NATIONAL CITIZENS INQUIRY

Red Deer, AB **Day 3**

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EVIDENCE

Witness 6: Dr. Jonathan Couey
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Shawn Buckley
We welcome you back to the third day of hearings in Red Deer, Alberta, of the National Citizens Inquiry. Our next guest is Jay Couey. Jay, can you hear me?

Dr. Jonathan Couey
I can, yes, sir.

Shawn Buckley
And thank you for joining us today. I'd like to start by asking you to state your full name for the record, spelling your first and last name.

Dr. Jonathan Couey
My name is Jonathan Couey, J-O-N-A-T-H-A-N, last name Couey, C-O-U-E-Y.

Shawn Buckley
And Jay, do you promise to tell the truth, the whole truth, and nothing but the truth, so help you God?

Dr. Jonathan Couey
I do.

Shawn Buckley
Now my understanding is you can be described as an academic neurobiologist, and you've been doing that for about 20 years before the pandemic.

Dr. Jonathan Couey
That's correct. I actually lost my position as an academic biologist as a result of taking a stand against the transfection and masking in 2020.

Shawn Buckley
Right, you went against the narrative and lost your teaching position at the School of Medicine at Pittsburgh University.

Dr. Jonathan Couey
Yeah, I was a research assistant professor, which means I was in the lab all the time. I taught only as an extra side thing.

Shawn Buckley
Right. Okay. And now you're teaching immunology and biology.

Dr. Jonathan Couey
Yes, just online, and I consult for a couple people as well, to make a little extra on the side.

Shawn Buckley
Okay, and we've entered your CV as Exhibit RE-11. And you've been invited here today because you've got a hypothesis to speak of, and my understanding is that you have a presentation, so I'm just going to invite you to launch into your presentation and share with us your hypothesis.

Dr. Jonathan Couey
Thank you very much.

I'm really pleased to hear previous witnesses pointing out so clearly that the principle of informed consent has been ignored for the duration of the pandemic. I want to point out that the last witness was very good at pointing out that you need to be able to say, "No." You do not have the possibility of exercising informed consent if no is not an option.

And the principle of informed consent from the perspective of me as a biologist, it requires that you understand. And I would argue that you can't really understand the coronavirus pandemic, given the biology that we have been provided with over the last three years on television and social media.

And because of the lack of the proper understanding of this biology across our medical communities in America and Canada and all over the world, doctors aren't even able to enable people to exercise informed consent because they themselves don't have the requisite knowledge. So these are the two topics I'd like to cover quickly tonight and then open for questions: the endemic hypothesis, and infectious clones defined.

I would like to put everybody on the same page by first just stating something that I want to justify through the rest of this talk.

The TV algorithms and NIH [National Institutes of Health] and CDC [Centers for Disease Control and Prevention] and all of these organizations like the WHO [World Health Organization] have convinced us that coronaviruses are a source of pandemic potential, and that this pandemic potential can be accessed through cell culture passage with a relatively benign virus being turned into a pandemic potential virus.

There's also the idea that you can passage it in animals and make it from a relatively safe virus to one that is pandemic potential. And the latest addition to this mythology is the idea that clever scientists can stitch together the right combination of genes and then these viruses can circle the globe for three years and do what we call pandemic. I believe that this mythology has been created over the last 20 or more years, especially with regard to coronavirus, with the idea of us having to surrender our individual sovereignty in a global inversion from freedom to some kind of fascism where you must have permission to do everything.

This mythology, I'm going to argue in this talk, is wholly unsupported by what we know about RNA [Ribonucleic Acid] versus DNA [Dioxyribonucleic Acid] replication possibilities and also just the behaviour of these entities that we are now calling RNA viruses in this talk. Not coronavirus, we're just saying RNA viruses, so we make that distinction.

So to put everybody on the same page, I just want to get everybody aware of where the endemic hypothesis fits in. Tony Fauci would have you to believe that in 2018—above my head—there was no coronavirus;

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2019 in September at some point, a coronavirus was released in Wuhan, and something like the fuse of a firecracker, it went around the earth and spread in many different directions: eventually became Alpha, Beta, Delta and eventually Omicron in South Africa, which then took over the globe, and now we are on some ancestral version or next ancestor of, or descendant of, rather, of Omicron.

In this model, the earth remains green because there were no health problems before the pandemic, and no health problems were caused by the lockdowns, the protocols, and the vaccines. Without those changes, many more millions of people would have died. In this scenario, we have defeated epidemics in the past with vaccination. Novel coronaviruses can jump from species and go around the world—they can pandemic. False positives are rare because PCR [Polymerase Chain Reaction] is good and specific, and variants are evidence of both spread and the continued evolution of a single pathogen. We spend money studying viruses using gain-of-function research. This is the basic TV narrative on one side.

And what they would like you to fight about, really, is whether or not it was a natural virus that just happened to fall out of a cave and get onto a train and a plane; or if it was a mistake made in a laboratory by some very arrogant scientist who either took a virus out of the wild and then infected his local town or a city; or that they, even worse, made something in a laboratory that otherwise wouldn't have existed. But again, green earth, there are no health problems, and then the pandemic comes along and here we are. Same difference.

The virus spreads. It changes to Omicron. It takes over the world and now we're at a new version of Omicron taking over the planet. In this scenario, again, the lockdowns don't have to have hurt anyone. Vaccines can have saved lives. The protocols were the best they could do, and the same thing holds true for all of these things. We used vaccination to defeat

epidemics in the past. Novel coronaviruses can jump from the wild. PCR works great. Variants are evidence of spread, and we spend money on gain-of-function research.

You can tweak this one a little bit if you want and say that the lockdowns and the EUAs [Emergency Use Authorization] caused some excess deaths, but the majority of people still died from a virus. And so there are many different ways to tweak this narrative.

Another way that this narrative has been tweaked is that there are no viruses at all. That measles doesn't exist, that there was never a coronavirus, that everything is a lie. This is, of course, not very— It's not very acknowledging of what we know of all of the molecular biological techniques and the synthetic viruses and clones that they can make. So there are these entities and we have studied them for a long time, and I think this scenario is one of those traps.

So you have three traps here. You have a natural virus, you have a lab leak virus, and you have absolutely no viruses at all.

And none of those three encompass the true biology that we knew already for basically the duration of modern medicine. If you go before the pandemic into a medical textbook and look up coronaviruses, they will tell you that between 25 and 35 per cent of all respiratory disease without a known cause is thought to be caused by coronaviruses, of which there may be up to 200 varieties which circulate in humans.

