Transcript
The End of COVID
Session 5 - The SARS-CoV-2 Genome & Variants

SPEAKERS
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The purpose of this presentation is to educate the public on everything there is to know about "the pandemic", and all the pandemics before it. That way, we can finally end this fictional show that's been on air since screens looked like this.

Jacob Diaz (00:00:29):

Welcome everybody, and thank you for joining us in this end of Covid Summit. Today we're going to be talking about the SARS COV two genomes and the SARS COV two variants. We're gonna get into the nitty gritty of genome sequencing with regards to viruses. Does genome sequencing prove that viruses exists? And if it doesn't, what are they doing? And joining me today is Dr. Andy Kaufman Stefano Scolio, and Dr. Mark Bailey, author of a paper that I highly suggest everyone read Farewell to Virology. Thank you guys for joining me. We're going to go into the questions immediately, and let's hope that, you know, people are gonna listen to these answers and truly understand and absorb them. And if you guys have anything else to add, please let me know. So, the first question I'm gonna gear towards Dr. Andy Kaufman is what exactly is a viral genome?

Dr. Andy Kaufman (00:01:25):

Alright, well, thank you. And I have to start off by saying that I have a problem with this question because since viruses don't exist, you can't have a viral genome, right? So it's a kind of a non-starter. But instead, let me answer what a genome is, and then I'll, I'll talk briefly about how it might be applied to the theoretical or imaginary viruses. So, according to, you know, the theory of genetics where said that each organism has a, you know, unique set of genetic material, okay? And so let's just say that this is mostly DNAfor most organisms, but supposedly some microorganisms might only have RNA and not d n a. And so this would be like for humans, we would have, you know, as is known, we have 23 pairs of chromosomes. And so the entirety of those chromosomes and all of the sequences or the lengths, the alleged genes that are represented on there, would make up our genome, like the entire sequence of all those pairs of 23 chromosomes.

(00:02:35):

And then for other organisms, it would be the same thing. And, you know, we're told at least or it's claimed that the, there are specific attributes of a genome that make it able to be identified as a species. So if you were, for example, given a complete genome, you could look at that and say, oh, this comes from a rabbit because it's, you know, x many base pairs long, and it's in so many chromosomes, and that only rabbits have that particular genome. And there would also be specific sequence sequences that you could say were characteristic. And usually that's kind of done by chopping up the DNAinto pieces, and then like seeing their unique things on the ends of certain pieces et cetera, et cetera. So let's say that

that's valid. And the way that this is determined is by, you know, let's say you wanted to determine the genome of a certain organism, right?

(00:03:35):

Like a chimpanzee. So you would go to a chimpanzee, take cells and out of a chimpanzee, and separate the nuclei from those cells and pull out the genetic material, you know, through a variety of different processes. And then you could characterize it, you could sequence it. And you could do that, by the way, in a number of different ways, because you're starting with a known, you know, origin of that genetic material. And then you could say, oh, you know, chimpanzees have so many chromosomes, and they're, so, you know, each one is, has a certain length and certain sequences or characteristic of chimpanzees. And then we could say that's the chimpanzee genome. But when it comes to viral genomes, they don't they don't find them that way. And they also often start out with particular assumptions. Like, for example, they might hypothesized that a certain virus is responsible for a certain illness.

(00:04:37):

And then when they look at samples from that illness, they would make an assumption, okay, it's this kind of a virus, and we know that this kind of a virus has a genome that's a certain length, or it's made of a certain material, right? Because it's said that there are DNA viruses and RNA viruses. And so we would be looking for one of those and that they have a certain length, right? Like it's been said that coronaviruses have a genome that's about 30,000 base pairs along, right? And so you might just look for that. But they never actually find that in nature or like, you know, take it from the organism. They do it by a different way. And I think that's gonna be answered in one of our subsequent questions. So just to summarize, or the take home point is that, you know, allegedly the genome of an organism can tell you things about that organism. Firstly, it can identify the species or the type of creature it is. And then it might also tell you other things, like for example you know, would they have Huntington's disease? Or, you know, would their eye color be a certain thing? I'm not saying all those things are necessarily proven, but you know, certainly that's the claims that are made about a genome.

Jacob Diaz (00:05:56):

Fantastic answer. Is there anything else you'd like to add mark or Stefano with regards to the genome where we can go into this? The next question,

Dr. Mark Bailey (00:06:04):

I think Andy's pretty much covered it there. And, and we should emphasize too, that Andy, myself and Stefano, we, we didn't invent these scientific terms. We're trying to apply them <laugh> and finding that these virologists are playing tracks. Because the term genome has been around for about a hundred years now, and it has always referred to the genetic material that belongs to a particular organism. It doesn't refer to other concepts, such as finding genetic material and environmental samples and putting it together and saying, Hey, I've found a genome. You have to know the provenance, as Andy said. So if you've got a genome of a rabbit, you have to identify the rabbit first, get the rabbit by itself and get a sample, get one of cells, and extract that genetic material. Now, with virology, we know the whole history is fraudulent because they never ever found these particles inside another organism.

(00:07:02):

So when they claim that they're getting viral genomes, in fact, all they're doing is detecting various bits of RNA in the case of sars Cov two, the fraudulent genome or DNA in the case of other invented viruses. So we, we will just, we'll keep harping on about this and keep them honest, that you have to show the provenance of the genetic sequences. It's no good running simulations. And then later on claiming that

because it fit together with your computer program, you've created a genome. That's not what it is. And we're not getting into discussions here about the relevance of finding genetic material inside organisms. For instance, in humans, we have what's considered mitochondrial D n a, which sometimes is considered separately from the human genome. But in addition to that, we've got all this other genetic material that is said not to be part of us, but is totally required for us to exist. You know, all of these bacterial and fungal species that coexist with us as well inside our gut. So, so yeah, let's I, I'll just say again, like, like we all do, we come back to the scientific definitions. Genome means from inside that organism have to show the organism, have to isolate the organism first. Otherwise, it's, it's a pointless exercise.

Dr. Stefano Scoglio (00:08:25):

I think pretty much they covered the the old thing. But I would add the following that, you know, there's also a big problem with genetics as such. In other words, the genetic science as such is based on the presumption that there's essentially only 20,000 active genes. Everything else is junk, d n a. But the, these other junk, DNA is actually almost 3 million you know, nucleotides, 3 million genes. And in reality, there's a lot of literature that these supposed junk, DNA is not junk at all. It is very active, is very relevant. And so, the old genetic thing I think as, as important questions to, to, to be asked regarding the, the viruses, the, the amazing thing is that viruses are just genetic, you know? I mean you have a, a rabbit or a human body where you have the genetic that actually codes for, for something, for a body, for, for functions, right?

(00:09:34):

The virus is just, just r n a, essentially an RNA sequence covered supposedly by a protein. And yet, for instance, you know the, the, as, as Andy was saying, the SARS Cov two is got 30,000 base pairs, you know, so but the big problem, you can do genetic with all these limitations on something that, you know, you know, like somebody that you've identified like an animal or, or, or a bacteria even. But when you apply to viruses, viruses have never been isolated, n never been seen. So whatever gen genome you do on viruses, it's always hypothetical, is always you know, you, you, you don't know what it is. So you guess, you guess with P C R and so forth, and and then we can talk about it later, probably.

