

# Why HART uses the virus model

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## *Arguments against “the virus doesn’t exist”*

*Also available on Substack ([https://open.substack.com/pub/hartuk/p/virus-model?r=2cly45&utm\\_campaign=post&utm\\_medium=web](https://open.substack.com/pub/hartuk/p/virus-model?r=2cly45&utm_campaign=post&utm_medium=web)) – Come and join the conversation with open comments*

There are two separate debates about interpretations of covid.

One is that there was no “novel virus”. The key point being about the **novelty**. This was used by governments to suggest a lack of prior immunity, with a number of far-reaching implications, so it seems justifiable to “hold their feet to the fire” and assess novelty on this basis.

The evidence, and previous pieces by HART (<https://www.hartgroup.org/a-possibly-unpopular-null-hypothesis/>), support a case that there was nothing exceptional about this virus in terms of the population’s immune defences compared with any previous respiratory virus. The observed excess mortality is therefore hard to explain, given the low mortality rate SARS-CoV-2 is known to have. This is particularly true among young people in New York City who reportedly died in the thousands in spring 2020, despite not dying elsewhere. Not everyone may agree with that argument — we do not all agree with each other on everything.

The second claim is that there was no virus at all and it is that claim that is addressed here.

In HART we do not believe that science can yet fully explain how and why viruses cause illness only in some people and at some times, nor details of how they spread, but to our knowledge there is no-one in HART who thinks that a virus or viruses (whether or not novel) are irrelevant to some of the respiratory illness experienced in 2020.

Why is that?

There are numerous reasons when looking at the evidence from every angle. Ultimately, in science there are always strands of evidence that cannot be explained. Scientists form a model that best explains the majority of the evidence. When new evidence emerges the model that best explains the majority can change. In the meantime, the best fit model is how the world is best understood. How does that relate to the virus model?

First of all, given that all life is based on a system of encoded replication, it would be extraordinary for there not to be viruses that can hijack that system. They have been studied in plants and animals as well as humans.

What about this particular virus? There are a series of observations that need explaining as follows:

1. **An environmental exposure predicted an illness.** Although a significant proportion of infections were not traceable to an outbreak, the majority were. Groups of people became ill with similar symptoms after having shared the same environment.
2. **A unique RNA sequence was detected in these people.** While PCR testing is far from perfect (especially the way it was rolled out and used as a sole indicator, overriding clinical judgement) the sequence being tested for is lengthy and specific. Yes, there were false positive test results. However, the fact remains that the likelihood of testing positive was orders of magnitude higher in people with the symptoms above than in the asymptomatic. There was therefore an association to particular sequences of RNA and these set of symptoms.
3. **The protein this RNA codes for was detected in these people.** The lateral flow tests that could be done at home detected the protein that the specific RNA sequence codes for.
4. **Crystallography** shows the shape of the spike protein and its exceptional affinity for the human ACE2 receptor (<https://www.nature.com/articles/s41586-020-2180-5>).
5. **Antibodies which reacted to those proteins were produced.** These same sick people went on to develop antibodies to the proteins produced by the RNA sequence.
6. **Lab grown virus.** Material thought to contain virus has been collected from patients and replicated in cell culture. The degree of cell damage done was in proportion (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7314198/>) to how strong the PCR test result was. Lab grown virus was also used to infect healthy young people, half of whom developed detectable virus after 2 days and symptoms of covid after 2 to 4 days (<https://www.nature.com/articles/s41591-022-01780-9>).
7. **Whole genome sequencing suggests viral evolution.** A huge amount of genomic (<https://nextstrain.org/sars-cov-2/>) sequencing has been undertaken, at great expense. From that family trees can be constructed demonstrating viral evolution over time across the world.
8. **Finally, There was an illness which some people regard as both viral in nature, and also characteristic.** This is of course subjective and opinions differ on this. Some claim it is unclear how different this actually was from the range of respiratory viral illnesses experienced before. It is possible that the unusual nature can be explained by observation and confirmation bias in an atmosphere of huge focus on this one illness – under other circumstances it might have been referred to only as a ‘some weird bug’ or a ‘nasty flu’.

Alternatively, doctors claim to have recognised particular symptoms and signs such as high clotting propensity and low white cell counts in the blood. However, these were not unique e.g. lymphopenia was seen in H1N1 influenza (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7102863/#:~:text=Lymphopenia%20has%20been%20observed%20in,A%2FH1N1%20is%20scarcely%20reported.>). Clinicians have also claimed they could diagnose it without any testing. Patients themselves seemed to be good at knowing whether they had had it because they, or someone they had been infected by, had characteristic symptoms such as loss of taste or smell, tinnitus or simply an exceptionally long duration of sickness and cough.

One notable observation in this regard is that although it is now accepted that whatever SARS-CoV-2 is, it had become widespread across many continents well before spring 2020, yet no clusters of unusual illness were reported or published **at the time** (as well as there being no excess deaths prior to the declaration of “the emergency”).

It should be emphasised that we are not here claiming that the above tells us anything about the impact of the virus on health or mortality — only that it existed.

The virus model explains all of the above in a way that no other proposed model can (yet).

There are two pieces of evidence on which the “no virus” proponents seem to place a lot of weight. The first is that, unlike say measles and polio, the SARS-CoV-2 virus does not replicate in cells, filling them with virus, before causing them to explode, releasing the particles. Instead, SARS-CoV-2 virus particles are claimed to bud from the cell surface one at a time. The same claim is made for influenza and HIV. It is true that there might therefore be interesting differences between these types of viruses worth exploring, but the umbrella term virus is still useful given their other similarities.

The second, is the fact that there has never been a pure isolate of SARS-CoV-2 virus (that means a solution containing only virus particles with no cells). This could be because no-one has tried hard enough to carry out this work. But let’s assume it is because it is not possible to isolate this virus. What would that mean? It would mean that there is something oversimplified about the explanation given for how viruses are formed and transmitted from person to person which needs more study. It is not enough to discount all the other evidence that the virus model is the best fit to explain this illness.

That does not mean that some aspects of the virus model might not be oversimplifications. For example, the idea that everyone is susceptible to viral attack is not supported by real world evidence. Host factors clearly have a major role to play in susceptibility. That knowledge can (and hopefully will) be adopted into the viral model of disease, adapting it to better fit the world.

Revolutions do happen in science, where an entire paradigm is overturned and a new model used to explain the world. Einstein’s work on relativity was revolutionary and expanded upon classical Newtonian mechanics (which is a special case where speeds are substantially less than the speed of light). However, Newton’s work is still used in all sorts of applications because its simplicity is a useful way to understand the world around us (and because humans do not tend to move around at speeds approaching the speed of light!). Perhaps we can learn something from the wave/particle duality of light. It is possible to disprove that light is a wave and to disprove it is made up of particles: both models are useful to understand the properties of light, but neither adequately explains all observations.

Navigating the terrain and germ theories of disease requires distinguishing between nuanced and extreme perspectives and taking on board the notion that uncompromising adherence to either of them is problematic. Commercial interests further complicate this landscape, with the pharmaceutical industry seemingly favouring germ theory for its potential to boost drug sales. Meanwhile, promoting holistic health approaches often faces scepticism, perceived as ‘alternative quackery’. Rather than take sides on a debate which has often lost nuance, it is better to keep gathering evidence to see which model (or models) provide the best explanation for how the world works.

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