Dr. Tom Cowan: Lab Created Viruses? Gain of Function Research? Bio Labs? – Smoking Gun or Bad Science?

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Truth Comes to Light editor's notes:

Below you will find a video presentation by Dr. Tom Cowan. The questions Dr. Cowan raises, the facts he presents, and the clarity he brings to the discussion of "viruses" and the field of virology are essential to our global conversation and quest to understand the truth. Truth Comes to Light has provided a basic transcript and added links to references for added clarity.

Over the past few years, we have shared many articles on this site related to this inquiry into the truth about "viruses" and the whole field of virology, including information on terrain theory vs germ theory. Find links here: Viruses, Vaccines & the History of Modern Medicine. At the end of this post you will find a selected list of related articles.

A few quotes from Dr. Cowan's video:

> *"Is there actually a SARS-CoV-2 virus? And, if there is, what is the genome? And how was it found?"*

> *"They never found a genome of this alleged virus. And so there is no possible way they could say that the Moderna patent was found in this virus. Because the virus simply doesn't exist.*

> *“Therefore, any attempt to say that this was a lab-created, engineered virus is simply anti-scientific because there is no genome that was actually found that it could have been made into.”*
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> *“So we have this published genome, fraudulent as it is, by a bunch of Chinese virologists. Right? They come up with this fraudulent, irrational genome. And, lo and behold, it matches a patent taken out by a company called Moderna in 2016.*
>
> *“So I ask myself how did they do that?”*
>
> *“What in the heck are these guys doing in these labs? What is gain of function research?”*
>
> *“Do we really know if mRNA is in these vaccines?*
>
> *“Where is the paper? Where is the evidence that there actually is mRNA in these injections?”*

Lab Created Viruses: Smoking Gun or Bad Science?

video presentation by **Dr. Tom Cowan**
March 25, 2022

Connect with Dr. Tom Cowan

Transcript provided by Truth Comes to Light:

Dr. Tom Cowan:

Okay, so before I get into talking about the question that so many people keep asking me: What about gain of function, lab-created viruses, bio labs now allegedly in the Ukraine?

So what is the science behind that?

So we'll get into that in a minute. And before that I have a very short, little clip to play.

So that clip pretty much sums it up. That was from our friend Dr. Sam Bailey and our other good friend Stefan Lanka.

So on that note, the reason I wanted to talk about this subject is there was a recent paper that was put out by Dr. Mercola…

The title is 'Moderna Patented Key COVID Spike Protein Sequence in 2016 – A recent study claims to have discovered something that matches a modified mRNA sequence by Moderna in 2016' by author Dr. Joseph Mercola.

[…]

So let's just read the first couple paragraphs there. So this is a summary:

> "A study published February 21, 2022, (so very recently) in Frontiers in Virology claims to have discovered that a sequence of the virus' spike protein is a 100% match to a modified messenger RNA (mRNA) sequence patented by Moderna in 2016.
>
> The genetic sequence patented by Moderna is part of a human DNA repair gene called MSH3. This patented sequence is found in SARS-CoV-2's furin cleavage site in the spike protein – the part that gives the virus such easy access into human cells.
>
> According to Moderna's patent application, the gene sequence was modified "for the production of oncology-related proteins and peptides," ostensibly for use in cancer research.

> According to the researchers, the chance that SARS-CoV-2 would have randomly acquired this furin cleavage site through natural evolution is 1 in 3 trillion."

Okay, so why is this important? So obviously, there's been a lot of attention in the political sphere and in the anti-vax community. There have been movies written about this.

There are many lectures, many prominent people in the "freedom" or "anti-vax" community who are investigating these patents, and saying that these patents – and as Dr. Mercola said, this study in Frontiers in Virology is literally the smoking gun proving that Moderna patented a sequence, which ended up in SARS-CoV-2, "the virus", and the only way it could have gotten there is, not through natural evolution (that is a one in three trillion chance) but if it was introduced into the virus by some laboratory technique.

This theory is crucial to our understanding, not only of whether there were crimes committed, but the whole theory of virology and gain-of-function research and all that.

So, obviously, and this should go without saying, that the most important part of this is: Is there actually a SARS-CoV-2 virus? And, if there is, what is the genome? And how was it found?

The rest of the article goes on to talk about what we know about this MSH3 sequence and the protein that it allegedly codes for.

But I want to emphasize again and again and again – the whole point of this is: This sequence which was patented by Moderna in 2016 is identical to the sequence found in SARS-CoV-2.

That is the point.

If we can demonstrate that there is no SARS-CoV-2 and this is not the genome of this alleged virus, then none of the rest of

this has any validity or is of any use at all.