Jacob Diaz (00:10:35):

Yeah, definitely. I mean, guys, you guys all provided great insight on this question, and Mark hit it on the head. It's virology way of skewing vernacular to fit their agenda where they say, oh, we isolated this. Oh, we have the genome of this. But in actuality, they have nothing of the sort, they're saying they do it, they don't. So going into the next question, we'll go into specifically the technology they're using or the methodologies they're using with regards to getting these genomes, you know, they are getting an effect in these computer models. How are they doing it, is the question. So this will be directed to Mark, and you guys can add after mark what is the difference between mainly the two technologies that are using with metagenomic sequencing and shotgun sequencing, which is directed to small sequence reads.

Dr. Mark Bailey (00:11:26):

We should be careful about conflating these terms, because metagenomics just simply means taking environmental samples. So that could be some soil, it could be some lung fluid or some snot from a human versus the sequencing technique that they use. So, shotgun sequencing is just taking small reads of genetic material. There may be a hundred to 300 nucleotides long, and seeing if they can assemble that into longer genetic sequences. So two different things there, but both of them problematic. And both of them relate to how the SARS COV two genome was invented by Fan Wu in 2020. So if we take

that as an example, a working example, the so-called Patient zero, or the, the first patient that was published, said to have this alleged new virus that caused this alleged illness. COVID 19 was from this 41 year old worker in Wuhan, and all they did was take some fluid from his lungs.

(00:12:39):

And then through a series of processes that did not involve attempting to isolate any virus, they simply saw what RNA sequences they could find in that sample. And the, that involved looking for every single RNA sequence. Now, if people read the paper, they might get confused, because these test kits will say things like the test kit extracted the viral RNA from the sample. Now, that's impossible because the chemical structure of r n A, what it is alleged to be made up of is exactly the same no matter where it's what animal or alleged virus it's supposed to be coming from. You know, it's got the same base piers. So the, the kits cannot possibly select out viral RNA as they claim. I mean, that's just a marketing gimmick. People like myself in this panel, we actually go and read those documents, and they're very boring, but they describe the steps, and there's nowhere in those steps where there's any proof that it comes from a virus.

(00:13:43):

They're simply molecular reactions, which would be the same no matter what you started with. So that's the first part. And so what they did with the sample in Wuhan was simply troll for every single r n a sequence that they could find. And that was using shotgun sequencing or next gen sequencing, where most of the reads, I believe were about 150 to 200 nucleotides. So that's very short in the scheme of things. And then they used a couple of de novo assembly platforms. One was megahit, one was Trinity. Interestingly, Trinity couldn't actually put together their alleged genomes, <laugh>, if they'd have just used Trinity, they would've said, no, there's, there's nothing in here. We couldn't find anything. But they used mega hit as well, which was able to assemble. And I put, put that in quotes there. 'cause This is like a a simulation basically based on probabilities.

(00:14:43):

That's the other thing that people sometimes miss, is that these programs, they're not putting things together like a puzzle and going, yep, that piece can only go there. They work on probabilities through rs is the technical term. And just see what is the probability that these sequences might fit together end on end. Okay. So it's a probability exercise. It's, it's a mathematical exercise. It, it does not link together actual RNA strands in the case of so-called coronaviruses. So then they come up with a sequence that was you know, 30,000 nucleotides long, and they claim that that was the quote genome based on these well, based on templates, and we'll get to that soon because I think we're covering that in, in other questions, I believe. But, but that, that is the, the short answer of the difference between the two.

(00:15:38):

So essentially, metagenomics, does it have any role? Probably, but not, not in this application. So if you were a soil scientist and you were looking for particular bacteria in the soil for various reasons, you could certainly use something like metagenomics to, to see which bacterial species you could find, or which fungal species, et cetera, or which worms might be present, all that, all that sort of stuff, that's fine. But those organisms all exist if you use metagenomics or fictional organisms, of course, you can invent anything you want because you're not having to show the provenance of where those genetic strands came from. So that is the big problem. Once again, we are not poo-pooing metagenomics, probably if you're a marine biologist or a soil scientist, et cetera, you may have some role doing metagenomics. But for what's happened, like many things that the virologists have done, is that they've used methodologies that are inappropriate for the field that they're studying.

(00:16:40):

And metagenomics, classic example here, shotgun sequencing. Is it, is it valid? Well, again, it could be, but not, not in this application. So if you already had a good handle on where the genetic material was coming from, so to use Andy's example where rabbit then shotgun sequencing might be okay, if you had these very specific sequences that you knew only came from rabbits, for instance. But in general shotgun sequencing is, is dangerous because you can make assumptions about what you've actually created. It's not as reliable as, say, saying a sequencing or o n t, this, this new stuff that they're using where you actually have to have the entire strands, you know, which may be a thousand or more nucleotides longs.

Jacob Diaz (00:17:29):

What did f w et all do with getting or developing the SARS two genome?

Dr. Andy Kaufman (00:17:36):

Well, they did essentially the steps that Mark described. So let me kind of give you a little bit of my spin on it to go through it, because a, as he described, right, they, they didn't start with a pure virus sample, right? Where they just had viral particles and they could extract genetic material because they've never been able to actually get a test tube of viral particles. And interestingly, even if you look up how to use next generation sequencing for viral genomes it describes starting with a pure virus sample as the way to go. And I, I do think actually that next generation sequencing is a valid methodology. If you start, actually, I think it's, you should be starting with a full genome, and then you use enzymes to chop it down into smaller oligonucleotides, because they can all be sequenced in parallel.

(00:18:33):

And if, if you did Sanger sequencing, for example, it might take three months with, if you do it this way, it could take three days. So, so it's advanced in, in convenience using technology, but you have to start with a known piece of material, and then you, and then you chop it down. So in this application, in the fan Wu paper, you know, the original alleged genome of SARS COV two, they start with just lung fluid from one single individual. And I wanna mention that of course, as with many experiments in virology, there was no control experiment where they tried to find the genome from, you know, someone else, someone else's lung fluid, whether they be healthy sick with a non-infectious lung disease, right? But you, in order to have a valid experiment, you need to have, of course, a control. Now, since there's no independent variable, it would be impossible to have a perfect control.

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But there was no attempt even at an imperfect control in this experiment. So once they took the the lung fluid, then they separated out only the shorter pieces of genetic material, specifically of r n a, they measured the concentration of it, and they were looking, I believe it was for one 50 or shorter pieces, but I could be wrong on the number. Mark said 200, it's in that range. And this is a very, very key aspect, is the length of these reads. Now, this is why the reads go much faster using that next generation sequencing. But in order they couldn't do that with r n a. So first they had to do something else, which is they had to reverse transcribe the RNA into DNA and make what they call a DNA library, which is make essentially complimentary copies in the form of DNA of all the short RNA strands that they found in the sample.

(00:20:32):

And then they did next generation sequencing to get the sequence of each one of those individual pieces of RNA that were in the lung fluid. Now, each one of those pieces of r n a, of course, we don't know where any single one came from. Did they come from human origin, from a bacteria, a yeast from

something in the air that was breathed in right before the sample was taken, right? It could be almost anything. Then once they were sequenced, and there were quite a number of sequence of, of pieces that were sequenced, you know, over a million, I believe, and these were just put into those computer programs, Trinity and Megahit as Mark described. And those programs are essentially anything that has an overlap in the strands, in the sequence with, you know, a minimum certain number of bases.

