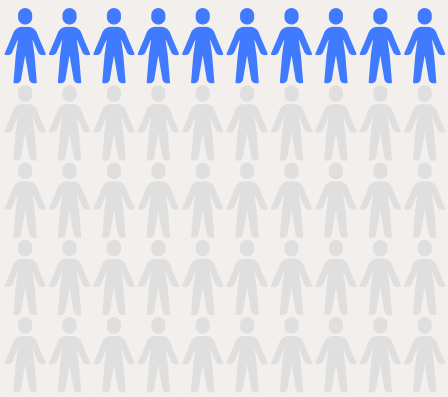


# COVID-19:

## Everything You Need to Know



## Analysis of the Scientific Study the World Health Organisation presents as Evidence for the Existence of the COVID-19 VIRUS.



The published Study is the singular most crucial document in the history of COVID. It identified the genomic sequence for the COVID virus, also known as SARS nCoV-19 and established it as a real virus. This Study led to a Global Lockdown and the ongoing global surveillance for COVID using PCR and Saliva testing, global vaccination, and digital passports.

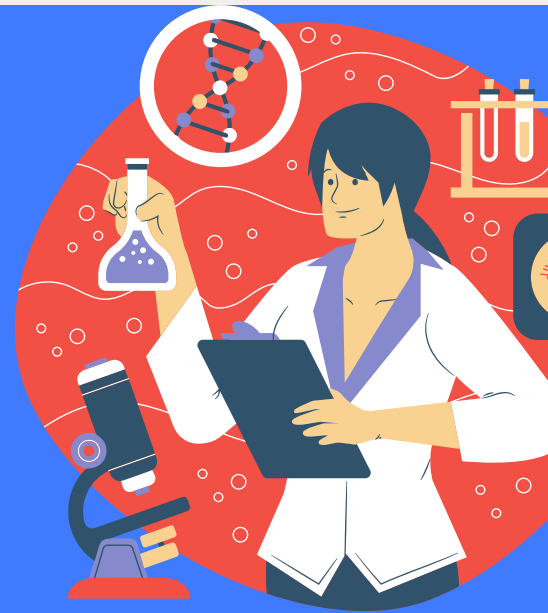
As you will see, the COVID virus is a **virtual virus** created in a computer program. **It is not a real virus and has never been isolated.**

**As our analysis will show, the Study is unscientific and fraudulent.**

## INTRODUCTION

We trust science because it uses tangible and replicable evidence to provide us with an understanding of the world. It relies on a scientific process to guide its Method.

The Car, Cell phone, Radio, Textile, Soap and just about any manufactured item are all produced following a scientific method, a repeatable process that will produce the same result all the time. And to declare a pandemic, there is also a scientific process to follow called KOCH'S POSTULATE.



KOCH'S POSTULATE is fundamental because it is the most logical outline for establishing a disease suspected of being caused by a microbe.

It is important to note that Modern medicine focuses on microbes as a major cause of disease while downplaying other significant causes of diseases such as contaminants, EMF's, nutrient deficiencies, and chemical sensitivities. It is necessary to establish this point because there may have been another cause of the pneumonia outbreak in Wuhan.

Since there were no evident attempts to rule out other causes of the symptoms observed in Wuhan Patients, it becomes crucial that strict scientific protocol is followed while establishing a microbial cause.

But as you would clearly see, due scientific process was ignored during the Study.

Every country should do everything to follow through on prioritizing, funding, and implementing preparedness interventions.

# KOCH'S POSTULATE



**Koch's Postulate is a scientific and logical process developed in 1890 by Robert Koch to establish that a particular organism is the cause of a disease or pandemic.**

