Email exhange with an evolutionary biologist

Mark Bailey [redacted] Mon, Jun 13, 2022 at 9:30 PM
Reply-To: Mark Bailey [redacted]
To: Christine Massey <cmssyc@gmail.com>

Dear Christine,

I was recently asked by a third party to engage in a "debate" with Dr Zachary Ardern, an evolutionary biologist at the Wellcome Sanger Institute. Ardern had claimed that after watching a podcast where I mentioned "viral" genomics, he was able to refute the points I made and provide evidence of viruses through his specialty of microbial genomics. I think you will find the email exchange amusing, if not interesting.

He declares that he is the "real" scientist and then proceeds to engage in *ad hominem* rants and other logical fallacies. You'll note how he avoids answering all the pivotal questions and keeps ignoring the lack of valid controls in virology's methodologies. He appears oblivious to the validity of the data he analyses as he constantly refers to "viral" sequences and proteins without showing how this was established. Apparently the scientific method can be ignored by the "real" scientists! In any case, his emails speak for themselves so please feel free to circulate them as you see fit.

Keep up the great work and best wishes from both Sam and myself,
Mark

Dr Mark Bailey
MB ChB, PGDipMSM, MHealSc
drsambailey.com

On Thu, Jun 9, 2022 at 2:45 PM [redacted] **(Moderator)**
<[redacted] wrote:

Hi everyone.

As you all know, I wanted to start this thread to help us nail down the usefulness/uselessness of modern genomics in supporting virus theory. You are all very busy so I understand that replies may be slow. But I think removing the middle man in the conversation is probably a good idea at this point.

Zachary as you know I passed on those papers you recently sent to Mark. Let's use his response as a springboard for this. How does that sound?

Marks Response
"These two papers don't add anything in terms of proof of a virus. I presume he still agrees with us that a virus is a replication-competent intracellular parasite consisting of a genome and a proteinaceous coat? (But where is it in these papers?...)

Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 In Vitro Infection

1. Was he involved in this paper, and if not, did he check what the authors meant by "mock-infected"? (We have FOIA material we are about to publish in our upcoming essay concerning the invalid "mock-infections" that the virologists are employing.) Unless it can be demonstrated their controls are valid, there is little point in further analysis of this paper as it is not following the scientific method.
2. *"Direct RNA-seq data was mapped to the combined genome (consisting of human/African green monkey genome from Ensembl (release 100), SARS-CoV-2 Australia virus (Australia/VIC01/2020, NCBI : **MT007544.1)"*** - they are using a reference genome as a template, which itself was templated against other reference genomes. Where is the paper that shows any of these sequences come from inside a pathogenic virus? (Remember my "turtles all the way down" comment - I have followed the "coronavirus genome" trail back to the start: there are no "viruses" demonstrated.)
3. *"differential polyadenylation, transcript usage and gene expression level changes"* - These findings do not require the existence of a "virus" and is almost certainly the reason why these authors and others are not comparing their results to valid controls.
4. The longer reads that can be generated with the ONT platform do not provide evidence of a virus. Obviously, nobody in our camp is denying the existence of nucleic acid sequences or proteins - it is the attribution to "viruses" that is fallacious. The virologist's methodologies are not scientifically valid for all the reasons we have written and talked about.

Direct RNA sequencing and early evolution of SARS-CoV-2

1. *"The genome sequence of SARS-CoV-2 was rapidly determined and shared on January 5th of 2020, being 29,903 nucleotides in length, and annotated based on sequence similarity to other coronaviruses (GenBank: MN908947.3)"* - We have already broken down this paper and why the methodology was invalid. As some people still don''t see the problems, my co-author and I are going to devote an entire section of our next essay to Fan Wu et al.'s declaration of a coronavirus, including the very sentence when they introduce the word "virus" without any demonstration of its physical existence.
2. *"Aligning to the genome of the cultured SARS-CoV-2 isolate **(MT007544.1)"*** - Again, they are starting with the premise that these sequences are viral by aligning it to a template that has been declared as the "SARS-CoV-2 genome".

All they have in these studies is the assumption that they started with a virus and from this unproven premise describe their findings, whether it be genomics, proteomics, or transcriptomics as being "viral" in nature. They are simply analysing tissue breakdown experiments *in vitro* and as I mentioned above, that is why they don't do valid controls with human-derived samples *sans* the alleged virus. And keep in mind, Dr Stefan Lanka generated almost the entire "SARS-CoV-2 genome" by simply adding yeast RNA to culture cells."

Note, I realise we have talked about the Lanka paper, hopefully we can source a copy of his work soon.

I know all sides here are passionate to learn more, so let's see if we can do that.

Thank you all again.

--

[redacted] **(Moderator)**

-------- Original Message --------
On Thursday, June 9th, 2022 at 15:16, [redacted] **(Observer)**
<[redacted]> wrote:

Hi All,

Thanks [redacted] for setting up the thread. I realise there is a lot for Zachary to reply to so I wondered if I could ask a quick clarification question to Mark?

Mark writes: Where is the paper that shows any of these sequences come from inside a pathogenic virus?
I'm sorry if it's been covered but it doesn't seem clear- what's the alternative explanation for the new sequences? I understand that you believe many of the images to be of vesicles, but cellular vesicles would have DNA/RNA that could clearly be shown to be from the host cells given that the genome has been sequenced. The same would be true with all of the additional contaminating DNA/RNA e.g from bovine serum- it would be of known sequences. I'm unclear about how the new sequences can be accounted for without a virus, particularly when they're derived de novo (or when there are long reads) as again, all the other fragments from cellular debris etc would be known sequences.

Stefan's paper doesn't appear to be published but I'd love to read it if the results are now available- the last version I saw showed cytopathic effects but had no results relating to sequencing after the addition of yeast.

Apologies if it's silly question- I'm a pretty broad biologist but don't work in genetics/virology. Clarification of this point would be really helpful.