(00:21:25):

So essentially, you know, kind of like letters the same. And I've, I've showed this in some of my slides before, they will put them together, but the problem is, is that it's not like a lock and key where there's one lock in one key. They can be put together in many different ways according to this procedure. And that's why you need the software, because essentially it's a number crunching operation, and it, it creates, you know, like one of those softwares created over a million possible combinations, right? The other one created several hundred thousand. So it it's just a simulation. And the reason why this is they need the short strands right? Each read has to be a short piece of sequence is because of combinatorics, right? It's a mathematical issue. So if you think about like all there's, you know, hundreds of billions of you know, bases, or the number is a extraordinary magnitude in more complex organisms.

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So that means contained in that large, large sequence is almost, if you, if you look at just, you know five bases, every single five base sequence is contained there, you can guarantee, right? If you look at 10 base sequences, every single 10 base possibility is contained there, right? So when, now if you wanna look at a 10,000 long piece, then no, it's probably not. You're not gonna find that everywhere, right? But, so if you have 151 150 long base pair, you could probably find it in many, many, many different places. And when some of these things you can put them in into a, a search, like a jaid database of genomes, for example, and you can find it pops up, oh, this sequence is not unique, right? Because it's short, it's, it shows up in a hundred different organisms, right? And so that's, that's where the problem lies, is that you can make all kinds of assumptions about the uniqueness of what you get, but the, it's all based on complete false assumptions, because you have to know the provenance of each of the pieces you start with, right?

(00:23:45):

And this is why other folks have done experiments on a control sample and been able to get a computer to create a viral genome out of that. It's because of the power of this mathematics. And we're, you know, we're all a little bit oblivious, right? Especially geneticists. They, they're not mathematicians. And a lot of times to do these experiments, it's an interdisciplinary team where you have someone who is the computer expert, and they might be a statistician, and they're doing that part, right? But they're not understanding the biology aspect of it. And then you have the geneticist who is probably not understanding fully the mathematical aspect, and this is how you can end up with results that essentially are meaningless, and they're just represent a simulation, but not reality. So I want to just state that once this computer programs generated, you know, millions of possible genomes, they chose one, they happened to choose the longest one because it matched that 30,000 number.

(00:24:54):

But you know, the second longest one was also 30,000. So, you know, why was that not it? But then they did an extra step. For some reason, they thought that what the computer spit out was not complete. So they went, they took what the computer spit out, they looked at both ends, and they made P C R primers based on the ends, then went back to their original sample and did P C R using those primers. And whatever they found there through their P C R process, they added that sequence onto the ends and said that was the ends. Now, I always ask the question, if the procedure they were doing was

correct, wouldn't they already have the ends in their sequence <laugh>? Now they do some further fine tuning based on what they think this is. So in this paper, they, they saw that it had 79 point something percent sequence homology to a bat coronavirus.

(00:25:57):

Now, that's not very close when it comes to genomes, right? Because we're about 88% similar to the house cat, supposedly as human beings, right? So that's more of a difference. But based on that, they said, well, coronaviruses have certain sequence motifs because of their, you know, genes like the spike protein, for example. And so they modified the sequence to sort of be more consistent with the coronavirus. Now then once that was all set, and they, you know, made their determination of what the final genome sequence was gonna be, and by the way, it was revised several times, then they, they turn that into a template. They publish it, you know, on the database. And then all the other labs who do a genome sequence of that virus subsequently, they essentially have a special kit that has a bunch of P C R primers that make up a substantial plurality of the entire genome sequence as a way to essentially hedge their betts and find it anywhere they look

Jacob Diaz (00:27:05):

To make it easier for people to understand <laugh>, because that was a lot, but I, I understood it. They took someone's lung fluid who they claimed had a pneumonia like disease. They took, like, was it 57 million strands of short r n a? They extrapolated all of that. They put it into a computer and a million different possibilities spit out. They pick the longest one, and then they take some stuff out, they add some stuff in they P C R it, and then voila, that is their genome in layman terms,

Dr. Andy Kaufman (00:27:38):

Essentially.

Jacob Diaz (00:27:39):

Yeah. Where, like, where in the heck are they grabbing this from antivirus? They're like, just hearing all of that stuff. Nobody can confidently say with integrity that this is coming from antivirus. Mark, is there anything else you'd like to add, or Stefano, anything you'd like to add? Yeah,

Dr. Stefano Scoglio (00:27:54):

I'd like, I'd like to say something because I think next generation sequencing is is not very frequent still, you know especially with the SARS COV two, most of it was regular genetic sequencing, Sanger sequencing done through P C R. In fact, there's an article by this guy, his name is Palu, and he is become a very important person in Italy because he is become the president, the director of the National Institute of Health of Italy, student superior Sanita. But he wrote an article in 2016 where, where he actually said, explicitly admitted, said, well, what are we gonna do when we have a new virus that we don't know? You know, how do you build a primers P c r primers for a virus that you don't know, you know? And he said, and then he said, well, maybe things will get better with next generation sequencing.

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So, which is, is like admitting, you know, that you are not doing anything with the, with the regular P C R because the problem is that you take the, you did you take the liquid of a patient you apply a P C R with primers that are just guesses, right? Because again, you are searching for something that you don't know, and somebody could say, oh, yeah, well, but you know, it's got similarity with the SARS COV two,

SARS COV one. So I'll use, you know, like a primer that primers that is short genetic sequences reverse and, and reverse that you know, resemble the SARS COV one. But the problem is not even the SARS COV one has ever been isolated, right? And so you can go back forever. There's never been a, a virus isolated. And so again, it is always been gases on gases on gases on gases, right?

(00:29:49):

And the point is so you take these material, I actually calculated that you know, in, in, in 15 microliter microliters of liquid, we have about 30 billion viral light particles, right? There are, and you throw down on these primers that are like 200, 400 nucleotides on 30 billion, you know particles. I mean, clearly, they, they will attach to something, right? Because there's so much material there they'll attach, but will be completely casual. And that's the reason why today you have at the G side more than 15 million genomes of the SARS COV two, because anybody can do their own experiment. Anybody can take, you know, its own primers and or even the same primers and get something different from the previous taste just because it's so, it's so casual. And so that's why, since there's no specific, you know, like real genome, you have 15 more than 15 million genomes of the SARS COV two.

(00:31:02):

Not to mention that. The other interesting thing is that as I joked you know, in my book it's you know, the, this SARS COV two was, was born one and trying like, you know, a, a higher power, because actually the the zoo article claims that it took three pe three different patients. He found a virus in each of the patients. They were different. So there were three different viruses, but at the same time, there were the sars, they call, they called all, all three of them sars COV two. So it's, you know, one and trying, so if we, if we talk about variants later on, I mean, this was already born into variants, you know, because they already had three. But I think the old thing goes back to, that goes back to the fact that when you have something that you don't know what kind of primers are you gonna use, you know, they're completely hypothetical and you, and, and the old game is completely casual.

Dr. Mark Bailey (00:32:08):

Yeah. Just to add to Andy's excellent description of, of what took place with the fan w patient, and yeah, these, what some people might say to us is that, hey, yeah, we admit that fan W's team didn't have to do a proper isolation because they were using templates based on previous isolations. But that's fraudulent because we know that, because some of us have actually followed the trail. So when they give an example like Andy of a so-called bat coronavirus, in the case of Van Wu, they went to Gen Bank and looked up a so-called genome that was deposited on the bank in 2018. And if you actually look at that paper, they certainly didn't isolate a virus. They just did more fraudulent virological techniques. In that case, they injected un purified biological muck into baby rats sprains. And because it injured some of them, they declared, Hey, that's, that's our evidence of a virus.