It's all just a sort of smokescreen or a way to throw us off the track about finding out what really is going on.

I cannot emphasize how important this is.

So for the next few minutes we're going to actually look at how the authors of the article in Frontiers of Virology – what were they claiming was the SARS-CoV-2 genome?

What were they claiming was the evidence that there is a SARS-CoV-2 virus that they could then compare the patent to?

Again, if there's no virus and there's no genome then they can't possibly have put this sequence into a virus or a genome. And it can't possibly be the thing that's affecting the world.

So, now let's be clear about the next step. There is no mention in this story by Dr. Mercola of how the Frontiers in Virology authors found the genome or found the virus.

[…]

In other words, there is no information in here of how Dr. Mercola actually knows there's a SARS-CoV-2 genome.

But the authors of the Frontiers in Virology paper said that they were comparing the sequence, the mRNA sequence patented by Moderna in 2016, to the genome found in our old friend paper by Chinese virologist Fan Wu.

So it isn't that we picked this paper by random. It isn't that I picked this paper to investigate how they found the genome or what their evidence for the virus was. This is the paper that the authors of the Frontiers in Virology use to compare the Moderna patent to.

So we're using their information and this is their evidence,

their proof that the virus exists.

So, let's look then at that paper and see what they found.

So this is about: Did the paper by Fan Wu prove that the virus existed – the SARS-CoV-2 virus exists – and that this is the genome of the virus?

Again, in order to say that the patented sequence matches 100% to the genome of the virus, obviously, obviously, you have to know that this is actually a virus.

So, this is an old friend, we've been through this many times, but let's see what they say.

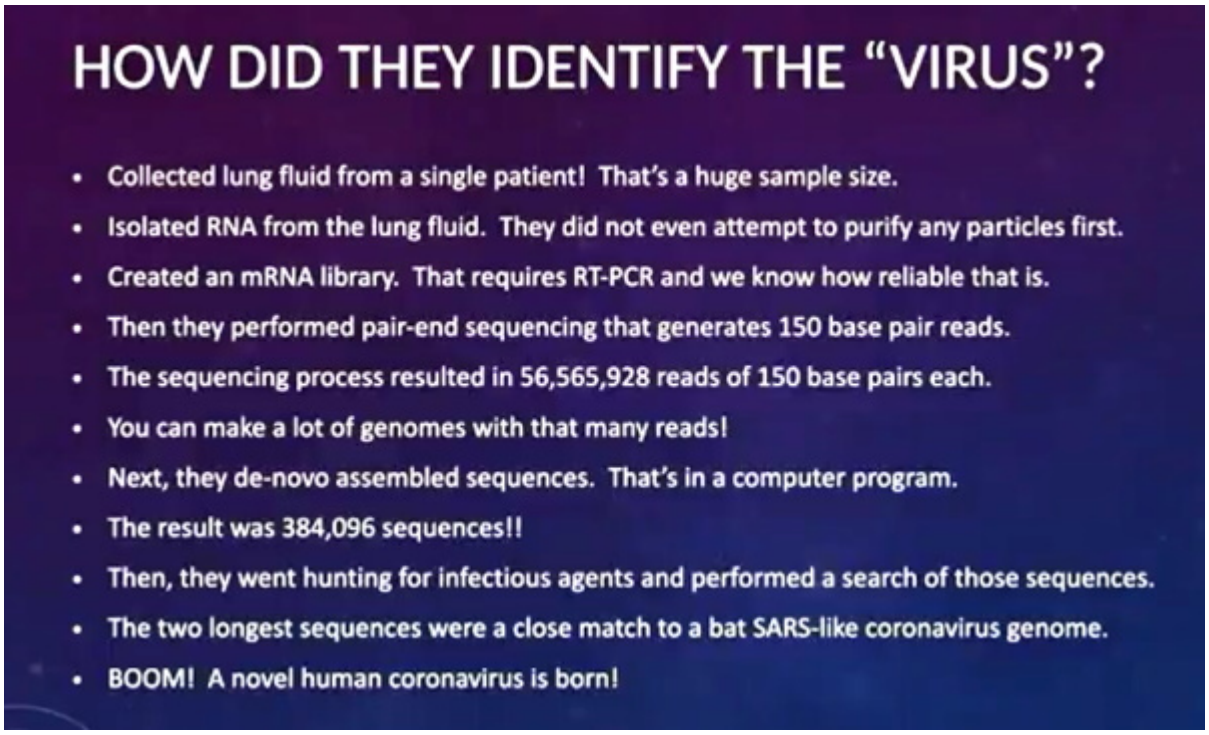
So here is the paper, published in the prestigious journal, I believe, Nature – February 3, 2020.