## THE POSTULATE

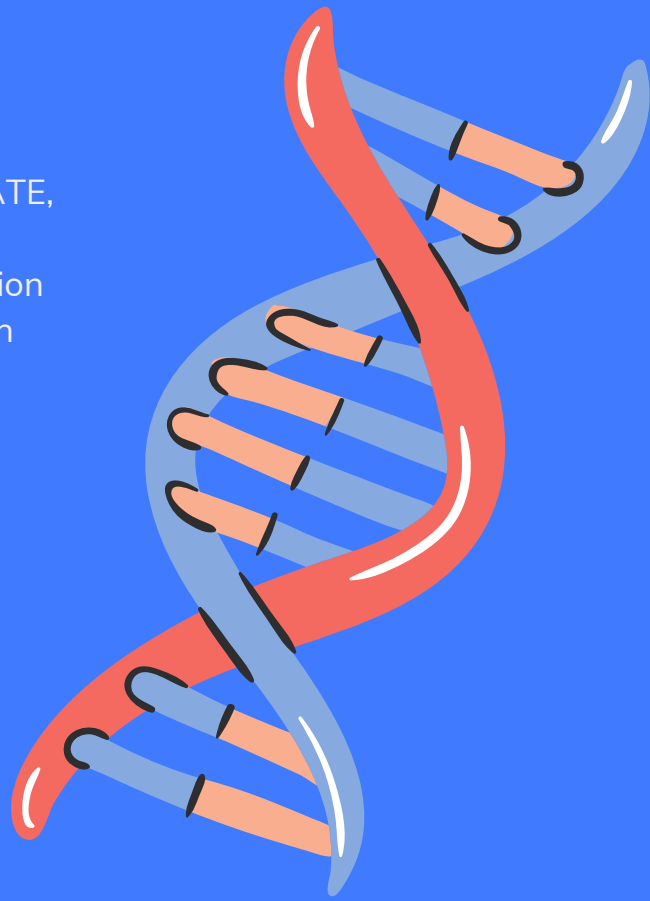
1. The microorganism must be abundant in all organisms suffering from the disease but should not be found in healthy organisms.
2. The microorganism must be isolated from a diseased organism and grown in pure culture.
3. The cultured microorganism should cause disease when introduced into a healthy organism.
4. The microorganism must be re-isolated from the inoculated, diseased experimental host and identified as being identical to the original specific causative agent.

## RIVER'S CRITERIA

RIVER'S CRITERIA is a modification of KOCH'S POSTULATE, proposed after viruses were discovered. It recognises the same criteria as KOCH, the only distinction being that viruses are cultivated inside cells rather than in Petri dishes.

### THE CRITERIA

1. The virus can be isolated from diseased hosts.
2. The virus can be cultivated in host cells.
3. Proof of filterability—the virus can be filtered from a medium that also contained bacteria.
4. The filtered virus will produce a comparable disease when used to infect experimental animals.
5. The virus can be reisolated from the infected experimental animal.
6. A specific immune response to the virus can be detected.



Koch's Postulate and River's criteria are logical and rational steps to take before declaring a global pandemic.

## A VIRUS CANNOT REPLICATE OR REPRODUCE OUTSIDE A LIVING CELL.

A VIRUS THAT IS TRANSMITTING AN INFECTION IS REPLICATING OR REPRODUCING, AND THIS CAN ONLY HAPPEN INSIDE A CELL.

To prove the existence of a novel virus, it makes sense to look for the virus inside a living cell. A virus can only replicate or spread from inside a cell.

Therefore, to prove the existence of a novel virus that is spreading, **you have to do so from an infected human cell, which is the only place to find a replicating virus.**



# THE PUBLISHED STUDY

## A NOVEL CORONAVIRUS FROM PATIENTS WITH PNEUMONIA IN CHINA

<https://www.nejm.org/doi/full/10.1056/nejmoa2001017>

Human cells are harvested from the sputum or saliva of infected people.

The Study starts by injecting infected sputum into a cell from a cancer patient.

### NOTES

**The logical first step should be to harvest infected cells from the sputum of a suspected case and then search for viruses inside the harvested cells because a virus can only replicate inside a living cell.**

**The Study has four main sections -  
SUMMARY, METHODS, RESULTS AND DISCUSSIONS.**

### REFERENCES AND COMMENTS

## SUMMARY

### STUDY

*"A cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan."*

### NOTES

There is no evidence that an epidemiological study proved that the pneumonia was of unknown origin. The only Study cited as evidence of the epidemiological Study done in Wuhan is unavailable online. In addition, there's no proof that the Study tried to rule out the commonest microbial cause of pneumonia – streptococcus and staphylococcus.

<http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989>

<https://www.diagnostictchnology.com.au/products/pathofinder-respifinder-2smart>

### STUDY

*"Human Airway Epithelial cells were used to isolate a novel coronavirus 2019 nCoV."*

### NOTES

The most logical and meaningful process is to isolate the virus from the Human Airway Epithelial cells filtered out from infected sputum. It seems illogical to recreate the infection by injecting contaminated sputum into cells harvested from a cancer patient.

You will soon discover that a novel coronavirus was never isolated. Instead, a computer program sequenced or rearranged over 20,000 pieces of genetic material from a contaminated sample to generate DNA with an 86% match to bat coronavirus. This computer-generated DNA is what is called the COVID virus.