(00:33:14):

Let's sequence it up and hey, we've got another coronavirus. But these, these are just, again, with the metagenomics, these are just sequences that are put together from crude samples in that 2018 paper that was just intestinal specimens from bats in China. And so nothing to do with showing, demonstrating that there was any virus. And that's why in my essay, I called that chapter turtles all the way down because I followed the trail. If you go to one gen bank or GSS a deposit after another, none of them show viruses. You know, we, we are talking the proper definition here of something that none of us on this panel have ever seen. And that's, that's a replication competent particle, an infectious particle genome surrounded by a prod nassis coat that causes disease. None of us have seen this, not even close. So we know what they call genomes in their fictional simulations and metagenomic techniques, but this is not corresponding to an actual entity that meets the description.

(00:34:22):

So I think we need to, people get confused with that because they think once the deposit is on gen bank, it must be all official. But this is like the most, and Gs a's terrible as well. Like Stefano says, we have 15 million of these processes, and here's another issue. We get them saying, look, we repeated the experiment 15 million times, and we keep getting similar results. Well, if the technique is fraudulent and scientifically invalid on the first time, it doesn't get better by repeating it 15 million times. It just shows idiocy will just keep propagating over and over again. So that, that's another issue you might see. They'll say, no, it is repeatable. But if you're not following the scientific method, it's, it's pointless. And as Andy mentioned, I think we should keep mentioning this, if, if you don't have controls, if you don't have valid controls, there's, there's no point to any of this.

(00:35:22):

And that's another thing I've taken pains to point out to people, is that we get sent papers and people say, no, they did do a control experiment for, for this genome. And then they'll show you the control experiment simply contained nuclease free water. Now, putting water in a sample. We don't expect to find genetic material in water <laugh>. So this is simply a negative control. It has nothing to do with validating what they claim as the genome. It's just saying that the pipeline they're using doesn't have contamination. Because if you check the water, you know, it shouldn't produce any of these sequences. So really important. And another thing I, I think we should emphasize too, which Andy touched on, is that they'll claim, oh, well, this was 79% or 89% similar to what we've found previously. Now this is the fraud that's been going on since they were able to do these procedures.

(00:36:19):

H i v another classic example. They allow 40% variation, and yet they're still calling it the same entity. Now, to give you an example, they say that we share 97 or 98% of genetic material with a chimpanzee. And I mean, we appear to be extremely different from chimpanzees. Whereas with these so-called quote coronaviruses, the variation is, is ridiculous. You know, it can be like 30%, and they're still claiming that they've got the same thing. And keep in mind too, that with a human, we're talking about 3 billion odd nucleotides to make up our entire genome with these so-called viruses. They're tiny, like relatively. So of course, you're more likely to be able to find these sequences and environmental samples. You're not going to find a human sequence necessarily. But if you've got a subset of some of these sequences, say H I V, which is about 9,000 nucleotides or alleged coronaviruses 20 to 30 kilobytes long, you're way more likely to find them.

(00:37:29):

It's just easier to find them because they're, they're very, very short sequences. So, so yeah, it's I know, and it's, I, I think the biggest problem is that we do have these gen bank and GS a data banks, which make it appear to people like, oh, you know, this, this has been done over and over again. But we can simply keep pointing out, if you don't know where the genetic material came from, if you don't run a control experiment, if the techniques are invalid to show your conclusions, then all of this stuff involving viral genomic genomics is, is meaningless.

Jacob Diaz (00:38:06):

Thank you for mentioning that, mark. And yeah, it's in, in, in my, you know, history with, with virologists, they always like to point out to the, the phylo tree and the <INAUDIBLE> databases and all that stuff, and if to the lay person, it would make it seem like, oh, yeah, they're doing this, this is real, they're getting results, therefore the virus is there. But when you actually go into it, no, they're just doing the same experiment over and over again. And then they try to perpetuate this whole evolutionary thing

about viruses changing, and that's why they're so different. There's a coronavirus here this year. And then the initial <inaudible>, as you mentioned it, Andy, I mean, 79% similar <laugh>, when I first read that, I was, I was like, what? And then they said in some other studies, oh, we got 85% similar, 86% similar, which is still not a lot. And you mentioned, mark in your answer that you had traced back all the genomes prior to SARS two. Were all of these genomes with all these, with all these other viruses in the coronavirus family and other families, were all, they done the same exact way, or the deviations in that?

Dr. Mark Bailey (00:39:12):

No. Well, certainly Jacob, when the virologists are at work, they have a, a certain number of tricks that they like to pull out of their bag. But so the various papers have different techniques. Sometimes they'll use a cytopathic effect to claim they've found a quote virus. Sometimes if we look at the common cold unit, which was apparently the first unit to find quote coronaviruses, their idea of finding a virus was simply taking a sample from someone who had a cold and putting it in a vial and claiming that that was the isolation technique. We have other people who just take the muck and inject it into baby animals' brains and say, well, that made the animal sick. So clearly the virus is at work. So there's a number of fraudulent techniques that they use. But importantly, what I did was I started following these trails back, starting with SARS COV two.

(00:40:04):

And if you follow things back, you get to SARS one, you know, the fraudulent creation from 2002, which they alleged caused the so-called SARS one pandemic. And if you keep following them back you get to the 1980s, which is when they first started developing these sequencing techniques where they said they were finding viral genomes. And back then it was much slower because of the techniques they didn't have next generation sequencing, et cetera. But the, the problems with the methodologies were exactly the same as what we have now. So I went back, found these papers from the 1980s, and they claimed that they had isolated infectious bronchitis virus, which is a, a famous coronavirus in the avian world, alleged to cause a whole lot of problems in chickens. The problem with their techniques were that they simply had un purified samples with chick embryos.

(00:41:04):

So they had mammalian tissue in their samples, and then they added samples from these chickens alleged to have infectious bronchitis virus. And in their mixture, they started generating sequencing, you know, se sorry. They started sequencing these mixed brews. And from this, they claim that they could piece together a coronavirus genome. But I, I could not, I, I spent a lot of time on this, and when the papers said purified variants, there was absolutely no proof that they purified anything. They did not provide electron micrographs showing that they'd found particles of the same size and purified them. They did not show that they had an infectious agent or something that was replication competent. So again, we've got this problem. You can't start with a biological brew and just say, oh, yeah, there's a virus in there, and now we're going to see what we can sequence.

(00:42:05):

And well, these sequences, they don't seem to come from here, so they must be from a virus, which is essentially what they did. So that is the whole basis to coronavirus genomes from 1987 when the I B V so-called genome was published through to the present day, when we have these 15 million fraud creations on G ss a. So I, I don't know how we can make it any clearer that at no stage from <laugh> when they first did it through to today, have they demonstrated that the genetic material comes from inside a replication competent particle. I mean, the material may come from inside a particle, it may come from inside a exosome or, or whatever name you want to call these particles. But at the moment, they have no proof whatsoever that they're viral.