"A new coronavirus associated with human respiratory disease in China". The lead author, his name Fan Wu.

So this is the paper, again, that was cited by the authors of Frontiers in Virology paper that is used as the reference genome.

So how did they do it?

So first we have a summary.



So how did they identify the "virus"? So I'm gonna run down the steps that they used and then we will show the clips, the actual wording from the paper, so that you know that this is actually the facts.

Okay, so we're looking to find a virus and then find the genome of that virus – a virus that had never been found before.

So first thing they take lung fluid from one person. That's a huge sample size (that's a little tongue-in-cheek). That's obviously just one person. That is a kind of ridiculous experiment to find a new virus.

Then they isolated the RNA, which is a genetic material, from the fluid in that person's lung. They did not attempt to purify any particles that they could say you were a virus. They did not do any pictures of any virus. They did not do any maceration, filtration, ultracentrifugation to see if they had any such particles. None of that.

They took RNA from the lung fluid, of which we have many possible sources. We have bacterial sources, fungal sources,

human sources, possibly viral sources, exosome sources, multivesicular body sources – many sources of RNA. We have no idea the source of that RNA.

Then they create what's called an mRNA library, which is a catalog of all of the RNA pieces that are in that lung fluid.

This requires that they amplify these pieces of RNA with the process called RT-PCR. And, as we have demonstrated over and over again. and is completely substantiated in the literature, doing PCR amplification of RNA cycles inevitably creates new sequences of RNA which weren't there in the original sample.

In some cases, if you do enough amplification cycles – up to even 80% of the sequences – after 45 cycles are made de novo, or anew, by the actual PCR process itself.

So now we have yet another source of our RNA. Not only do we have potential viruses, exosomes, multivesicular bodies, apoptotic bodies, human lung tissue, human epithelial lung tissue…, fungal RNA, bacterial RNA – we also have new pieces of RNA generated by the test itself.

Then they performed pair and sequencing that generates 150 base pair reads. That means they matched the sequence by pairing the ends. And you end up with sequences that are basically 150 base pairs long. That's a fairly small amount. And this results in 56.5 million of these 150 base pair sequences known as reads.

So to be clear, they take this mass, not knowing any idea the origin of these mRNA, they chopped them up into sequences that are 150 base pairs (that's fairly short) long by pairing the ends. They have 56.5 million of these reads. And then they start doing what's called de novo assemble.

So there is no sequencing here. There is assembly. And, as it says, you can make a lot of genomes with that many reads.

So they put these 56 million, 150 base pair, reads in aa assembly computer program and… they actually put it in two different computer programs. And one of the computer programs generated 384,000 different sequences. The other one generated over a million sequences.

So now these sequences – all 384,000 of them – are meant to be the possible genomes of this virus. For some reason, they threw away the program that made over a million of these sequences and said the one that made 384,000 – I think that was Megahit – one of those must be the right sequence, the actual sequence of the virus.

Just to be clear, at no point did they ever find a particle. At no point did they purify or isolate a particle.

At no point did they find in any particle… an entire string of RNA, which they then sequenced one by one to find out the sequence of the genetic material of this particle.

None of that was done. All they did was chop up RNA from many different possible sources, put that in a computer program, generate 384,000 and a million in another, and then they went hunting for infectious agents and performed a search of those sequences.

The two longest sequences were a close match to a bat SARS-like coronavirus genome, found 15 years ago or so, that was made in exactly the same way – never having isolated or purified a particle, never having found an intact genome, never having sequenced the genome.

They just did the same sort of assembly, no sequencing of RNA from God knows where. And, this one, the longest one was a 89% match to the previous SARS coronavirus that they did in the same way.

And, as we say: Boom! There is the new novel human coronavirus – even though, as we've said over and over again, humans and

chimpanzees are about a 96% match. So to say it was an 89% match is essentially like saying there's no way this could have been anywhere similar to the previous bat SARS-like coronavirus.

In other words, they never found a virus. They never found a genome of this alleged virus. And so there is no possible way they could say that the Moderna patent was found in this virus. Because the virus simply doesn't exist.

Therefore, any attempt to say that this was a lab-created, engineered virus is simply anti-scientific because there is no genome that was actually found that it could have been made into.

And that are simply the facts.

Now, I just want to say I'm going to read from a pre-publication article from the Lancet Respiratory magazine.

The title is Exosomes in False-Positive Covid-19 PCR tests: non-specificity of SARS-CoV-2 RNA in Vivo Detection Explains Artificial Post-Pandemic Peaks.

This is a manuscript draft and I don't know when it will be published.

When I read this, just remember that all these articles that go into The Lancet have to pay homage to the virus god. But I will explain what they mean here.

