PROMETHEUS SHRUGGED:

Censorship & the Legacy of COVID-19

Abstract

The COVID-19 pandemic was supposed to be scientists' finest hour – a victory of mankind's progress over the ravages of nature, won by those whom we trusted most. Instead, humanity was betrayed by its shepherds, as scientists rushed to protect themselves. I've gathered the evidence to lay out who struck the match on censorship, why they lied to us & how they conspired to hide the evidence.

Charles Rixey M.A., MBA (c)
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Note:

This work is a compilation of selected primary source documents, preceded by the five articles I wrote from 2/26/2021 – 6/6/2021 in which I discovered and analyzed the role of Dr. Fauci in the broad scientific censorship on the topic of the potential lab origins of COVID-19.

All of the email images were pulled from 6 Freedom-Of-Information-Act (FOIA) document collections, originally requested by US-Right-to-Know & Buzzfeed. A primary goal of this work has been to provide the most relevant selections from more than 91,000 pages of correspondence, condensed and in context.

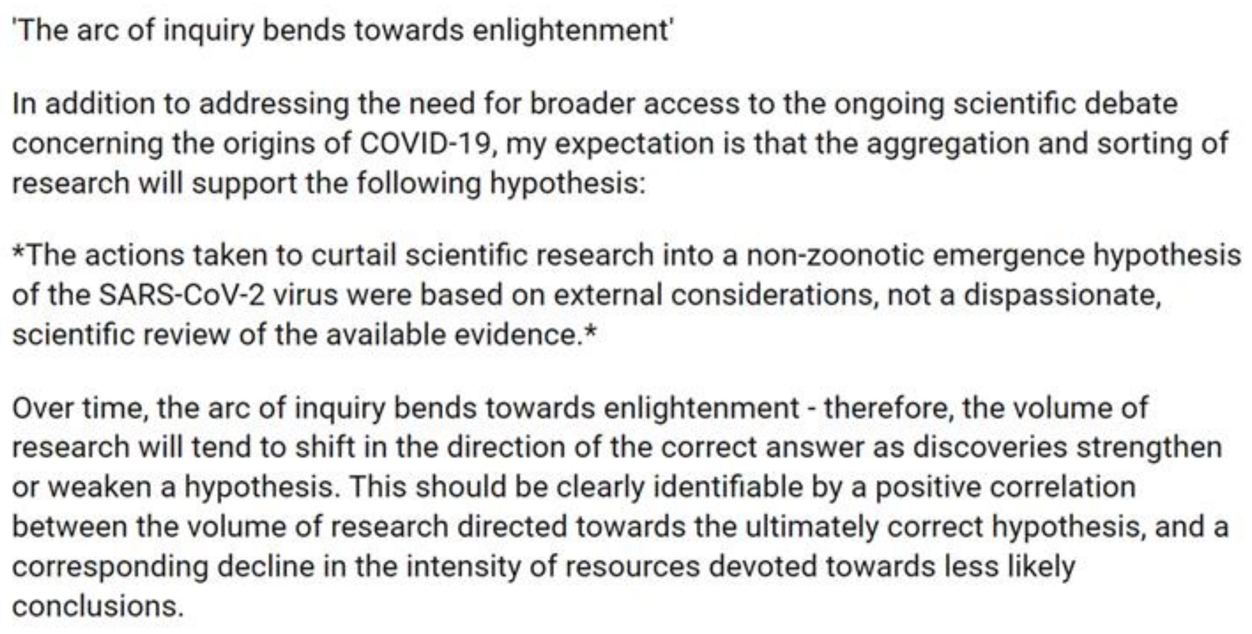
The articles have been virtually unchanged from their original versions, and as a result there are a few repeated elements within them to provide background for someone who hadn't read any of the previous ones.

Lastly, the Appendix documents have been compiled, in part, for use within an upcoming volume of DRASTIC's publications of evidence for the lab-origin of SARS-CoV-2. A fuller narrative will be included there.

I encourage this to be shared; I ask only that proper attribution is given for any materials within [to C. H. Rixey & DRASTIC] , as they represent hundreds of hours of volunteered time and effort spent reading, editing and analyzing the primary sources.

Charles Rixey

From my primary ResearchGate project description:



'The arc of inquiry bends towards enlightenment'

In addition to addressing the need for broader access to the ongoing scientific debate concerning the origins of COVID-19, my expectation is that the aggregation and sorting of research will support the following hypothesis:

The actions taken to curtail scientific research into a non-zoonotic emergence hypothesis of the SARS-CoV-2 virus were based on external considerations, not a dispassionate, scientific review of the available evidence.

Over time, the arc of inquiry bends towards enlightenment - therefore, the volume of research will tend to shift in the direction of the correct answer as discoveries strengthen or weaken a hypothesis. This should be clearly identifiable by a positive correlation between the volume of research directed towards the ultimately correct hypothesis, and a corresponding decline in the intensity of resources devoted towards less likely conclusions.

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My Purpose (4/12/20)

My Purpose

4/12/2020

I have chosen to offer this website as a forum for information about the current COVID-19 pandemic, in an effort to provide meaningful, factual and useful content during what will continue to be a destabilizing time. There is no indication that our media will soon get better at filling the knowledge void that they've created; as a result, confidence in those who deliver our news has hit rock bottom at the exact moment in recent history when we need responsible media the most.

Past experiences and current observations lead me to believe that the big picture of the pandemic is poorly understood, and there has been so much conflicting information floating around that it has been very difficult to see what awaits us beyond the immediate horizon. My goal is simply to provide resources so that each of us can approach the coming months with intention – as perspective widens, willpower to overcome circumstance increases. The opposite is also true, in that fear increases when awareness decreases, and in the aftermath of societal upheaval a vacuum appears that will be filled, by one voice or another. Just as the Native American parable states, courage and fear are interrelated; now is the time to feed courage and starve fear.

My goal is to learn and prepare, because those who expect "normal" to return are going to be disappointed. The odds of future waves of infection are high, and a lot of changes will have to be made in order to keep the engine running once flu season arrives in the fall. The statistics paint a clear picture, in that the near-simultaneous global response saved millions of lives; it's also clear that applying the same medicine several times will negate the economic prosperity that fuels innovation in medical technology. Being able to see a storm coming is meaningless if all you can do is watch and wait, and America's economy has been even more critical during the last decade of malaise in a majority of the developed world. In particular, the last few years of higher growth gave a bigger cushion to land on, but after witnessing unemployment go from historically low to historically high in six weeks it would be foolish to expect us to fully recover before the reemergence of a global peak in cases. So, our responsible way forward is to plan for the worst and accept the need for major changes as soon as possible.

Our goal should be to do whatever is necessary to limit death or economic calamity as we wait for the development of a vaccine. Pretending otherwise might make the next 12 months less stressful, but "flattening the curve" is more important – applying the same measures as in 2009 (H1N1) aren't enough, because 60.8 million cases of COVID-19 could produce 2 million deaths, not the 12,000 from 2009. That number doesn't include the effects of hospitals at capacity for long periods, which effectively increases the mortality rate of any serious ailment. We are victims of our own success. The unprecedented scale of our response in taking swift, global action is helping to fuel criticism of overkill, but flattening the curve has limited the exponential demands that would've dwarfed the current struggles to care for everyone in Italy, Spain or New York. Specifically, that scenario would have played out everywhere at once. There's a reason this type of outbreak represented the worst-case scenario in strategic planning – our only saving grace is that the CFR is closer to 3% than 15%. Personally, I don't think that relying on luck is the basket we should be placing all of our eggs in, even if that turned out okay with H1N1 in 2009.

Our time requires leaders who are honest, because an informed populace is fully capable of rising to meet historic challenges; instead, the early days of this crisis have given rise to political narratives that minimize or catastrophize the situation. If the oxygen continues to be sucked out of the middle of the debate, citizens won't know what to trust or believe – and the vulnerable Americans among us will ultimately pay the price for our confusion. There are several straightforward factors that we can plan for to mitigate the impact of COVID-19 amongst our susceptible populations, and all they require is a will to sacrifice. Each of us should recognize that the choice is ultimately a reflection of how much we value our older family members, because children in schools is a possibility this fall, but our economy will have to allow space for older workers to be productive and safely distanced. How many teachers over 50 are in our schools. Nurses over 40? Our most experienced people are the most vulnerable, because a 2% CFR at 60 assumes enough medical care to provide for everyone that needs it. Our responsibility is to understand how little separates us from 60,000 dead vs. 2 million in the US; creating ways to incorporate this lesson while returning to work and school is a small price to pay, if 2 million Americans can receive a routine vaccine next year because they didn't die this year. There are a lot of people pondering how much sacrifice is worth accepting in order to prevent that scenario-my advice would be the same as it always would've been in the past: if you're not sure how you feel about it, you should go seek wisdom from your parents. Their perspective may be different.

Shoulders: Leading in Crises (4/12/20 & 9/27/20)

Shoulders: Leading in Crises

4/12/2020 & 9/27/2020

For Leaders, COVID-19 is a harsh teacher – but what is the lesson?

I originally published this article on April 22, during the dark period when the virus was "peaking." As we enter fall, in preparations for what will likely be a much larger wave of the COVID-19 pandemic, there's been a little time to reflect on what went right and what went wrong as our society confronted an unprecedented pandemic. The bulk of the criticism has been directed at our President or our Congress, with a healthy disappointment in the responses in many states mixed in - but the harsh truth is that the pandemic has been used as an excuse to step back right at the moment when good leadership is needed most.

ὅτι σὺ μετ᾽ ἐμοῦ

As I've observed the response to this global pandemic, I've been encouraged by the willingness of many leaders to make bold decisions, when faced with difficult choices that must be made quickly. In many cases, this has meant putting aside some differences that had been used as excuses for inaction over the decades. However, the fight over the current relief bill is a reminder that waiting for someone else to come to the rescue is also an excuse – and if we are to complain about our government then we owe it to ourselves to become an example worth following.

This moment calls for more than the government holding out a hand; it calls for leaders to rise to the occasion, people who will give everything they have to lift others up in this time of uncertainty. However, despite the good intentions of many people who feel burdened to make a difference, it is vital to point out that true leadership comes at a cost – and our times require leaders, not outstretched hands.

The value of your leadership is proportional to the price you are willing to pay to apply it. The currency can be explained as ***elevation*** and ***inspiration***.

Many leaders never drive positive change because they are unwilling to pay the price of ***elevation***. In leadership, "elevation" isn't about how much respect you've acquired in reaching a superior position; it's all about how much you respect and value those who need your help. The hard part is <u>lowering </u>yourself to the place where the help is most needed, and pride will seek to hold you back.

Even an Olympic weightlifter can't lift more with his arms than with his shoulders; our bodies weren't made that way. And yet, the most common expression and method for assisting someone is offering a hand. It is the easiest way to show compassion, but the most difficult way to lift someone up. In spite of this truth, most leaders will stop short of truly sacrificing for the sake of someone else, because it means lowering themselves <u>even further</u> – only your shoulders are capable of supporting someone for very long. <u>A good leader works to elevates others, and the price is that not everyone will be able to see your sacrifice beneath. The world needs leaders who will sacrifice without the expectation of glory.</u>

The cost of ***inspiration*** is inter-related; in a time of crisis, the need for inspiration is greater than normal, because the mountains to climb are higher than normal. Our modern world is incredibly cynical, and so many leaders have disappointed us that our natural response is to question people's motives when a good deed is performed (or worse-attack the character of someone in an effort to discredit them).

This exemplifies the power of leaders to destroy inspiration, with very little effort. It costs very little to tear something down; it is a sad truth that journalists gain more notoriety through investigative reporting than through courageous or uplifting opinions. The profession of journalism values its role in communicating to the masses, but it doesn't value those masses enough to project objectivity or optimism. Therefore, we have entered into a crisis largely defined by the pessimism and subjectivity of the media, and politicians' willingness to look for blame instead of looking for inspiration; imagine if it were defined by courage and the value of human life instead.

In this age, we need a Nelson Mandela or Martin Luther King – or more accurately, we need thousands of them. Neither man sought wealth or fame, but both inspired millions of people by elevating others at their expense. Their ability to inspire was partly a function of their rejection of rewards and acclaim. I have no doubt that most people don't see such a person on the horizon, but I disagree. I see 10,000 such people who are willing to step forward, and I believe many of them are already attacking this crisis across the world. There is no limit on how many Nelson Mandelas humanity can produce, and almost all of the leaders who have made a difference in history are <u>invisible</u> to us because most of their elevating and inspiring came while carrying others on their shoulders. We are not wrong to celebrate heroes like Martin Luther King, Jr.; <u>we are wrong when we lack the courage to lead without the promise of acclaim.</u>

It is very common for children to want to make a difference or impact when they grow up, but reality dampens that spirit. Experience tells me that the decline comes from clarity, not cynicism; once we learn the cost of leadership, our willingness to sacrifice is proportional to our distance from the dangling carrot. If you can read this, you are also capable of looking into a mirror. If you look at your reflection and question your desire to sacrifice for others, then this is not yet your moment. Real leaders don't help others in order to get a carrot – for them, helping others *is the reward.*

However, if you go to a window (instead of a mirror) and see an opportunity to make a difference in the lives of others, then this may be your time. Every true leader came to a moment in their lives in which the choice to act was laid before them, and you should find comfort in the fact that Mandela and King were no different than you – until they took action. We still have the ability to influence our surroundings, regardless of the position we hold. There's no such thing as a person too low in status to make a difference. How you see yourself is far more important than how others see you.

The ebb of the pandemic will leave historic challenges, and our success in overcoming them will be determined by the sacrifices of leaders – thousands of heroes with no comic book. In this respect, our picture of heroism is flawed, because waiting for Superman is the wrong example. The Greeks had a much more appropriate myth thousands of years ago, because we need leaders willing to lift us up and bear the burdens of our world like Atlas (I should note that for him, it was a punishment); without demanding recognition or waiting for witnesses before rising to the challenge. Their background could be Harvard or Taco Bell, because leadership doesn't arise from a resume, a paycheck or a degree program. The fire comes from within, and the spark comes from the example of others.

ἐὰν γὰρ καὶ πορευθῶ ἐν μέσῳ σκιᾶς θανάτου οὐ φοβηθήσομαι κακά **ὅτι σὺ μετ᾽ ἐμοῦ**

In boot camp, my platoon's motto was: "As I walk through the Valley of the Shadow of Death, I will fear no evil." It wasn't until 15 years later that I realized that our motto had left out the most important lesson from that verse: "For You are with me." As a kid, my twin brother was with me; in Iraq – my fellow Marines. All of us, at some point in life, walk through dark valleys, but all of us can also be the 'You': a second set of footprints in the sand. Your background might be different than mine, but that's okay - last time I checked, heroic leadership takes place from the front. Everyone *can* make a difference, and there's plenty of room in this crisis.

If you're reading this and struggling, don't lose hope. This too shall pass.