**Consider that Chimpanzees and Bonobos share 99% of human DNA**

<https://www.scientificamerican.com/article/tiny-genetic-differences-between-humans-and-other-primates-pervade-the-genome/>

### STUDY

*"In late December 2019, several local health facilities reported clusters of patients with pneumonia of unknown cause epidemiologically linked to seafood and wet animal wholesale market in Wuhan, Hubei Province, China".*

### NOTES

The link provided to verify the epidemiology study no longer exists.

<http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989>

In the absence of a Study, we cannot verify that other factors that could have caused pneumonia were considered. It is well documented that the earliest cases of COVID did not transmit their infection to close contacts.

## STUDY

"We report the results of this investigation, identifying the source of the pneumonia clusters, and describe a novel coronavirus detected in patients with pneumonia whose specimens were tested by the China CDC at an early stage of the outbreak. We also describe clinical features of pneumonia in two of these patients."

## NOTES

The coronavirus was never detected.

The clinical features of COVID-19 initially described - Fever, Cough, Chest Discomfort, Respiratory Distress, are shared with many other microbial infections, particularly staphylococcus and streptococcus infections.

**Ironically Streptococcus and Staphylococcus were not tested for as a cause of pneumonia.**

# The first case and his family



The first patient in Wuhan was identified with symptoms on December 1, 2019. None of his family members developed fever or any respiratory symptoms.

No epidemiological link was found between the first patient and later cases.

Every country should do everything to follow through on prioritizing, funding, and implementing preparedness interventions.

Huang C et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet. 2020 January 24.

[https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(20\)30183-5/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30183-5/fulltext)

# Chinese Heart Patient



A young woman in Guangzhou, China, with congenital heart disease was hospitalised for a long time without suspicion that she was COVID-19 RNA-positive. By the time she tested positive, 455 people had contacted her, including hospital staff, other patients, and family members. All contacts were traced, and despite 8 having respiratory symptoms, all 455 tested RNA-negative.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7219423/>

# METHOD

## VIRAL DIAGNOSTIC METHODS



## STUDY

"Sputum was collected from 4 patients with pneumonia who had been to the Wuhan Market. Sputum was also collected from 7 patients with pneumonia of known cause from other hospitals".

## NOTES

It is important to note that the Symptoms of the 4 patients suspected of a novel infection were not different from those of the other 7 control patients. There was no clinical reason to suspect a disease of unknown cause.

There is no explanation of what was done with the samples from the control experiment. It was only mentioned in the Study.



## Study

"Nucleic Acid or DNA was extracted from the Samples using a Viral Nucleic Acid Kit from Roche."

## Notes

A fact of biology is that viruses can only replicate (reproduce) in living cells. Therefore, any process for isolating a contagious virus should start from an infected human cell. Nucleic acid should be extracted after infected human cells are filtered out from a sample.

## Study

"Extracted Nucleic Acid was tested for bacteria and Viruses using the RespiFinderSmart22 kit and the Light Cycler 480 real-time PCR system".

## Notes

A fact of biology is that viruses can only replicate (reproduce) in living cells. Therefore, any process for isolating a contagious virus should start from an infected human cell. Nucleic acid should be extracted after infected human cells are filtered out from a sample.

# NOTES



What is very clear from the kit manufacturers is that it only checks for 22 microbes - 18 Bacteria and 4 Viruses. The microbes tested for does not include 2 of the most common cause of pneumonia in the world Streptococcus and Staphylococcus.

## STREPTOCOCCUS AND STAPHYLOCOCCUS ARE THE COMMONEST CAUSE OF PNEUMONIA



<https://pubmed.ncbi.nlm.nih.gov/19368345/>



### STUDY

"High-Throughput Sequencing was used to discover sequences not identified by the means above".

### NOTES

High-Throughput Sequencing uses computer programs to analyse and arrange tiny pieces of DNA until a close match to a known viral DNA is found. It is not an isolation process for viruses.

### STUDY

"Real-time RT-PCR was used to detect specific genomic sequences using primers".

### NOTES

PCR detects only a tiny proportion of a known genomic sequence or DNA. In other words, the genomic sequence of a virus must be known before the PCR can be applied. PCR cannot detect an unknown virus.

In addition, the primers designed by the Study to detect regions specific to the COVID virus also detect hundreds of other microbes.