And now instead of this being the baseline, we start with a baseline where there are coronaviruses. And then in 2019, it doesn't even matter. Was there a release? Was it a natural one? Did a few people get sick in Wuhan? It doesn't matter because the PCR can't differentiate between any of these coronaviruses.

This is the illusion that they've placed on you because all they needed to do was accentuate different coronaviruses found in the background and claim a phylogenetic progression. Sounds wizardry, but it is one of the only ways in which this molecular signal will be shared so beautifully. The lockdowns, protocols, vaccines, account for the total excess deaths in the pandemic. There, nothing unusual happened until we stopped treating respiratory disease the usual way.

The interesting thing about this endemic background hypothesis is that the PCRs are not

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having false positives in the way that you think, all the time. Yes, you can over-cycle a PCR test, but if the background is hot for homologous genes from endemic coronaviruses that they are pretending are not there, you have a situation where a vast majority of the good positives are still picking up background coronavirus and not whatever they purport to have been released.

Shawn Buckley
Now, Jay, can I just interrupt you just to make sure that people understand what you're saying? What you're saying is that there are a number of coronaviruses that we just live with, and have lived with all of our lives. And that the PCR test is not specific to what governments call COVID-19. The PCR test is just testing for genetics that are already in this background of coronaviruses that we live with. Is that what you're saying?

Dr. Jonathan Couey
I'm saying that, yes, that is the scientific literature at this stage. The ability to pinpoint a particular coronavirus is not a level of fidelity that they had before the pandemic. And there's no reason to believe, from looking at any of the PCR tests and the primers that they've put forward, that they've come up with a unique and highly specific PCR test that can differentiate between one coronavirus and the hundreds of others that are in the background and rare.

Shawn Buckley
So sorry for interrupting. I just thought that was important for people to understand.

Dr. Jonathan Couey
Absolutely. It's not a problem at all.

Additional harms were also caused by the response and including the lockdown, including use of specific agents like midazolam and remdesivir. The point of this of this hypothesis is to remind everyone that your gut feeling that the PCR test was one of the primary ways that the hood was pulled over our eyes, you are absolutely correct.

And the one trick that they still have up their sleeve is the idea that there was a novel virus for which you had no previous immunity. Even in the worst-case scenario here, where there is a release from a laboratory, you still would have had previous T cell and B cell immunity from previous coronaviruses because of the homology between these genes had a great chance of overlapping. And so the concept of this being a novel virus is also cancelled out in this hypothesis. It's not possible.

And people were making that argument in 2020 from March on, and they were just ignored. Mike Yeadon is one of them. So if we move forward, then let's think about how this could be possible.

In the United States, the total number of deaths is in sky blue here behind my head. And the number of pneumonia deaths is in light blue down here on the bottom. And I hope you can see this arrow. The very yellow at the bottom here are identified flu virus deaths. And so what you see here at this part is the beginning of the pandemic. This is 2014 to the pandemic. And what you see is: Although year on year, it seems like we got pneumonia under control—remember, ladies and gentlemen, these are pneumonia deaths; many, many, many more people get pneumonia, but don't die—and then suddenly after 2014, '15, '16, '17, '18, '19, '20, '21, What? Up to three times as many people in the United States started dying of pneumonia in a way that they've never done before. And that is a number of deaths which correlates precisely with any possible excess deaths. It is extraordinary, really, that this correlation is so high, and people have still ignored it.

And I know everybody here is familiar with Denis Rancourt's work, and he has done an excellent job of dissecting how the all-cause mortality in America was organized in different places around different times. And John Bodeman [Note: Researcher's name cannot be confirmed] is another researcher in the United States, who's done excellent work correlating these new causes of death. And what happened during the beginning of the pandemic was simply a mismanagement of respiratory disease in hospitals.

And it's been done with one particular methodology, right? They said there was a dangerous novel virus. It could be detected by a PCR test. And they correlated that PCR test

with detrimental health protocols, where they took away antibiotics from people who probably should have just had antibiotics.

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They didn't allow people to be treated with repurposed drugs, and instead insisted on remdesivir. They ventilated people to prevent spread; and these detrimental health protocols were encouraged by giving hospitals $35,000/a patient that got on a vent. That enabled a larger portion of all-cause mortality than PnI—that's pneumonia and influenza—to be prioritized as a national security threat. That's what you're referring to, your previous speakers are referring to, when they say that this is a military operation. This was identified as a national security threat caused by a novel virus. Therefore, we could execute a plan that we had, and it is still in motion.

My argument would be that if you need a molecular signature, which would have seeded this event around the world, it could not have been a point release of a coronavirus because its genetic signature would have changed sufficiently in different directions around the world so that none of this uniformity in variance could have ever occurred. And yet somehow or another, we are told this story of a clean progression of variants around the world, sweeping, sweeping, sweeping in these waves and colors. There's no precedence—none, zero precedence in biology—for any phenomenon of an RNA virus to do such a thing. And yet without any questioning at all, we just took it.

And I'm saying to you now that I think the only way this could have happened is if they purposefully planted these— these molecular signatures in the places that they were going to blame and call part of the pandemic because a natural coronavirus swarm cannot do this.

And then the goal again is a total surrender of individual sovereignty and removing these basic human rights granted permissions.

The way that they did it with four basic ideas: they did it by changing the way you think about respiratory disease. We just got through saying that there used to be hundreds of causes of respiratory disease, and now we have all basically saying it's either not that one or it's that one.

They also changed how we think about all-cause mortality. That's why I show you that picture with the blue and the blue, because in America, we never saw the light blue. Nobody ever looked at all-cause mortality and said, "Okay, let's put this in perspective. We're in America. Three million people die every year." Nobody said that. Nobody told us that every week, between 50 and 70,000 Americans die. So when they say that, "wow, a thousand people died of COVID," it sure sounds crazy.

Then they changed how we think about our immune response to disease. This was very diabolical because it was part of the way that they sold us on the shot. Antibodies are what you need. They had to change the way you think about your immune response to a respiratory disease.

And then they changed the way that you think about vaccination so that you don't question the applicability of transfection for immunization. That's what these are. These are transfections. Everybody should be calling them that because this technology has been around for more than two decades, and it's never been called anything else.
That's why I originally got in trouble with my job and got too much attention was because of speaking out about transfection because I used it on mice for many, many years.

