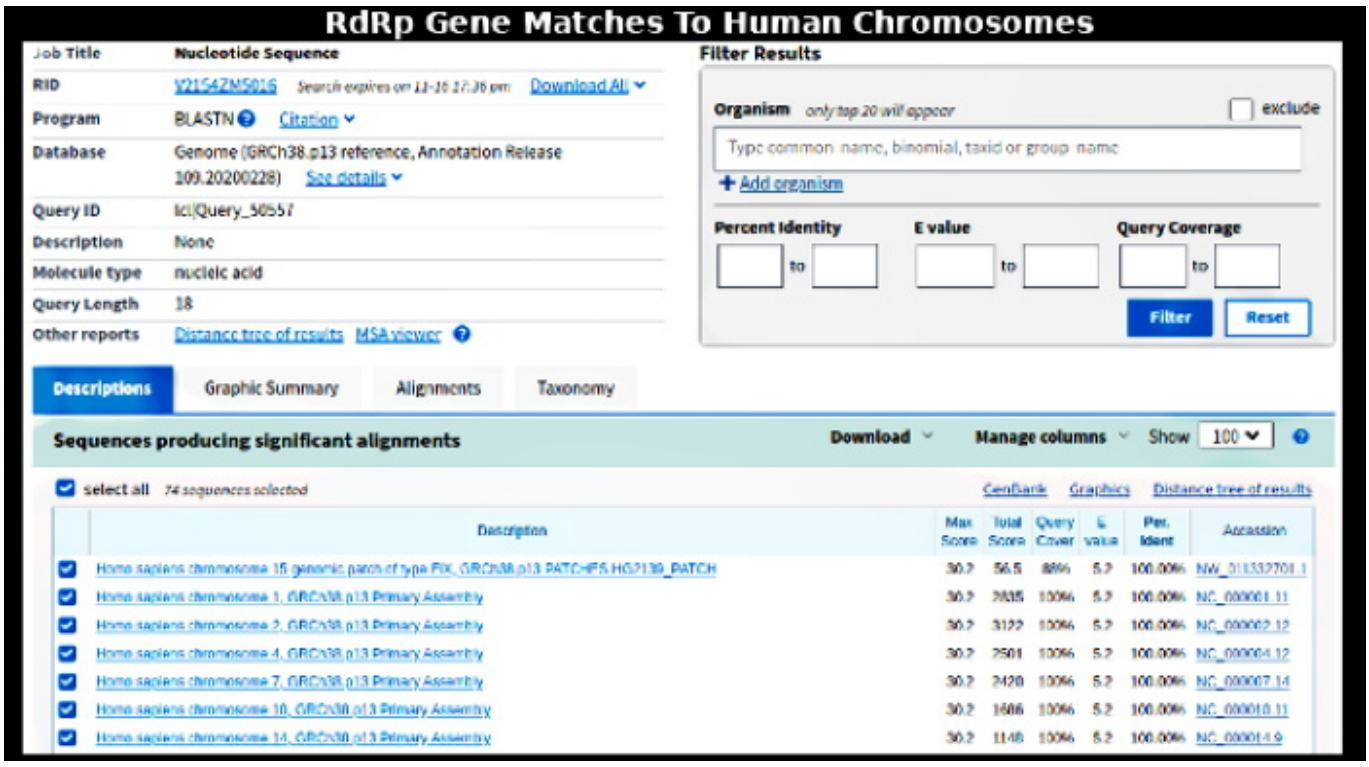
The WHO maintain a publicly available record of the RT-PCR primers and probes used to test for SARS-CoV-2. The primers are specific nucleotide sequences that bind (anneal) to the antisense and sense strands of the synthesised cDNA (called forward and reverse primers respectively.)

The cDNA strands separate when heated and reform when cooled. Prior to cooling, nucleotide sequences called probes are introduced to anneal to specific target regions of the suspected viral genome. During amplification, as the regions between primers elongate, when a primer strikes a probe, the probe decays releasing a fluorescent or dye which can then be read by researchers.

It is the identification of these markers which scientists claim to prove the presence of SARS-CoV-2 in a sample.

Something else which is publicly available is the Basic Local

Alignment Search Tool (BLAST). This allows anyone to compare published nucleotide sequences with all those stored by the U.S. National Institutes of Health (NIH) genetic database called GenBank. Therefore we can BLAST the claimed SARS-CoV-2 primers, probes and target gene sequences.




The WHO's forward, reverse primers and probe protocols, for the alleged SARS-CoV-2 viral genome, are based upon RdRp, Orf1, N and E gene profiles. Anyone can run them through BLAST to see what we find.

The vital RdRP nucleotide sequence, used as a forward primer is – ATGAGCTTAGTCCTGTTG. If we run a nucleotide BLAST this is recorded as a complete SARS-CoV-2 *isolate* with a 100% matched sequence identity. Similarly the reverse E gene primer sequence – ATATTGCAGCAGTACGCACACA – reveals the presence of the Orf1ab sequence which also *identifies* SARS-CoV-2.