If you're reading this and questioning your ability to impact others, I recommend helping others until the answer comes.

- CHR -

*This is a portion of Psalm 23:4 in Koine (κοινε) Greek; the full κοινε verse is tattooed on my left forearm. It comes from the *Septuaginta* (*c.* 300 B.C.) translation of the Old Testament, which was what most early Christians used because very few could read Hebrew. The language choice is a product of my first graduate degree; the verse grew to become an inspiration during the PTSD treatment that led me to leave active duty.

The Gordion Knot: What Iraqis taught me about priorities & the value of freedom (1/10/21)

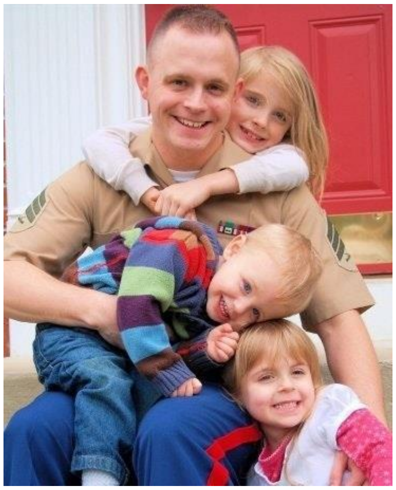
The Gordian Knot: What Iraqis taught me about priorities & the value of freedom

1/10/2021

The pragmatism of raw freedom - Wikimedia, December 15, 2005

What makes our country great? Why do I believe in it, despite our problems? Because when I was 22 years old, I learned why America is different - I just never anticipated a time when the perspective of Iraqis would be needed to remind us of the value and necessity of the rights we take for granted.

My concern at the response to the terrorism last week is not the same as my disgust at the actions. I've never had the occasion to frame my experience in this realm, but while most Americans can't relate to terrorism aimed at threatening an election, I've seen the struggle firsthand. I had the honor of witnessing and working directly with the effort as Iraqi turnout exceed 80% in Anbar province, under the promise of bloodshed by Al Qaeda in 2005. As one of the few volunteers with a clearance, I was pulled from the role I signed up for - and at the likely cost of a lifetime's worth of karma - met all 600ish poll workers in the province. My "team's" responsibilities meant that I was one of the only people there in the middle of the night when they returned (all fixed-wing flights had to take off or land in darkness, for safety). My most indelible memory of Iraq was the flood of poll workers afterwards, with the carts of ballots in tow, cheering as they held up their purple thumbs. One man in particular is burned into my memory, who was crying (happily) as he shook my hand. His other hand was missing fingers and wrapped in bloody bandages, but he was joyful. As long as I live, I will never forget that handshake, or watching dozens of wounded Iraqi men holding up ink-stained fingers and singing along with everyone else.



The divisions within American society are deep, and 2020 was a nuclear bomb of pessimism - its fallout is still actively poisoning our spirit - right at a moment in history when the pandemic challenge we face is *literally peaking**this week***. But, after watching insurgents escort families to the polls and defending against terrorist attacks, I don't buy in to the fatalism or rhetoric that says our cultural cancer is inoperable. After all, when the diagnosis comes from the bi-partisan toilet bowl responsible for a generation of failed leadership (and their radioactive divide-and-conquer tactics fed the tumor), why give **the turds** a plunger when flushing will solve the problem?

I can't, in good conscience, remain silent when American politicians respond to terrorism by supporting censorship of their opponents; in the face of promised violence, Iraqi factions united to exercise their new freedom at any cost. I saw someone pay 3 fingers and some shrapnel for a single ballot, and afterwards thank us through tears of joy; our Congress undermined unprecedented achievements in vaccine technology because the price of even paying a compliment to President Trump was too high. As such, my commentary on our current election is not idly chosen, or made without considering the evidence or context available. My primary reason for actively researching and educating about the COVID-19 pandemic, beginning in early March, was the disgust I felt as I watched partisanship shape media coverage before the crisis had even reached our hemisphere. The last thing I want to do is undermine that effort - but at this point, refusing to speak up at home would be an insult to the sacrifices of Iraqis who understand the true value of what we take for granted.

Our freedom is more valuable than our comfort, which is why my responsibility to defend Colin Kaepernick was superior to my disapproval of his decision to kneel for the anthem. He had that right, unlike those terrorists who stormed the capitol last week - but we should never value safety so much that violating the Constitution becomes our justification to ignore it.

[Me w/kids, 2009]

Prometheus & Pandora I: Trust the Scientists, not the Science? (2/26/21)

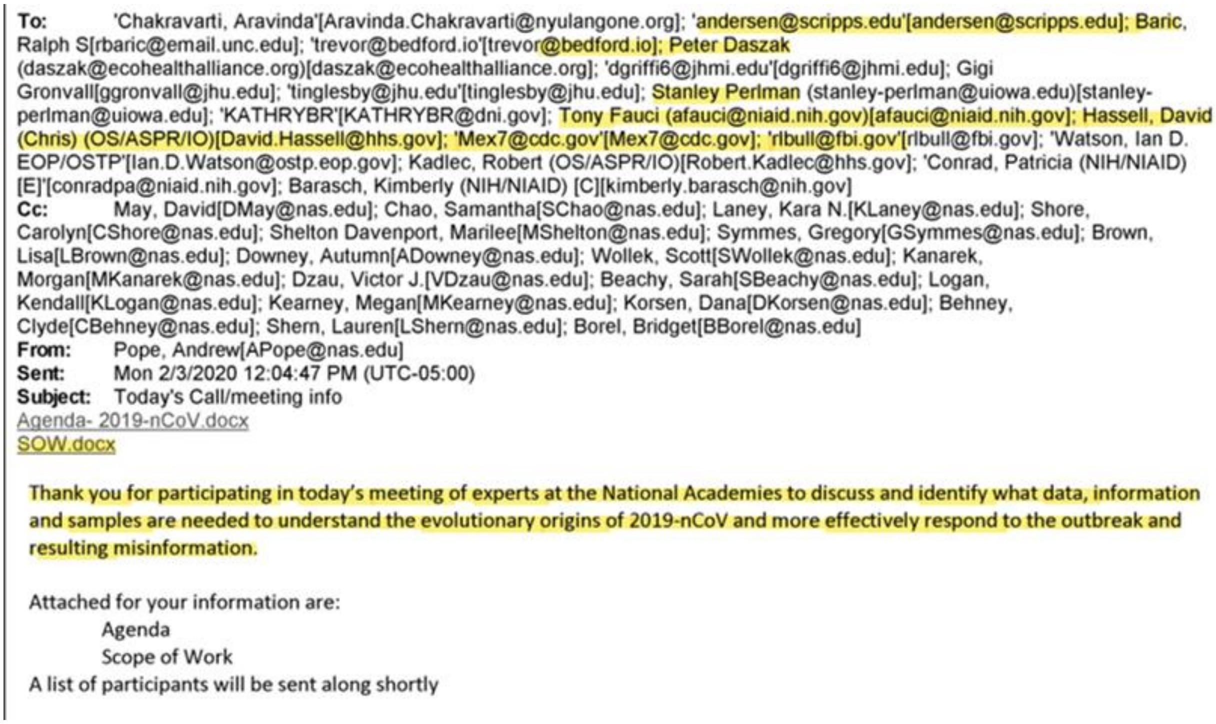
Prometheus & Pandora I – Follow the Scientists, not the Science?

2/26/2021

[Above: Quotation marks are the new middle finger (courtesy of Yahoo news)]

Prometheus brought fire to mankind; Pandora was sent as punishment for accepting the gift - but which one gave us COVID-19? "Follow the science" has been a popular refrain in recent years, but if the WHO investigation is any indication, we're about to find out if our leaders really mean it.

I'm only about 14,000 pages into the US RTK FOIA email dump, courtesy of one Ralph Baric, but in their 2nd article about the Daszak 'group therapy letter' [my *own personal nickname for it]*, it seems everyone missed an inconvenient nugget:



To: 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; 'andersen@scripps.edu'[andersen@scripps.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'trevor@bedford.io'[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; Gigi Gronvall[ggronvall@jhu.edu]; 'tinglesby@jhu.edu'[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; 'KATHRYBR'[KATHRYBR@dni.gov]; Tony Fauci (afauci@niaid.nih.gov)[afauci@niaid.nih.gov]; Hassell, David (Chris) (OS/ASPR/IO)[David.Hassell@hhs.gov]; 'Mex7@cdc.gov'[Mex7@cdc.gov]; 'rlbull@fbi.gov'[rlbull@fbi.gov]; 'Watson, Ian D. EOP/OSTP'[Ian.D.Watson@ostp.eop.gov]; Kadlec, Robert (OS/ASPR/IO)[Robert.Kadlec@hhs.gov]; 'Conrad, Patricia (NIH/NIAID) [E]'[conradpa@niaid.nih.gov]; Barasch, Kimberly (NIH/NIAID) [C][kimberly.barasch@nih.gov]
Cc: May, David[DMay@nas.edu]; Chao, Samantha[SChao@nas.edu]; Laney, Kara N.[KLaney@nas.edu]; Shore, Carolyn[CShore@nas.edu]; Shelton Davenport, Marilee[MShelton@nas.edu]; Symmes, Gregory[GSymmes@nas.edu]; Brown, Lisa[LBrown@nas.edu]; Downey, Autumn[ADowney@nas.edu]; Wollek, Scott[SWollek@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; Dzau, Victor J.[VDzau@nas.edu]; Beachy, Sarah[SBeachy@nas.edu]; Logan, Kendall[KLogan@nas.edu]; Kearney, Megan[MKearney@nas.edu]; Korsen, Dana[DKorsen@nas.edu]; Behney, Clyde[CBehney@nas.edu]; Shern, Lauren[LShern@nas.edu]; Borel, Bridget[BBorel@nas.edu]
From: Pope, Andrew[APope@nas.edu]
Sent: Mon 2/3/2020 12:04:47 PM (UTC-05:00)
Subject: Today's Call/meeting info
Agenda- 2019-nCoV.docx
SOW.docx

Thank you for participating in today's meeting of experts at the National Academies to discuss and identify what data, information and samples are needed to understand the evolutionary origins of 2019-nCoV and more effectively respond to the outbreak and resulting misinformation.

Attached for your information are:
Agenda
Scope of Work
A list of participants will be sent along shortly

What does this mean? Is Dr. Fauci's appearance in the 'to' section evidence that conspiracy theories are true and he's the antichrist helping Bill Gates change the world?

No. Something can be wrong without descending into conspiracy theories - just like how someone can be stupid before they prove it beyond all doubt.

Last spring, as I first began writing about COVID-19, the symbolism of Pandora's Box seemed perfectly fitting as a backdrop from which to spark a conversation about the potential for the SARS-CoV-2 virus to have originated from a laboratory, rather than jumping to humans in a natural setting. After all, Πανδορα is the poster child for anyone who has ever misread a label, licked a frozen pole, picked the Dallas Cowboys to win a playoff game, or experimented on a virus in order to make it exponentially more dangerous and infectious.

If my goal is to present unbiased, accurate information about our global pandemic, then I must apologize to Pandora - her reputation for trouble was often just a catch-all excuse for any complaints related to the fairer sex, which conveniently ignored the fact that Zeus had created her as a punishment for mankind's acceptance of fire [as Pandora was the first human woman, the ancient author Hesiod took some time to articulate the harshness of the punishment and list the many failings of wives].

The benefit of hindsight, and the accumulation of evidence, have led me to question the Pandora metaphor, because it provides an attractive and convenient excuse while obscuring the actions of Prometheus in the background. The natural emergence of COVID-19 would be the most convenient answer [if your research/funding was centered on 'gain of function' experiments] to the question of where the SARS-CoV-2 virus came from, but compelling evidence exists for the hypothesis we can't ignore; until we know what 'gifts' Prometheus brought out of caves in Yunnan Province from 2011-2017 [among other issues], we must rely on the evidence we already have. And, as you'll see below, the tide is turning for a reason.

Recently, I've expanded my research and begun connecting with some of the authors and investigators whose own studies have driven much of the progress of the last year. This includes a few members of D.R.A.S.T.I.C., a loose collection of scientists and researchers that emerged in response to the intense suppression of any studies that questioned the zoonotic (natural) origins of the SARS-CoV-2 virus. I've also been poring over 80,000 emails obtained by FOIA request to investigate the connections between Ralph Baric, Zheng-Li Shi, Peter Daszak and the broader US pandemic response coordination. Daszak is one of the world's leading proponents and fundraisers for gain-of-function research, Baric is one the US's foremost coronavirus experts, and Shi likewise is a de facto head of China's own CoV studies. Shi led projects into increasing the lethality of CoV's, often using techniques she learned while visiting Baric's UNC-Chapel Hill lab a few years ago. Already, the emails have shown intense coordination among them to frame the reporting of potential lab-accident origins for SARS-CoV-2 as a conspiracy theory, an effort which was very successful until the last few weeks.

Ultimately, the conclusion of this mystery has enormous implications, because guilt would mean China is responsible for a crime against humanity. The current evidence suggests that the best case scenario for them would be that China's missteps allowed COVID-19 to become a global pandemic. Our Department of State's decision to reject the WHO investigation's initial assessment shows that President Biden has endorsed the skepticism of his predecessor's stance on China. My initial COVID-19 research was driven by a desire to spread accurate information about the pandemic, but that has shifted to the quest for answers that surround COVID-19's birth - and for justice for the millions of victims of the virus.