So after they changed their mind about these four basic biological principles, they were able to ventilate people to prevent spread. They used remdesivir and midazolam to kill old people and young. The untreated bacterial pneumonia went up by at least three to four times: shutting down schools; masking children; and social distancing, even people who were married for 50 years, and let them die apart.

And at the same time in *Scientific American*, the WHO just recently in March put out an article, which stated, of course, "mRNA vaccines are safe, powerful, and effective." Those are exact words. Masks work; indoor air quality matters; wastewater tracking is useful; and genomic surveillance is key.

They are doing exactly what they planned. They are going in exactly the direction that they planned to go. So they haven't wavered at all.

So how can we get them to— How can I help you, rather, to understand this endemic hypothesis and what it really means? I think you got to understand the infectious cycle and the infectious clone, and what it is. So that's what we're going to do here. And then I'll be done.

The infectious cycle is depicted in this cartoon here. You have a viral particle, it binds to its receptor, it comes into the cell and releases its RNA,

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and then the RNA needs to get translated into proteins, and then those proteins start copying the RNA into different segments. And then this long genomic RNA gets packaged into new viruses and those new viruses go out into the wild to infect other people. You've seen lots of versions of this, this cartoon, in all of the news programs.

You may have even seen a cartoon where they show you in three dimensions, the RNA and the N protein and the invagination of the viral particle and the formation of the full variant inside of an endosome.

But this is a lot of hand waving in terms of what they know about what happens here, and they know about what the fidelity of this, it's all hand waving; because up until now, these are RNA viruses. The only way to look at them is to use reverse transcriptase to turn them into DNA and then do PCR. And once you do that, you really only find what you're looking for because your PCR is pulling up things that are specific for the primers. So if you don't choose the primers correctly, you're not going to see everything that's here. So up until this stage, it was pretty hard for them to say, "What are these viruses that get produced look like? How many of them are there? How uniform are they? What is the genetic variation between the particle that you get infected with and the particles that get produced by supposedly the hundreds or the thousands during infection?"

And so if I simplify this a little bit, the TV and Fauci has told you that you get infected with the coronavirus. The coronavirus goes into your lungs. It makes copies of itself. And if it makes too many copies of itself, you start coughing those out on people around you, and then they also get sick from the variant that you're sick with. That's why all these virions are yellow. The question is, why do they have so much trouble culturing these viruses?

You're going to hear a lot of people say, "Oh, they don't have trouble culturing them." But they do. They have to use a 96 well plate and they look for cytopathic effects and they

might find it in two wells. And then they call that a viral isolate. They can do a PCR test on that. Maybe find an E protein. “Oh, see, now there’s definitely a coronavirus there.” That’s the isolate; that’s culturing. It’s not like growing mushrooms, and then you grow some more, and give them to your friends so they can grow them, or give them a tomato cutting. Or, say, give them a couple of breeding pair of mice, so that they can have the same mice that your laboratory invented.

If you find a novel coronavirus, the only thing you can do to share it with somebody is to give them the sequence. Because you can never grow enough coronavirus from a magic bat swab to, let’s say, divide it between four labs and let them do their thing with it. That’s not how RNA viruses work.

Unfortunately, not very many virologists are adequately informed of the limitations of their work. A lot of them are not adequately informed about how this is a particular limitation in coronavirus. The reason why this is, is because a large majority, if not the vast majority, of the particles that are produced during a coronavirus infection are in fact replication incompetent. What that means is they have a mistake. They’re missing genes. Their genome did not get completely run, but it still got packaged. And so even though they look like a virus, when they bind to the next cell and release their contents in there, those contents won’t have all the doodads and gazoos ready to go, all the genes present in order to make copies of itself. Therefore, in the cartoon above my head, it now becomes more obvious why it’s difficult to culture coronaviruses; because not all the particles that you detect that might be PCR positive for an N protein are going to be infectious. Now you might think, where’d you learn that?

[The witness plays a brief video of Robert Malone stating that “in most cases, a large fraction, if not the majority, of the virus particles that are produced are defective. They’re not good for anything.”]

So I learned it from Robert Malone. Once you once you know this, you can go back into the literature before 2020, before they were trying to obfuscate all this lack of fidelity. And you can see them plainly complain about it. In fact, describe looking for coronaviruses using pan-coronavirus PCR primers because it’s very, very difficult to find a particular coronavirus.

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And so the people that have known this— Everybody knows this, but this all started way back in the 80s with Vincent Racaniello and David Baltimore, because they did this technique with the polio virus.

But since then, almost everybody that works on coronaviruses from coronaviruses in plants, in salmon, in mice, it doesn’t matter. They never start with a wild sample that they went deep into the forest to get. They start with a sample that they cloned. So what does that mean?

Well, as I explained, the wild virus here depicted as a cassette tape is lacking fidelity because DNA versus RNA. Basically, you can copy DNA because it’s double-stranded. You can also check and proofread it. And there are a whole host of secondary enzymes that are very good, optimized at doing that.

With RNA, because it’s single-stranded, although it is purported that there is proofreading in coronaviruses, the biology of coronaviruses requires them to be able to have a certain

mutation rate. And even more, it requires a regular recombination rate because of the subgenomic RNA production. Therefore, there is a great fraction because of errors in recombination, because of shortened genomes, which are called defective genomes in other viruses, where you get essentially a large portion that are replication incompetent.

But when you use PCR to sequence this group of viruses that you might find in a bat, you can get a consensus sequence. And that consensus sequence can be translated into DNA. And you can think of that as a CD [Compact Disc]. And you can make lots of copies of a CD because CDs are digital. And DNA can kind of be thought of high fidelity like that. You know, one in a million bases is a mistake, maybe even less than that. And so if you use bacteria, you can actually make a bunch of this CD. You can make a bunch of this CD in a bacterial culture.

And keep in mind, this is exactly how they make the RNA for the shot. They make a circular DNA that encodes the spike protein RNA. And they make lots of copies of that DNA in a bacterial culture. And then they add an RNA polymerase and that produces the genomic RNA, or for the shot, it would produce the spike RNA. And that spike RNA that needs to be separated from that plasmid DNA before they inject it in your kids. But apparently, they didn't do that very well.

Now, this process here, very similar, you use circular DNAs to encompass the entire genome of the coronavirus. You add RNA polymerase to make lots of RNA copies of that same clone. One sequence, that's it. It's not going to be perfect.