Dr. Stefano Scoglio (00:43:00):

No, I just wanted to say that the fact that there are 15 million genomes deposited, you know, cannot be taken as a proof that, you know, or they keep replicating because the, the, the old point is exactly that. You know, all these, all these genomes are different. And one thing that one should ask is, you know, when they, they, they started deciding 'cause was a political decision as we'll discuss later to launch the variants, right? The old thing of the first terrible variants, the alpha variants from, from England was a deletion of one nucleotide, right? Which made it so terrible. Now we've got 15 million where 15 million genomes where the difference is 10, 5, 10, 20, 30%, 40%. And, but there's not been a, there's not been an explosion of terrible variants killing everybody in the world. I mean, clearly these 15 million variants, because they are variants essentially, otherwise you wouldn't deposit it, right? I mean, if it wasn't different from, from another, another genetic sequence, you wouldn't deposit it. So they wouldn't accept it as deposit. So that means there's 15 million different variants, but they didn't make any difference now, except for two or three. Why, of course not, nothing of this is explained. So the point is the fact that there are 50 million variants is not approved that they repeated it. It's a proof that it's completely casual.

Dr. Andy Kaufman (00:44:45):

I if I could, I just, I'd like to add something onto that because I mean, I know we, we might talk a little more in depth about variance, but I think it's completely misinterpreted, right? Like Mark rightly reported how that that's given as proof that they were able to, you know, find the genome in other people. But in order to give validation to an experiment by being able to repeat it, you actually have to get the same results, not different results that are similar <laugh>, right? They have to be the same. So, so the way to properly interpret all of these genome variant sequences is actually that you're index sequence was incorrect because you're unable to validate it by getting the same results. But of course, you know, they, they spin a story, which in order to create fear to reinterpret the results and, you know, give the appearance of, of something really happening, when in reality all, all it is, is you know, fraudulent misinterpretation of an obvious results.

Dr. Mark Bailey (00:45:52):

That, that, that's why, and on this panel, we are signatories of the settling the virus debate statement, because we actually challenged the virologists to take, we take a sample and split it five ways and send it to five different labs and see what their results are, because they should all get exactly the same result, shouldn't they? But they wouldn't probably, and if they got different results, I guess they'd make up some fictional story, like the virus quote mutated on the way to the lab and caused a different result. <Laugh>. And here in New Zealand, our colleague Michael s had a, I'm pretty sure he put, he's put a lot of foer requests to agencies in New Zealand, and he suggested to one of them, don't you take a sample, split it into 10, and then run it through your sequencing platform 10 times in a row and see what the result is. Because like Andy's saying, I think it would just fire out different results, and then that, then they'd claim that what the virus is mutating halfway through the procedure, or, or we've found, no, we've found variants. There were 10 variants within that one sample because they just keep making up backstories and whatever challenges we can throw at them to point out, it's not scientific. They just create another backstory such as variants or mutants, et cetera.

Jacob Diaz (00:47:16):

To add on a little bit to what you were saying, mark, about the lack of controls, they, they're not doing any controls to check if these, these pieces of these genetic materials, genomes, whatever, aren't found

in other organisms. And they're not, like for <inaudible>, a proper control would've been what? To get a healthy person to try to see if they can develop a genome from their healthy fluids or another viral genome of sorts. But they didn't do any of the sorts.

Dr. Andy Kaufman (00:47:44):

It's not possible in these experiments to, to really do a scientific control because, you know, a control would have all of the experimental, all the experimental conditions in place except for the independent variable, which would have to be a vi a pure virus particle. But since there's no pure independent variable in any of these experiments, you can't devise a control where you include everything but that. So you could only approximate a control, really. And I, I think if you had an individual's lung fluid who was ill, but not with an infectious illness, like, let's say Ill from lung cancer for example, or sarcoidosis or something, and then probably you could in addition to that have, you know, healthy. But the thing is, the experiment's designed wrong, because if you want to do this properly, you have to have first find the viral particle in nature, right? In a sick individual, then separate it out, and then take the genetic material directly from it. And we, we would not be, you know, on here criticizing that approach, because that is how to apply the scientific method to this problem. And that's what is used to analyze the genome of every other type of organism that I'm aware of other than viruses. So, you know, really we're, we're just pointing out that this procedure is not scientific.

Dr. Mark Bailey (00:49:17):

A specific fan w example, what they would've had to have done is taken the first sample, which they alleged contained the coronavirus and run their geno genomic simulation, and then removed the so-called viral particles <laugh>, and then run it again, because that's the independent variable that they're claiming. But we know that they're, they're not able to do that. Now, if you were doing it with bacterial species, you could do that because you could take the lung fluid from someone, you could remove all the bacterial cells and then run the, the procedure again. But we know with the quote viruses, the unable to do that. Now, the other option would be, yeah, to take a, a series of controls, and one could be with a healthy person, but like Andy, I would suggest taking someone who's got pneumonia, but not so-called coronavirus pneumonia, to see if we can find these sequences. And, and importantly too, it would ideally you'd do a sequence of these tests, like for instance, that patient zero if we want to call 'em that out of Wuhan, you could run the simulation six months later and see what happens, and then run it a year later and then two years later keep doing it. And seeing how many times can you pick up these sequences because, you know, what is the, is the quote virus coming and going <laugh>. But yeah, it, it makes no sense whatsoever. So,

Dr. Stefano Scoglio (00:50:44):

Yeah, but, but you know, you know what would happen if you were that type of control? And you get like a, a, a person who has a, a, a lung disease different from the, the supposed virus that when they found in the, in the genetic sequence, a difference of 30% in the genome, they would say that it's, it's, it's not a coronavirus, it's something else <laugh>, because it's completely, it's a completely political decision. That's all it, that's all it is, you know, is like,

Jacob Diaz (00:51:13):

Good segue, Stefano. 'cause I'm just gonna ask you straight up. So we know that they're doing basically very similar things with the SARS Cov two genomes. What are the variants? So you mentioned it's like a

political decision, it's all these things. What is a variant? Is it truly a variant of a genome, or is it just a different result altogether?

Dr. Stefano Scoglio (00:51:31):

No, the a a variant is a, is a, is a political statement, because the point is you have 15 million variants, right? But none of them became relevant except for genomic registering at G Zs when they started, the ones that became, started becoming relevant was because at some point what happened with with C O V I D was that at the beginning you had all these people dead because of other things like you know, like bad, bad medical procedures and so forth, or, or IPA vaccination. Then you add as positive asymptomatic, right? Asymptomatic positive people for six months. You went on with that, then you started killing some more people with vaccination in November with flu vaccination. Then in 2021 you started to needing, needed needing something else. And so what they did, the first variant that became relevant happened in England.

(00:52:38):

It was the alpha variant, and this is the way it happened. They started talking about this variant in December, 2021, and a, an article was published by an, by a neke from Hong Kong, which shows that there was a, a, a, an overall world coordination through world led organization and so forth. And the article stated that this variant among the many variants that were found in the laboratories in in England at that time was becoming dominant. And the reason why it was becoming dominant, not because they did any, any epidemiological inquiry, right? But only because this, these people this author stated because there were more sequences of that variant deposited at the G Z than others. I don't know if it's clear. In other words the reason why this be, this, this variant was, was be becoming dominant is because the researchers were focusing more on that than rather than other variants.

(00:53:48):

So no, no connection whatsoever with epidemiology. Then what they do is they take about 35,000 of these genomes done the Public Health England, and they found that about four 1,400, 1400 belong to this variant. So four, 4% this, this dominant variant was 4% of the old, of the old variants that they found, right? And then, and then the, the, the, the most beautiful thing is that they said, how are we going to monitor the development of this variant in the population? Because, you know, if you have to do full genomes, you know, it takes two weeks, only a few laboratories do it, you know, it would be impossible. So, so we need, we need a proxy marker, something that tells you quickly why, you know, you, you are affected by this variant. And this was the marker that they used. If you remember at the beginning when they were testing for SARS COV two with with a P C R test, with molecular test, they were testing for the n gene, the S gene, and the OR gene, something that all three of them, the genes of the, the supposedly formed the, the virus, right?