So this is the interpretation of the entire article. I won't go through their methods.

> "The RNA code counted in PCR tests, previously attributed to SARS-CoV-2, belongs instead to a respiratory-virus-induced immune system response by human cells that liberate exosomes, and that vitiate PCR test results. PCR tests have zero specificity in vivo due to the exosome RNA."

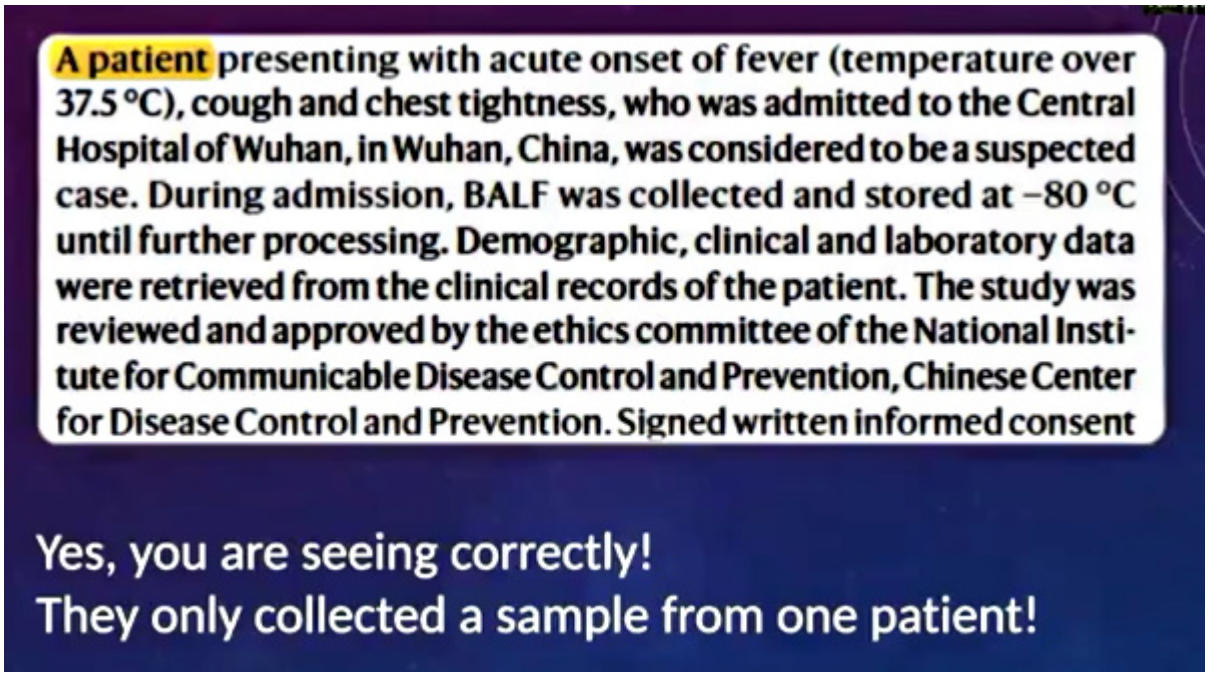
[…]

And they go on in this article, just as we're saying – the reality is all of these RNA sequences, all of these reads which were assembled into a viral genome, actually when you do careful analysis, come from human epithelial lung cells.