Thanks in advance
[redacted]

On Thu, 9 Jun 2022 at 06:56, Mark Bailey <[redacted] wrote:

[redacted] **(Moderator)** ,

I'll get to the point - I'm not here to give tutorials to people who are new to the virus existence debate. Particularly as the material is freely available from the likes of Stefan Lanka, Sam and I, The Perth Group, David Crowe, Andy Kaufman, ViroLIEgy, etc. In fact, even more groups here.

Thousands of hours have gone into this work and yet we still get asked to go over the same material!

I have just pointed out that the genomic sequencing experiments have no valid controls, which should be a red flag for any scientist and [redacted] asks for an, *"alternative explanation for the new sequences"*. Find out what "mock-infected" means and exactly what their methodology involved. (Hint: they don't use a human-derived sample *sans* the alleged virus.) Admittedly you probably haven't seen the number of institutions we have pinned down on this issue - we are writing a follow-up essay to this: https://drsambailey.com/covid-19/the-covid-19-fraud-war-on-humanity/ - The second essay is much bigger and we will be publishing the responses with a whole section on virology's anti-scientific practices through their lack of valid controls. You may also want to look into Barbara McClintock's work demonstrating that new sequences can be expressed "*de novo*" by cells through various "shocks".

The burden of proof is not on us to prove there is no virus: we can't prove a negative and have no obligation to provide alternative explanations. The virologists invented the theory of viruses so whatever method they employ to prove their existence, it must satisfy that definition. *In vitro* genomic experiments that attribute sequences of unproven provenance to "viruses" are not proof of a replication-competent obligate intra-cellular parasite, that transmits between hosts and causes disease. Asserting a "virus" must be responsible (or citing antibodies, clinical observations, etc) is not the required proof.

"I understand that you believe many of the images to be of vesicles" - which images are you referring to and what do you mean by "believe"? How do virologists distinguish EVs from viruses? *"cellular vesicles would have DNA/RNA that could clearly be shown to be from the host cells"* - if that is the case why don't the virologists simply settle the issue once and for all and show us the "viruses" and their contained DNA/RNA? (We have been asking for this proof for years.)

They will not publish Stefan's paper in any scientific journal for reasons you can probably understand - I believe that the lab technician that did the experiments would also likely lose her job.
Stefan talks about the experiments here: https://odysee.com/@DeansDanes:1/cpe-english:f

Moderator [redacted] - this is not "Terrain theory vs Genomics": it is whether the methodologies of the virologists are sufficient to prove their claims concerning the physical existence of their postulated particles. Terrain theory and genomics do not necessarily clash although you have probably noticed that many of us in the terrain camp do not view genomics as particularly informative with regards to health and of course dispute "the central dogma of molecular biology".
Genomics is probably virology's last stand - all of their traditional methodologies are being abandoned as the virologists refuted themselves by employing them. Hopefully you will see in the next essay the corner they are in from the preposterous FOIA responses, etc.

If anyone has further questions, please do so after familiarising yourself with the debate. The Perth Group's "HIV – a virus like no other" goes over many of the virology techniques and is worth reading if you haven't already.
And if anyone has a virologist who is prepared to defend one of their papers purporting to show a virus, we would love to have them on Sam's channel.

Regards,
Mark

-------- Original Message --------
On Friday, June 10th, 2022 at 02:51, Zachary Ardern [redacted] wrote:

> Hi everyone,
>
> The reason I am interested in this discussion is that I saw some videos from Sam and Mark, where the relevant genomics was misrepresented, misunderstood, and/or generally butchered. This is perhaps not surprising given that they're not scientists and seem to have very little relevant training but it was all in a remarkably sarcastic tone, dismissive of actual scientists (apparently so as to poison the well for their audience, and discredit real science). I am curious whether they are willing to learn or at least attempt to justify their extreme claims. Having them purporting to explain genomics (and the scientific method more broadly) in the way they have done is a great disservice to the public understanding of science and to public health. I'm not here to give basic tutorials in genomics, but I will attempt to do so if necessary to get a straight response or for them to admit that they actually are way out of their depth.
>
> I am not a virologist (though I have published actual scientific papers on COVID, rather than just blogposts), but am an expert in microbial genomics (largely from an evolutionary angle), having spent many thousands of hours on it. The group I now work in is a world leader in genomic epidemiology in bacteria and viruses. If Mark, Sam, et al. actually want to engage with scientists, this is their opportunity. It should

> not be necessary to have to read hundreds of pages of material in non-scientific sources in order to get an answer to [redacted]'s very reasonable scientific question.
>
> Observer's
>
> <u>A few major problems with Mark and Sam's approach:</u>
> - Mark demands proof, but actual science is based on multiple corroborating lines of evidence, rather than 100% "proof"
> - Science is actually about comparing hypotheses, and the virus hypothesis clearly accounts for a large amount of data. The alternative is very murky indeed, but there is in fact an obligation to give a clear alternative if you want scientists to take you seriously (I don't think you do though, it seems clear that your target is non-scientists).
> - Sam and probably Mark have claimed there is ***no*** evidence for viruses. This is patently absurd, and a basic misunderstanding of "evidence". The genomes, for example, clearly count as evidence of some type for the virus theory.
> - The genetic material in question is known to encode proteins (see via ribosome profiling and mass spectrometry). The structure of these proteins can be determined in the lab, or inferred straight from the sequence (with e.g. AlphaFold). The mechanism of action of many of these proteins is known in some detail through laboratory studies. The structures also match what is seen in e.g. electron micrographs. So, there is a clear connection between sequence, structure, and pathogenic behaviour in cells. My interpretation of the rhetoric here is that Mark and Sam attempt to obfuscate what is actually clear to those with relevant scientific training.
> - Long sequences of nucleic acids which encode proteins don't just pop out of nowhere - they contain a lot of specific information, which is closely tied to the virus proteins and their structure and function.
> - Real science is done with experiments by people with relevant training, peer-review, and published papers, not FOIA requests, conspiracy theories, and blogposts.