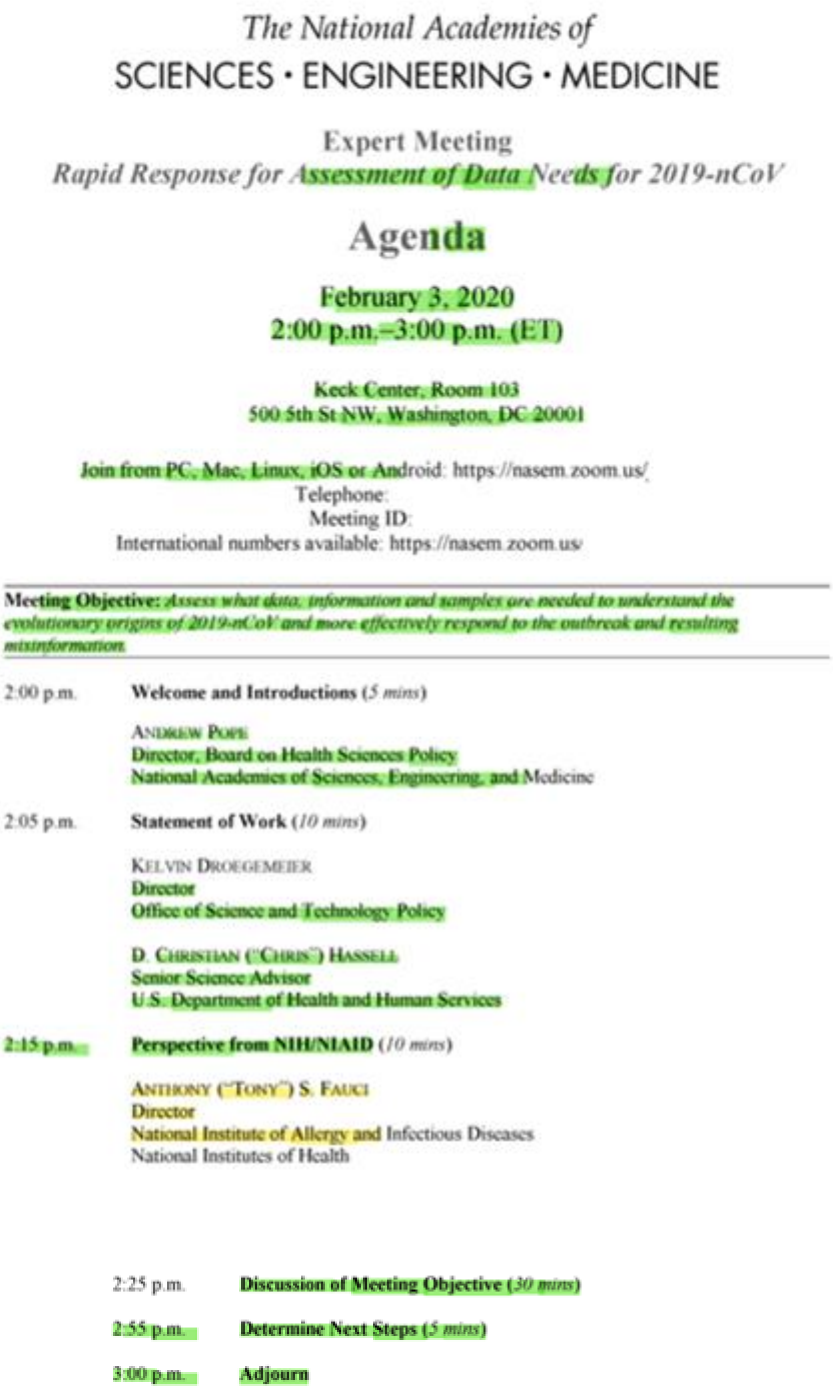
Protecting the Shepherd or the Flock?

The January 29th publication of a pre-print article, which claimed to have discovered elements of the HIV genome suspiciously placed within that of SARS-CoV-2, sparked a wave of concern amongst scientists after the hypothesis quickly fueled speculation about the potential for the virus to have emerged from a laboratory, rather than by crossing the species barrier (zoonoses), which certainly leads to more disturbing implications, in diplomatic terms. That first paper questioning the legitimacy of the natural origin of SARS-CoV-2 was published within a week of Zheng-Li Shi’s own paper that introduced the sequence to the world, so it isn’t terribly surprising for scientists to have been concerned about further breathless speculation that could obscure other vital research trying to reach the global audience.

What is surprising, however, is how drastic and intense the crack-down came to be, given that record-breaking numbers of articles have been published (103,012 as of 2/25/21) about COVID-19 and before 2021 less than 10 (by my count) contained arguments in support of the lab origin hypothesis.

One of the counter-arguments has been that the quantitative difference between the two sides speaks for itself, but the absence of opposing data is illusory, since most of those first articles had waited 3-6 months for publication, delaying public debate on a credible topic and emboldening the scientists under the greatest suspicion. Zheng-Li Shi didn’t bother addressing the absence of any record of a 2012-13 outbreak in Yunnan Province until November 2020, even though it directly led to a much more intensive volume of study within her lab. This would be like Fleming discovering Penicillin and waiting 7 years to announce that could it kill bacteria, or that it grew on bread.

Given the documented history of lab accidents across the globe, and the magnitude of our current pandemic, rejecting the possibility of lab escape mentions intentionally ignoring the known evidence without having a viable alternative. And yet, that's exactly what happened after this [all documents from emails below were pulled from US Right-to-Know's recent FOIA request]



The National Academies of
SCIENCES · ENGINEERING · MEDICINE

Expert Meeting
Rapid Response for Assessment of Data Needs for 2019-nCoV

Agenda

February 3, 2020
2:00 p.m.–3:00 p.m. (ET)

Keck Center, Room 103
500 5th St NW, Washington, DC 20001

Join from PC, Mac, Linux, iOS or Android: https://nasem.zoom.us/
Telephone:
Meeting ID:
International numbers available: https://nasem.zoom.us/

Meeting Objective: *Assess what data, information and samples are needed to understand the evolutionary origins of 2019-nCoV and more effectively respond to the outbreak and resulting misinformation*

2:00 p.m. **Welcome and Introductions** (*5 mins*)

ANDREW POPE
Director, Board on Health Sciences Policy
National Academies of Sciences, Engineering, and Medicine

2:05 p.m. **Statement of Work** (*10 mins*)

KELVIN DROEGEMEIER
Director
Office of Science and Technology Policy

D. CHRISTIAN ("CHRIS") HASSELL
Senior Science Advisor
U.S. Department of Health and Human Services

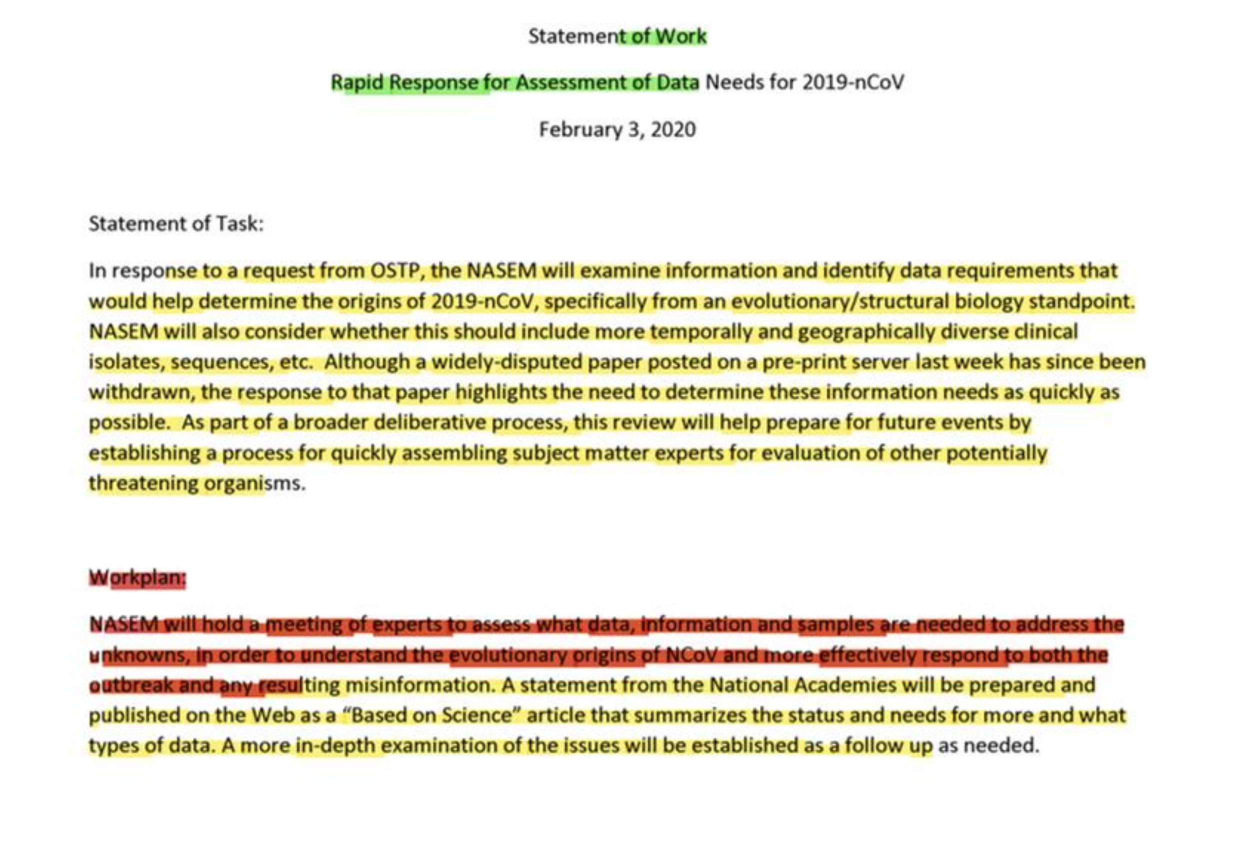
2:15 p.m. **Perspective from NIH/NIAID** (*10 mins*)

ANTHONY ("TONY") S. FAUCI
Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health

2:25 p.m. **Discussion of Meeting Objective** (*30 mins*)

2:55 p.m. **Determine Next Steps** (*5 mins*)

3:00 p.m. **Adjourn**



Statement of Work

Rapid Response for Assessment of Data Needs for 2019-nCoV

February 3, 2020

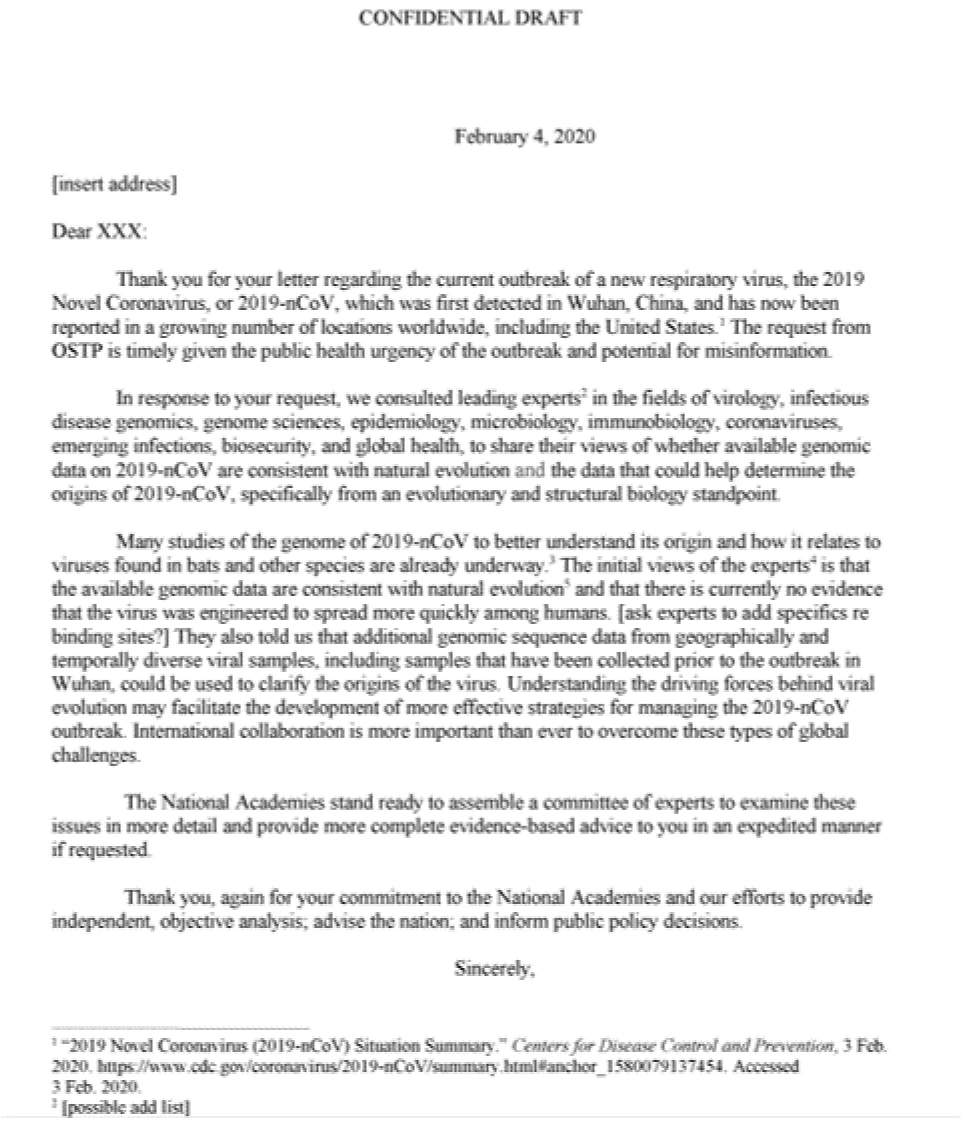
Statement of Task:

In response to a request from OSTP, the NASEM will examine information and identify data requirements that would help determine the origins of 2019-nCoV, specifically from an evolutionary/structural biology standpoint. NASEM will also consider whether this should include more temporally and geographically diverse clinical isolates, sequences, etc. Although a widely-disputed paper posted on a pre-print server last week has since been withdrawn, the response to that paper highlights the need to determine these information needs as quickly as possible. As part of a broader deliberative process, this review will help prepare for future events by establishing a process for quickly assembling subject matter experts for evaluation of other potentially threatening organisms.

Workplan:

NASEM will hold a meeting of experts to assess what data, information and samples are needed to address the unknowns, in order to understand the evolutionary origins of NCoV and more effectively respond to both the outbreak and any resulting misinformation. A statement from the National Academies will be prepared and published on the Web as a "Based on Science" article that summarizes the status and needs for more and what types of data. A more in-depth examination of the issues will be established as a follow up as needed.

The 'Statement of Task' directed the National Academy of Sciences, Engineering & Medicine to deliberate and respond with current knowledge and future discoveries related to SARS-CoV-2, to fill the gaps most likely to fuel misinformation about the 'evolutionary/structural' origins of the virus. Notably, the initial request did not rule out a non-natural origin for COVID-19, but Daszak, Baric and others were determined to include specific language to that end in their response [3rd paragraph]:



CONFIDENTIAL DRAFT

February 4, 2020

[insert address]

Dear XXX:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the public health urgency of the outbreak and potential for misinformation.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health, to share their views of whether available genomic data on 2019-nCoV are consistent with natural evolution and the data that could help determine the origins of 2019-nCoV, specifically from an evolutionary and structural biology standpoint.

Many studies of the genome of 2019-nCoV to better understand its origin and how it relates to viruses found in bats and other species are already underway.[3] The initial views of the experts[4] is that the available genomic data are consistent with natural evolution[5] and that there is currently no evidence that the virus was engineered to spread more quickly among humans. [ask experts to add specifics re binding sites?] They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus. Understanding the driving forces behind viral evolution may facilitate the development of more effective strategies for managing the 2019-nCoV outbreak. International collaboration is more important than ever to overcome these types of global challenges.

The National Academies stand ready to assemble a committee of experts to examine these issues in more detail and provide more complete evidence-based advice to you in an expedited manner if requested.

Thank you, again for your commitment to the National Academies and our efforts to provide independent, objective analysis; advise the nation; and inform public policy decisions.