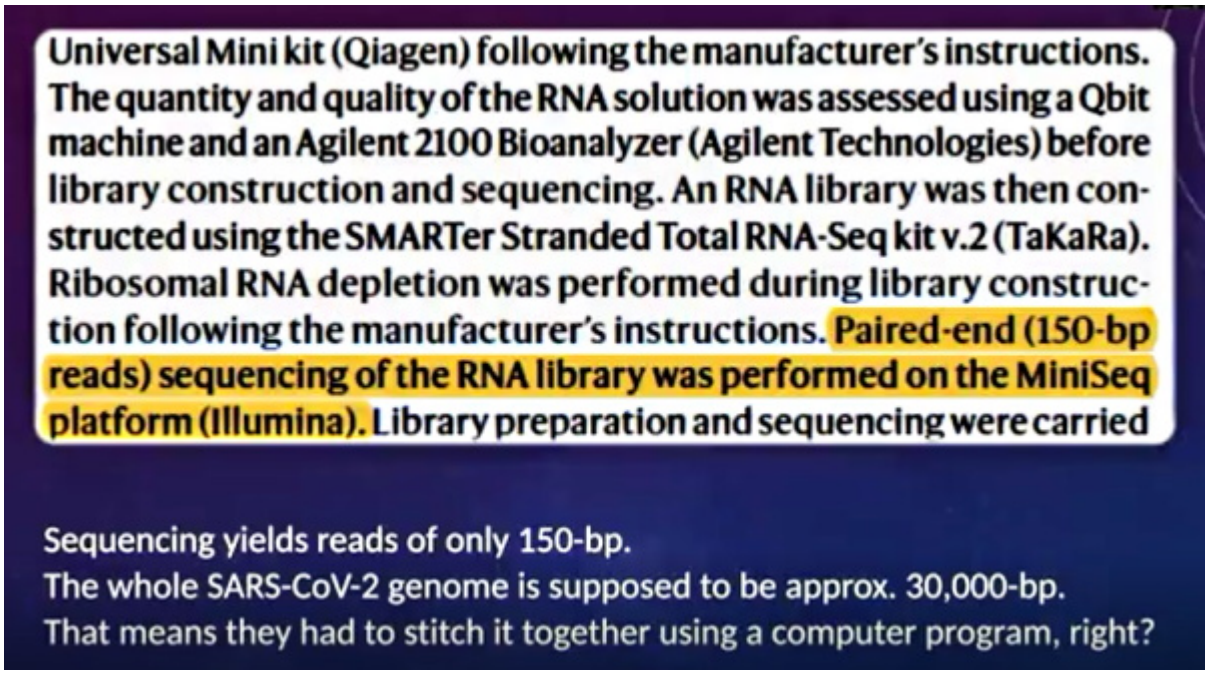
In other words, just as we've been saying all along, these are not viruses. These are breakdown products of our own tissue. And the misconception in calling them a virus needs to stop.

And this idea that they put this patented sequence into a virus can't possibly be true because, simply, there is no virus.

And all the rest of the article is for not – because nobody put a RNA sequence, patented or otherwise, into a virus.

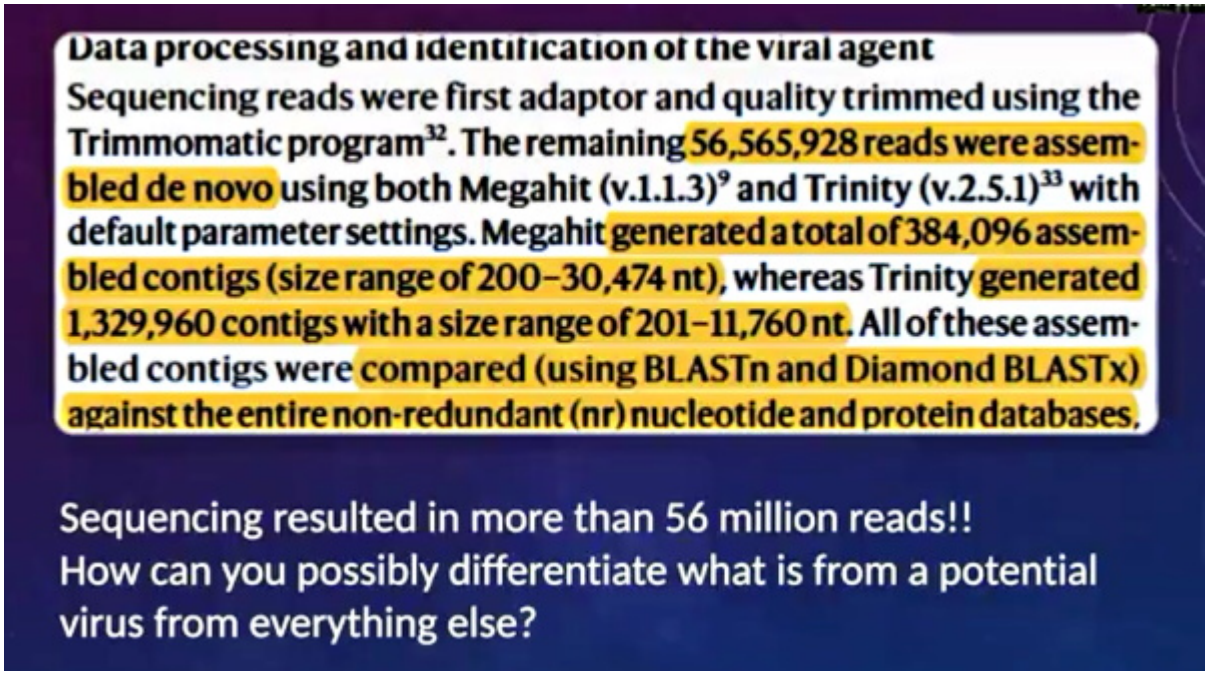


Now just to show you that we got this from the article – so here is the one patient presenting with cough, etc. So that's the evidence that we were correct about the one patient.