# LIST OF PRIMERS AND PROBES DESIGNED BY THE STUDY

[https://www.nejm.org/doi/suppl/10.1056/NEJMoa2001017/suppl\\_file/nejmoa2001017\\_appendix.pdf](https://www.nejm.org/doi/suppl/10.1056/NEJMoa2001017/suppl_file/nejmoa2001017_appendix.pdf)

## CHECK THE PRIMERS AND PROBES WITH THE BLAST PROGRAM

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>



### STUDY

### ISOLATION OF THE VIRUS



*"Bronchoalveolar-lavage fluid (Sputum) was collected in a sterile cup containing a virus transport medium".*

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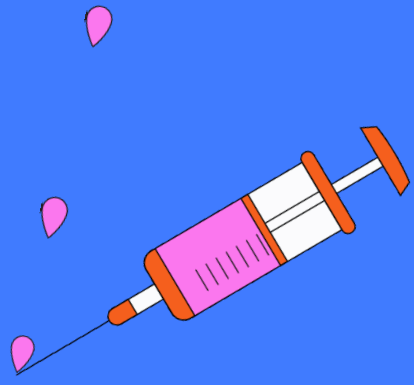
### NOTES

The virus Transport Medium Contains Antibiotics (Gentamicin and Amphotericin) and Serum from Cattle. These antibiotics will destroy living cells in the collected Sample and release a variety of DNA from different sources.

The contaminated Sample will likely contain DNA from Human and Animal Tissue, Bacteria and other microbes.

# VIRUS TRANSPORT MEDIUM

<https://www.copanusa.com/sample-collection-transport-processing/utm-viral-transport/>



## STUDY

"Samples were centrifuged to remove cell debris, and the Supernatant was inoculated on human epithelial cells".

## NOTES

The Supernatant contains DNA from several different microbes, human and animal tissue. It seems irrational to inject the concoction into a cultured cell to prove the existence of a novel virus.

On its own, Centrifugation can be a direct way to isolate viruses from cells. You can read about the process below.

<https://www.beckman.com/resources/reading-material/interviews/fundamentals-of-ultracentrifugal-virus-purification>

## STUDY

"... Cells were incubated at 37 C for 2 hours and washed with phosphate-buffered saline. The process of washing and incubation continues for 48 hours, and the cells are harvested...".

## NOTES

This process will negatively impact the cells capacity to survive. While the Study tries to demonstrate cell death or 'cytopathic effect', there is no control study to show that cell death doesn't occur from the cells' treatment.

## STUDY

"Cells are monitored daily for Cytopathic effects and with RT-PCR to detect viral nucleic acid"...

## NOTES

Cytopathic effects mean cell death. Cells injected with a concoction of DNA from a variety of sources will most likely die. Besides, no control study shows that the chemicals added to clinical samples and the treatment that the cells undergo do not cause a cytopathic effect on their own.

RT-PCR is used to detect a known virus. The PCR probes designed for the Study is not specific, and it identifies over 100 different microbes.

VIDEO DESCRIBING DR STEFAN LANKA'S EXPERIMENT TO PROVE THAT CONTAMINATED SAMPLES ARE NOT REQUIRED TO CAUSE CYTOPATHIC EFFECT



<https://www.bitchute.com/video/Z32sPQZFz99r/>



# TRANSMISSION ELECTRON MICROSCOPY

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## STUDY

"... Supernatant from human airway epithelial cells that showed cytopathic effects are collected inactivated and fixed with 2% paraformaldehyde, 2.5% glutaraldehyde, 1% osmium tetroxide, dehydrated with grade ethanol and embedded with PON812 resin. The stained grids and ultrathin sections were observed under an electron microscope"...

## NOTES

Notice the number of chemicals and the processes that the cells undergo before observation with an electron microscope. During preparation, these chemicals and processes will denature and distort the cells and introduce artefacts that interfere with a clear cell picture.

# VIRAL GENOME SEQUENCING

## STUDY

"Extracted RNA from Sputum was used as a template to clone and sequence the genome".

## NOTES

"The sputum sample used in the Study was not filtered to remove contaminants and isolate infected human cells containing the virus. A virus transport medium that contains antibiotics and bovine serum were added to the mixture before Centrifugation. The resulting Supernatant will contain DNA from cows, humans, bacteria, and other microbes.

## STUDY

"Primers were designed for PCR .... although the cycle threshold value was higher than 34 for detected samples..."

## NOTES

A known fact is that PCR cycles above 20 are meaningless. The Study acknowledges using over 34 PCR cycles to achieve a result.