But let's say the RNA polymerase is pretty good. So most of these are going to be fairly long transcripts. And they're all going to be the transcript that you built out of this DNA. Then you take that, and you use electricity or a centrifuge or any other number of ways. You take that pure genomic RNA for that virus, and you put it in a cell culture. And then what that cell culture makes will make animals sick. What that cell culture makes will cause cytopathic effects. And you can do plaque assays and all that stuff.

But you can always send the DNA. You can always send the DNA to your friends. You can put the DNA in the freezer. You can print the DNA. You can order it from companies. You can order these five plasmids from companies, and they'll print them right up. And then you put them in your bacteria and grow as many litres as you want. And then convert that litres to as much RNA as you care to make over and over again. This is gain-of-function. Not the mixing and matching. Not going into bat caves. It's making pure versions of what they detect in the wild using PCR and sequencing. This is how they get around it. This is how RNA virology is done and especially coronavirus biology.

And Ralph Baric's lab is famous for the techniques that are necessary to assemble these long genomes and produce infectious clones that can be used in laboratories.

So the point is that if we could do that, right, we can look at this, we can ask ourselves what kind of viruses are produced? Can we look at that infectious versus non-infectious?

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Can we look at that fraction and see it?

Up until now, it's been very hard because we use PCR, which means we have to convert these RNAs to DNAs, and then we have to amplify them up. And then all the fractions and all of the relationships between which was more abundant, is lost. So they have recently

come up with a way of doing it where they can sequence the RNA directly, which means that they can just look at, well, are you going to take all the viruses that are supposed to be in this culture and we're going to dump them through a nanopore and we're going to see how many of these different RNAs we find.

So in a virus, when the virus makes copies of itself, it makes copies of the whole genome, which is 30,000 bases long, but it also makes skip copies with a leader sequence that then skip down to these TRSB [Tandem Repeat Sequence B] sequences and make what is called subgenomic RNA. And these subgenomic RNAs turn out to be several orders of magnitude more abundant than the genomic RNA, which should be the RNA that gets packaged in the new viruses and sent out to infect other cells. So if we use a clone of SARS-CoV-2 and we put it in a cell culture and we watch it replicate, what we see is 400–600,000 copies of the N protein.

I think I got one more click here. No, I don't. So I'm going back. Sorry about that. I thought this zoomed in a little bit, but it doesn't.

So here you can see on this map, they're doing coverage of the genome here on the bottom. You don't have to look at these two on the bottom. I should have covered these up. We're just looking at this one "B" figure right here. This is the genome on the bottom, nucleotide 0–30,000. And as this black line rises, they find more sequences of this part of the genome. And so it's way down here at under 1,000 over here. And it starts to rise. The S protein is above 50,000. And then we get up to 200,000 with the E and the M. And then we get up above 400–600,000 with the N protein. So 600,000 copies of the subgenomic RNA for the N protein.

And how many copies of the full genome did they find? The longest tags correspond to the full-length genomic RNA. And they found 111: 111 full genomes and about 600,000 copies of the N protein and thousands of copies of these other subgenomic RNAs. So interestingly, this breakdown, where you have hundreds of thousands of these subgenomic RNAs and only a handful of full genomes that are supposed to be the new infectious virus that you've been culturing: this has been known for decades.

Ever since they've been able to isolate the RNA from a picture like this, or purporting to isolate the RNA corresponding to a picture like this, when they try to isolate these viruses here, they don't find a pure— You know, these are all really long genomes, and we sort through them and sequence. There's never been an experiment done like that. When they do this, they find this crazy ratio of almost no genomes, and thousands and thousands of copies of these partial subgenomic RNAs.

Now, the argument that the virologist will make is that you need a lot more N protein and S protein and M protein in order to package new virus. And so that's why you need hundreds of thousands of those RNAs and only a handful of the full genome.

But that still doesn't jive with the known amount of non-infectious particles that the right side of virology often will acknowledge. So again, if you look at this and you think about what's really being packaged here, they have no—they have none—experimental evidence that it's only full genomes being packaged.

And in fact, by the abundance of the RNA, by what they found in all previous experiments, it's very likely that the vast majority of the particles that are produced are having incomplete genomes, if not even subgenomic RNA.

So just to be sure

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you don't think I'm crazy, right before the pandemic, they did this with a human coronavirus called 229E. They made a clone of it. They grew it in a cell culture. They did exactly the same measurement. Here's the entire genome on the bottom. Here's 10 to the fourth, 10 to the fifth, of N protein. And then all the way down here, if you look at the last figure of the paper, you find that they found two whole genomes in that clone. Two.

So we're not getting thousands of viral particles being produced when we do these culture experiments.

And I think coronavirus— People have known this for some time and they just kind of hand wave it. Because here's a paper from 2001 where you can see the full genome is barely a ghost. And the N protein and the E protein and the S—these guys are gigantic overexposed blots.

So they've known that this ratio occurs no matter how they set up these clones, no matter how they do it. They know that these partial genomes get packaged. Since before the 80s and 90s they've been looking at the replication and packaging of coronavirus infections, bronchitis, defective RNAs. It's essentially how come there's so many of these viruses that just have like junk or partial what we thought were the genome of these.

That's because that's the way this works. That's the best fidelity that these things are able to usurp from our own cell's machinery.

Here's a paper from 2023 acknowledging the generation and functional analysis of defective viral genomes during SARS-CoV-2 infection. Those are non-infectious particles. And if you read this paper here, right here in the importance, "Defective viral genomes are generated ubiquitously in many RNA viruses including SARS-CoV-2. Their interference activity to full-length viruses and interferon stimulation provide potential for them to be used in novel antiviral therapies and vaccines." This has been known for some time in flu, although the flu field seems to like to ignore this.

So infectious clones defined is, simply put, that RNA viruses are tricky. They've been very hard to understand and study, because they are often only observable as what is an indirect shadow of a genetic signature found through reverse transcriptase PCR. And that ability, or lack of ability, lack of fidelity, has opened this door for people to say that, "look, they haven't isolated the virus. The isolation doesn't work. These experiments are nonsense. Therefore, there are no viruses at all." And this is a very, very dangerous place for us to be.

We need to wake up and realize that we've never really understood coronaviruses with the fidelity portrayed on television. We've never been able to tractably manipulate them in the lab the way it's been portrayed on television. And they certainly do not travel the globe in the fidelity that has been portrayed on television.

So has it actually been cultured?

Just to address this quick before we stop, let's look at this paper. This paper actually became famous because a correlation between 3,790 quantitative polymerase chain reaction, positive samples, and positive cell cultures. It says here that, "up to the end of

May, 3,790 of these samples reported on a positive nasopharyngeal samples were inoculated and managed for culture as previously described."