Some starting questions for Mark:
- what do you think was done to the "mock infected" cells that makes them a bad control? (In any case, this is a red herring, given that clearly there is new genetic material seen e.g. in patient swabs, that was not found prior to the pandemic).
- where is the genetic evidence of SARS-CoV-2 being able to be derived from natural yeast cells? (clearly this is nonsense). Show me the sequence data, please.
- where does Barbara McClintock show completely **novel**, highly specific, genetic material representing what scientists call viruses being produced by shocks to cells?
- if the highly specific RNA sequenced across millions of patient samples is a result of tissue breakdown, why was it never seen before late 2019?
- do you accept that the results of genomic epidemiology (in diverse bacteria and viruses - e.g. Ebola) show transmission chains of the genetic material between people? If not, why not?
- do you accept that these transmission chains correlate with disease? If not, why not?

Thanks

Zachary

On Fri, Jun 10, 2022 at 9:43 AM Mark Bailey <[redacted]> wrote:

Zachary,

You've made no attempt to address the body of our work or other groups - in fact, you do not appear familiar with it at all.
We are back to the same fundamental problem: steering the discussion away from the physical proof of particles that fit the description of a virus, particles that are disease causing.

"If Mark, Sam, et al. actually want to engage with scientists, this is their opportunity." - Yes, would you like to come on our platform to put forward your case to the audience? I would be happy to engage in a debate. We could start with the scientific method and valid controls.

(Moderator) [redacted] I'll leave it up to you whether Zachary's response, resorting to ad hominem and appeal to authority arguments has any merit. To me it is irrelevant to the discussion.

Zachary - can I confirm that this is you: https://www.sanger.ac.uk/person/ardern-zachary/
We would like to include you in our next essay.

Mark

------- Original Message ------- **(Moderator)**
On Friday, June 10th, 2022 at 11:49, [redacted] wrote:

> Thank you both.
>
> Yes, Appeals to authority aren't logical or useful in debate, neither are personal attacks. We want to come to a common understanding of our physical reality, so let's try to keep personality etc out of it and assume each other's motives are pure. Having spoken to you both, I do believe they are. But there are different incentives at play, this I think we can acknowledge.
>
> Just to clarify as well, this is to **discover the relevance of genomics in proving/disproving a physical virus**.
>
> I'd like to attach two bits here. One is a clip from Dr Richard Smith from our interview with him, who I think addresses peer review, and its proven usefulness. Not directly useful but still helpful to the broader cause of disagreement here I think
> Secondly I'd like to hear your comments @Zachary Ardern on this attached paper regarding structural analysis of sequence data regarding SARS-CoV-2. From my understanding this is exactly your wheelhouse? Is it useful? Is it wrong? How?
>
> Zachery, if you had to explain to your Grandma, in one or two sentences, how your field of study proves the physical existence of viral particles, how would you formulate your response to her? Without saying "trust he peer reviewed PhD's" She needs to understand its relevance to the claim clearly.
> I've been attempting in my head to find the best way to steelman your position in simple terms, and am struggling due to its complexity. A more simple explanation might help us find the best way to address it. I am still at a loss as to how detecting genetic material in populations is logically necessarily connected to proof of a virus. How does finding new genes in a population prove to us that they belong to a tiny parasitic ball? It appears to

me that we can find that same information in other things.

Steelmanning the position(on both sides) is useful to us.(us being the human race)

To the point of engagement in a public platform, is there a "neutral territory" that could be suggested, that could allow for both Zacharys understandable desire for anonymity and also provide neutrality?
Ivor Cummins comes to mind, as he is of the opinion that viruses likely do exist, but that the core driver of the bodies response to them is the Terrain. How would you both feel about engaging on his platform, I can attempt to line it up if that is agreeable?

Thanks again, your engagement is honestly very much appreciated.

DrRichardSmith_PeerReview.mp4

(Moderator)

On Sat, 11 Jun 2022 at 02:29, Mark Bailey <[redacted]> wrote:

Hi [redacted] Moderator

Sam or I would be happy to go on Ivor's platform - people were requesting back in 2020 for Sam and Ivor to do something together. If Zachary doesn't want to join, we're happy to talk to Ivor about "viruses" anyway.

We also have a development that should be of interest to all.
A group of us in the "no virus" team are putting together a public challenge for the virologists. For over a century, the virologists have failed to fulfil their own postulates regarding the proof of a particle that meets the definition of a virus. Hence we are going to meet them halfway and are proposing a series of experiments using their own current methodologies to see whether they have any validity. We are putting together a document that is easy for the public to understand and I'll let you know when we publish it. In the meantime, Dr Tom Cowan provides a rough outline of the proposal here (starting @8.10).

Zachary - you are yet to provide the specifics of what the Baileys and others have got wrong in our publications. Can you elaborate on "the relevant genomics was misrepresented, misunderstood, and/or generally butchered" and "they actually are way out of their depth"? How does this relate to our work concerning the existence of viruses? We are all here to learn but it is unclear what your argument is.

Your "starting questions" indicate you are probably not familiar with the virus existence debate. To briefly address a key point:
So far you have produced two papers which do not provide any evidence that the sequences are viral in origin. To get to the fundamental problem in "Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 In Vitro Infection" the experimental cells were alleged to be "infected with SARS-CoV-2

Moderator

Australia virus (Australia/VIC01/2020, NCBI: MT007544.1). The MT007544.1 "isolate" was obtained by Leon Caly et al. in 2020. Their paper is another uncontrolled experiment and no part of it demonstrates a particle that meets the description of a virus. Their culture mixture (aka "viral isolate") becomes the basis for the Long-read paper. There is no mystery why the same sequences are found in the brew but none have been shown to come from inside a virus or be disease-causing at this point or any other. The "mock-infected" line is invalid as a control as it is not altering one variable (the "virus") - there needs to be a human-derived sample *sans* the "virus". In other words it needs to be consistent with the scientific method.