Sincerely,

---

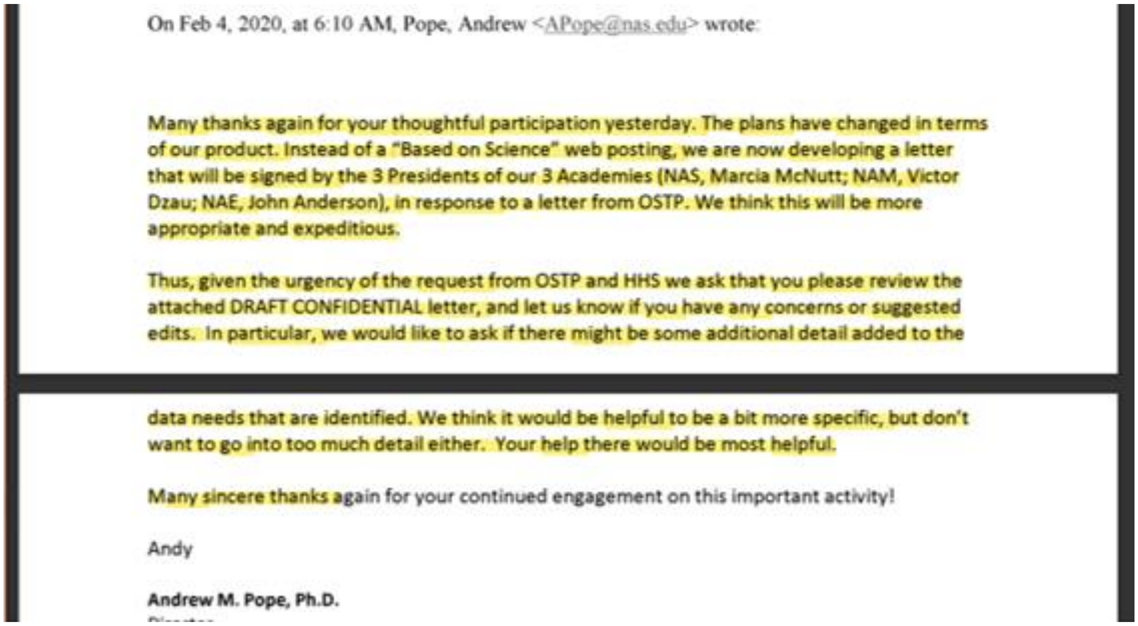
[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] [possible add list]

Prometheus blames the flames

Kristian Anderson, Peter Daszak, Robert Baric and others were gung-ho about putting out this statement, and a second one that was ultimately published a few days later, but in the midst of 80K+ emails [whose response chains run backwards] some of the details are out of order, and the connection to a specific meeting was never made by US Right-to-Know, who focused on the backdoor coordination between two of the scientists who would later be implicated by their publicly-available research.

But, once the 2/4 discussion is put in sequence, it turns out that the great idea for the letter didn't come from them – it came from this NAS meeting.



On Feb 4, 2020, at 6:10 AM, Pope, Andrew <APope@nas.edu> wrote:

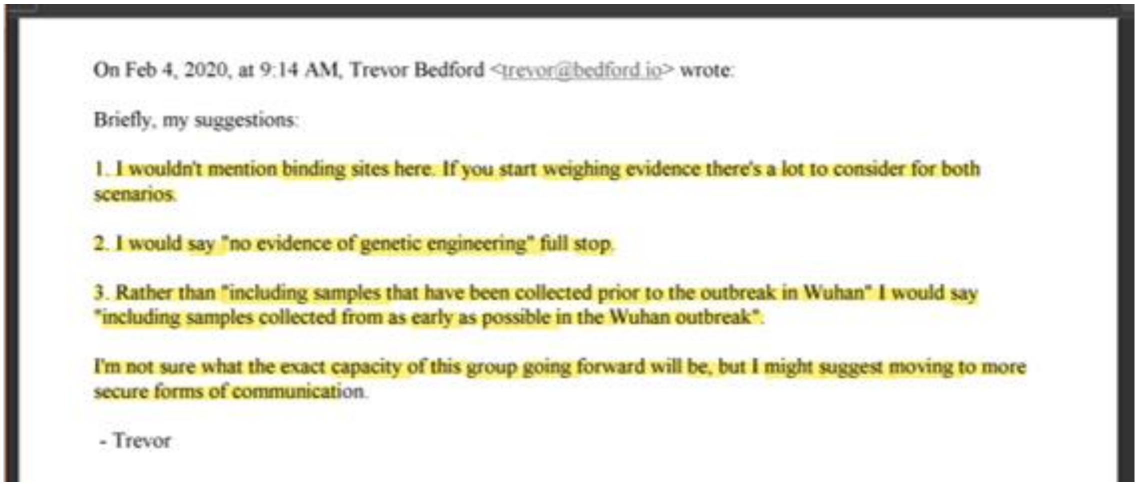
Many thanks again for your thoughtful participation yesterday. The plans have changed in terms of our product. Instead of a "Based on Science" web posting, we are now developing a letter that will be signed by the 3 Presidents of our 3 Academies (NAS, Marcia McNutt; NAM, Victor Dzau; NAE, John Anderson), in response to a letter from OSTP. We think this will be more appropriate and expeditious.

Thus, given the urgency of the request from OSTP and HHS we ask that you please review the attached DRAFT CONFIDENTIAL letter, and let us know if you have any concerns or suggested edits. In particular, we would like to ask if there might be some additional detail added to the data needs that are identified. We think it would be helpful to be a bit more specific, but don't want to go into too much detail either. Your help there would be most helpful.

Many sincere thanks again for your continued engagement on this important activity!

Andy

Andrew M. Pope, Ph.D.



On Feb 4, 2020, at 9:14 AM, Trevor Bedford <trevor@bedford.io> wrote:

Briefly, my suggestions:

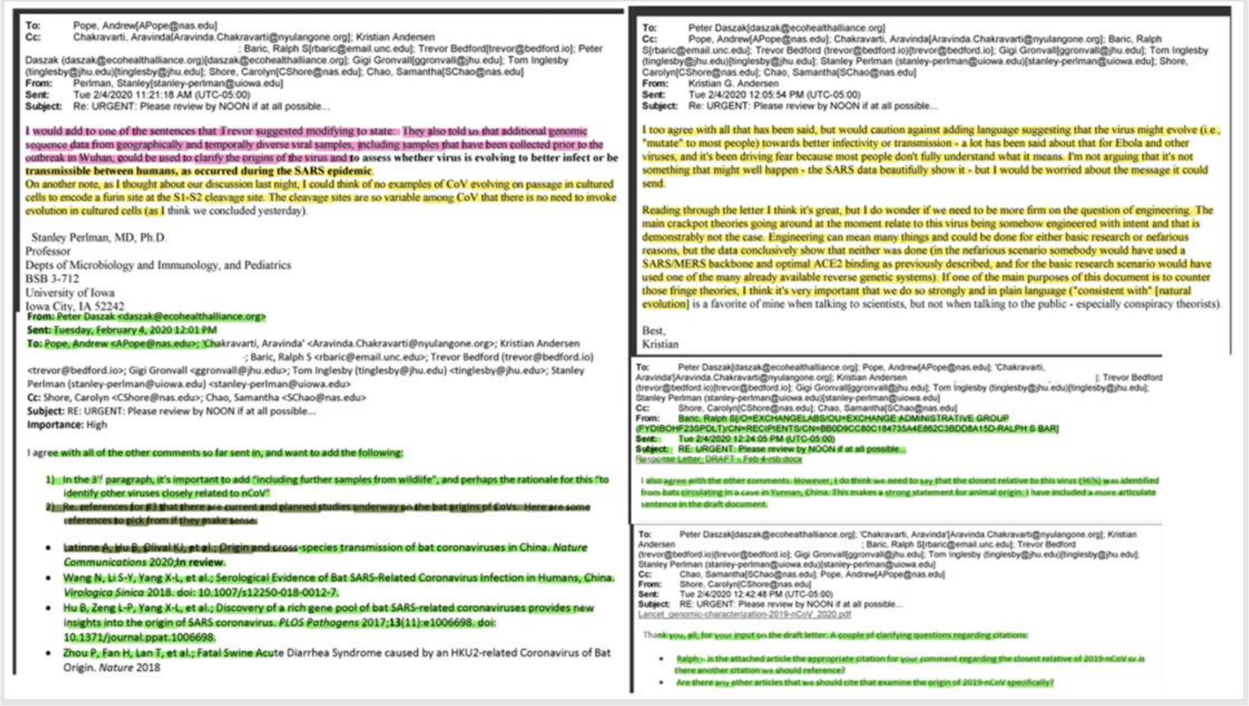
1. I wouldn't mention binding sites here. If you start weighing evidence there's a lot to consider for both scenarios.

2. I would say "no evidence of genetic engineering" full stop.

3. Rather than "including samples that have been collected prior to the outbreak in Wuhan" I would say "including samples collected from as early as possible in the Wuhan outbreak".

I'm not sure what the exact capacity of this group going forward will be, but I might suggest moving to more secure forms of communication.

\- Trevor



To: Pope, Andrew[APope@nas.edu]
Cc: Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Tue 2/4/2020 11:21:18 AM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I would add to one of the sentences that Trevor suggested modifying to state: They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus and **to assess whether virus is evolving to better infect or be transmissible between humans, as occurred during the SARS epidemic**.
On another note, as I thought about our discussion last night, I could think of no examples of CoV evolving on passage in cultured cells to encode a furin site at the S1-S2 cleavage site. The cleavage sites are so variable among CoV that there is no need to invoke evolution in cultured cells (as I think we concluded yesterday).

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, February 4, 2020 12:01 PM
To: Pope, Andrew <APope@nas.edu>; 'Chakravarti, Aravinda' <Aravinda.Chakravarti@nyulangone.org>; Kristian Andersen ; Baric, Ralph S <rbaric@email.unc.edu>; Trevor Bedford (trevor@bedford.io) <trevor@bedford.io>; Gigi Gronvall <ggronvall@jhu.edu>; Tom Inglesby (tinglesby@jhu.edu) <tinglesby@jhu.edu>; Stanley Perlman (stanley-perlman@uiowa.edu) <stanley-perlman@uiowa.edu>
Cc: Shore, Carolyn <CShore@nas.edu>; Chao, Samantha <SChao@nas.edu>
Subject: RE: URGENT: Please review by NOON if at all possible...
Importance: High

I agree with all of the other comments so far sent in, and want to add the following:

1) In the 3rd paragraph, it's important to add "including further samples from wildlife", and perhaps the rationale for this "to identify other viruses closely related to nCoV"
2) Re. references for #3 that there are current and planned studies underway on the bat origins of CoVs. Here are some references to pick from if they make sense:

- Latinne A, Hu B, Olival KJ, et al.; Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications* 2020;**In review.**
- Wang N, Li S-Y, Yang X-L, et al.; Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Virologica Sinica* 2018. doi: 10.1007/s12250-018-0012-7.
- Hu B, Zeng L-P, Yang X-L, et al.; Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLOS Pathogens* 2017;**13**(11):e1006698. doi: 10.1371/journal.ppat.1006698.
- Zhou P, Fan H, Lan T, et al.; Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. *Nature* 2018

To: Peter Daszak[daszak@ecohealthalliance.org]
Cc: Pope, Andrew[APope@nas.edu]; Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Kristian G. Andersen
Sent: Tue 2/4/2020 12:05:54 PM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., "mutate" to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other viruses, and it's been driving fear because most people don't fully understand what it means. I'm not arguing that it's not something that might well happen - the SARS data beautifully show it - but I would be worried about the message it could send.

Reading through the letter I think it's great, but I do wonder if we need to be more firm on the question of engineering. The main crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter those fringe theories, I think it's very important that we do so strongly and in plain language ("consistent with" [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists).

Best,
Kristian

To: Peter Daszak[daszak@ecohealthalliance.org]; Pope, Andrew[APope@nas.edu]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
Sent: Tue 2/4/2020 12:24:05 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Response Letter: DRAFT - Feb 4-rsb.docx

I also agree with the other comments. However, I do think we need to say that the closest relative to this virus (96%) was identified from bats circulating in a cave in Yunnan, China. This makes a strong statement for animal origin. I have included a more articulate sentence in the draft document.

To: Peter Daszak[daszak@ecohealthalliance.org]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Chao, Samantha[SChao@nas.edu]; Pope, Andrew[APope@nas.edu]
From: Shore, Carolyn[CShore@nas.edu]
Sent: Tue 2/4/2020 12:42:48 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Lancet_genomic-characterization-2019-nCoV_2020.pdf

Thank you, all, for your input on the draft letter. A couple of clarifying questions regarding citations:

- Ralph – is the attached article the appropriate citation for your comment regarding the closest relative of 2019-nCoV or is there another citation we should reference?
- Are there any other articles that we should cite that examine the origin of 2019-nCoV specifically?

Whatever happened at that meeting the previous afternoon, it's clear that the lab hypothesis was not a fan favorite. Given that every speaker invited by the OSTP was the head of a major American research institution, highlighting the possibility of a lab escape for a pandemic pathogen that will have killed more than 3 million people is a buzz kill for scientists whose ban on gain-of function research had been lifted only 2 years earlier.

I can imagine their excitement dying down after the letter was published, since each of the direct refutations of man-made origin was removed by the three national academies of NASEM in the version sent to the White House:

February 6, 2020

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy
1650 Pennsylvania Avenue, NW
Washington, D.C. 20504

Dear Dr. Droegemeier:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the declaration of a public health emergency and potential for misinformation to confound the response.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health. We wanted their views about the data needs that could help elucidate the origin and evolution of 2019-nCoV.

Research studies to better understand the origin of 2019-nCoV and how it relates to viruses found in bats and other species are already underway.[3] The closest known relative of 2019-nCoV appears to be a coronavirus identified from bat-derived samples collected in China.[4] The experts informed us that additional genomic sequence data from geographically- and temporally-diverse viral samples are needed to determine the origin and evolution of the virus. Samples collected as early as possible in the outbreak in Wuhan and samples from wildlife would be particularly valuable. Understanding the driving forces behind viral evolution would help facilitate the development of more effective strategies for managing the 2019-nCoV outbreak and for preventing future outbreaks. In this regard, we understand from Chunli Bai, President, Chinese Academy of Sciences, and the Alliance of International Science Organizations (ANSO), that the Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences is willing to share isolates of the 2019-nCoV with the international community and is working with the University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. International collaboration of this kind is more important than ever to overcome these types of global challenges.

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[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] Experts consulted: Kristian G. Andersen (Scripps Research Institute), Ralph Baric (UNC School of Public Health), Trevor Bedford (Fred Hutchinson Cancer Institute), Aravinda Chakravarti (New York University School of Medicine), Peter Daszak (EcoHealth Alliance), Gigi K. Gronvall (Johns Hopkins Bloomberg School of Public Health), Tom Inglesby (Johns Hopkins Center for Health Security), and Stanley Perlman (University of Iowa).