(00:55:08):

Then at some point, the were let organization stated that was not necessary to find all the three genes anymore, right? But only one was sufficient, right? So you could be positive to SS or positive only two n or positive only two rf, and you'd be positive to sars COV two. So public health England in December, 2021, state that since the very, this variant had a deletion of the, in the E SS gene anyone would be positive to the other two, but not to, to the S gene would be positive to the new variant. Now, to, to understand what this means, means that all the people in the past that had been positive to N O F and not to s would've been affected by the variant before the variant was even found, right? Which is completely ridiculous, but that's actually what was used everywhere to, to monitor for the variant, okay? And I mean, more clear, more, more clear than this, that this is just a political decision, you know, manipulating data the way you want. I, I, I, I, I can't really see why, you know, more than this,

Dr. Andy Kaufman (00:56:30):

The reason why that is so important for the government, right? You said it's a political decision, is because before that point in time when they announced this variant, right, all of those P c R tests would've been negative, but now they only need one out of three markers. So all those negative tests are gonna be positive, and that will allow them to increase the numbers. It's like if we said, okay, you know, there's a hundred millionaires in the city of London, but now we're gonna change the definition, a millionaire that you only have to have 500,000 dollars in the bank to be a millionaire, right? So overnight, the number of millionaires goes up through the roof. And that's what they did. And they did the same thing with Omicron where they allowed two out of three markers instead of the full three out of three. So they could buy manipulating, using the preexisting, you know, p c r kits invent, you know, new pretend or fake cases overnight by announcing this kind of strategy.

Dr. Mark Bailey (00:57:29):

If I could just add too that again, we'll, we'll come back to definitions and what, what does variant actually mean in this world? And I think probably to date, Andy's come up with the best definition, which is a failure of the experiment to replicate properly <laugh>, which I think should go in the virology textbooks. But if you actually look up a virology textbook, you can't even find satisfactory definitions of the term variant. So they seem to be just arbitrary declarations that slightly different sequences were found. And they don't even claim that they're so-called pathogen, which, you know, they're claiming they have a virus and it's a pathogen. They don't even claim that it has any particular new properties or anything. They're simply saying, oh, some of the sequences were a bit different, but this is, this is just like saying, you know, you, you got a car and it's, it, now it has a scratch on it, and we better call it, it's not A B M W anymore. We better call it something else. It, it's just, you know, it's completely ridiculous. So I'll just point out again that when, when we're asked to comment on things like quote variance, we say, well, what, what is it that you want us to comment on? It's again, these, these are imprecise terms, and virology is used, this kind of thing like isolation and pathogenicity, when in fact they don't, that's not what it means on scientific terms.

Dr. Stefano Scoglio (00:58:59):

I just want to add something, and that is the political decision to use variants, which lasted all throughout 2022, was parallel to vaccination. Why? Because of course, you could not claim that you vaccinated all these people and people would still get sick with SARS COV two, right? So invent the variants because the variant allows you to say, oh, well, you know, maybe the vaccine didn't cover the variant, you know? So they, they covered all the sickness that was due, of course, to the vaccine, them themselves, to the toxicity of the vaccine themselves through the variant. So that's why it was so important to start, start the variants exactly at that time, December, 2021, January, 2022, when the vaccination program was, was starting to pick up.

Dr. Andy Kaufman (00:59:53):

Stefano, there's proof that you're correct, because just now since the, in the United States, they're officially ending the emergency, the emergency use authorization of the first generation of of vaccines is expiring, right? And they said, they said also, you can't use that anymore because now they have the approved vaccine is for different variants that didn't exist at that time. Right? So, so right there, it's exactly what you said.

Jacob Diaz (01:00:24):

So, and, and Andy, I know you, you're tied on time, so I'll ask you very quickly with regards to these genome assemblies, the results we're getting, the variance, all that stuff, are these genomes actually present in the sample of these sick people, or are they just a complete artifact of the process?

Dr. Andy Kaufman (01:00:44):

Yeah, well, no, clearly they're not present, and I don't think anyone has looked for them. There have been, I think one or two published studies where they have done, I believe Sanger sequencing or micropore sequencing and found longer sequences than, you know, 150 to 200, but never to my knowledge that a complete genome because it doesn't exist in nature. So they couldn't you know, find it. Actually, but, but you know, they, we talked about the next generation sequencing requiring short reads, right? 150, 200 around that at most. And but if you, if you were looking at an unknown sample and you wanted to find, you know, something that at least you could say, came from one single organism, now you still wouldn't be able to identify what that organism was unless it was already known and it matched, you know, precisely. But it, if you find a 10,000 long base, long strand, at least, you know, that came from one place in nature. Like it didn't just assemble in the test tube spontaneously, right? So you know, but like I said, it's of, it couldn't be done. And it's never been done because why would you even conduct that experiment when you can just buy the kit and, you know, find the 15 million and one variant you know at will pretty much

Jacob Diaz (01:02:19):

Do these virologists and scientists, are they checking themselves to see if their genomes don't have proportions in them that are coming from other factors like the supernat of a cell culture? Or you mentioned the chicken embryo cells being used, or fetal bovine serum being used. How do we know that all of that genetic material isn't being found within the genome and they're, that's what they're claiming is a viral genome? Are they checking that or are they just running with it?

Dr. Andy Kaufman (01:02:48):

If you look back at the fan w paper, right, they did claim to try and remove human sequences, known human sequences, right? They, they claimed that, but they did not describe specifically which sequences were removed. And when a group tried to replicate their procedure later on, they, it was a black box. They couldn't get the same exact results because they didn't know what to leave out. But, you know, it all depends on the length of the sequence too. Because once again, if you, if you try to remove sequences that are known, well, how long are those pieces that you're removing and how short are they? Because if the shorter it is, then you're gonna find 'em everywhere. And, you know, if you remove them all, you can't make anything. But if they're long, then they only match something that a computer assembled they didn't match, right? Something that was originally in the sample. So with that, I'll let mark give a more complete answer.

Dr. Mark Bailey (01:03:53):

There's one answer. No, <laugh>, I don't, but yeah, this is the problem. I mean, and this is why we're grilling the virologists, because they're not really, you know, the, the whole idea with the scientific method is that you look for other explanations and you put forward a hypothesis essentially, and say, okay, everybody now attack it in every way you can and see if there could be other explanations for this. And so, when you look back at all of their experiments involving alleged coronaviruses, we keep getting the same problem is that what they have is things like you can take, say papers where they have tissue culture breakdown experiments, and then they find these various sequences that they attribute to

coronaviruses. And we would just argue and say, well, no, you, you don't have a methodology that showed that you have a particle that fits a description of a virus.

(01:04:47):

You essentially just have a tissue breakdown experiment. And yes, maybe during the tissue breakdown, these various sequences are generated. And I think also we should point out the fact that things like genomes are not something that's completely stable. So if you take a sample from a human, it, it's going to vary the sequences you can find, depending on which tissue in the body you go to over time. Like if you take a sample 10 years later, it could be, it could be different. And this comes back to the whole problem, this fraudulent idea that we have these fixed genomes, like a computer code that gets input at the start, you know, that we inherit or whatever, and then it forever stays that way unless it mutates in a certain direction. But that, that's not what happens. We know that this is a dynamic process.