Dr Richard Smith's comments outlined what many of us have talked about with regards to virology: the methodologies described in the published papers are not adequate to make their conclusions. We have outlined the insufficient methodologies including "culturing", "isolation", animal experiments, etc extensively in our work. We have also addressed the "genome" issue - Zachary's evidence for viruses relies on the assertion that sequences are "viral" in nature and starts his arguments with this unestablished premise which leads to circular reasoning regarding whether the viral particle exists.

In any case, I believe that the challenge we are proposing will be a great way to move forward - [redacted] it may tie in with the documentary?
Zachary - you can possibly pull some strings with your contacts to help make the challenge possible? Help make it "real" science for people like yourself.

As Tom points out, the "debates" are rarely productive. In the video, his mention of me is with regards to a live "debate" I had with Dr Kevin McCairn. Kevin made a spectacle of himself in trying to prove the existence of SARS-CoV-2 through *ad hominem* attacks and his unwillingness to discuss the failed methodologies and lack of controls in virology. It seems to happen every time it's been tried sadly.

Regards,
Mark

------- Original Message -------
On Sunday, June 12th, 2022 at 11:59, Zachary Ardern <[redacted]> wrote:

> Dear all, I'll respond to various points, apologies for the length, it is necessary as details were requested.
>
> I don't know what you mean by your publications Mark.

Do you mean your self-published blogposts, or the book?
Either way, I haven't read these (I don't want to pay you for this disinformation), I have just listened to the same material most of your followers get - videos. If you don't stand by these, please remove them from the internet and post an apology.

Let me give you all some specific examples of the Baileys' butchered interactions with genomics.

1) Viral Mania podcast - Mark - https://odysee.com/@VirusManiaFilms:b/Podcast_01:0
Around 18:50 you focus on genomics. You say there are millions of small fragments, and we need to pick a template, and picking the template is arbitrary.
There are multiple basic problems here.
- you ignore the existence of long read sequencing
- you ignore the results of de novo assembly from long reads (you completely misrepresent this as being literally "from nothing")
- you ignore the fact that the human genome is known and these sequences can be extracted, so it's not a mess of many millions of random reads
- critically, you ignore the extreme specificity of even 150bp long sequences. Specific sequences of this length aren't obtained by chance. I suspect you know this to at least some extent, hence prefer to avoid or misrepresent the genomics.

20mins: claims that it is "not like looking at a human genome, or a bacterial genome, where you know exactly where the genetic fragments came from". Actually the process is the same in bacterial and viral (and other) genomics. That is why I can run exactly the same scripts for standard analyses in both.

There are lots of other issues, including fundamental and blatant inconsistencies in how you approach genomic knowledge from different taxonomic groups.
You claim bacteriophage do exist (fascinating!) but aren't pathogenic (around 7:15). But of course they are pathogenic for their bacterial hosts - they lyse cells, and the processes are observed and known in extreme detail. You say they are a stage of development of bacteria. Remarkable claim, but I can only assume you felt free to make stuff up in this interview and were freestyling.

14:40 - you say there's no evidence of transmission even in bacteria. This is false, of course - genomic epidemiology (using whole genome sequences) clearly shows transmission of various pathogenic microbes, including in animal studies e.g.
https://journals.asm.org/doi/full/10.1128/IAI.00071-20 , as well as e.g. in hospital studies. Given that you accepted in this interview that bacterial whole genome sequences are legitimate, you don't seem to have much to stand on here.

Of course, Sam's videos are full of similar claims.

I'm curious, as I look at the different associated revenue streams you've built up around this, how much money you're making from this con (almost certainly more than my salary - despite all the intimations about how the actual scientists are the ones motivated by money), but that's a side issue. Maybe Luke can investigate it in his forthcoming expose of the virus denialist movement.

##########
Moderator's
Now, to[redacted]questions
I don't have time to properly dig into the unpublished essay from an anonymous mathematician. I have already spent too long on this for free. I can't see much point to doing this either, given that it's anonymous so details can't be checked, and any technical issues raised won't make sense to you.
Anyway, in summary it seems they find that if you allow an absurdly low similarity threshold (minimum 0.6% similarity??) with no biological relevance you can get short reads from the original SARS-CoV-2 samples to "map" to other viruses. Feel free to explain to me why this is not a pointless exercise intended to impress non-scientists.

You asked me to explain how my field of study proves the existence of viruses. I have already said that science is not about proof, it's about evidence, so in future please use "evidence" instead.
Here is an explanation of some key points, again, which are connected in a logical order:
1) The virus sequence, which can be obtained by multiple different sequencing approaches, demonstrates the existence of **highly specific long RNA sequences** in recent samples from infected patients which were **not present in human samples prior to late 2019**.
2) This genome sequence encodes specific proteins not found in the human genome or of mammalian origin, which **we can predict the structures** of from the sequence alone using methods such as AlphaFold. We can also **experimentally determine the structures of individual proteins**, after expressing them separately. We can also **detect the existence of these proteins (including in patient samples) using mass spectrometry**.
3) These **detailed structures e.g. for the Spike protein match the structures observed in the virus particles in cell culture, observed with various forms of electron microscopy**. This is another link to "particles" aside from the mass spectrometry - **the proteins encoded by the RNA have a specific, observable structure** (also able to be predicted straight from the RNA sequence), and form e.g. the virus outer coat (along with other components of the virus).
4) The full **genomes allow detailed tracing of the course of transmission of the viral RNA** (which demonstrably encodes the particle-forming and pathogenicity-causing proteins) between patients, using very similar methods of inference as those used in paternity tests, or other genetic studies.

I'm not very interested in engaging on this in public at the moment as the Baileys have no scientific credibility and I don't feel either a need to lend them mine or a massive desire to spend more unpaid days on this preparing to debate a baseless conspiracy theory. If I did engage in some form it would just be because they have quite a few misled fans who are wasting their money and time on this and risking their health.

Zachary

On 12. Jun 2022, at 03:17, Mark Bailey <[redacted] wrote:

Some comments...

Zachary continues to be unable to address the fundamental issues but seems happy to declare that he hasn't read the body of work that has been presented.
Interestingly he also made no comment on the proposal from our wider group to test virology's current methodologies in a blinded trial.

