



CORONAVIRUS SARS-CoV-2

Science 101

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"Today virology is in danger of losing its soul, since viruses now show a strong tendency to become sequences ..."

~ Prof André Lwoff, Microbiologist,
Nobel Laureate in Medicine

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QUICK TIP

Researchers simply removed the unwanted sequences from the sample, assembled what was left, and filled in the gaps.

It isn't isolation.

THE "ISOLATION" STUDY OF THE SARS-COV-2 VIRUS: HOW WAS MADE?

CORONAVIRUS or SARS-CoV-2 is a mix of human and computer generated sequences and it was never isolated.

<https://pubmed.ncbi.nlm.nih.gov/32004165/>

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THE "ISOLATION" STUDY OF THE SARS-COV-2 VIRUS: HOW WAS MADE?

Researchers overlooked some matches with the **HERV-H_Chr_2q24 LTR repeat region of the Homo sapiens endogenous virus**. They should be more careful the next time.

```
XZESKJ6B013-Alignment - Notepad
File Edit Format View Help
Query: Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome Query ID: MN908947.3 Length: 29983

>Homo sapiens endogenous virus HERV-H_Chr_2q24 LTR repeat region
Sequence ID: MT992309.1 Length: 670
Range 1: 600 to 670

Score:132 bits(71), Expect:4e-26,
Identities:71/71(100%), Gaps:0/71(0%), Strand: Plus/Plus

Query 1540 ACGTGCTAGCGCTAACATAGGTTGTAACCATACAGGTGTTGGAGAAGGTTCCGAAGG 1599
          |||
Sbjct 600  ACGTGCTAGCGCTAACATAGGTTGTAACCATACAGGTGTTGGAGAAGGTTCCGAAGG 659

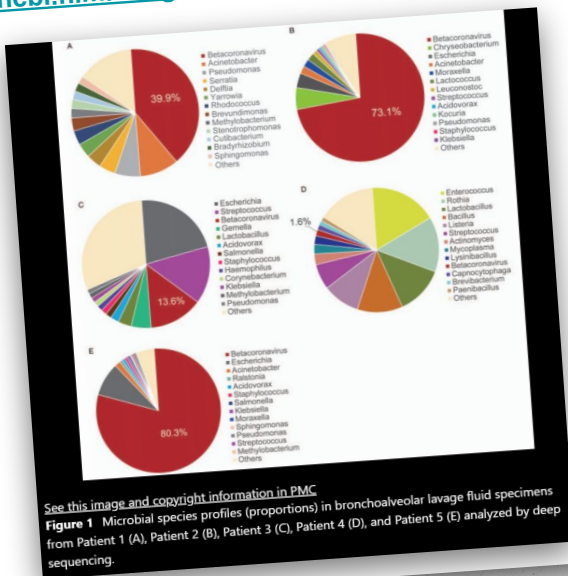
Query 1600 TCTTAATGACA 1610
          |||
Sbjct 660  TCTTAATGACA 670
```

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THE "ISOLATION" STUDY OF THE SARS-COV-2 VIRUS: Was there anything else in the sample?

There were numerous other pathogens in the sample that could cause the same symptoms. So, how is it accepted as a new disease?

<https://pubmed.ncbi.nlm.nih.gov/32004165/#&gid=article-figures&pid=figure-1-uid-0>



See this image and copyright information in PMC
Figure 1 Microbial species profiles (proportions) in bronchoalveolar lavage fluid specimens from Patient 1 (A), Patient 2 (B), Patient 3 (C), Patient 4 (D), and Patient 5 (E) analyzed by deep sequencing.

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QUICK TIP

COVID-19 patients are classified as such solely on the basis of a flawed test. No other factors are taken into account. When patients test positive for other pathogens, the results are ignored.

Fun Fact

COVID symptoms are nearly any symptoms.

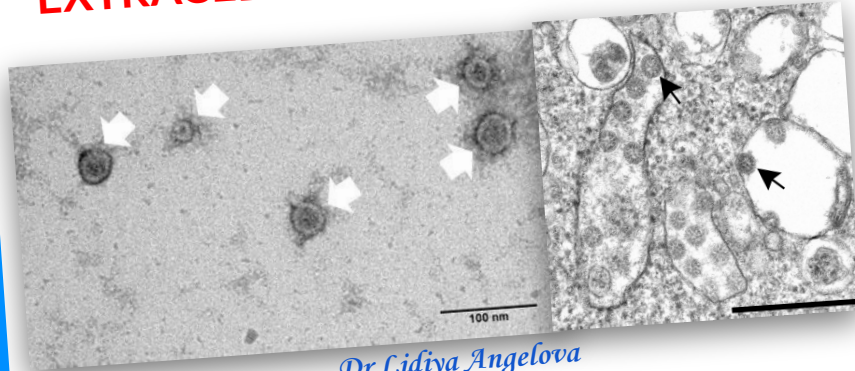
YOU'RE TOLD IT'S A PICTURE OF SARS-COV-2, BUT IT'S ACTUALLY AN EXTRACELLULAR VESICLE!