Interesting. Let's go to where they're previously described.

This is the paper that they previously described it in. You can see that they're almost all the same authors, just in different order. A total of 183 samples tested positive by RT-PCR [Reverse Transcription Polymerase Chain Reaction], including nine sputum samples, 174 nasopharyngeal swabs from 155 patients were inoculated in cell cultures. SARS-CoV-2 RNA positivity in patient samples, was assessed by real-time PCR targeting the E gene. Not the S, not the RNA-dependent RNA polymerase, not the N protein, the E gene. That's it.

So listen carefully. This is culturing coronavirus at the beginning of the pandemic and showing 3,000 positives. All patients, 500 micro liters of that swab fluid, or sputum, were passed through a 0.22 micrometer pore filter. That's to remove bacteria. And then were inoculated in four wells of 96-well culture microplates

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containing Vero E6 cells. After centrifugation, that's to get the stuff to go into the cell culture.

After centrifugation at 4,000 Gs [Gravity], microplates were incubated at 37 degrees. They were observed daily for evidence of cytopathogenic effect. Two subcultures were performed weekly. That means every week they split them, so they moved, whatever was growing they moved it into a new fresh well with cells next to it. Two subcultures weekly, presumptive detection of virus in supernatant showing cytopathic effect was done in a scanning electron microscope. No images shown.

So if there was cytopathic effect, they assumed that there was a virus and they put it under the microscope to see, but they didn't show you anything. And they don't tell you how many of those they found anything in. There's no data from that. And then confirmed by specific PCR targeting the E gene. It's a loop. Don't you see? It's just a loop.

I tested positive for an E gene, then they made me cough into a dish. And then if any of those cells died, they said, wow, that's pretty cool. That's the coronavirus because he tested positive for the E gene.

Now they tested again in that culture and find the E gene again. The E gene is not proof of a coronavirus. The E gene doesn't prove that a coronavirus caused the cytopathic effects. These are the objections that the no virus people bring to the table.

And these objections are very solid for a vast majority of these papers, during the pandemic. It is just an insufficient level of scrutiny. It's an insufficient level of control. And it is a giant pile of assumption that is instead, interestingly enough in this paper, confusing people by saying hydroxychloroquine and azithromycin were effective at shortening the duration of this read. And so this is another aspect of the immune-mythology you've got to be very careful of. So many of these repurposed drugs were given in combination with other drugs and then over and over sold as the drug.

For example, this paper was pushed as evidence that hydroxychloroquine can work, without acknowledging that azithromycin is given with it. The games that they have been playing are many.

If we go back to before the pandemic to a guy like Marc Van Ranst, who was the flu commissioner for Belgium for the 2009 flu, and has got his own infectious disease lab where he works on testing for coronavirus. Here he is arguing why we need— Coronaviruses can't be found without using pancoronavirus primers. He's got a whole book chapter about how pancoronavirus RT-PCR assay for detection of all known— This is how they did it.

It's not specific, ladies and gentlemen, and these people have known that.

And so they tell you these stories about these imperfect genetic ghosts in the wild that have potential to become permanent circulating pathogens. They talk about how if you let the wrong guy like Peter Daszak into the wrong bat cave, he can passage those viruses in cell culture and pull out pandemic potential on the other side. They might also do it with ferrets someday. Or worse yet, somebody like Ralph Baric will stitch a bunch of things together that should have never been there, and we'll have a pandemic.

In reality, the only potential danger that could be used and weaponized against us is the production of RNA viruses using DNA clones. That is the danger.

That is the reason why they don't ever talk about it. They talk about gain-of-function as a way of making sure that you don't understand that that's not the danger. There was never a danger from coronavirus. Coronaviruses were always largely— If they are part of this causes of respiratory disease yearly, then they are part of a very benign set of somethings that float around. They are not part of this never-ending source of pandemic potential.

So this is what I think they did. They declared a pandemic of a

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dangerous novel virus for which the PCR was not specific, and yet they applied a unique and mostly detrimental protocol for respiratory disease to those people that tested positive; and they enforced that with financial incentives. This was all part of a military plan in the United States, which was ready to be executed when the excuse was given, and the excuse was given when these protocols were changed. It could have been an infectious clone.

You could have used a clone to see the same sequence in Iran and Wuhan and in Italy, and that unique and identical sequence around the world would have been a molecular selling point for there being an ongoing pandemic. And if it was required in order to fool these governments in Europe and in Italy (like Italy's not Europe), but to fool these governments around the world, if that was required, a clone of a wild coronavirus would have been more than sufficient for us to have seeded these things, and then let the plan roll on forward with just using this a-specific PCR test.

Again, I want to plug Denis Rancourt's data, because it's so important to understand how, if there was a novel respiratory disease for which no one had any immunity, then there would have been a predicted impact on all-cause mortality. And those predicted impacts were not seen at all, and his analysis is fantastic.

And then finally I just want to make sure I remind you one more time that nobody should be using "transfection." I was so excited to hear someone say that earlier today. There's no

debate. It should not be used in healthy humans, and up until the pandemic, it was only used on people who were likely going to die anyway.

So please stop transfection because they want to eliminate the control group. Once everybody's been transfected a few times, all of these ailments, all of these increases in illness and autoimmunity, will all just blend into a background of increasing public health problems, rather than being able to be identified as, "Wow, the people who have triple transfected themselves are having worse and worse outcomes, year on year." Which I think is the truth that has already emerged, and can only emerge in greater and greater numbers as we move forward.

Thank you for your patience. I hope that was okay. That was the end of my presentation.

Shawn Buckley
That was really interesting. I'm just hoping to clarify a couple of things with you and ask you something new. You use the term transfection, which for most of us is a new term. We think of mRNA [Messenger Ribonucleic Acid] technology, but that's a new term for transfection. You're saying transfection instead of mRNA vaccine, because transfection is the correct term.

Dr. Jonathan Couey
Yes, that's correct. So if I can add to that a little bit, for the academic bench biologist, that means somebody that plays with mice or monkeys in a laboratory, and they want to change the local protein expression, upregulate it, downregulate it, maybe even knock down a gene. There are ways that that's done, and that's ways that's been done for about 20 years.

One way to do it is to use an adenovirus, where you put the DNA of interest, encoding the protein that you want to express in that adenovirus, then you put that adenovirus in the brain of the mouse, and it will go where it's going to go and express that protein. Using DNA to express protein in a cell is called "transformation." And if you use mRNA to do the same thing, you can use electricity to put the mRNA in, you can use lipids like they're doing now, sometimes people use gold particles.