None of the points he raises have anything to do with showing the evidence of a virus. We have asked him to show us a paper where the provenance of the sequences were established as "viral" but he is unable to do so. He appears unfamiliar with where the "virus" template trail leads - where is the original "virus" in the creation of the templates?

A brief response to his latest email:

"Specific sequences of this length aren't obtained by chance. I suspect you know this to at least some extent, hence prefer to avoid or misrepresent the genomics."
- Specificity does not equal virus, how is that being misrepresented?

"20mins: claims that it is "not like looking at a human genome, or a bacterial genome, where you know exactly where the genetic fragments came from". Actually the process is the same in bacterial and viral (and other) genomics. That is why I can run exactly the same scripts for standard analyses in both."
- Again Zachary: how were the sequences declared as "viral" in the first place? If we take a blood test from you, we don't then mix it with other people's blood and then start our analysis, we only want your blood. There needs to be a step where the provenance was originally established.

"You claim bacteriophage do exist (fascinating!) but aren't pathogenic (around 7:15). But of course they are pathogenic for their bacterial hosts - they lyse cells, and the processes are observed and known in extreme detail."
- Please send us a paper that shows this "pathogenic" property, I suspect you are referring to the headlines and not looking at the methodology.

"14:40 - you say there's no evidence of transmission even in bacteria. This is false, of course - genomic epidemiology (using whole genome sequences) clearly shows transmission of various pathogenic microbes, including in animal studies e.g. https://journals.asm.org/doi/full/10.1128/IAI.00071-20 , as well as e.g. in hospital studies. Given that you accepted in this interview that bacterial whole genome sequences are legitimate, you don't seem to have much to stand on here."
- Yes, I believe we were talking about the claim that "pathogens" pass between humans to cause disease. We've never claimed that microbes don't pass between organisms and you've missed the point again. What does your murine study show? Did the mice make each other ill? If you bothered to

look through our work you would see we have dismantled these types of animal studies. Are you aware of the 100 years of failure in clinical experiments to show H-T-H transmission of influenza?

It is a continuation of these kinds of arguments being employed:

"The alternative is very murky indeed, but there is in fact an obligation to give a clear alternative..."
- Who says so? Can't something be wrong although no one knows which other idea is right? Study the history of pellagra for example. What's important is not to pursue a hypothesis that is wrong, even if no one cannot think of another. You only need one anomaly to sink a hypothesis.

"The genetic material in question is known to encode proteins (see via ribosome profiling and mass spectrometry). The structure of these proteins can be determined in the lab, or inferred straight from the sequence (with e.g. AlphaFold). The mechanism of action of many of these proteins is known in some detail through laboratory studies. The structures also match what is seen in e.g. electron micrographs. So, there is a clear connection between sequence, structure, and pathogenic behaviour in cells. My interpretation of the rhetoric here is that Mark and Sam attempt to obfuscate what is actually clear to those with relevant scientific training."
- Interesting and testimony to the marvels of technology. But irrelevant if it's not a virus Zachary. Once again you have missed the point.

"Real science is done with experiments by people with relevant training, peer-review, and published papers, not FOIA requests, conspiracy theories, and blogposts."
- How did Archimedes get on with your worldview? Did you listen to Richard Smith's comments or read Peter Gøtzsche's work regarding the corruption and control of the scientific journals?

"Science is actually about comparing hypotheses, and the virus hypothesis clearly accounts for a large amount of data."
- Science is actually about comparing hypotheses, and the virus hypothesis clearly generates huge amounts of data. Except data on what stuff is inside the alleged virus particles. And upon this every claim depends, including diagnosing viral infections.

"if you want scientists to take you seriously (I don't think you do though, it seems clear that your target is non-scientists)."
- How do you know our targets? Our targets are anyone with a brain and curiosity. Do you only target scientists?

Moderator [redacted] did in fact take the time to find out about our situation - he knows the price we have paid in the past few years. We gave up well paid work in the medical system to pursue our own research and wouldn't want it any other way. What "con" are you referring to? We ask money from nobody - almost all of the content is provided for free and people are free to donate if they wish. Your comments in this regards are puerile. Thousands of people around the world contact Sam to say that she has been the most important factor in improving their health over a lifetime. We also give local talks for free and field thousands of questions related to health matters. Curiously you say they are "risking their health" - that's not the feedback we've received and I'm not sure how you would be able to advise them about health matters? (Attacking the Baileys won't help them with their wellbeing.)
The barrage of *ad hominem* arguments has only served to reveal your fear and I suspect a lack of wisdom.
You appear to be in danger of losing touch with humanity - perhaps read the last verse of 'The Sounds of Silence'. Technology can be very seductive but not all of us pray to a neon god.

Moderator [redacted] - I'm still happy to go on Ivor's platform.

Cheers,
Mark

------- Original Message -------
On Sunday, June 12th, 2022 at 23:43, Zachary Ardern [redacted] wrote:

> I'm not avoiding the key issues - I'm focusing on the genomics, the intended topic and why I'm here. I'm not going to play other games which distract from this.
>
> There's no need to get hung up on using the word "virus", since you're allergic to it. It's just a word. We can just talk about the entities we observe and what we can see they do.
> There's also no need to worry about "templates" (reference sequences) because assemblies can be created fine without them. I know you want to try to go down a rabbit hole here which any nonscientist will get lost in.
> And there's also no need to worry about tissue culture (I know you also love to go there as you can label it as artificial), as most things of interest here can be shown straight from patient samples.
>
> **Mark, please clarify what exactly you disagree with, if anything, in this simple straightforward list:**
> Moderator [redacted], please ensure that you understand each of these points, and see if Mark gives an answer.
>
> 1) The specific, reproducible, RNA sequences seen in patient swabs since late 2019 (and not before), coinciding with the rise of a novel respiratory illness, produce specific known proteins such as "Spike" and "Nucleocapsid".
>
> 2) We know the structures of these proteins from both sequence-based predictions and structural biology techniques such as cryo-electron microscopy. We can observe these same proteins at the whole virion level in electron micrographs (and I believe also more specifically with various immunofluorescent techniques - I haven't delved into the literature on the best methods for these).
>
> 3) We can detect these highly specific sequences at the protein level in patient samples with mass spectrometry and at the RNA level in patient samples with nucleotide sequencing (short or long read - direct RNA sequencing or via cDNA). We do not observe these sequences in samples prior to late 2019.
>
> 4) We can study this highly specific genetic material being transmitted between people and animals with genomic epidemiology. The RNA is not just native to the mammalian cell, produced some kind of mysterious "tissue breakdown" but is clearly transmitted between people.
> Example: If I get sick after contact with my office mate after his family are all sick, I will see that their RNA sequences are the same as mine or differ only very slightly, while others sequences from across the world or earlier in the pandemic will be different at more positions. The natural inference, of course, is transmission of the material among his family and to me.
> - Luke, please let me know if you need more information on how we can confidently trace the transmission, I would be happy to explain this as it relates to my area of expertise, and can dig up specific papers showing transmission chains if necessary.

> 5) We understand in extreme molecular detail the way that these proteins (which are not naturally found in mammalian cells) interact with host cells, as part of the replication of the entity e.g.
> - the binding of Spike to ACE2
> - the replication of the viral RNA with the encoded RNA polymerase
>
> Another question from a friend for Mark (but please don't let this distract you from the main list above) - what is your take on checking blood transfusions for viruses like HIV? Would you be happy accepting blood which hasn't been checked?
>
> Thanks

On Mon, 13 Jun 2022 at 00:23, Mark Bailey <[redacted]> wrote:

[redacted] Moderator,

this is farcical behaviour from Zachary and he has wasted a great deal of time by not familiarising himself with our work and the work of many others.

"I'm not going to play other games which distract from this."
- He has been on several *ad hominem rants* and committed other logical fallacies throughout his emails. Last time he declares he doesn't want anything to do with the Baileys who according to him, *"have no scientific credibility"* and now wants us to dignify him with a response again.

"There's no need to get hung up on using the word 'virus', since you're allergic to it. It's just a word. We can just talk about the entities we observe and what we can see they do."
- This is completely disingenuous, patronising, and anti-scientific. 'Virus' has a specific meaning which is a replication-competent obligate intracellular parasite consisting of a proteinaceous coat surrounding a genome. If it exists it must have a physical existence and shown to be infectious and the *causal* agent of disease in a host. His disingenuous argument is further revealed when he then goes on to use the terms 'virion', 'viral', and 'viruses'. Words are the means by which we communicate and understand each other - if the definition of words don't matter, then how can one have this conversation?

- He expects me to answer all of his questions and when his points are rebutted he simply moves to another question without any acknowledgement.

- He has not responded adequately (or at all) to other issues that been put to him such as:

1. The lack of valid controls in the methodologies of the virologists - this is the fundamental issue. For example, the long read RNA paper (Chang et al.) he proffered as evidence is not a validly controlled experiment and it derives its material from Leon Caly et al.'s paper, which also lacks valid controls. It is nonsense built on other nonsense and is inconsistent with the scientific method.
2. The inconsistencies found by the Hamburg mathematician in Fan Wu at al.'s SARS-CoV-2 sequencing data and why there were better matches for other "viruses". Zachary has assured us of his expertise in this area so I invite him to provide a formal response and we will ask Dr Stefan Lanka to present it to the mathematician. After all, Fan Wu et al.'s paper was the basis of the declaration of a "novel coronavirus" and COVID-19.
3. Dr Richard Smith's comments on the major problems with peer-reviewed journal publications relating to how "scientific" narratives are controlled.
4. Where we can find a paper demonstrating the establishment that any of the sequences he refers to come from inside a virus particle.
5. The proposed challenge headed by Dr Tom Cowan where the current methodologies being employed by the virologists, including sequencing, are put to the test in a blinded trial involving multiple laboratories.

- He's now introducing questions from his "friend", revealing more ignorance to the material already covered in *Virus Mania* and elsewhere. How do you check blood for "viruses like HIV" Zachary? You've indicated you won't read *Virus Mania* so here's some comprehensive information that you and your friend can start with: http://theperthgroup.com/SCIPAPERS/HaemophiliaHIVAIDS.pdf and http://theperthgroup.com/HIV/TPGVirusLikeNoOther.pdf

Moderator [redacted] - I outlined at the start, I'm not doing this to provide tutorials for people who are new to this material. As you know I'm doing this "debate" with both hands tied behind my back as you asked me to focus the discussion on Zachary's field of genomics. If he wants to expand the scope into our other areas such as the history of virology, virus "isolation", HIV/AIDS, antibodies, clinical diagnostics and treatment, PCR, epidemiology, electron microscopy, cell culturing, animal studies, vaccines, etc then I would be more than happy to refute virology that way.)

Moderator [redacted] and team,
you have said you want to find out if genomics could provide the evidence for the existence of viruses so I'll respond to Zachary's email for your benefit.

To answer his points:
1) *The specific, reproducible, RNA sequences seen in patient swabs since late 2019 (and not before), coinciding with the rise of a novel respiratory illness, produce specific known proteins such as "Spike" and "Nucleocapsid".*

- Specific and reproducible sequences do not equal a virus no matter how "novel" they appear. See above definition of 'virus'.
- What *"rise of a **novel** respiratory illness"* - How is it novel? A case of COVID-19 is confirmed by circular reasoning with a PCR that has no established diagnostic specificity: https://odysee.com/@drsambailey:c/what-is-a-covid-19-case:9 and https://odysee.com/@drsambailey:c/covid-19-behind-the-pcr-curtain:b and https://drsambailey.com/covid-19/the-covid-19-fraud-war-on-humanity/
- Spike and nucleocapsid proteins have been described for decades, can you show us the paper where it is demonstrated by the methodology that they belong to any viruses?