Here is the evidence that the paired and 150 base pair reads sequencing of the RNA library was performed on this computer platform. So the sequencing yields reads of only 150 base pairs. The whole SARS-CoV-2 genome is supposed to be 30,000.

That means they had to stitch it together using a computer program. This was an assembled genome, out of little bits from God knows where.

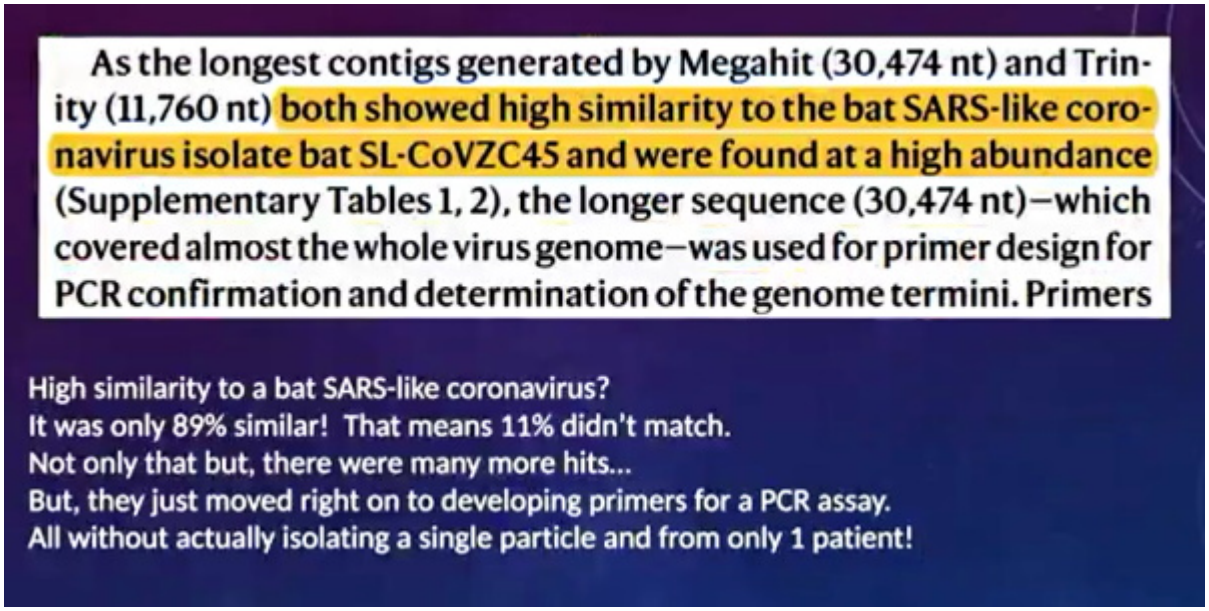


And here we see the 56.5 million reads were assembled using

Megahit and Trinity. Trinity, they got over a million. They generated a total of 384,000 contigs (that's sequences).

Trinity generated 1.3 million. They don't like those because they weren't long enough. They compared those with the database and compared and found that it was somewhat, although not really similar to a previous bat coronavirus. So, as he says, sequencing results in more than 56 million reads.

How can you possibly differentiate what is from a potential virus from everything else? The answer is you can't.



And finally… The longest contig is generated by Megahits. The longest one by Trinity is 11,000. How come they didn't use this one?

Both showed similarity to bat coronavirus. They were found at high abundance. It was only 89 percent similar. That means 11 percent didn't match. That is a huge amount.

Then they just moved on to develop primers all from this one assay without isolating anything, and from one patient.

And, my friends, that is not science; that is propaganda, as is the entire story of a lab engineered virus.

Now, the real issue here and one of the reasons why this, to

me, is so important, is if you go by this unscientific theory that there's a lab-created virus, you actually miss what I would say are the three most important questions to be asked, and then answered, about this situation.

And so now I'm talking – I would say theory. Where everything else was what I would call simply facts.

So the question that should be asked (and it would be nice to have answers for, and which I don't have the answers for, but I have some theories) is, to me, the most interesting thing is –

So we have this published genome, fraudulent as it is, by a bunch of Chinese virologists. Right? They come up with this fraudulent, irrational genome. And, lo and behold, it matches a patent taken out by a company called Moderna in 2016.

So I ask myself how did they do that? How did they make – like there's two theories, there's two ways of looking at this.

One is: They don't want that to happen and so it was a mistake.

But, if we think, which I'm inclined to do, that "they" (meaning Moderna and other people) wanted this to happen so that they could throw people off and essentially create a kind of patsy out there, how did they do it?

So I have three possible theories as to how they did it.