There's lots of different ways to do it, but regardless of how you do it, you use mRNA, it's called transfection. If you use DNA, it's called transformation.

And so if you go on the website of Sigma or Thermo Fisher and you just look for transfection products, they'll have a whole web page on it. And there's no difference between the mRNA shots that they're giving and any previous transfection technology, except for maybe the proprietary bubble that they put it in. But it's the same technique, with the same lack of tissue specificity and dose control that they've never been able to replicate in any other application of it.

Shawn Buckley
Now you've said that that we shouldn't use transfection in humans. And can you explain, give your reasons why we should not use transfection—

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or as most of us know, mRNA technology—in humans?

Dr. Jonathan Couey
The proof is in the use. So in a laboratory animal, for example, if your using transfection, you're inevitably going to get autoimmunity. Animals that are transfected are not intended to live long, healthy lives. They're always sacrificed and then their tissue is used to look at the changes that you made. And so up until very recently, I don't think anybody's really thought about this as a very viable technique, except to use for somebody who's already going to die from, like, cancer or something like that.

And the trick is to realize, and I think that this is a very true statement, although this is more of a gut feeling to me—but it's a gut feeling that a lot of other people have had for a long time—it doesn't matter, really, if you expressed a particular toxic protein. It doesn't have to be the spike. If you've expressed a foreign protein in your cells, and it's random cells in your body, your immune system only can do one thing. It can unleash the neutrophils, destroy those cells, and clean them up.

Now if those are your heart cells, it's permanent damage. If it's endothelial cells, you have endothelial damage. If it's ovary cells, you have ovary damage.

And this is a known downside of transfection. It's a blunt tool. It's been used for a long time in academic medicine, and for 20 years, people have been dreaming about making it into a viable therapeutic methodology, but they've never even come close to getting it to work in single examples, never mind on a scale of billions. And there is no other conclusion to come to, that if you want to treat, beneficially, a mammalian, like a human that you want to live for 20 more years, transfection is not a therapeutic option. And anybody that has sold it as such has either been telling us lies or has been just really wrong. It's not to be done. It's not fit for purpose.

They would like you to believe that it is, but you cannot usefully augment someone's immune system by transfecting foreign proteins randomly in their body. It's just ridiculous.

Shawn Buckley
Okay, and your opinion on that is based on animal study after animal study after animal study after animal study, and some use in a very small subset of humans who are, you know, terminal with cancer and things like that.

Dr. Jonathan Couey
Yeah, and also very anecdotal personal experience: I can tell you one three-second story. I was asked to help do an experiment in squirrel monkeys where they wanted to express an algae protein. It's a long story about why they would do that, but they wanted to express this protein in the brain of the monkey so that they could manipulate some circuitry, and then go back to that brain region afterward and see what neurons they manipulated and see how they were connected anatomically, and maybe that was going be a good idea.

But, when we started this experiment, I suggested to these primate neuroscientists that, look, when we transfect a mouse, I've got a window of, like, let's say three to four weeks where I can do my experiment and everything is okay; but if I wait any longer than that, the place where I initiated the transfection starts to have problems, and starts to have an immune reaction which leads to a lot of neuronal death. So I tried to tell these primate scientists that, like, if we do this experiment, we got to do it on an animal that you're all done with, and that's already scheduled to be sacrificed because otherwise, you might just lesion that area of the brain in four months and then you won't even know what you did.

Well, what did they do? Monkeys are expensive, so you can't just sacrifice them. So they let this experiment run—I think, for, I think they let it run for 12, but it might even have been 18 weeks—and then when we did the anatomy and we cut into that area, almost all the neurons were gone. And that's because, again, transfecting neurons and getting them to express foreign proteins is eventually a challenge that your immune system can't ignore.

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And that is true no matter where transfection is done, and in any current application of it, it should be an expected outcome. And so yes, it's not fit for purpose.

Shawn Buckley
Right. Now, I wanted to go back. You've made the point, and I think it's important for people to understand, is, coronaviruses are part of, just basically the environment that we live in. There's a number, there's hundreds and hundreds of coronaviruses, and so many that the conventional wisdom is that—what did you say?—20 or 30 per cent of our flus, annual flus, are considered to be caused by one or another of these hundreds of corona viruses. That's— I've got that right?

Dr. Jonathan Couey
Yes, correct.

Shawn Buckley
So what my question is: this started with just a bang in the media in early 2020; and all of a sudden, we seem to be using the PCR test for a specific coronavirus that we're told is SARS-CoV-2, or named COVID-19. Is it possible that there was a specific PCR test for a specific new virus at that time?

Dr. Jonathan Couey
It's not. I don't think that it is possible for them to have had the fidelity to use the— The PCRs that they designed, were not designed, cannot be designed to be specific the way that they were designed. As far as I understand, for example, in Canada, after talking to Dr. David Spector, they didn't have nested primers for your PCR, which means that any overlap on the PCR sequences, or partial overlap, would likely result in amplification, which again makes them a-specific for the genes that they're amplifying. And because this was a national security issue, the goal would not have been to be as specific as possible, but of course, as you guys know in Canada, to rope in all possible suspected cases.

And so again, the more specific the test would be, I think the less appropriate it would be for the national security threat. So there's motivation for them to have not made a specific test. And more importantly, the background and lack of fidelity means that they could not have made such a specific test.

Shawn Buckley
So the technology of the PCR, would it be your opinion then, that they were basically, that PCR test would just be identifying a family of coronaviruses?

Dr. Jonathan Couey
At best. And again, remember, it's only identifying small fractions of the genome being present, which does not in any way, shape, or form indicate infectivity, or even the presence of a contiguous virus, but just the presence of these genes, which are homologous across lots of coronaviruses. So it's a very, very different lack of fidelity relative to what is portrayed.

Shawn Buckley
So you know, if we had a multivitamin with 100 different vitamins in it, this is really a test for one vitamin and then pretending that there's a multivitamin there.

Dr. Jonathan Couey
Uhhh...

Shawn Buckley
Just using an analogy that maybe people might understand, right? So think about that.

Dr. Jonathan Couey
It's a bit more like saying that there's a— That not telling anybody that there are any automobiles in the world, and then saying, "Oh, there's a pandemic of KIAs, and if we just test we can—" Lots of people end up having KIAs. And it's like wow, that's pretty crazy. And then, "Oh, yeah. Look, now we have Toyotas, and now we have Hondas," and as we change what we're identifying with the test, it seems like, wow, it's spreading all around the world. But those cars have always been there.