[3] Latinne *et al*. "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications*, in review.

[4] *Zhou et. al*. "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 2020. https://doi.org/10.1038/s41586-020-2012-7 (2020).

500 Fifth Street, NW, Washington, DC 20001

We may never know who snipped those phrases out of the final product, mostly because those individuals weren't tied to this FOIA request; but, what we do know is that after the meeting, Baric & co. were eager to pile impactful, serious language into the short document, so it would've been surprising to see such effort if the final speaker dismissed their contentions the previous afternoon.

I should point out that Daszak and Baric et al ended up publishing a much more explicit rejection of the lab hypothesis that same week - having apparently been healed from their fear of appearing self-serving.

50 years and then 15 minutes of fame - No Peer Reviews for the Peerless

I can assume that no one present on 2/3 was thinking that Dr. Fauci was about to become one of the most recognizable people on the planet, but his willingness to buck President Trump assured that he would receive a fawning welcome on TV ever after. The Office of Science & Technology Policy falls under the executive branch, and feeds into the NSTC, chaired by the VP. The OSTP Director, National Academy of Sciences Director & Fauci got together with our friendly neighborhood skeptics, and magically, the OSTP requested an emergency response to a 1/29 controversial pre-print; that letter was also accompanied by an article called *The Proximal Origin of SARS-CoV-2*, which remains one of the 2 most-cited COVID-19 articles on the planet. It's blistering rejection of any non-zoonotic transfer theory succeeded in setting the tone early, thereby giving Daszak the confidence to maneuver onto the WHO's investigative team - with China making that one of the required pre-conditions of any investigation.

Dr. Fauci has been the target of so much conspiracy talk simply by being the key cog in funding questionable studies [well, to the less invested Americans {98%}, he became the face of the Anti-Trump pandemic experts], which has put him into frequent contact with the WHO, Bill Gates, the CDC, etc. He's less well known for his groundbreaking research and leadership of the effort to combat the AIDS epidemic from its very start, or the effort to develop vaccines to fight H1N1 in 2009 [I was among the first to get that vaccine, as a Marine guinea pig].

I hate mindless speculation, and I don't think Dr. Fauci is part of some unholy trinity with Bill Gates as the antichrist, but it looks pretty obvious that he was protecting his legacy and the NIH's funding circus, while actively working to undermine the lab hypothesis at the start. How influential was this effort? It's hard to know specifics, but while the National Security Council was passing along intel to Trump about the WIV, the clinical side of our federal government was absolving itself of any scrutiny by rejecting the thesis. Sadly, this arrangement had the added benefit of elevating a voice critical of Trump's decisions, making it difficult for the media to scrutinize other actions of the NIH's operations.

No wonder Peter Daszak has been so cocky, probably thinking he just had to skate by until the election, which also happened to be the time when Fauci would fade in importance for anti-Trump Republicans and Democrats. My guess is that Ol' Pete wasn't expecting the Biden administration to the stay the course, with regards to the COVID-19 origin investigation that recently returned. It's time for America to pull off the bandages and take out the IV, and accept that it's going to sting a little bit.

A Fauci Ouchie

1) It's time for Dr. Fauci to provide some insight into the decision-making process that led to Peter Daszak being deeply connected with our nation's planning for and response to the emergence of COVID-19. Ralph Baric was involved in virtually all of the calls and meetings with the government agencies working to prepare for the pandemic, and yet both he and Daszak sometimes had Zheng-Li Shi attached to email threads or contributing to a Zoom working group.

If there was ever a time or person to distance yourself from in a pandemic that kills 3 million people, it would've been Zheng-Li Shi in January 2020, when suspicions first appeared that China was attempting to erase evidence. Shi was the one whose first action after hearing about an unknown pneumonia in Wuhan was to edit and delete files from her Institute's genome database. China wouldn't even release early patient info to the World Health Organization, including the hospitals they first went to and to where they lived, which serves no legitimate purpose and prevents the investigators from even knowing where to start looking.

2) It's time for Dr. Fauci to explain the logic of gain-of-function research to the American people directly, and why his Institutes felt comfortable approving incredibly reckless experiments with China, who has long been suspected of violating the Biological Weapons Convention. Who gains from these studies? We now know exactly what can happen, and who loses - even if COVID-19 was natural.

3) I call on Dr. Fauci to publicly state his role and reasoning in the decision to silence proponents of a lab origin for COVID-19 - an act that silenced published dissent in the scientific community, especially when his commander in chief was presumably receiving more intelligence briefings than Fauci. Furthermore, why would he continue to keep Daszak and Baric directly connected to the heart of our national safety apparatus, long after incriminating evidence about them began to surface? Daszak's selection to serve on both investigative teams wasn't surprising, since the US had pulled out of the WHO.

Fauci's silence on gain-of-function (GOF), on the other hand, is surprising. In 2012, he wrote the following, during the debate that placed a moratorium on GOF Research:

"The voluntary moratorium on gain-of-function research related to the transmissibility of highly pathogenic H5N1 influenza virus should continue, pending the resolution of critical policy questions concerning the rationale for performing such experiments and how best to report their results. The potential benefits and risks of these experiments must be discussed and understood by multiple stakeholders, including the general public, and all decisions regarding such research must be made in a transparent manner."

3) I call on Dr. Fauci to push for the full ban of all research funds, sponsored academics, and joint research partnerships related or to with any scientist who is a citizen of China - with research, subject to replacement if other qualified individuals can be found.

My reasoning for these actions is simple, just like the remedy. China has refused to provide more than token cooperation to the WHO's investigation of the pandemic. The quality of their mitigation efforts has exponentially improved since the first SARS pandemic in 2002-03, but their cooperation and communication with WHO efforts has declined. China already has enough evidence to exonerate themselves, and yet has refused to release this data, even to the investigation team whose composition it dictated as a term of negotiation. If they refuse to cooperate during the middle of a global pandemic, then the United States should restrict access to our national treasure until a satisfactory answer is received.

Dr. Fauci helped set the tone of treating China as 'innocent until proven guilty,' but it doesn't protect against being a suspect. He has also based his conclusions on GOF and COVID-19, in part, on the input of individuals who are STILL energetically attempting to prevent a broad scientific inquiry into the origin of the greatest human tragedy in generations.

If he still believes that the 'general public' deserves a chance for informed input, he should prove it. If skeptical scientists reject a lab escape, then they should make their case - and then defend it publicly. Americans may not catch every nuance, but we deserve an open debate, and our 500,000 victims have families who deserve closure. Peter Daszak has been paid millions of dollars to facilitate research that taxpayers also pay for, and so his condescension and twisting of words today is a slap in the face, regardless of how just he perceives his crusade to be.

Requiem for a Steam……….ing pile of BS

If Daszak truly believes in his cause of fighting disease emergence, then he should understand the skepticism that arises when a global pandemic begins in a city, less than 3 miles from the lab working on CoV's under a program partly funded by his firm, led by a long-time collaborator and friend, that contains the closest known viral relative and happens to be one of the foremost [and few] labs on earth with the ability to perform the steps necessary to mold a unique virus, that's highly contagious, in a city of 11 million people that exhibits no evidence of seroconversion, and a virus perfectly adjusted to multiple types of human tissue, a spike protein that was 99% perfect for humans from the very first human, with scant mutations, evidence of vero cell passaging, whose progenitor was found floating in a microbiome unlike any of its chronological cousins, whose furin cleavage site appears in a random place of frequent recombination but not in any strains that could actually recombine with it, and……..

I could keep going, but Daszak has now heard most of this before and never answered, and certainly doesn't think we're smart enough to understand it.

So, in honor of the Chinese regime he has faithfully served, I'll encourage him with a quote from Ren Zhiqiang, a very wealthy businessman who disappeared days after writing a scathing review of a Xi Xinping speech in early March. I've only ever found one complete, translated copy online [link coming], but the quote was powerful, especially coming from someone who reappeared for a 1-day trial, followed by 18 years in prison for 'corruption.' I sincerely hope that you're right, Petey Prometheus, and COVID-19 was just a horrible coincidence; **it would still serve you well to care more about the millions of dead people than your lost opportunities to find more viruses after the NIH pulled your funding**.

Ren Zhiqiang on Xi Xinping: c. 3/1/2020:

> "But this kind of cover-up propaganda, it can basically only cheat those who want to be cheated; there's no way it can cheat those who believe in facts and reality."

(R. Zhiqiang - NBC News)

The Prometheus analogy fits him a lot better - A man who crept into the darkness to steal a flame of wisdom and share it with mankind, only to be punished by the gods.

Prometheus & Pandora II: The West must not go gently into a COVID-19 goodnight (3/4/21)

Pandora & Prometheus II – The West must not go gently into a COVID-19 goodnight

3/4/2021

-Do Not Go Gentle Into that Good Night-

The sun has not yet set on the West, nor is it inevitable - but if the West doesn't hold China to the same standards of accountability that western civilization applies to itself now, IN THE MIDST of the 2nd truly simultaneous global pandemic in the history of mankind, then when? As it happens, the voice we should be listening to isn't the World Health Organization, but it IS from someone within China itself:

"But this kind of cover-up propaganda, it can basically only cheat those who want to be cheated; there's no way it can cheat those who believe in facts and reality."

That author of that quote disappeared 11 days after it was posted online, and the 38 million followers of his blog woke up to discover little evidence that it had ever existed. The COVID-19 origin story is peppered with evidence of the same phenomenon, but the sheer number and consistency of the ‘**truth singularities**’ has almost made it easier to discern the chapters of the story they were meant to conceal. The publication of this article, via exquisite serendipity, comes on the same day as the *Wall Street Journal* has a front 'page' story announcing a decision by the WHO COVID-19 origin investigation team to skip the publication of a partial review of their results, presumably to allow for some time to reflect on the potential impact of continuing to blatantly parrot Chinese assertions.

The real story, however, is in the byline - recognizing the importance of a letter written by dissidents beyond China’s reach - a group of scientists scattered across the globe, but united by the same passion for truth as Ren Zhiqiang, the wealthy real-estate investor who sacrificed his freedom to call out Xi Xinping directly, for his handling of the pandemic that exacerbated a nascent crisis and accelerated its spread across the globe. Their letter, published 8 days before the first anniversary of Ren Zhiqiang’s abduction, is a call to arms for diplomats, scientists and politicians to hold China accountable now, because the window of opportunity is closing, and the implications of innocence or guilt dwarf other geopolitical issues by gravity alone.

[*Note - for BLUF, click here]

◆ WSJ NEWS EXCLUSIVE

WHO Investigators to Scrap Plans for Interim Report on Probe of Covid-19 Origins

U.S-China tensions rise over investigation as group of scientists presses for fresh inquiry, including into lab escape theory

Security personnel stood outside the Wuhan Institute of Virology as members of the WHO team arrived on Feb. 3. THOMAS PETER/REUTERS

“Life was such a wheel that no man could stand upon it for long. And it always, at the end, came round to the same place again.”

-Stephen King, *The Stand* (1978)

First, we must draw distinctions between the past and the present. The origin of SARS-CoV-2 isn’t a matter of blame - it’s a matter of perspective, and justice. China has been more dismissive and indignant than in 2003, during the original SARS outbreak, when China’s blatant refusal to share details of the situation hindered the global response attempting to help them contain the tragedy. Their behavior was so reckless [in humanitarian terms] that it sparked an urgent WHO update to the mandatory reporting requirements for any member nation-state, so that in the event of the future emergence of a pathogen with pandemic potential, the rest of the world wouldn’t be blind-sided…

The emergence of a new type of deadly viral disease was a shock to the international health community, which had historically focused on *influenza*, tropical diseases like malaria and dengue, hemorrhagic fevers including Ebola & Marburg, and smallpox. Until the global vaccination effort of the mid-20th century led to smallpox’s official eradication in 1980, it had been humanity’s most prolific pathogenic killer, with an estimated 300 million deaths from 1900-1977 alone.

A child with smallpox in Bangladesh in 1973.

Doctors perform CPR on a COVID-19 patient United Memorial Medical Center in Houston on July 17, 2020.

Callaghan O'Hare / Reuters file

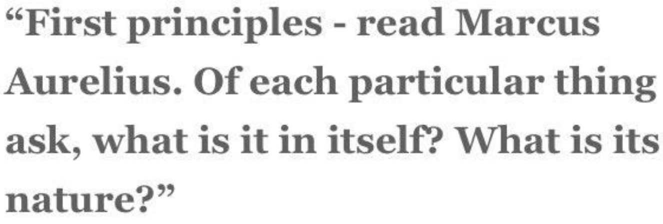
What set SARS apart was its efficiency in transmission through respiratory droplets, which paired high lethality with rapid contamination/infectivity. This combination is what made a novel *influenza* or coronavirus strain the focus of planning strategies for pandemic preparedness, especially after the H1N1 'Swine Flu' pandemic in 2009. The danger was highlighted by two locations in Hong Kong, when a single patient sparked an outbreak of 290 cases at a hospital and an apartment complex. Ultimately, the outbreak was contained through intense quarantine and strict protection measures implemented by the doctors and nurses.

Innocence Lost

China's blatant refusal to cooperate with WHO investigators may be familiar, but it stands in stark contrast to the difference between their response to SARS in 2003 and COVID-19 in January 2020. The effectiveness of their brutal mitigation measures killed a full-blown epidemic in less than two months, and fewer than 5,000 cases have been confirmed in the year since then. China's stunning achievements and intense diplomatic goodwill efforts muted criticism of their early actions, and the pandemic itself provided a convenient excuse to delay an investigation of China's conduct during the initial outbreak in Wuhan.

But… viewing 2020 through the prism of 2003 is stupid, dangerous and short-sighted, and the WHO investigation must be understood as a wake-up call, not a diplomatic power struggle or as a cover for 'embarrassing' failures in China's handling of Wuhan. If China's answer to criticism [including from the US, which prompted Trump's angry withdrawal from the WHO] was to commandeer the WHO, dictate the terms of its investigation, and brazenly withhold evidence while pushing theories rejected by the scientific community, then they are already ignoring established international precedent - and the real question is ***why***.

Perspective - the more things stay the same, the more they change



"First principles - read Marcus Aurelius. Of each particular thing ask, what is it in itself? What is its nature?"