Now, let me be clear.

What I'm trying to figure out is these guys Fan Wu and others, Chinese virologists, having, I don't think, any connection with Moderna, come up with a bogus, anti-scientific genome and for some unbelievable coincidence – let's say for now – it actually matches exactly one of the patented sequences from the Moderna patent of four years prior. How did that happen?

So possibility number one: It was dumb luck. They just made this sequence and it just so happened to match the Moderna patent. And, frankly, I don't think that's actually the right answer.

The second possibility: … Somebody from Moderna or somebody – I don't know who – calls up Fan Wu and says 'I want you to make a genome out of nothing and I want it to have this particular sequence in it so some day people will find this out and say "you see, they genetically engineered this sequence"'. Got it? In other words, there was collusion between the patenters (that's Moderna) and Fan Wu and his team.

Now I gotta tell you, I actually don't think that's true. I would actually love to find out if it is true and if there is a phone call from doctor head of Moderna saying, you know, 'Hey Wu, would you put this sequence in there so that we can – people find out that it was a genetically engineered sequence?' But I just don't think that happens.

And then I came up with a third possibility which is: Once I discovered all these people who are looking into all these patents, that there was at least 70 different patents taken out, of different sequences of RNA, that could end up in a genome. Now, my guess is … I would think it's a good possibility that one of those sequences may end up in the final genome. And then you would then implant the story that this was a genetically engineered organism and there you go.

So you wouldn't have to rely on luck, you wouldn't have to actually have collusion, you could just patent a whole lot of different sequences, for instance, that came in the SARS-1 genome. You could patent all kinds of sequences knowing that, at the end of the day, when somebody makes up this new fraudulent genome it's bound to have one of them in there. Somebody will find it some day, say it's the smoking gun and you then implanted the story of the century which does nothing

but throws people off.

So those are my three options. I'd be happy to hear about any other possible options. But those were the only three that I could come up with.

Now, the final question then is: **What in the heck are these guys doing in these labs? What is gain of function research?**

And, I must say, I don't know what they're doing in the labs and I don't think really anybody knows – including in the Chinese labs or Ukrainian labs or North Carolina labs or any other labs.

So again, I have some possibilities.

One is the following …

Screenshot image from BrandNewTube video (specific video source unknown)

They're doing this.

In other words, what the virologists do is they dress up in hazmat suits and they go on to their computer and start making

sequences. And the hazmat suits are crucial, because, as we all know, it's very possible for the sequences to jump from the computer into their eyes. So it's very important, as you can see, that they wear goggles and protective head gear to prevent the computer sequences from jumping directly in their eyes.

In other words, they may be just doing nothing and it may be just a whole lot of hooey to get people to worry about things. And to implant in their minds that there is this horrible engineered virus, that we should all be scared of viruses, etc. So that's one possibility.

Another one is they're making some sort of proteins or genetic material which can be injected into people. In other words, they're making toxins. And that is certainly possible.

So those are the two main categories that I came up with. Either they're just doing nothing and they're just a front, or a smoke screen, or they're actually making stuff which isn't good for people.

And that gets into my final thing that I want to point out.

… This section right here. this is something I've been very interested. So this is again from the Mercola article:

> "For clarity, this may have nothing to do with Moderna's patented MSH3 sequence specifically, because the RNA code in the jab is not identical to the RNA code of the actual virus. (I'm not going to get into that.) The RNA in the jab has been genetically altered yet again to resist breakdown and ensure the creation of abundant copies of the spike protein. [11]"

Now, I have been asking the question now for months: **Where is the paper? Where is the evidence (a) that there actually is mRNA in these injections?** They say there is. That's the whole point. But when people look there either seems to be not there

or in variable amounts depending on which injection and which batch.

So it could be that even the whole mRNA in the jab is a actual smokescreen or cover for what's really in these injections –which is a lot worse stuff like self assembling nanoparticles which we've heard about a lot.

And the Baileys, Mark Bailey just did another show on that.

So I was very interested to see that this was… stated as fact, because I can't find a paper, and my friends can't find a paper, that confirms that abundant copies of this protein are actually made when you inject this sequence.

And this would be like saying – if I wanted to get investors for my new pencil factory, my investors might ask me to see the pencils that we make. And so it would be natural for me to produce copies of the pencils – maybe tens or hundreds or thousands or millions of them – to show that my technology for making pencils actually works.

One would think that if the whole point of these jabs is to make you make spike proteins that, therefore, "confer immunity", there would be scores, hundreds, thousands of papers showing here's the amount of spike proteins in an unjabbed person. And then you jab them and then 10 minutes, half an hour, three hours, two weeks, six months, 12 years later, here's the amount of spike protein. That would prove that the concept is real and that you can actually genetically alter a human being.