(01:05:38):

We know that within our own bodies, and we know that even within test tubes, for instance, in the 1960s, Barbara McClintock started showing that you could just stress cells in a test tube and they would start producing new sequences that you couldn't find before. So we've got a problem here, you know, with this whole viral theory, is that they don't have a way of showing that these sequences are not simply coming from, say, say, in the case of coronaviruses, classically, they'll use mammalian tissue to, to find these sequences, whether it's you know, from cow tissue or humans et cetera. And, and from the kidney cell lines that they use tend to come from mammals as well. So absolutely, there's plenty of other explanations, but it's not our job. We don't have necessarily the facilities to go out and check these things. This is the job of the, the virologists who are making the claims. We can simply analyze their papers and say, what you have doesn't prove a virus at all. So yeah, I'll see if Stefano wants to add anything.

Dr. Stefano Scoglio (01:06:46):

No, I completely agree. I would say that unfortunately, it's not just shortcomings of virology. I think it's it's fraudulent behavior. Because essentially, for instance, I did a, a presentation recently on this a paper on the Alpha Omicron. I don't know if you heard Boston University came out with this new variant, alpha omicron generated in the laboratory. And in Italy. Everybody was talking about the fact that this alpha omicron killed 80% or 100% of the mice. So it was, you know terrible. Everybody was scared by this. Then you go look at the paper, and no mice died on its own. They, they established parameters like weight loss raffled fur and stuff like that. And, and if they re-entered in this parameters, then they killed them. And they said, oh, the virus killed 80% of the, the, the alpha omicron variant killed 80% of mice.

(01:07:54):

Now, what is interesting about the study is that there are other interesting facts. One is they actually create a new type of virus, which is the the recombinant wild virus. In other words, they talk about they test three different whatever vivir viruses. And one of them is the recombinant wild, in other words, is the wild type from Wuhan, right? But recombinant done in done in lab laboratory, which I think it's also approved, but there is no wild type, because why would you have to make it in the lab if you add actually an a, a a real wild type, right? So this oxymoron, which is, you know, the artificial wild, you know, that's the thing. It's approved that there's no virus to begin with. The other thing is when they tested this wild type, this alpha omicron variant where they added some extra protein spike protein or whatever, and then the, the fluid from a from an omicron infected patient, right now when, when they tested for pathogenicity, and if they kill the mice, the one from the, the, the, the liquid from, from the, the sick omicron sick person, how many, how many mice killed 0% had no effect whatsoever.

(01:09:26):

And even on, on the, on the cell lines, didn't have almost no cytotoxicity at all. So again, this is now proof that, you know, it's, it's all, it's all created in the lab through adding toxins, all, all sort of toxins and so forth. And it's clearly fraudulent because how can you not know this? How can you not be aware of the fact that you are actually spray send out, sending out the news that there's a new omicron alpha omicron variant that kills 80% of the mice, and you kill them yourself? I mean, you know that, right? So,

Jacob Diaz (01:10:10):

And thank you for mentioning that because I, I kinda lost my mind. But for people listening, this is what they do in their gain of function sciences where it's really gain of fiction. It's creating a virus in their eyes, which with a chimeric culture, where they combine one culture with another culture, and then they do sequencing of it, and they say, oh, we have a new alpha variant of this or that. But in actuality, they don't have anything. It's nothing what Stefan Lanka's famous quote, they have nothing. They don't have anything. It's taking supernat for one experiment and another experiment. You're combining it. You're taking small, tiny pieces of, of reads and RNA and you're claiming you're making these vast claims that this is a variant that's gonna kill millions of people when it couldn't even kill a couple mice in the laboratory.

(01:11:01):

So it's, it's like, what are we, what are we actually talking about here? And, and, and Mark mentioned it, and he also wrote about it in his paper, where they get these genomes and these experiments, it's, it's Frankenstein science. They're taking poop from a bat and then injecting it into a culture and putting it in a rat brain and then saying, oh, this is a virus. Show us the virus first before conducting these abusive animal experiments where you're just killing these animals in the name of science with poison cell cultures and fluids that you don't know prove, have viruses in them. Mark, do you have anything to add to that?

Dr. Mark Bailey (01:11:39):

Yeah, well keep in mind that along with my wife Sam, we're doing a whole presentation for the end of Covid on the gain of fiction narrative. So we, we'll certainly cover that. But yeah, once again, it's bringing it back to this whole alleged SARS Cov two genome, injecting biological muck into animals', brains and abdominal cavities, and then claiming that there's a virus in there because you detected various genetic sequences. Again, just another fraudulent wing of this whole genomic scam, basically. So yeah, essentially, I, I think Jacob, you, you hit on the head there, <laugh>, show us the virus, don't show us genetic sequences and claim that that's a virus. And you know, I remember it may have been back in 2020, Sam actually made a video quoting an Australian virologist who in the middle of a public interview on the radio said, after all, a virus is just a piece of r n a.

(01:12:43):

And we were like, what <laugh> is this what virologists are now claiming that we don't need to? And I have seen this from other people who are feeling the heat from the pushback that we've been giving them are saying that well, forget about showing all these other properties that the old school virologists we're, we're looking at, we're in the, the next generation, now we're in the, the modern technological era, and all we need now is sequences. And this is absolutely ridiculous because a virus is not a sequence. <Laugh>, bacteria are not a sequence. A human is not a sequence. You know, that's, you need a lot more than that. So than I agree. Show us the virus, don't show us sequences.

Jacob Diaz (01:13:27):

Yeah, I think it's, it's pretty damning as well as you guys have mentioned, you know, even pretending there's a genome out there of a virus, which there isn't, they can't pull it out from A to Z. They simply can't, you can't find a coherent, complete genome from beginning to end and show us that that has a process and disease, which we've been asking for 2, 3, 4 years now, and they can't provide the proof. So where is it? It's not there. And you know, I I I I, I made an example a couple, like a year ago in one of our projects where they're, they're assembling, essentially. You're just, you're taking these strands and you're making something that was never there, there, and then you're claiming that it was always there. Kind of like if you go to a trash dump and you build a building out of all this trash, and then you claim the building was always in the trash, it was never there. You made it out of the trash that you had. So this is what they're doing for people listening and watching. This is what they're doing with all of their genomes in terms of viruses, all, all of their variants. It's not there, it never was. And to use this as proof of any virus is completely erroneous, unscientific, especially when they can't even show us the virus. Stefano, anything you have,

Dr. Stefano Scoglio (01:14:45):

I think I, I think the key point is what Mark was saying. In other words, the, what I would say, the escape from the co postulates, right? Because they, they, since they, they've never satisfied the co postulates, never, of course, what is the, the way of solving the problem, killing the co postulates. And so now they're saying that, you know, you don't need to prove anymore pathogenicity, isolate the virus test it on you know, inject it on a, on a, on a Guinea pigs and see if it's reproduce the, the disease and so forth. No, you just do a sequence, a genetic sequence, and that proves the existence of the virus. And then the way you prove the pathogenicity, you put in a culture with a lot of toxic stuff, you know, the then killing the cells and say that it was the genetic sequence. But, but I think this is the key point. So I think we need also to, to defend and protect the, the co co postulate. Not because CO was a, a big fraud himself, but the, the postulate that he, he posited, which actually were coming from somebody else before him are actually what should be the, the quintessential proof of, of existence of pathogens. And they've never been proven.

