

What Does a Virologist Know About SARS-COV2 as of March 21, 2021?

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by [Dr. Tom Cowan](#)

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A virus is a particle wrapped in a protein coating containing genetic material, either RNA or DNA. A virus is considered to be a physical thing.

How do virologists find a new virus, in this case, SARS-CoV-2?

Lay people and most medical providers assume virologists take fluid samples from the nose or lungs of many sick people with the same symptoms and examine them under a powerful microscope. They assume that the virologists actually see a virus that they've never seen before in these samples.

How do they know that virus causes the disease in question, in this case, Covid-19?

Most people – again, including medical providers – would assume that virologists prove causation by exposing nothing but the pure virus to healthy animals in the normal way that viruses supposedly spread.

In fact, here's what they do, and here's what they did again with SARS-CoV-2. Virologists took bronchoscopy-guided lung samples (BAL fluid) from people with pneumonia from an unknown cause. They "washed" and filtered this fluid to remove large

cellular debris, fungus and bacteria. Here's where people's assumptions of what happens and what actually happens diverge: They never examined this fluid under an electron microscope (the only type that can visualize something as small as a virus). In fact, virologists always skip examining this fluid under a microscope.

They then took this unpurified soluble fluid from the person with pneumonia of unknown origin and inoculated it onto tissue taken from an animal or human source. But first they added a variety of other fluids, including amniotic fluid, horse serum, bovine fetal serum, all of which are themselves rich sources of proteins and genetic material. They do this because the "virus" they're looking for won't grow otherwise. In addition, the nutrients supporting the growth of the tissue in the culture were withdrawn. In other words, the tissue was starved. Antibiotics, such as gentamicin and amphotericin, were added to the culture, both of which are known to be toxic to kidney tissue.

They then measured the ability of this unpurified mixture to lyse (or kill) the animal or human tissue in the culture. To date, the **only** tissue that was killed (called a cytopathic effect) came from Vero cells, which are taken from monkey kidneys. When the cultures contained only human or other animal-sourced tissues, little to no cytopathic effects were seen.¹

The Vero cell culture did, indeed, break down into millions of different sized and shaped particles. The virologists took an electron-microscope picture of it, saw particles they said were budding out from the Vero cells, and they called those particles isolated SARS-Cov-2.

How do they know those particles in the culture are the culprits?

Here's the problem: In reality, no accepted scientific

protocol can distinguish a particle that emerges as a result of the breakdown of Vero cells or the other sources of genetic material added to the culture from a “virus” coming from the outside.²

It gets worse. As of today, no particle with the characteristics or appearance of SAR-CoV-2 (as seen in electron micrographs) has been found in the results of this “culture” procedure, until a protein-digesting enzyme called trypsin is added to the mix.³ This enzyme digests the outer protein coating of these particles, resulting in the characteristic “spike” protein appearance of the alleged SARS-CoV-2.

The next step for virologists is to do a genetic analysis of the results of this “viral culture.” Virologists have NOT and can NOT find any complete sequence in that culture that would represent the entire genome of any known virus. Rather, the genome sequencing is performed inside a computer, which is called in silico genome.

In this culture, they find billions of various sized pieces of genetic material. They chop these pieces into smaller bits, and some are discarded if they are alleged to originate from human or other microbial origin. These small sequences are “aligned” inside the computer, meaning, they are reconstructed into a long genome that would be the size of a coronavirus genome, which has been previously published.⁴

In other words, a complete genome is sequenced based on the template of other such in silico genomes, thereby guaranteeing that the computer will “find” SARS-CoV-2 in this new sample. Inevitably, there is some divergence in the new genome sequence as compared to the template. This is called a variant. At no time has the virologist found the complete sequence of either of SARS-CoV-2 or the variant in the BAL fluid. It exists only in the computer.

The only reasonable conclusion that anyone examining this process would come to is that no evidence exists that a real particle in the real world that causes what they're calling Covid-19 has been found.

Sources:

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2 Gianessi, et al Viruses 2020 May; 12(5): 571. The Role of Extracellular Vesicles as Allies of HIV, HCV, and SARS Viruses

3 Caly et al, Med J Aust 2020, June; 212 (10) p. 459-462 PMID 3223727. Isolation and Rapid sharing of the 2019 novel coronavirus (SARS-CoV-2) from the first patient diagnosed with Covid-19 in Australia.

4 Ibid

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