QUICK TIP

Can you tell which image contains viruses and which contains extracellular vesicles?

Fun fact

A lot of "viruses" look like it.



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SCIENCE FACT

>Extracellular vesicles (EVs) are lipid bilayer-enclosed entities containing proteins and nucleic acids that mediate intercellular communication, in both physiological and pathological conditions. EVs resemble enveloped viruses in both structural and functional aspects. In full analogy with viral biogenesis, some of these vesicles are generated inside cells and, once released into the extracellular milieu, are called "exosomes".<

<https://pubmed.ncbi.nlm.nih.gov/32456011/>

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The closest SARS-CoV “virus” has been “isolated” in the same way. Researchers simply removed the unwanted sequences, assembled what was left, and filled in the gaps. It isn't isolation.
<https://pubmed.ncbi.nlm.nih.gov/12690091/>

QUICK TIP

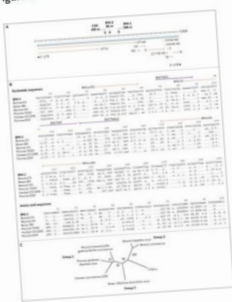
Christian Drosten, the author of the bogus PCR test, is also the author of the SARS-CoV sequence.

What a strange coincidence!!!

Article Figures/Media

About 20 distinct DNA fragments were obtained and sequenced. The resulting sequences were subjected to BLAST data-base searches. Most of the fragments matched human chromosome sequences, indicating that genetic material of the cultured cells had been amplified (Vero cells are derived from monkeys). Three of the fragments did not match any nucleotide sequence in the data base. However, when a translated BLAST search was performed (comparison of the amino acid translation in all six possible reading frames with the data base), these fragments showed homology to coronavirus amino acid sequences, indicating that a coronavirus had been isolated. Two of the fragments were 300 nucleotides in length and identical in sequence, and the third fragment was 90 nucleotides in length (sequences BNI-1 and BNI-2, respectively, as reported on the Web site of the WHO network on March 25) (Figure 1A). Detailed sequence analysis revealed that both fragments were located in the open reading frame 1b of coronaviruses and did not overlap with a 400-nucleotide coronavirus fragment identified by colleagues at the Centers for Disease Control and Prevention (CDC) (sequence CDC, reported on the Web site of the WHO network on March 24) (Figure 1A).

Figure 1.



Genetic Characterization of the Novel Coronavirus.

QUICK TIP

The research confirms the presence of bacteria that cause pneumonia.

Why, then, is it claimed that it is caused by a new virus - a "virus" made up of random sequences?!

OTHER PATHOGENS CAUSING THE SAME SYMPTOMS WERE FOUND IN THE FIRST SARS-COV SAMPLE AS WELL.

"Paramyxovirus-like particles were seen in throat swabs and sputum samples from the index patient by electron microscopy. Electron microscopy of cells in a bronchoalveolar-lavage specimen from the index patient showed a severe intracellular bacterial infection, and the bronchoalveolar-lavage cells reacted in immunofluorescence analyses with a monoclonal antibody directed against *C. pneumoniae*."

<https://pubmed.ncbi.nlm.nih.gov/12690091>

gures/Media

Paramyxovirus-like particles were seen in throat swabs and sputum samples from the index patient by electron microscopy. The particles were scarce. However, several PCR tests specific for virus species of the family Paramyxoviridae were negative (including tests for human metapneumovirus), as were PCR assays based on primers designed to react broadly with all members of that family.

C. pneumoniae was not detected by PCR or antigen ELISA in sputum of the index patient from day 9. However, on day 11, electron microscopy of cells in a bronchoalveolar-lavage specimen from the index patient showed a severe intracellular bacterial infection, and the bronchoalveolar-lavage cells reacted in immunofluorescence analyses with a monoclonal antibody directed against *C. pneumoniae*. Consistent with this finding, there was an increase by a factor of four in the *C. pneumoniae* IgA titer in the index patient between day 10 and day 13.

There's no doubt about the fact that SARS-CoV-2 is a sequence. However, it raises additional questions about testing, cross-immunity, sequencing, data, death rate, science studies validity and so on. I'll make separate flashcards files for each. Follow my blog to ensure you don't miss anything, but keep in mind that explaining something so complex in simple terms takes a lot of effort. Please visit my website <https://genuineprospect.com/> and make a donation to help support my work. Nobody else does what I do.

REFERENCES

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<https://pubmed.ncbi.nlm.nih.gov/12690091/>