Jacob Diaz (01:16:11):

And even though Coke was a fraudulent, a fraud, he was fraudulent. But the actual postulates themselves are pretty reasonable and logical for anything really almost sense. They, they, they're common sense, and they, and they can't adhere to these. So they, so then Thomas Rivers goes ahead and adjusts them to fit viruses. And even then, they still can't succeed with those postulate. I believe in one sars, one paper, the initial one, I think Andy, Andy made a video on it, A rooster and a river of rats, that's what it was called. They said that it, it fulfilled coax postulates, but they then said, modified by rivers. So they actually used rivers postulates, and then they acknowledged that it didn't fulfill rivers postulates altogether. So it's like, what are we, what are we doing? Guys like it, it's just, it's fra on top of fra

Dr. Stefano Scoglio (01:17:00):

I don't think river really modified the cock postulates because he only added the condition that, you know, as opposed to bacteria that grow in, in a culture on their own, you need to grow viruses on a tissue. 'cause They need a tissue to proliferate, right? But still, the rest of the po of, of the postulate were there. They were there. I think the big jump was done in the nineties with that article by Frederick, and I forgot the name of the second daughter where they actually said, oh, we don't need anymore these postulate, because now we have sequencing

Jacob Diaz (01:17:35):

And are you talking about molecular co postulates? Something like that, right? Is that what

Dr. Stefano Scoglio (01:17:39):

It called? Yeah, something like that. And yeah, now we have, we have sequencing. Through sequencing. We know the, the presence of the virus regardless of purifying it, isolating it, and, and testing for pathogenicity.

Jacob Diaz (01:17:57):

Anything else to add? Mark? I think we've covered pretty much everything regard to the questions. Anything else? Any closing comments?

Dr. Mark Bailey (01:18:04):

Yeah, I think, I think we've covered it pretty well, but yeah, one final thing is just to say, you know, you mentioned whether or not the SARS cov genome exists in nature, and it, of course, we leave open the possibility that a 30 kilobyte sequence may exist in nature, and, but it should not be called a SARS COV two genome, because it has not been shown to come from a particle that fulfills the description of a quote virus. So I've, I've always left that open that possibility. But the, I think there are some major problems with it. And because they say it's an RNA virus, they have no independent way of checking a 30,000 nucleotide RNA sequence, because they don't they can do that with D n A, they can show very long strands, but it's not possible with r n a.

(01:18:53):

So again, we've got this convenient story going on for the virologist and say, oh, well, unfortunately we can't check whether this thing exists or not. And the, the other issue is, even if with say Oxford Nanopore technology se sequencing where they can actually, like Andy say, do much longer sequences into the thousands and thousands of nucleotides, e even say, if they did manage to find it, I, I'd say, well, you still have to show that it relates to an actual virus, because Stefano and I, we don't dispute that there are classes of proteins that they, that they've called spike proteins or nucleocapsid proteins. That's fine. They can call them what they want that there are these genetic sequences and that there are these various proteins, but it doesn't mean that they've come from viruses. And that's the major problem, because we've seen, you know, you go back to say 1990, you can see experiments where they describe the quote spike protein, but again, it's just a tissue breakdown experiment.

(01:19:57):

And we say, sure, these proteins may appear, but you have to show that they're part of an organism that you're call it calling a virus. So, yeah, I think we should as scientists, we should leave open the possibility that they may find one of these 30,000 long nucleotide sequences you know, made up of R n a, but that would still not mean that they've got a virus. And that, that's the most important thing all comes back to providence. Find the organism, prove that it exists, isolate it by itself, and then come up with your genome, not this backward system that they've got where they're coming up with the genome. Basically, that's all they're doing now, is coming up with the sequences and then making up a backstory about what that means, completely anti-scientific.

Jacob Diaz (01:20:49):

I wonder what it'll be next when they realize that genomes are fraudulent, so they're gonna do something else, whatever trick they have in a couple years, <laugh>, we'll see.

Dr. Mark Bailey (01:20:57):

Well, well, there's always epidemiology. We know that they, they like to use that, and, and we know that that epidemiology helps produce a hypothesis about what might be going on. But we've seen any number of people, including your neighbor, who might say to you, wow, you know, why did everyone down at the local school get sick at the same time? And that for them, that's the, that's the probably the oldest quote, proof of virus that we've seen, is just humans trying to create these explanations in their own mind. But I, I agree, Jacob, that's why in a farewell of virology, I suggested that metagenomics is probably virology final stand. I don't think they've got anything else. We know that all of their techniques last century have basically showed that the virus hypothesis is incorrect. So, you know, we saw huge attempts, particularly I think around the 1970s when they were trying to purify viruses.

(01:21:51):

Really, they, they were actually trying to do it, you know, it was serious business developing a whole lot of techniques with centrifugation, et cetera, to try and get these particles. But what happened was that whenever they came up with these purified mixtures, they didn't do anything. They <laugh>, they, they didn't have all these nasty pathogenic disease causing behaviors. It just didn't work out for them. So I think what we've seen is a systematic failing, failing over, you know, over a century now with the methodologies failing. And I think this is it. We're, we're at genomics now. So I think this, this has been a most important topic to discuss because I think it's the, it's, it's virology last gasp. It's, it's all I've got before the whole virus model disappears, hopefully for good.

Dr. Stefano Scoglio (01:22:39):

I think I just wanna add one thing, and that is you know, the real problem I think is coming for, for virology from the field of ex exosomes research, because now they do purify exosomes. They don't really purify exosome, but they concentrate them a lot through n nano oral filters, right? Nanopore filters. They could do the same with viruses, right? The problem is the researchers in, in, in in exosomes, they don't need to prove any pathogenicity. So they can purify them and that's it. But if they virologists apply the same technology and concentrates whatever they think is the virus, then they, they would've to prove pathogenicity and they would actually discover the viruses are just exosomes, non-pathogenic exosomes. That's why they don't do that. And they keep going with the cell cultures, with the, you know, and telling you that isolation means cell cultures in microbiology, which is of course bss.

Jacob Diaz (01:23:47):

All of it's bss. I mean, I mean, we covered this in other sessions as well with the idea that exosomes, micro vesicular bodies, cellular debris, all of them, they look the same, but it, it, it's all point in the clear stuff. You point to something and you claim that it's doing something that you can't even prove that it does, which is all a virology. And unfortunately it is rampant in academia nowadays. So I really hope that everyone watching and listening was able to get through all the scientific vernacular and all that stuff and really understand why genomes, variants, all of that pertaining to virology on top of what we've discussed earlier in this summit with isolation and all that stuff, isn't science. It's not real. They have nothing. It's artwork. You know, Peter McCullough, you know, a couple months ago used a study. He said, oh, look, this is a work of art.

(01:24:40):

These, these virions or whatnot, they're exact, this is exactly what they're doing. It's a work of art. It's all fake. They're making things in a lab. They're making things in their test tubes. They're making things in their, in sical models, and they're pushing it as reality when none of this has ever been proven to be real in the first place. So everyone listening, don't be afraid the next time that they announce a variant of

another virus, because we guarantee you it does nothing to worry about. So thank you for tuning in to the end of Covid summit session end of variant and the end of genomes as we know it. Regarding to viruses. I'm Jacob Diaz. I'm leaving you with Dr. Mark Bailey and Stefano Scoglio and Andrew Kaufman. Thank you guys for joining me. I really appreciate it.