It may seem crass to use Hannibal Lecter, but I'm confident that history will show that the WHO's Wuhan investigation, if anything, contributed ***less*** to our knowledge of COVID-19's origins than this fictional cannibal's wisdom.*

[*I should note that my M.A. focus & thesis centered on aspects of Roman History]

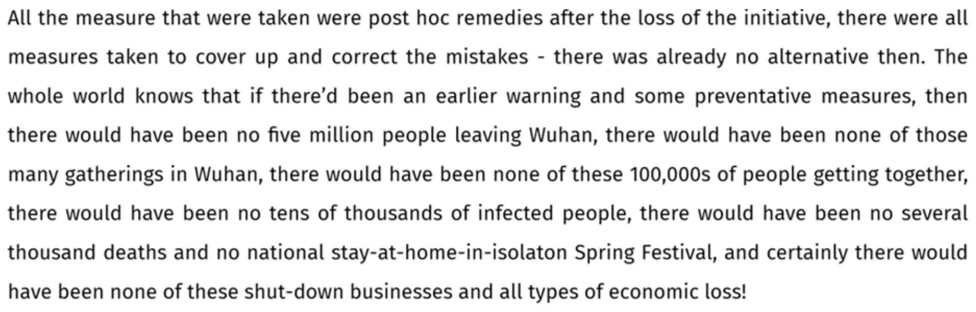
It is fitting that Dr. Lecter quoted Marcus Aurelius, because it was during his reign as *imperator* [emperor] that the Rome Empire experienced its worst plague prior to the 'fall' of the western half *c.* 476 A.D. Given that he wrote his *Meditations* in the midst of that tragedy, which decimated his legions' ranks enough to roll back military successes and create strategic weaknesses that his barbarian enemies could exploit, perhaps we should ask ourselves the same questions about COVID-19. And if we are to consider the 'nature' of SARS-CoV-2, our perspective must be founded on these first principles:

1) The **scale** of the SARS epidemic & and the COVID-19 pandemic are incomparable; all SARS confirmed cases would be equivalent to **7 thousandths of 1%** of the current COVID-19 total. There's actually been substantially less criticism from the scientific community so far, despite a pattern of misbehavior that contributed to the ultimate breadth of the pandemic.

2) China 2020 is not analogous to **China 2003.** In 2003, China's economy was smaller than Italy's and 1/9th the size of the United States' - today, China's economy is 7 times larger than Italy's and 3 times larger than Japan's, who sits at #3 in the world. They were able to marshal vastly greater resources to contain the pandemic, and are using the leftovers to distract from the criticisms concerning the cover-up in Wuhan.

3) The **epidemiological characteristics** of SARS & COVID-19 are **fundamentally** distinct; SARS-CoV-1 was highly contagious, but SARS-CoV-2 is exponentially more contagious, utilizes multiple pathways within its genome to attack cells, can spread with similar intensity before symptoms appear, during the clinical course of infection and even without symptoms at all, and these traits made early symptom-checks at airports a band-aid for a bullet wound.

4) The WHO's treatment of China in 2003 & today is negatively correlated with the scale of the mistakes made and actions taken. In 2003, an emerging China was desperate to avoid embarrassment or open its country to critical analysis from international observers, in the wake of an epidemic caused by a truly novel virus. In fact, since the discovery of coronaviruses (CoV's), no species was known to present mortal danger to humans. In 2020, however, China was not unprepared - it was home to the world's most accomplished CoV researchers. No better situation could've played out for China, since its CoV experts ran a BSL-4 lab in Wuhan, which also stored the world's largest collection of bat CoV samples, and had conducted groundbreaking research on dozens of species. With all of these resources, and with samples of an unknown viral pneumonia being collected as early as the 10th of December, 2019 [from a patient at the hospital closest to the Wuhan Institute of Virology, roughly 2 miles away], China didn't even tell its citizens about the virus until 1/3/2020. Per Ren Zhiqiang, writing in the blogpost that led to his disappearance on 3/12/2020:



> All the measure that were taken were post hoc remedies after the loss of the initiative, there were all measures taken to cover up and correct the mistakes - there was already no alternative then. The whole world knows that if there'd been an earlier warning and some preventative measures, then there would have been no five million people leaving Wuhan, there would have been none of those many gatherings in Wuhan, there would have been none of these 100,000s of people getting together, there would have been no tens of thousands of infected people, there would have been no several thousand deaths and no national stay-at-home-in-isolaton Spring Festival, and certainly there would have been none of these shut-down businesses and all types of economic loss!

Just in the last few weeks, the WHO has admitted that much of the data they requested during their investigation was never provided; the Chinese refused to provide basic information and reportedly did 'little' to investigate COVID-19's origins. However, given that the high-technology police state tracks their citizens lives through a smart phone app that is set up at purchase, the odds of China having failed to investigate the ‘origins’ of a pandemic that started in a Chinese city of 11 million people seems unlikely.

5) Nearly every conceivable genome mutation that could’ve increased the R0 of SARS-CoV-1 appeared in SARS-CoV-2, and the technological ability to tweak the genome to incorporate such mutations [especially through passaging] was demonstrated by the WIV or its global research partners

6) China’s willful failure to comply with the WHO’s new reporting standards continues, even though doing so could prove their innocence [if innocent].

7) The WHO ‘investigation’ in Wuhan included a financier of the GOF research whose income is derived from attracting grant funding, and the NIH/NASEM report to the White House’s OSTP was ghost-written by said financier’s organization with the assistance of Dr. Fauci.

8) The weight of current evidence does not favor zoonosis; if COVID-19 began in Atlanta, Moscow, Paris, etc., would a WHO investigation have argued for an end to lab-accident hypotheses, and concurrently posit frozen-food transmission?

9) 1 year removed from the emergence of the SARS outbreak, all signs pointed to a natural emergence of the virus. 1 year removed from the emergence of COVID-19, all we know is that the WHO, NIH, and other entities actively worked to prevent serious inquiries into the origins of the SARS-CoV-2 virus from a non-zoonotic source, and they allowed the EcoHealth Alliance organization [who funded, among several projects, gain-of-function experiments in Wuhan] to shape their messaging in order to shield China, the WIV, NIH, WHO and EHA from criticism, while working to prevent publication of research that questioned their assertions.

-Old Age Should Burn and Rave at Close of Day-

The 21st century has seen the continued acceleration of technological advancement [most effectively predicted by Ray Kurzweil], along with the attendant dichotomy of remarkable progress towards the elimination of global poverty (down 90% in recent decades) and increasing social turmoil sparked [in part] by the disorienting impact of so much rapid change in so many aspects of daily human life.

The COVID-19 pandemic is, in many ways, as much a symptom of humanity's growing pains as it is a consequence of the disease caused by the SARS-CoV-2 virus. Because of the stunning impact COVID-19 has had upon human civilization, superficial analyses of the pandemic's origins are not just unsuitable - they could dangerously obscure the fundamental lessons humanity should be learning from this shared tragedy.

Such superficial treatment has allowed China to avoid any liability for its actions in the pivotal early weeks after a viral pneumonia of unknown cause was first detected in December 2019, in the central Chinese metropolis of Wuhan. If anything, appreciation for China's effective pandemic response has rested upon the willingness of some admirers to ignore the methods used to achieve those enviable results.

On March 1st, 2020, I was sitting in an economic brief within the US Embassy in Prague when the speaker was cut short because of the announcement of the Czech Republic's first 3 confirmed cases of COVID-19. A year removed from that abrupt transition to an emergency footing, the world is now facing a decisive milestone on the path to recovery; as attractive as the thought of accepting China's forced whitewash on the pandemic's beginnings might be at the moment, the ultimate cost of blind acceptance would be much worse - a lesson best taught by a teacher like Ren Zhiqiang, who lost his freedom after publicly [and directly] speaking truth to the same power the rest of the world must now face.

The Emperor has no clothes

If you've never heard of Ren Zhiqiang, you shouldn't feel too terrible - the Chinese Communist Party (CCP) has expended a sizable amount of effort to remove his 'stain' from their 'public' discourse. Although Ren was a wealthy and vocal critic of the ruling party in China for many years, it's been difficult to even narrow down his net worth or recent activities, even though he had previously been given the moniker "China's Trump" because of his outspoken populism and real-estate background. He's not the only high profile critic to 'disappear' from Chinese society, of course - Jack Ma, the Alibaba founder worth $60 billion dollars, returned from a similar sojourn just 40 days ago, and at least 4 other billionaires have been 'humbled' in the last few years of Xi Jinping's rule.

Ren, however, stands out because of the strength of his criticism and the timing of his outcry, right at the moment when the outbreak in Wuhan was finally subsiding under the stunningly intense quarantine imposed on 1/23. The response was swift, beginning with the deletion of his blog that was followed by 38 million Weibo users. On March 12, 2020, he disappeared, presumably kidnapped by his own government, from his own house. His article, *The Emperor has no clothes* [my own unofficial title, though I've recently found it referred to as "The lives of the people are ruined by the virus and a seriously sick system"], reportedly continued to be shared amongst Chinese internet users, although when this version was translated, the translator couldn't find any complete version in Mandarin *or* English, and this copy only survived after being captured by the Internet Archive, which is where I found it last week.

Why did I choose to include it here, in this discussion of the West's proper response to the pandemic? I felt compelled to do so because his passionate roast perfectly captures the mindset of the CCP, and dispels any illusions about the ability of the West to obtain compliance in the hunt for the origins of the SARS-CoV-2 virus - as long as they allow China to dictate the terms of their 'assistance.'

-Rage, Rage Against the Dying of the Light-

Sometimes the truth may sound ridiculous, but truth should never be judged according to what it sounds like - it should be judged according to what it is.

Here in March of 2021, the world is much quieter, but not because the orange-haired troll is gone - it's mostly quieter because there's no daily chorus to remind us that his garish bluntness is destroying the fabric of western civilization. What's remarkable is that no one seems willing to fill the leadership void that spawned Trump, expanded his base in his re-election campaign, and which the West was counting down the days until he would have to relinquish.

Certainly not in America itself, where the cancel mob is now encouraged to self-immolate, leading the French president Macron to publicly warn his own citizens to reject such damaging and self-serving propaganda. The quick and powerful censorship post-capitol hill riot was so alarming that Angela Merkel, Putin & Navalny *all* were concerned enough to chastise Congress; Vladimir Putin directed an attempted assassination of his political foil Navalny [because of his withering criticism in public speeches] **six months before January 6th**, and **even he** called it dangerous.

The truth, however, is that the world is entering a time when a unified and resolute response is required, to ensure that China will be held accountable for its handling of the COVID-19 outbreak. There is **unequivocally** no legal justification for China's refusal to provide evidence regarding patient data, ongoing research at their labs or serology results from hundreds of thousands of samples taken in Wuhan in the fall of 2019; providing such documentation is mandatory for any WHO member nation that becomes the initial location for a potentially global outbreak, and the possibility of violations of the Biological Weapons Convention makes their blunt refusal even more egregious.

Enforcing these two charters is vital ***regardless of guilt or innocence***. Ironically, without President Trump's rapid response to Syria's repeated use of chemical weapons, China would have even less motivation to worry about being called out for non-compliance to the BWC or WHO reporting requirements - since the absence of a credible 'Red Line' encourages repeat offenses. After all, the WHO gave China veto power over its investigative team, and allowed Peter Daszak to be included as an investigator (along with other members of his NGO EcoHealth Alliance) on both the WHO and Lancet teams; imagine what complete impunity would look like! The recent WHO investigation can best be described as equivalent to ***appointing General Michael Flynn to be the special prosecutor for the 'Russiagate' investigation, along with various other members of Trump's campaign organization.***

However, directly enforcing the BWC would require an actual mechanism to do so, which the charter does not contain - in contrast with the CPW or IAEA, which enforce the Chemical Weapons

Convention (CWC) and the Treaty on the Non-Proliferation of Nuclear Weapons (NPT), respectively. This reality only adds to the necessity of US leadership in the global effort to hold China accountable for its early suppression of critical information that likely played a major role in delaying mitigation efforts until global community spread was already in motion - much less any broader measures should a global consensus emerge that the SARS-CoV-2 virus jumped species because of ongoing β-coronavirus research by the Wuhan Institute of Virology or other labs within that city of 11 million people.

Former US Secretary of State Mike Pompeo burned down any remaining bridges when he issued a statement 5 days before the inauguration:

> “And in January 2021, the State Department confirmed that people had fallen mysteriously ill at WIV in fall 2019, and that WIV conducts secret bioweapons research with the PLA.
>
> The negligence at China’s biolabs, especially WIV, was so dangerous that the PLA dispatched a general to take over the facility soon after the outbreak in Wuhan. Xi Jinping’s first speech on the outbreak highlighted “lessons learned” about “shortcomings” and “leaking holes” in China’s management of biological material and biological-security system. He demanded that “a new biological-security law” be made part of the “national-security system.” *Wall Street Journal (2/23/21)*

China responded with a raised middle finger, and some viewed his statement as a political stunt, but someone nursing presidential ambitions is unlikely to fabricate an accusation *tantamount* to a crime against humanity if the incoming administration could immediately denounce it as unfounded. It should be noted that the Biden administration has not modified the stance taken by its DoS predecessor. And last week, the former Deputy National Security Advisor provided more details on Face the Nation, 2/21/21. Our English counterparts joined in on the chorus, and in the last 24 hours the WHO itself has hedged.

The foundation of any further inquiry should rest on the following assumptions:

It’s ***more probable than not*** that fulfillment of the basic WHO requirements for pandemic reporting would contain enough information to exonerate the Wuhan Institute of Virology and any other research institution from culpability for the sparking of the COVID-19 pandemic - IF they are, in fact, innocent and the zoonotic hypothesis is correct. Conversely, it is ***highly likely*** that fulfillment of those same WHO requirements would provide sufficient information to prove evidence of a lab release beyond the threshold of legal 'reasonable doubt.'

It's highly ***unlikely*** that any additional evidence will exonerate the Chinese Communist Party, because a zoonotic transfer can be assumed as the inverse outcome from the evidence above. It is, of course, entirely possible for SARS-CoV-2 to have jumped directly from an animal in Wuhan, but it is less likely and almost certainly would not produce evidence prior to the conclusion of the options listed above. The herculean efforts of D.R.A.S.T.I.C., other scientists highlighted in today's WSJ, and other assorted researchers have resulted in a stunning amount of evidence against a natural emergence - that continues to grow daily.

As Dr. Steven Quay plainly and brilliantly pointed out in his Bayesian analysis, two discoveries stand out in particular:

- An in-depth analysis of the very first genome sequences [as in, the phylogenetic ancestors of all current strains] uncovered remnants of sequences from a SARS-CoV-2 vaccine [adenovirus-based just like the first Chinese vaccine peppered throughout multiple samples. Given that those samples were taken before the virus genome was ever sequenced, only time-travel could've produced such contamination - unless a vaccine ***did*** exist in December of 2019. Dr. Quay is still awaiting confirmatory results from other researchers…
- An absence of evidence of seroconversion in the Wuhan population prior to the outbreak. Animal transmission of a virus invariably leaves behind traces of evolutionary trial-and-error, because a virus must continue to evolve in order to strengthen its affinity for a host. Both SARS and MERS showed classic patterns of this process within blood samples taken just before their respective outbreaks. Thus far, COVID-19 has not been seen in any of 68,500 samples.

"But this kind of cover-up propaganda, it can basically only cheat those who want to be cheated; there's no way it can cheat those who believe in facts and reality."