Because I have my doubts. So I'm looking for a reference to show this is true. And, lo and behold, here is the reference. Number 11. *[see page 3 of Mercola article]* So where is the reference from? CBS News.

Now, I could say – I would say if it was from Fox or MSNBC then I would be skeptical. But the fact it's from CBS, that

must mean it's true. And obviously I'm kidding. Let's see the reference.

If the whole point of this is to put RNA into injections, make you make a spike protein which is allegedly from the virus, let's actually see that it works. And here's a quote saying there's at least 73 patents.

My guess is one of them was bound to show up in the imaginary sequence. Bingo! We've got proof that it's there, that it was a genetically engineered virus.

And the whole thing, hopefully you now see, comes crashing down like a house of cards if, as we showed, there was no virus genetically engineered or otherwise in the first place.

[At this point in the video, Tom takes questions from the viewers.]

Question: So this one is related, but it has to do with Dr. Bush's reference to 10 to the 30th power of viruses within our blood, as well as in the oceans, in the soil. His purpose is to provide constant flow of updated genomic information that we need to in order to adapt and survive. And they're not pathogens. That we need not fear, etc., etc.

Answer: So he also has said that, of course, viruses are pathogens. The real issue here is how did they find these 10 to the 30th power viruses? And I've gone over this, especially in reference to a paper, and I don't remember the name, but it's called the ….something to do with the renaming or the re-evaluating of viral…virome…viral world or something like that.

The reason people say this is because they don't realize that t**hey're not talking about actual organisms or particles called viruses. They're talking about liberated pieces of either RNA or DNA – little snippets of RNA or DNA which then get amplified in what's called metagenomics sequencing and so there are billions and billions and billions of these**

breakdown products. None of them have anything to do with a virus. They're simply little bits of genetic garbage that are coming off of our cells and tissues all the time. They have no particular meaning or function that anybody has been able to prove. They're just little bits of garbage. **And the misconception that they're somehow actual particles and could possibly hurt you or could possibly help you is just a misunderstanding of how they found viruses in the first place.**

They don't find particles. They don't purify particles. **There haven't been 10 to the 30th purified particles. We're talking about little pieces of DNA or RNA that get amplified, called viruses, which is a misconception big time.**

[Additional questions include speculation about the patent links to the Fan Wu team "discovery" as well as a question about allergies.]

Articles mentioned in this video presentation:

Moderna Patented Key COVID Spike Protein Sequence in 2016 by Dr. Joseph Mercola [originally published March 7, 2022 at this link – https://articles.mercola.com/sites/articles/archive/2022/03/07/moderna-patented-spike-protein.aspx – and was mirrored around the web. It can still be found at Dr. Mercola's paid archive membership.] Dr. Cowan has provided a pdf file of the article here: https://brandfolder.com/s/fv2q4h7fp84bm5vb3ppn37

Frontiers in Virology paper: **MSH3 Homology and Potential Recombination Link to SARS-CoV-2 Furin Cleavage Site**

Chinese virologist **Fan Wu**'s paper published in **Nature**: **A new coronavirus associated with human respiratory disease in China**

Lancet Respiratory magazine article: **Role of Exosomes in False-Positive Covid-19 PCR tests: non-specificity of SARS-**

CoV-2 RNA in Vivo Detection Explains Artificial Post-Pandemic Peaks

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Related articles:

Dr. Stefan Lanka & Dr. Tom Cowan: How We Got Into This Mess – The History of Virology & Deep Medical Deceptions

Dare to Ask: Dr. Tom Cowan, Dr. Stefan Lanka & Dr. Andrew Kaufman on Freedom, Fear, and False Science About Viruses and the Nature of Reality Itself

Dr. Stefan Lanka 2020 Article Busts the Virus Misconception

Dr. Tom Cowan on the "Spiked Protein Toxin" & "Virus Created in a Lab" Stories

The Contagion Fairy Tale

The Non-Existent Virus; an Explosive Interview With Christine Massey

The Contagion Myth: No Virus Has Ever Caused Disease

The Fraudulent Use of PCR / RT-PCR Techniques for the Manipulation, Harm and, Ultimately, the Destruction of Humanity

Warning Signs You've Been Tricked by Virologists

Jon Rappoport: My Bottom Line on the Existence of the Virus, Its Isolation and Sequencing

Exposing the Lie – Hippocratic Hypocrisy: A Tale of Two Snakes [*A collaborative film by Spacebusters and Dr. Andrew Kaufman about how authentic medicine was hijacked by the power elite and turned into a deadly, sickness-for-profit industry.]*