2) "*We know the structures of these proteins from both sequence-based predictions and structural biology techniques such as cryo-electron microscopy. We can observe these same proteins at the whole virion level in electron micrographs (and I believe also more specifically with various immunofluorescent techniques - I haven't delved into the literature on the best methods for these).*"

- Electron microscopy does not demonstrate the biological function of any imaged vesicles, they are photographs of stuff that has been embedded in resin and then cut into very thin slices - whatever is visualised in these images is dead. Their particles certainly don't replicate and evidence for that must be sought elsewhere. https://odysee.com/@drsambailey:c/electron-microscopy-and-unidentified-viral-objects:f
- How can a "virus" be labelled with immunofluorescent techniques or similar if the particles being labelled are not known to fulfil the criteria of a virus? Vesicles don't become viruses because an antibody attaches to them. Several of us have dealt with this circular reasoning before, for example: https://viroliegy.com/2021/12/07/june-almeida-and-the-first-coronavirus-em-images-1967/

3) *"We can detect these highly specific sequences at the protein level in patient samples with mass spectrometry and at the RNA level in patient samples with nucleotide sequencing (short or long read - direct RNA sequencing or via cDNA). We do not observe these sequences in samples prior to late 2019."*

- You are basically repeating point 1. See my response to that - not a virus.
- Yes, we have all seen the 'S', 'N' and 'E'-protein "phylogenetic trees" featuring humans and other animal "coronaviruses". You need to get to step one first: establish that they belong to a particle that meets the description of a virus.

4) "*If I get sick after contact with my office mate after his family are all sick, I will see that their RNA sequences are the same as mine or differ only very slightly, while others sequences from across the world or earlier in the pandemic will be different at more positions. The natural inference, of course, is transmission of the material among his family and to me.*"

- Yes, nucleic acids are everywhere, including up your nose and can pass around. The detection of which sequences are reliably related to being "sick" though? The PCR kits in use have never been clinically validated. Many of us pointed out in 2020 that they had already invalidated themselves by studies such as this: https://onlinelibrary.wiley.com/doi/full/10.1002/jmv.25786 (See also the links provided in my point 1 response.)
- I have been trying to tell you that our investigations and FOIA responses have revealed that the "viral" genome sequencing has not been done with valid controls. There have only been negative controls with water and 'positive' controls with already known sequences. My next 'COVID Fraud' essay with Dr John Bevan-Smith will dedicate a whole section to exposing this and I will send you a copy. In the meantime, Dr Stefan Lanka has already outlined virology's control problem, for example: https://www.researchgate.net/publication/316280466_Virology_State_of_the_Art and https://wissenschafftplus.de/uploads/article/wissenschafftplus-the-virus-misconception-part-1.pdf

5) “We understand in extreme molecular detail the way that these proteins (which are not naturally found in mammalian cells)”, *“the binding of Spike to ACE2” and “the replication of the viral RNA with the encoded RNA polymerase”*

- Not naturally found - what does that mean? The proteins can be detected in asymptomatic mammals as well as tissue breakdown experiments.
- Interesting area we are now in. Can you show me the evidence for the ACE-2 receptor? I used to think I knew about it too, until I went looking for it. Suggest you look into some of the issues with cell theory that has become dogma. (Harold Hillman’s work for example.) In any case, you haven’t established you have a virus, and certainly not that any spike protein belongs to such a postulated virus.
- You are making assertions about the RNA being “viral”. One more time - where was the step that showed the RNA came from inside a particle that fulfilled the definiton of a virus?

Moderato[redacted] thank you for the opportunity to participate but I don't think Zachary has the temperament or breadth of knowledge to make this worthwhile. I'm happy to help your team with any other questions.

Best wishes,
Mark

------- Original Message -------
On Monday, June 13th, 2022 at 8:09 PM, Zachary Ardern [redacted] wrote:

> Let's stick with the 5 questions I raised. We're making some progress with these "responses" and I think Mark is getting nervous.
>
> Quickly though, regarding the anonymous mathematician's paper, as I recall it doesn't claim that other viruses give a better match than SARS-CoV-2 does - see their table 4. They claim, as I recall, that other viruses give a better match than other coronaviruses do. I'm not going to waste time on a full review but think their methodology for mapping to other viruses is meaningless, given the extremely low similarity threshold.
>
> 1) we seem to agree these RNA sequences are real, and no evidence has been provided that they're not novel. The specific forms of Spike and Nucleocapsid have not been described for decades - homologs but not identical proteins are known in other coronaviruses. I think you know this Mark, and are trying to obfuscate.
>
> 2) what we see in the particles which scientists label virions is the same proteins encoded by the RNA of interest. This is confirmed not just visually but e.g. with immunogold labelling of patient samples. https://www.mdpi.com/1999-4915/13/9/1816/htm. These observed particles are not just random vesicles which Mark can brush aside, but show a direct connection with the RNA of interest, which (see below) is being passed around between people. Now we're making progress.
>
> 3) we seem to agree, these very specific RNAs and proteins are real and detected in patient samples. Great!
>
> 4) Mark seems to be accepting that these RNAs of interest (including the information of Spike, Nucleocapsid, etc.) are being passed around and this can be tracked. Remember, these are not random RNAs, but encode specific proteins, which we can show form into particles encapsulating the RNA.
>
> 5) These specific proteins are **not** found in "tissue breakdown experiments". This is nonsense.
> And Mark is now denying not just viruses and germ theory but also cell theory - this is quite funny. I'll let Moderato[redacted] look into the literature for the ACE2 receptor.
>
> We know the RNA is "viral", because it encodes specific proteins which produce an outer coat, and which are involved in replicating the RNA. In order to get around this, Mark needed to pretend in his videos that genomics is all a mess and made up, but that is not true, and I think he knows it. There are real, specific
>
> RNAs being transmitted, and they are encoding proteins which fulfil the different roles required for a virus. Genomics thus provides excellent evidence for the existence of SARS-CoV-2 and other viruses.
>
> If you read these questions and responses carefully, you will see that Mark is (perhaps inadvertently) admitting rather a lot, which together adds significantly to the case that SARS-CoV-2 is a real novel entity which is being replicated in cells and passed around between people. This already is a massive result which fans of the Baileys should hear.
> The correlation with sickness is of course clearer with more deadly diseases such as Ebola or HIV - the same principles apply there regarding the genomics. I'm not an epidemiologist so can't immediately give all the best studies regarding disease, but I think it is clear that my expertise in genomics helps to clarify some things which are very relevant to the existence of SARS-CoV-2.
>
> Zachary

From: [redacted] Mark Bailey

To Zachary Ardern[redacted]

Date: Tuesday, June 14th, 2022 at 00:03

Zachary,

your arguments are that of the destitute. Your proffered EM study reveals you didn't do your homework with the references I sent you and don't realise that the methodology of the paper doesn't support its headline.