3-RACE was used to fill in the gaps from Sanger sequencing. Multiple sequence alignment and reference sequences were performed with the MUSCLE program to determine the genomic sequence of 2019 – nCoV

The genomic sequence of COVID was generated with a computer program called MUSCLE.

# RESULTS



## STUDY

### PATIENTS

"3 Patients were admitted with severe pneumonia on December 27 2019, with varying degrees of fever, cough and chest pain".

## NOTES

Note that the symptoms of the patients are not unique. The same symptoms occur in chest infections due to bacteria, fungi and parasites.

## STUDY

A diagnosis of pneumonia was made based on X-rays and CT scans. 2 of the patients recovered, and one died.

## NOTES

A diagnosis of pneumonia is typically made from microbial analysis and not through X-rays and CT scans.

# DETECTION AND ISOLATION OF A NOVEL CORONAVIRUS



## STUDY

"Samples from 3 patients were collected on December 30, 2019. No specific pathogens were detected using the RespiFinderSmart22kit."

## NOTES

The RespiFinderSmart22 kit detects 22 microbes, viruses and bacteria. It does not test for the most common causes of Pneumonia – Streptococcus and Staphylococcus bacteria.

<https://www.diagnostictechnology.com.au/products/pathofinder-respifinder-2smart>

## STUDY

*"RNA extracted was used to clone and sequence a genome using the illumina and nanopore sequencing technology 20,000 Reads were obtained and showed an 86% match with Bat Coronavirus."*



## NOTES

Genomic Sequencing means arranging pieces of DNA and finding the closest match to a known DNA. Finding a close match to something is not the same as identifying it.

## STUDY

*"Positive results were also obtained using real-time RT-PCR assay for the RdRp region; however, this was after 34 cycles."*

## NOTES

Using the PCR test without first Sequencing the virus is fraudulent because genomic sequence must be known before using the PCR technology. Furthermore, a 34 cycle PCR exceeds the recommended limit of 20 cycles, after which the results are no longer valid.

## STUDY

*"Virus Isolation from the clinical specimen was performed with human airway epithelial cells and Vero E6 and Huh-7 cell line".*

*"Infected Human epithelial cells and mock-infected epithelial and COVID infected human airway epithelial cultures are examined with light microscopy daily and with electron microscopy for Cytopathic effects".*

## NOTES

It is illogical that the virus is searched for in a laboratory prepared cell inoculated with infected sputum rather than from an actual infected human cell.

## STUDY

*"Cytopathic effects were observed at 96 hours with human airway epithelial cells and after 6 days for the Vero E6 and Huh 7 cell lines".*

## NOTES

Prof Stefan Lanka, a German virologist, has proven that cytopathic effects are caused by the chemicals used during analysis and can occur in the absence of an infected sample.

# STUDY DISCUSSION



"We report a novel CoV (2019-nCoV) identified in hospitalised patients in Wuhan, China, in December 2019 and January 2020. Evidence for the presence of this virus includes identification in bronchoalveolar-lavage fluid in three patients by whole-genome Sequencing, direct PCR, and culture. We report the isolation of the virus and the initial description of its specific cytopathic effects and morphology".

## NOTES SUMMARY

In reviewing the Study, we make the following observation.

The patients in the Study had no unique symptoms.

The Sample from infected patients (sputum) was not filtered to collect epithelial cells that may contain the virus.

The Extracted DNA from the unfiltered Sample possibly contained DNA from other sources such as bovine serum, human tissue, bacteria and other microbes.

The PCR primers designed for the Study are not unique to COVID-19 and can identify over 100 other microbes.

A computer program produced the genomic sequence that describes the novel coronavirus.

## STUDY

**"Further development of accurate and rapid methods to identify unknown respiratory pathogens is still needed. Based on the analysis of three complete genomes obtained in this Study, we designed several specific and sensitive assays... The primer sets and standard operating procedures have been shared with the World Health Organization".**

# NOTES

The primers that were designed can identify over 100 different microbes when studies with BLAST. In other words, the PCR scan that uses these primers are testing for over 100 different microbes.

# STUDY

***Although our Study does not fulfil Koch's postulates, our analyses provide evidence implicating 2019-nCoV in the Wuhan outbreak.***

**While it has been mentioned that KOCH's Postulate is outdated, we cannot help but observe that the scientists referred to it.  
a heading**



<https://community.freedomvillage.me/signup/HwYYMC>

email: [logictree@protonmail.com](mailto:logictree@protonmail.com)