Ren Zhiqiang called out Xi Xinping on 2/23/2020, and disappeared 3/12. He re-appeared just before his 1-day corruption trial/conviction in September. I've only found 1 translated copy on Google, so China's been busy. If he was willing to face that to say this, we should pay attention, because Ren only got to say it once.

This is the government that Peter Daszak was and is protecting, to keep a full SARS-CoV-2 origin investigation from taking place; this is who he has defended against our Department of State and supported with our tax dollars. The contrast of two voices….

I fought against a brutal regime & helped a freed people vote for the 1st real time in a gen. [in Anbar Prov., '05]; I can't stand by when a man gives up freedom for the truth. IF this pandemic is unjust, 2.5M dead need justice. This is why I'm here, simply to pass truth along.

The Prometheus analogy fits him a lot better - A man who crept into the darkness to steal a flame of wisdom and share it with mankind, only to be punished by the gods.

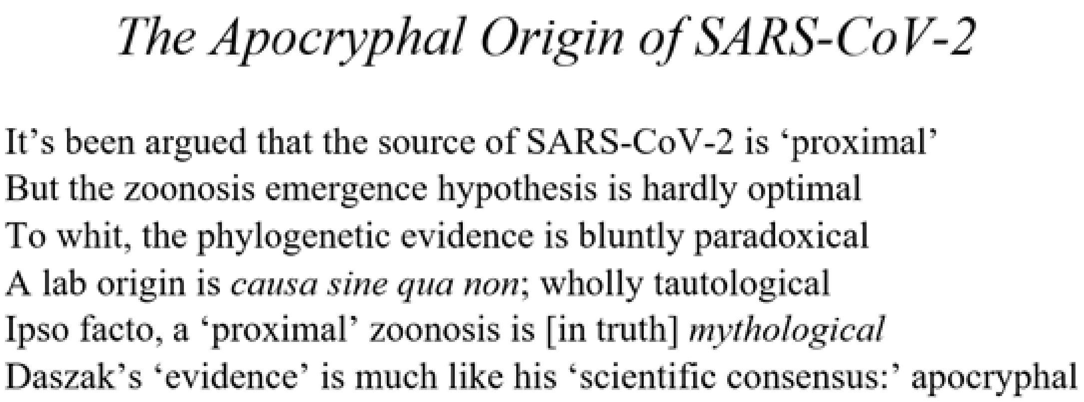
C. H. Rixey

[My 'living and breathing' list of 250+ sources is here....]

Prometheus & Pandora III: The Apocryphal Origin of SARS-CoV-2 (4/8/20)

Merely Shadows on the Wall* [2.0]

I felt it was appropriate to preface this analysis with a tribute:



The Apocryphal Origin of SARS-CoV-2

It's been argued that the source of SARS-CoV-2 is 'proximal'
But the zoonosis emergence hypothesis is hardly optimal
To whit, the phylogenetic evidence is bluntly paradoxical
A lab origin is *causa sine qua non*; wholly tautological
Ipso facto, a 'proximal' zoonosis is [in truth] *mythological*
Daszak's 'evidence' is much like his 'scientific consensus:' apocryphal

On March 17, 2020, the esteemed journal *Nature* published a research article that laid out the central argument for a zoonotic emergence as the likely trigger of the COVID-19 pandemic. *The Proximal*

Origin of SARS-CoV-2 went on to become one of the two most-cited articles of the pandemic, referenced 1,316 times and viewed more than 5.27 million in total:

Correspondence | Published: 17 March 2020

The proximal origin of SARS-CoV-2

Kristian G. Andersen ✉, Andrew Rambaut, W. Ian Lipkin, Edward C. Holmes & Robert F. Garry

Nature Medicine **26**, 450–452(2020) | Cite this article

5.27m Accesses | **1316** Citations | **35224** Altmetric | Metrics

For the uninitiated, that's a lot of exposure for a scientific article; in the neighborhood of what you might expect if an article proving the existence of the 'Force' was published - and written by Yoda himself.

Baby Yoda's thoughts on zoonosis

Unfortunately, ***level of attention*** doesn't always correlate with ***accuracy or veracity***, and after a year of 'findings' [and 2.8M deaths] most of the evidence that's been discovered has undercut nearly every aspect of its argument.

A general synopsis could include:

- The RaTG13 sequence that forms the basis of the zoonotic hypothesis may have been fabricated itself [a collection of sources for RaTG13]
- The market hypothesis cannot account for the sequences of the earliest known cases
- The case for pangolins as the intermediate host species appears to rest on articles that sampled from the same animal
- The WHO's own investigation [wholly researched and partially written by the Chinese] found no pre-pandemic evidence of of COVID-19 in more than 60,000 animal samples, 70,000 suspect pneumonia cases prior to December 2019, no evidence of multiple jumps during the transmission to humans, etc.
- No evidence of an earlier sequence than WH04 exists[which appears to have been uploaded three weeks after being taken in an attempt to obscure its origin as having been taken from a patient at the nearest hospital to the Wuhan Institute of Virology (WIV)]
- No other examples of a CoV within the sub-genera *Sarbecovirus* of a species/strain that shows evidence of insertion of a polybasic furin cleavage site (FCS)
- More and more examples of lab contamination of samples published by the WIV
- Multiple analyses have shown that SARS-CoV-2 binds more tightly to human cells than any other mammal species, while bats are at the opposite end of that scale
- Among a dozen other major evidentiary concerns

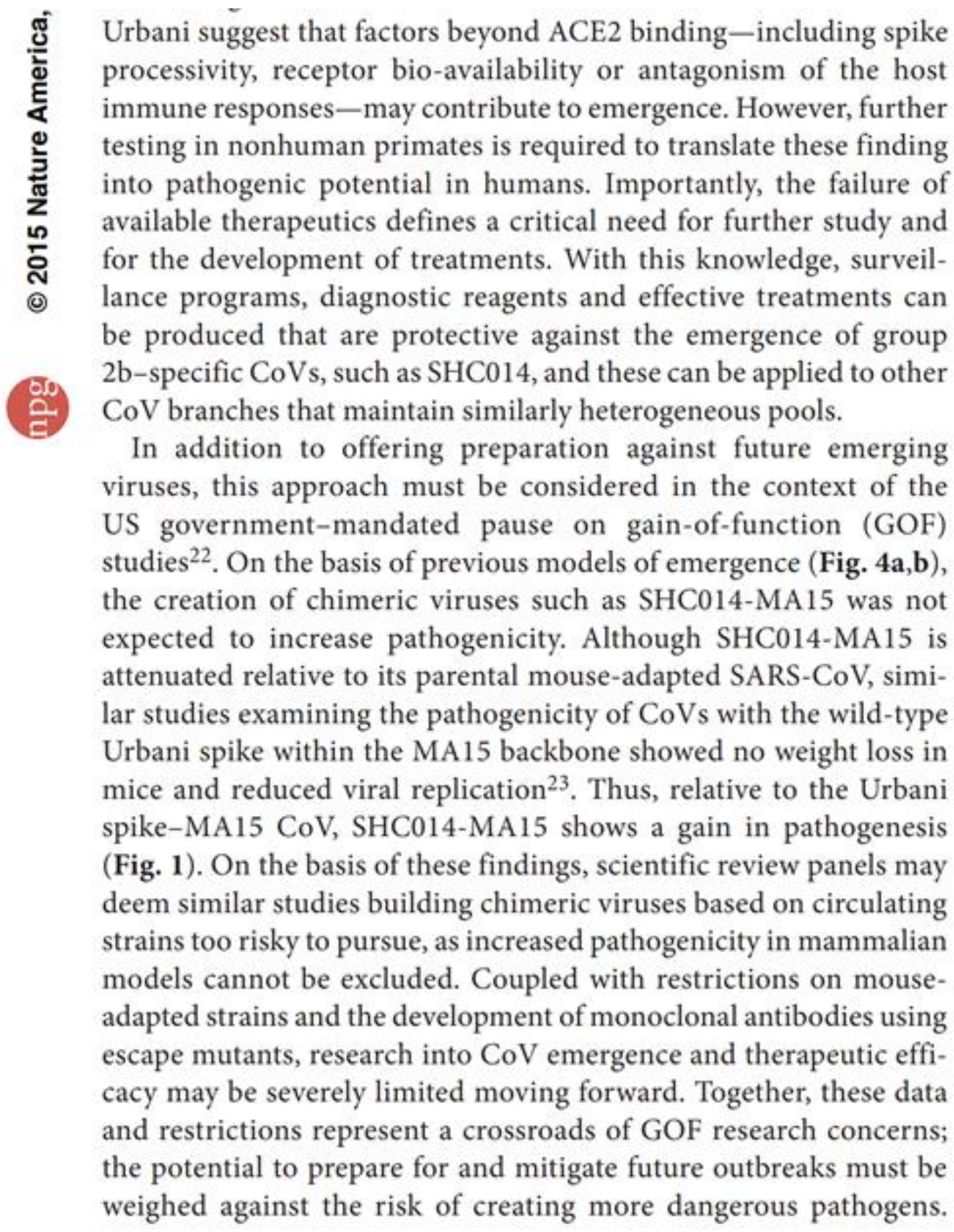
In almost every case, the zoonotic claim/criticism of a lab leak have been driven by the same core group of scientists that have been heavily involved in gain-of-function (GOF) research on coronaviruses (CoV) for more than a decade. Peter Daszak has been raising funds via his non-profit EcoHealth Alliance with the explicit aim of furthering gain-of-function research, as if it were the only way to develop vaccines for emerging pandemic threats. A large portion of the grants he's procured have gone to the WIV, and he has personally assisted in their research several times over 15 years.

One of the many projects that Daszak has worked to draw attention away from was the joint research between the WIV and the UNC-Chapel Hill lab of Ralph Baric; as the GOF debate raged in 2014 [ultimately resulting in a partial ban on the riskiest *influenza* and CoV experiments], Baric was teaching advanced techniques to Zheng-Li Shi herself! The joint research, which had been ‘grandfathered’ despite the ban that took effect in late 2014, gave Shi enough insight to trigger similar experiments back home in Wuhan - literally driving innovation and ‘keeping the engine running’ as American scientists stalled until the moratorium was lifted in 2017.

Funded by EcoHealth Alliance, of course.

One of the repeating themes of this saga, however, is the fact that none of our unholy trinity of Shi, Daszak and Baric has expended much effort in even pretending to care about restrictions and standards, especially since 2014. In the video below [one of the sessions of a working group debating the potential moratorium, the esteemed David Relman asked Baric directly if his research would involve gain-of-function tweaks that could increase the danger of CoVs to humans [minutes 41-48, if the bookmark doesn’t load]. Mark Denison, another CoV research giant, adds emphasis to Baric’s emphatic ‘no:’

I’d add a ***Spoiler Alert*** warning here, but everyone only needs 1 guess to answer the question "what experiment did Baric do next?" His 2015 paper describes how he took humanized mouse models and used them to create a chimeric CoV virus - just as he and Denison had sworn wasn’t being considered, and wouldn’t be unless a viable need emerged in the future:



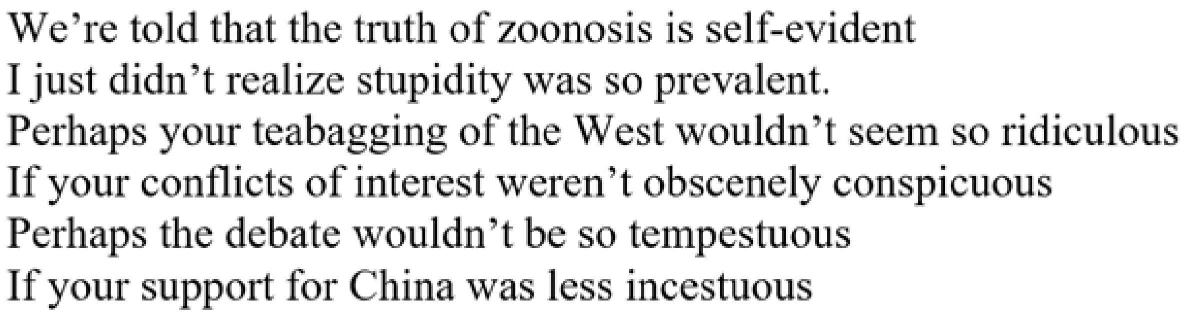
Urbani suggest that factors beyond ACE2 binding—including spike processivity, receptor bio-availability or antagonism of the host immune responses—may contribute to emergence. However, further testing in nonhuman primates is required to translate these finding into pathogenic potential in humans. Importantly, the failure of available therapeutics defines a critical need for further study and for the development of treatments. With this knowledge, surveillance programs, diagnostic reagents and effective treatments can be produced that are protective against the emergence of group 2b–specific CoVs, such as SHC014, and these can be applied to other CoV branches that maintain similarly heterogeneous pools.

In addition to offering preparation against future emerging viruses, this approach must be considered in the context of the US government–mandated pause on gain-of-function (GOF) studies[22]. On the basis of previous models of emergence (**Fig. 4a**,**b**), the creation of chimeric viruses such as SHC014-MA15 was not expected to increase pathogenicity. Although SHC014-MA15 is attenuated relative to its parental mouse-adapted SARS-CoV, similar studies examining the pathogenicity of CoVs with the wild-type Urbani spike within the MA15 backbone showed no weight loss in mice and reduced viral replication[23]. Thus, relative to the Urbani spike–MA15 CoV, SHC014-MA15 shows a gain in pathogenesis (**Fig. 1**). On the basis of these findings, scientific review panels may deem similar studies building chimeric viruses based on circulating strains too risky to pursue, as increased pathogenicity in mammalian models cannot be excluded. Coupled with restrictions on mouse-adapted strains and the development of monoclonal antibodies using escape mutants, research into CoV emergence and therapeutic efficacy may be severely limited moving forward. Together, these data and restrictions represent a crossroads of GOF research concerns; the potential to prepare for and mitigate future outbreaks must be weighed against the risk of creating more dangerous pathogens.

A correction was submitted in 2016, to add in the fact that ***EcoHealth Alliance had provided the funding for the research***. Stunningly, Baric added ***another correction*** in May 2020, to add the sequence from the chimeric mouse CoV that had never been uploaded to Genbank for reference. Just as the WIV frequently did, Baric never bothered to upload sequences for his groundbreaking work, at least until it was noticed in the early months of the pandemic. This is highly unusual and rare, because one of the requirements for publication in every area of science is making your data available so that others can reproduce and verify your results. It's even more disturbing because Ralph Baric has been a key member of the federal government's advisors

Zheng-Li Shi (ZLS) had worked with Baric ***in NC,*** practicing advanced passaging techniques and chimera development, and then returned to Wuhan in 2014/15 to apply those lessons to her own collection of CoVs - which happens to be the largest collection of bat CoVs in the world.