Here is a "cell culture"/tissue breakdown
experiment: https://www.microbiologyresearch.org/content/journal/jgv/10.1099/0022-1317-71-2-263#tab2

Thanks, we're happy to go public with your "massive result" - we can let others decide who couldn't answer the questions in this exchange and who is nervous.

Mark

Final emails in the "debate"

Mark Bailey <[redacted]> Wed, Jun 15, 2022 at 5:57 PM
Reply-To: Mark Bailey <[redacted]>
To: Christine Massey <cmssyc@gmail.com>

Dear Christine,

I have attached the final few emails in the "debate" I had with Zachary Ardern. You will see he still doesn't appreciate the invalid methodologies being used by the virologists. I sent him the 1990 paper, "Primary structure of the S peplomer gene of bovine coronavirus and surface expression in insect cells" by Parker et al. (https://doi.org/10.1099/0022-1317-71-2-263), as an example of an invalid tissue culture experiment that attributes a spike protein gene to a "coronavirus".

His response is *"It shows if you culture a specific, known, **virus**, you can find out things about the proteins."* - how does Zachary know it's a "virus"? Because the paper states *"the Quebec strain of bovine coronavirus (Dea et al., 1980) was propagated in Madin-Darby bovine kidney (MDBK) cells, obtained from the American Type Cell Culture collection"* (The 1980 experiment was performed with Vero and MDBK cell lines with the usual fallacious methodologies and claims you are familiar with regarding "virus isolation".)

He completely fails to see the circular reasoning being employed once again. Genetic sequences and proteins are being called "viral" without a step to show how this was established. The experiments are not providing the required evidence for a virus as they do not demonstrate infectious, parasitic particles that result in more of the same particles. And once again it is astounding how he simply will not address the lack of valid controls.

You can see that the moderator is not impressed with Zachary's efforts and his ongoing logical fallacies. In my opinion, it's even worse for Zachary, as he doesn't even focus on the alleged *particles* - his argument is based on detected sequences and proteins only.

Best wishes,
Mark

Sent with Proton Mail secure email.

Final emails.pdf
24K

------- Original Message -------
On Tuesday, June 14th, 2022 at 00:43, Zachary Ardern <[redacted]> wrote:

I don't know why Mark is emailing me off list like this, but if I go public on this topic it will be on my own terms, not being doxxed by these people.

The linked study, of course, does nothing to justify the absurd claim that "The proteins can be detected in ... tissue breakdown experiments." It shows if you culture a specific, known, virus, you can find out things about the proteins. Specific RNA and proteins don't pop out of nowhere.
Do you agree with your esteemed mate "Dr" Tom that the pandemic is caused by 5G? This stuff is a joke, not science.

I am doing this for the sake of[redacted]et al. As far as I can tell Mark, you're not persuading anyone here who wasn't already persuaded, and you might be turning off those who were on your side. Whoops.
This is nothing personal (though I think your claims and attitude in your videos do a great disservice to the public), you've just chosen to adopt an ideology which is nonsensical. I hope you eventually realise, if you are indeed sincere, that empirical reality is not on your side.

[redacted] feel free to follow up on any of the 5 questions I raised, or any of the other points I have raised.

Zachary

On 13. Jun 2022, at 22:22, Mark Bailey <[redacted]> wrote:

Hi Zachary,

that was to let you you know we're more than happy for your "massive result" to go public. If you want [redacted] and [redacted] to know, that's fine and I've copied them in.
The scientific method should employ valid controls among all the other fundamental issues you've avoided in this exchange. You need to understand the methodologies of virology before believing the headlines.
Perhaps take some time to look at the material you've been sent.

Mark

Observer
BTW [redacted] is not working for the documentary crew currently as she is back working on her own project.

On Wed, Jun 15, 2022 at 8:43 AM Zachary Ardern <[redacted]> wrote:

By the way, where is the magical yeast-derived SARS-CoV-2 genome that I was assured totally exists?

Was it produced by 5G too? Please make sure you discuss this question in your upcoming videos Mark/Sam.

Thanks

Zachary

From: [redacted] Moderator
To Zachary Ardern[redacted] CC [redacted] Mark Bailey
[redacted]
Date: Wednesday, June 15th, 2022 at 09:22

Thanks guys.

I've enjoyed reading through this, and it has definitely helped me refine my thoughts around it all.

Zachary, as I said earlier, and this has been again confirmed from your two recent emails, you are still affirming the consequent. A logical fallacy that really doesn't help your case at all imo. And it astounds me that an entire field of study appears to have fallen into the same trap, though given the very hierarchical structures now in place, it makes sense that it eventually would happen. As I've said, I still think the best claim you can make with the evidence you have provided is "we find these particles and there is an inferred association with sickness" to jump to the conclusion that "this particle causes sickness" is unfounded in my estimation. But we will let the viewers decide, once we get some virologists to join the conversation.

"Was it produced by 5G too? " Silly straw man claims like this don't do the virus side any good, my friend. I think you can do better.

Anyway, thank you all again, I think we should just leave it here for now. IF anyone has anything new to add in the future, feel free, but I think for now this thread is closed.