However, BLAST also enables us to search the nucleotide sequences of the microbial and human genomes. If we search for the RdRp SARS-CoV-2 sequence it reveals 99 human chromosome with a 100% sequence identity match. The Orf1ab (E gene)

returns 90 with a 100% sequence identity match to human chromosomes.

Doing the same for these sequences with a microbial search finds 92 microbes with a 100% match to the SARS-CoV-2 E gene and 100 matched microbes, with a 100% sequence identity, to the vital SARS-CoV-2 RdRp gene.

Whenever we check the so called unique genetic markers for SARS-CoV-2, recorded in the WHO protocols, we find complete or high percentage matches with various fragments of the human genome. This suggests that the genetic sequences, which are supposed to identify SARS-CoV-2, are not unique. They could be anything from microbial sequences to fragments of human chromosomes.

So called fact checkers, like Reuters' *Health Feedback* project, have been quick to dismiss the claims of those who have noticed the apparent lack of specificity in the supposed SARS-CoV-2 genome. Using a slew of strawman arguments like, *"this claim suggests every test should be positive,"* (which it doesn't) their *debunking* attempt runs something like this:

*Primers are designed to bind to specific nucleotide sequences that are unique to the virus. The forward primer may bind to a particular chromosome but the reverse primer doesn't bind to the same chromosome and so the chromosome is not present in the SARS-CoV-2 virus. Moreover because the forward and perverse primers envelop the sequence to be amplified the cDMA sequence between primers is unique to the virus.*

This seems to deliberately misrepresent the significance of these findings by forwarding an argument that no one, other than the fact checkers themselves, are making. BLAST searches show that these target sequences are not unique to SARS-CoV-2. Nor do all targets need to be found for a result to be deemed positive.

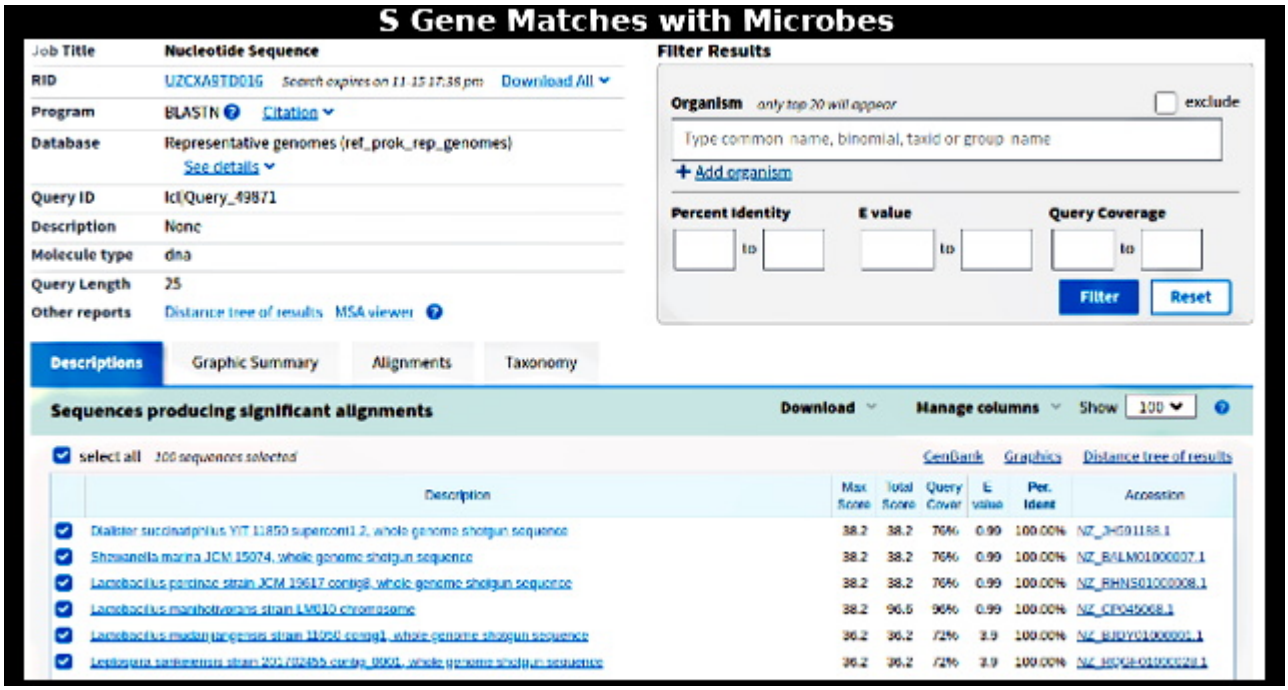
Moroccan researchers investigated the epidemiology of Moroccan alleged *cases* of SARS-CoV-2. Nine percent were positive for three genes, eighteen percent were positive for two genes and seventy three percent for just one. As we have just discussed, many may have been positive for none.