And so in this case, they told us, I guess, that there's an epidemic of Teslas, which can be tested for by looking for wheels and four doors and a windshield. And so when people tested their garage, they go wow, I guess I got a Tesla too.

And it's probably closer to something like that, where the specificity is implied, when in reality they're testing for things that all automobiles have. And so there is no pandemic of a particular kind of automobile. It's just that the test is confirming everybody's got a car, or there are a lot of cars around.

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Shawn Buckley
So just so that we're clear: so if the test is non-specific, and even because it's just testing for a part that doesn't even tell us we have a whole genome, conceivably, then, they could just come up with another virus name, start running a bunch of PCR tests, and convince us that we're in the pandemic again.

Dr. Jonathan Couey
Absolutely. Absolutely. I think this is the one you should almost assume that's what's going to happen. That's their plan. That's what PCR has been established as, they can— That's what the WHO said in that article that I shared. Genomic surveillance is a good way of

following these things. So they would like to sequence the sewer all the time. They would like to, yeah, they would like to swab you monthly if they could. That's what they want. Definitely.

Shawn Buckley
Right, but it's really just a tempest in a teapot, it's a phantom.

Dr. Jonathan Couey
I mean, think of it this way, like rhinoviruses are a virus that we all know are very common, part of the common cold bouquet, and we're not sequencing and doing PCR for rhinoviruses right now, but they could. And as soon as they rolled those tests out at people that were asymptomatic and then cycled them too far, you'd get a lot of false positives right away. And if they told you it was one rhinovirus instead of a-specific for many, they could also convince you that, "look, it's changing." So it's very tricky game they played on us.

Shawn Buckley
Right, now do you have any information— We've heard about people taking antibody tests for SARS-CoV-2, and do you have any information on whether or not those are realistic tests, or whether, to use your term, they would have high fidelity?

Dr. Jonathan Couey
I think they're probably, if done correctly, they're actually probably very good identifying people with previous immunity and recent exposure. It's tricky, right, because they, I think, use the antibody test as a way of emphasizing the seroprevalence to the spike protein.

So they get to choose what they search for when they say that they're going to build this antibody test. If they were going to be honest with it, we would look at these papers that we looked at today, and we see that the N gene, or the N RNA, is produced in the most abundance. So the loudest signal to look for, if you were going to see if someone recently exposed to a coronavirus, would be that N protein. But there's almost no tests can find the N protein epitope immune response in people that are vaccinated because they don't have a natural response to the virus anymore, which would be to respond to the RNA that gets produced the most and the protein that gets produced the most.

They are responding to the protein that they were forced to respond to. And that illusion was partially seeded by the idea of saying, "here's an antibody test for the spike protein. It can show you if you've been infected."

And so people got it in their head that all the spike protein antibodies that tell if I'm infected, when in reality, you'll have T cells to the RNA dependent RNA polymerase and T cells to the N protein and B cells to the N protein, all from overlapping previous infections. So you could have tested positive before the pandemic, too, because you had natural immunity and were exposed.

Shawn Buckley
So I guess to refine my question. I mean, I'm just wondering if it's possible that there's an antibody test specific to what were called, this you know, COVID-19 or SARS-CoV-2, as opposed to an antibody test, really, for just this background group of coronaviruses that—

Dr. Jonathan Couey
I think we're really— I think you and I would be buying in to their simplified biology if we said that there was a SARS-CoV-2 to separate from all of these other viruses.

Shawn Buckley
No, it's just interesting, because I live in the drug approval world regulation part. In Canada, we didn't have an emergency order the government came out with, or rather, we don't have an emergency pathway that they could use. We hear in the U.S., this emergency approval. So we had an interim order that didn't define a specific virus. So they define COVID-19 as relating to something that was not a specific virus. And that got me very suspicious about our ability to identify a specific virus.

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Dr. Jonathan Couey
I mean, much of the literature supporting this panoply of viruses that's circulating in the wild: if you look through this literature before the pandemic, you will find that entire papers are written about the diversity of coronaviruses in bat caves by looking for a 296 base length part of the RNA-dependent RNA polymerase. And if they find it, well, that's a coronavirus; they find another one, that's a coronavirus. And we find all these and then we make a little chart of how they're related. And this is a phylogenetic tree of bat coronaviruses: no spike proteins, no full sequences, and no viruses cultured, just genetic sequences found using pan-coronavirus primers for the RNA-dependent RNA polymerase.

And so to go from a literature which is so amorphous, to "now we can definitively tell you that this is the sequence and this is you, positive or negative," all this stuff is just smoke and mirrors, they do not have that fidelity.

Shawn Buckley
Thank you. Those are my questions. I'll ask if the commissioners have some questions for you.

Commissioner Massie
Thank you, Dr. Couey, for this very interesting presentation. I mean, you certainly did a lot of effort to make it somewhat accessible for a layperson, because I mean, what you're discussing is fairly complex. I have a background in biology, and I've developed adenovirus vaccines, and all kind of things, so I understand where you're coming from. But there's a few questions that popped in my mind. Do you have experience growing viruses, either small scale or large scale, or different type of viruses in your lab?

Dr. Jonathan Couey
I only have had the privilege of working with somebody who does it for me. So no, I've never enriched adenovirus, for example, or anything like that. It's stuff that I take for granted that has been commercially available since, I guess, since I had my first lab. For me, I take a lot of things, especially with adenovirus production and the transformation experiments that I've done, I just take it as very commercially accepted that adenovirus can be made, and it can be packaged with the DNA that I want in it.

Commissioner Massie
My question has to do with your very interesting concept of infectious clone. I mean, to me it's not a big surprise because I know that even DNA viruses based with adeno-AAV, when you actually go to the trouble of doing deep sequencing and you isolate clone based on plaque formation and you're very careful to make sure that it's clonal and you grow it just one cycle, you'll see variants immediately after one cycle of replication. And as you pointed out, the fidelity of replication for DNA is way higher than RNA. So I've always thought of RNA viruses from any source, would it be plant or bacteria or mammalian viruses, as kind of quasi-species, I mean the extreme being the HIV [Human Immunodeficiency Virus] where I mean, where hepatitis, I mean, you find a lot of variation, which makes the characterization of a clone that much more difficult.