This is entirely in keeping with WHO's test guidelines. They state:

> ***"An optimal diagnosis consists of a NAAT [nucleic acid amplification test] with at least two genome-independent targets of the SARS-CoV-2; however, in areas where transmission is widespread, a simple single-target algorithm can be used……One or more negative results do not necessarily rule out the SARS-CoV-2 infection."***

Regardless of the spurious arguments of well funded *fact checkers,* if the forward and reverse primers identify junk, perhaps one being the fragment of a chromosome and the other a microbial sequence, then the amplified region between them is probably junk too.

The argument that RT-PCR only finds RNA is specious. Natural transcription (the separation of DNA strands) occurs during gene expression. No one is saying whole chromosomes or microbes are sequenced in the alleged SARS-CoV-2 genome. Though they may, for all we know. They are saying the alleged markers, used to test for this supposed virus, are not fit for purpose.




RT-PCR tests do not sequence the entire genome. They look for incidents of specific probe florescence to indicate the presence of sequences said to exist. These sequences are defined by MN908947.1 and the subsequent updates. These primers and probes could reveal nothing but RNA matches extracted from non-coding, sometimes called *"junk,"* DNA (cDNA.)

For example the SARS-CoV-2 S gene is meant to be highly specific to the SARS-CoV-2 virus genome. The target sequence is – TTGGCAAAATTCAAGACTCACTTTC. A microbial BLAST search returns 97 microbial matches with 100% identity sequence match. The lowest identity percentage match, within the top 100, is 95%. A human genome BLAST also finds a 100% sequence match to 86 human chromosome fragments.

No matter where you look in the supposed genome of SARS-CoV-2, there is nothing in the WHO's test protocols that clearly identifies what it is. The whole genome could be false. The tests do not prove the existence of SARS-CoV-2. All they reveal is a soup of unspecified genetic material.

If so, as there are no isolates or purified samples of the virus, without a viable test, there is no evidence that SARS-

CoV-2 exists. Therefore, nor is there any evidence that a disease called COVID 19 exists.

This infers that there is no scientific basis for any claims about COVID 19 case numbers, hospital admissions or mortality figures. All measures taken to *combat* this *deadly virus* are quite possibly founded upon nothing.

## Conclusive Fraud

Fraud is a criminal act. The legal definition of fraud is:

*"Some deceitful practice or willful device, resorted to with intent to deprive another of his right, or in some manner to do him an injury."*

The Legal definition of a conspiracy is:

*"A combination or confederacy between two or more persons formed for the purpose of committing, by their joint efforts, some unlawful or criminal act"*

It seems, those who claim we face a pandemic have not provided any evidence to show that a virus called SARS-CoV-2 causes a disease called COVID 19. All of the information strongly suggesting this possibility is readily available in the public domain. Anyone can read it.

For there to be a fraud the deceit must be wilful. The intention must be to deliberately deprive others of their rights or injure them in some other way. If there is evidence of collusion between individuals ad/or organisations to commit fraud, then this is a conspiracy (in Common Law jurisdictions) or a Joint Criminal Enterprise (JCE) under International Law.

It seems COVID 19 has been deliberately used as a *casus belli* to wage war on humanity. We have been imprisoned in our own homes, our freedom to roam restricted, freedom of speech and expression eroded, rights to protest curtailed, separated from loved ones, our businesses destroyed, psychologically

bombarded, muzzled and terrorised.

**Worse still, while there is no evidence of *unprecedented* all cause mortality, there were unseasonable spikes in deaths. These correlate precisely with Lockdown measures which saw the withdrawal of the health services *we pay for* and a reorientation of public health services to treat one alleged disease at the exclusion of all others.**

Further, it is proposed by those who have forwarded the COVID 19 story, that this alleged disease provides justification for the complete restructuring of the global economy, our political systems, societies, cultures and humanity itself.

To be *allowed* to participate in their so called *"new normal,"* which is the wholesale transformation of our entire society without our consent, they insist we submit to their conditions.

These include, but aren't limited to, bio-metric surveillance of everyone, the centralised control and monitoring of all of our transactions, oppressive business and social restrictions and an effective demand that we have no right to sovereignty over our own bodies. This constitutes the condition of slavery.

There is no doubt that we have been deprived of our rights and injured. In Common Law jurisdictions innocence is presumed, but the evidence that harm has been deliberately caused by an international conspiracy is overwhelming. Destructive policies, enacted by governments across the world, clearly originated among globalist think tanks and supranational institutions long before the emergence of this non existent pandemic.

In Napoleonic Code jurisdictions, guilt is presumed. In order for the accused conspirators to prove their innocent they must show that, despite their immeasurable resources, they have collectively been unable to access or understand any of the

freely available evidence suggesting COVID 19 is a myth.

Those responsible for the crime of conspiracy to commit global fraud should be tried. If found guilty they should be imprisoned while the rest of us get on with trying to repair the damage they have already inflicted.

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*Author Iain Davis is an independent researcher and short filmmaker and the author of the new book, A Dangerous Ideology. See more of Iain's work at his blog site In This Together and follow him at Twitter & Steemit & MINDS.*

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