Having said that, we now have tools to do that, and I've noticed that you were citing a paper from Didier Raoults' lab that has done— I've been following his work for more than three years now, and he has done a large number of clonal isolation and tried to characterize it, doing deep sequencing to confirm that it's not just PCR sequence that they were looking at; they were very thorough in order to do phylogenetic tree and so on.

Are you wondering whether when you actually isolate a clone from an individual that is sick—and now you're trying to identify within this individual a clone or variant, and now they've called it "variants of concern" and stuff like that—are you questioning that the moment you start to grow it in culture, after a few cycles, you might end up with something that has already started to evolve, or have differences in the overall sequence because it's a long genome and the fidelity of the replication is not so great?

Dr. Jonathan Couey
So I assume that that happens, and that's the argument that pervades my head when I think about the idea that we were told that

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from Wuhan to Washington to California to New York and Italy, there were less than three amino acid differences for four months. And thousands of people, hundreds of thousands of asymptomatic infections, were supposedly spreading around the world, but the virus was keeping a fidelity of a ridiculous level. And the original SARS [Severe Accute Respiratory Syndrome] virus that was tracked in 2002 had an average of between 33 and 50 amino acid changes per patient for the first six months. And then this one changed 10 amino acids in the first six months.

So the stability of the portrayed sequences has no previous biological precedence. So the only way that this could have happened is if somebody seeded this level of fidelity around the world, like put a clone in, so that everybody that they tested would have a culturable virus for a little while, and it would be a sequence of very high homology with the ones they released elsewhere. And then they slowly drifted away. They slowly recombined with the background. I don't even think that they would have to do it with very many patients.

If you look through the literature, you will find a very large paucity of actual, and I'm talking about experiments now, like from 2020, where they really isolated the virus sequence and then said, "Wow, it's pretty much the same." It's not based on very many observations like that. America's entire pandemic is based on one sequence collected in Seattle from the Snohomish County man, and that's it. Every other sequencing reaction that was ever done was done behind CDC closed doors, and the sequences were reported only

after the CDC decided to report them. There's no open sequencing in America, and there never was.

And so if these sequences are real, as we are here now, the point is what happened in 2020 was a portrayal of something that couldn't have happened. Now we're talking about a background sequencing coronaviruses when we've never sequenced them with this rigor before 2022. It doesn't surprise me that we find all of this stuff. But to say that this is evidence of a pandemic is very, very different; and I don't think that that's evidence of a pandemic. It's evidence that those genetic sequences might be there. But he's got no data from 2019, so he doesn't know if he would find the exact same data set had he started looking then.

Commissioner Massie
So what we're seeing right now, though, I mean, in this Omicron era is that it seems that when you do a rigorous analysis, you do find other types of variants that seems to be more prevalent, in the sense that I understand there's going to be a very wide diversity of different sequences of the SARS-CoV-2 virus. But the one that seems to be growing better in a given population, in a given time, will eventually be, if you want, sampled more frequently, and in the end you will have an over-representation of this variant until another one will supersede that. So that's kind of a cycle. And it's probably, it has probably been like that before we started to analyze the coronavirus. I just didn't know about it.

Dr. Jonathan Couey
That's it. There you go. There you go. You just said it. If it was like this, and this pattern existed before the pandemic, and they just announced it now, then we are being bamboozled. It's like saying that, where there's a pandemic of automobiles, while forgetting that we've always had them.

Commissioner Massie
So your hypothesis in terms of the endemic state is that we have been, the human population, have been in an endemic state of coronavirus that could give respiratory infection as other viruses could, like rhino and even adeno and RSV [Respiratory Syncytial Virus], you name it. And somehow emerged, or decided, that these atypical respiratory infections was triggered by this particular new virus that has come in the environment, and now was spreading all over the world. And it was almost the same kind of virus everywhere.

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And you find that difficult to fathom with the way normally coronaviruses will actually be in the environment. Is that your thesis in terms of a pandemic versus having local reproduction of coronaviruses in a population?

Dr. Jonathan Couey
Right. Remember, the pandemic definition is a virus that starts in a room and then spreads around the world without being able to be stopped. And that is a very, very specific set of biological claims. And so the idea that there are these many, many stories of people having an interesting respiratory disease is completely and wholly disconnected from the idea that

a pathogen, or a virus, is moving around the world with high fidelity, and is tracking with that disease. Because that is the illusion of the PCR.

If you assume that a PCR test identifies a case, knowing that the PCR can be false-false positive, and also positive-false positive, in the sense of a wrong coronavirus gene, then we have a really huge problem because the statement that a virus was released at a point and is still circulating the globe is not possible. And that requires an extraordinary amount of evidence. It's an extraordinary claim. It requires an extraordinary amount of evidence, way beyond doctors saying, "I've seen a few people with a new sickness. And so I decided not to give them antibiotics and throw them early on the ventilator and give them some remdesivir and they died." That's not an atypical respiratory disease.

And you can't differentiate from that, and mistreating it, if you changed your protocols across the entire nation. How can you call that a unique respiratory disease when you stop treating the respiratory disease the way you used to? And you started giving remdesivir, or midazolam, or not giving them steroids?

All of these changes that were made, and the autonomy taken away from doctors, caused unique respiratory symptoms. That's the more likely explanation than an RNA virus maintaining fidelity for three years, and now having a slightly different hat on that we call Omicron.

Commissioner Massie
So if I understand what your hypothesis is, is that the SARS coronavirus COV2 exists and it can potentially induce diseases, but it was this kind of disease—among all of the other disease you can find from respiratory viruses—was not the unique cause of this so-called pandemic. And what we see in excess mortality is more likely attributed to what we've done in terms of lack of treatment, and also all of the things that we've imposed to, quote-unquote, control the spread of the virus. Is that your working hypothesis?

Dr. Jonathan Couey
Absolutely. Because if you talk about how people died, you don't have to talk about very much virus. Absolutely.

Commissioner Massie
Thank you very much.

Dr. Jonathan Couey
You're welcome.

Shawn Buckley
Dr. Couey, those are the questions of the panel. This was very illuminating. On behalf of the National Citizens Inquiry, we sincerely thank you for attending today and providing your testimony.

Dr. Jonathan Couey
It was my honour, thank you very much. And I wish you guys the best of luck in this most important endeavor.

[01:19:06]

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The evidence offered in this transcript is a true and faithful record of witness testimony given during the National Citizens Inquiry (NCI) hearings. The transcript was prepared by members of a team of volunteers using an "intelligent verbatim" transcription method.

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