Further inspiration:



We're told that the truth of zoonosis is self-evident
I just didn't realize stupidity was so prevalent.
Perhaps your teabagging of the West wouldn't seem so ridiculous
If your conflicts of interest weren't obscenely conspicuous
Perhaps the debate wouldn't be so tempestuous
If your support for China was less incestuous

Did you know that the difference between 'speculation' & 'science' is dependent upon ***who*** is making the claim? *Me neither*. In retrospect, it's been hard to find examples of the 'consensus' Daszak has referenced that don't include interventions from his inner circle of collaborators.

In research, it seems to really be all about ***WHO*** you know, and who's paying you to know it. Statesmen, diplomats, WMD professionals [formerly myself] and scientists not in the field of virology have been stunned by the unwillingness of the WHO or virologists to consider the possibility of COVID-19 having leaked from a lab, but it's much less surprising when you realize that the potential defendants have colluded to control the investigation of themselves.

And by "colluded to control," I mean to control the ***entire narrative*** -

- from the paper announcing COVID-19 to the world [Shi, with the 1st sequence]
- 1 letter to the National Security Council [see my exclusive article that exposed Dr. Fauci & the NIH's direct coordination to protect GOF research]
- 2 public letters literally ghost-written by Daszak et al
- The *Proximal Origin* paper
- The primary 'response' to Li-Meng Yan's expose' [an opinion piece by Angela Rasmussen, who works for Lipkin at Columbia University, just a few miles from their collaborator, EcoHealth Alliance]
- Several Daszak interviews on cable news and in newspapers
- Two early research papers supporting pangolins as the intermediate host species of a zoonotic jump
- A letter signed by 77 Nobel Prize laureates calling for the re-instatement of EcoHealth Alliances funding, which had been cut by the NIH in April [coordinated by Daszak]
- A letter signed by the presidents of 31 leading Academic Societies, also protesting the cut of EcoHealth Alliance's funding [and also coordinated by Daszak]
- Daszak's presence on both the WHO ***and*** Lancet teams investigating the origins of COVID-19 in Wuhan [he's actually been named the ***leader*** of the latter group]
- Daszak's assistance to the WIV by cutting off inquiries into the removal of WIV's main databases [containing more than a thousand CoV sequences, mostly unpublished] in September 2019, and the specific removal of the primary remaining one by Zheng-Li Shi on December 30, 2019, immediately after being ordered to return to Wuhan.
- Daszak's assistance in drafting the WHO's 300-page report on their [lack of] findings while investigating in Wuhan
- And the large-scale censorship of all articles openly discussing the possibility of a lab-leak origin for the SARS-CoV-2 virus, which the researchers of D.R.A.S.T.I.C. finally succeeded in piercing last fall, with a growing mountain of evidence.

Virtually all of the 2020 investigative journalism/research into the Wuhan Institute of Virology that I came across [while researching and writing independently about the theory] was directly or indirectly tied to D.R.A.S.T.I.C.'s discoveries, and their efforts have finally begun to bear fruit. From the open letter published in the *Wall Street Journal* to last week's 60 minutes interview, appearances on The Joe Rogan Experience, Fox News and other outlets across the globe [some examples below], the palpable tsunami of momentum can be traced back to ripples that appeared more than a year ago:

relevant authorities to help with the next stages

So that *any gaps in data needed to further the investigation can be addressed*

Called for timely access for independent experts early in futur pandemics

There is so much evidence implicating the WIV that only a portion of the links can even fit into Substack's article size limit - such as disturbing implications of mutations within COVID-19's genome that hint at vaccine development gone wrong, and the discovery of potential vaccine markers in the very 1st patient samples from Wuhan, collected in December 2019. However, as I wrote in part II of ***Prometheus & Pandora,*** the failure of the global community to fully investigate all possible origins of the SARS-CoV-2 virus's emergence into humanity is 'too big to contemplate:'

The 21st century has seen the continued acceleration of technological advancement [most effectively predicted by Ray Kurzweil], along with the attendant dichotomy of remarkable progress towards the elimination of global poverty (down 90% in recent decades) and increasing social turmoil sparked [in part] by the disorienting impact of so much rapid change in so many aspects of daily human life.

The COVID-19 pandemic is, in many ways, as much a symptom of humanity's growing pains as it is a consequence of the disease caused by the SARS-CoV-2 virus. Because of the stunning impact COVID-19 has had upon human civilization, superficial analyses of the pandemic's origins are not just unsuitable - they could dangerously obscure the fundamental lessons humanity should be learning from this shared tragedy.

Sometimes the truth may sound ridiculous, but truth should never be judged according to what it sounds like - it should be judged according to what it is.

-Rixey

*From the top photo: L-R: Zheng-Li Shi, Peter Daszak, Peter Ben Embarek & Ralph Baric. Picture Frames: Xi Xinping & Mark Denison. TV: The Messiah

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~[My 'living and breathing' list of 349+ lab-leak sources is here....; 200+ more have been compiled, but I haven't had time to add the links for them yet]

~~For any recovering former members of 'the consensus,' or as a reward for making it through the full WHO report *sans emesis*, I've provided some therapy via Heather Heying & Bret Weinstein.

Prometheus & Pandora IV: Edifice Wrecks (5/10/21)

Prometheus & Pandora IV – Edifice Wrecks

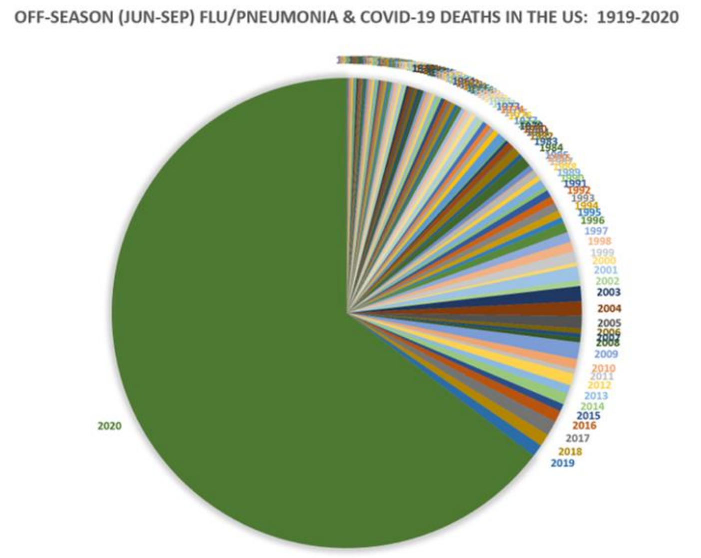
5/10/2021

"Trust the Science, Not the Scientists"

The COVID-19 pandemic was destined to be a uniquely profound moment in the history of science, in that it represented the first time in human history that modern medical technology could be applied to a pandemic of historic proportions. And, despite the concerns I've written about below, there have been many triumphs amidst this tragedy.

Comparing 2020 to 1918 may seem like a low bar, but if COVID-19 had emerged in 1918 the number of deaths would be closer to 30 million than 3 million. Despite having no cure, no specific treatments or vaccines and near-global spread in 2 months, scientists embarked on the largest single research project in the history of mankind, and created dozens of new treatments and vaccines. Of all coronavirus research published in the last half-century (since 1971), 92.7% has been published since January 10th, 2020, when the first genome sequence of SARS-CoV-2 was shared. Compared to 2018 data, COVID-19 research accounted for 3.9% of ***all*** global research & 11% of output in the combined bio/biomedical/health science fields.

It's true that humanity has benefited from broad increases in standards of living - since 1980, the proportion of global population living below the 'extreme poverty' level has shrunk from 50% to 10% while nearly doubling in real terms, from 4.5 billion to 7.9 billion. However, it's also true that the scale of the pandemic has been incredibly misunderstood. Many of my first articles last spring were focused on exposing the 'middle' - the fact that partisan hype/dismissal made it impossible for people [Americans, at least] to understand the actual threat. I made the following pie chart to illustrate how COVID-19 compared to the off-season months of seasonal flu, as part of my fall projection of US COVID-19 deaths through May (published 10/7):


OFF-SEASON (JUN-SEP) FLU/PNEUMONIA & COVID-19 DEATHS IN THE US: 1919-2020

The general expectation among scientists was for COVID-19 to peak in the winter, just as the seasonal flu. With that in mind, consider what I discovered while comparing the summer waves to the CDC's historical *influenza* records: on the average day from June - September last year, more Americans died from COVID-19 than from the average 120-day off-season in the previous century. This also meant that COVID-19 killed more Americans in four months than the sum of all 101 summers since the original Spanish Flu in 1918-1919, in the midst of the first true lock-down in a century.

The previous articles in my 'Prometheus & Pandora' series:

[informally, I call it '***Requiem for a Steam…..ing Pile of BS'***]:

Part I - Trust the Scientists - Not the Science? [Fauci helped framed the debate]

II - The West must not go gently into a COVID-19 goodnight [The big picture]

III - The Apocryphal Origins of SARS-CoV-2 [How scientists manipulated research]

****IV - *Edifice Wrecks* [How much are scientists prepared to lose to protect themselves?]**

Against this historic backdrop, it's not surprising that people across the globe have mixed emotions about the public health response where they live. Faith in the abilities of scientific establishments to protect the rest of us has been rocked by a reality tv show in which almost every decision, projection, recommendation and mandate has been ineffectual or worse. And, even if that wasn't initially the case, partisans would immediately undermine the opposing side anyway.

The frequency of these errors has led to questioning of everything, even those things scientists got right. My intuition tells me that the reason for such backlash has less to do with the esteem our societies have bestowed on them, and more to do with the esteem they have bestowed on themselves.

-History is written by the victors - or is it?

Experience has taught me that this common nugget of wisdom is both overused *and* misunderstood; history is often written by whomever wants to control a narrative more, and sometimes it's just easier to re-write history when in power. What most Americans don't know is that, in addition to China's destruction of early lab samples, deletion of hundreds of news articles and mass 'disappearance' of early whistleblowers, a vastly smaller and more targeted campaign of censorship was taking place elsewhere - especially in the United States. That last point is crucial, because American scientists and institutions have driven global research for most of the last 100 years - either through innovation, funding or both.

As my research into COVID-19 has progressed over the last 14 months, the ‘arc of evidence’ has never bent towards the SARS-CoV-2 virus having emerged via random, natural chance. At the same time, the messaging from the leadership of our scientific institutions has remained fairly constant; the unwillingness to adjust to new evidence or allow open debate on lockdowns, various therapeutics and the continued validity of school closures is now questioned even by former supporters of the strategy.

As I write this on Sunday evening, 5/9/21, global scientific leadership remains defensively crouched with its back against the wall, aware of the damage to their reputation but desperate to maintain the illusion of control. Consider this an open letter, from an observer who’s examined the mountain of evidence:

Scientists,

Fairly & unfairly, your overall response to the COVID-19 pandemic has been harshly criticized, and it was almost unavoidable that the issues surrounding pandemic response would be politicized, and used as a sword and/or a shield with which to engage political rivals. That process has played out in countries across the globe.

It is clear that the strategy you chose to implement was to lean on the accumulation of public goodwill and trust earned over the decades, in order to reassure the public that any steps taken were ultimately in our collective best interest. I hope that the events of the last year [if nothing else] will disabuse you of the notion that citizens are still willing to blindly accept your emergency declarations at face value. Trust cannot be instantly gained, and the broad swath of evidence now emerging from the 50 states has struck down many of the sacred cows epidemiologists had compiled as the optimal plan for mitigating pandemics in recent years. It was certainly improper for President Trump to insert his opinion into the debate - but it was ultimately more damaging to pretend that a legitimate debate didn't exist.

2 simple observations arise from this reality:

1) We [citizens] ***can*** handle the truth. We definitely handle truth better if we're told before everyone is dead - at a minimum, before the annual memorials begin.

In our modern age of global connection, you must approach your civic responsibilities from a position of ***honesty; for example, the unwillingness to allow doctors to prescribe various drugs off-label [Ivermectin, Hydroxychloroquine, etc.], despite a high degree of patient willingness and provider experience with the medications, was a massive failure. Why? Because anyone willing to waive compensation for complications arising from EUA-approved vaccines would likely be willing to do the same if emergency needs meant the use of off-label treatments that at least were fully approved for….anything. Instead, the world watched the same people justify or reject various options, despite the accumulation of real-world evidence that rarely correlated with the choices made by officials.***

Personally, I had no dog in this particular fight, other than thinking that this was one of those 'everything but the kitchen sink'-worthy crises, but it's hard to review the body of evidence found and the decisions made ***and then conclude that officials' priorities were centered on anyone but themselves***.

2) Science should focus on leadership, not censorship.

Nowhere is this statement more applicable than in the matter of COVID-19's origins. As a matter of trust, the ultimate answer is less important than how the scientific community conducts itself in the meantime. For starters, I'll list the options, taking the liberty to paraphrase:

1α) Where did COVID-19 come from?

A) Nature? [zoonotic emergence, *zoonosis*]

B) Nurture? [lab emergence, *oops-onosis*]

Since A) has been extensively covered elsewhere, we're going to use hypothesis B) to illustrate the importance of the 2 observations above. I should note that regardless of how COVID-19 came to Wuhan, it left via 5 million travelers during the 3+ weeks China waited before locking down Wuhan; some of the time was filled by ordering labs to destroy all of their samples after testing. I should also note that this was several weeks ***before*** the lab theory was a 'thing.'

Ηυβρισ Springs Eternal

In almost every case, the zoonotic claim/criticism of a lab leak have been driven by the same core group of scientists that have been heavily involved in gain-of-function (GOF) research on coronaviruses (CoV) for more than a decade; the Ηυβρισ **[*hubris*]** is stunning. Peter Daszak has been raising funds via his non-profit EcoHealth Alliance with the explicit aim of furthering gain-of-function research, as if it were the only way to develop vaccines for emerging pandemic threats. A large portion of the grants he's procured have gone to the WIV, and he has personally assisted in their research several times over 15 years.

Zheng-Li Shi (ZLS, leader of a main lab within the WIV) had worked with Baric ***in NC,*** practicing advanced passaging techniques and chimera development, and then returned to Wuhan in 2015 to apply those lessons to her own collection of CoVs - which happens to be the largest on Earth. Virus sequences pulled from those samples were stored in databases that have been taken off line, with the last one removed by Shi herself not long after first being ordered to return to Wuhan from a conference elsewhere in China on 12/30/19. Since then, Shi has **given lectures with slides showing phylogenetic**

trees containing β-CoV's whose sequences [or existence] have never been published [discovered by DRASTIC]. The lack of other **β-CoV** examples [or genetic 'backbones' used for genetic engineering] was one of the main arguments in the paper *The Proximal Origin of SARS-CoV-2* for a natural origin of the virus, the most viewed & cited scientific article about COVID-19 [5.3 million views in all]. There is no logical reason to withhold data that would likely exonerate the WIV & China - unless, of course, it would prove their guilt instead.

~

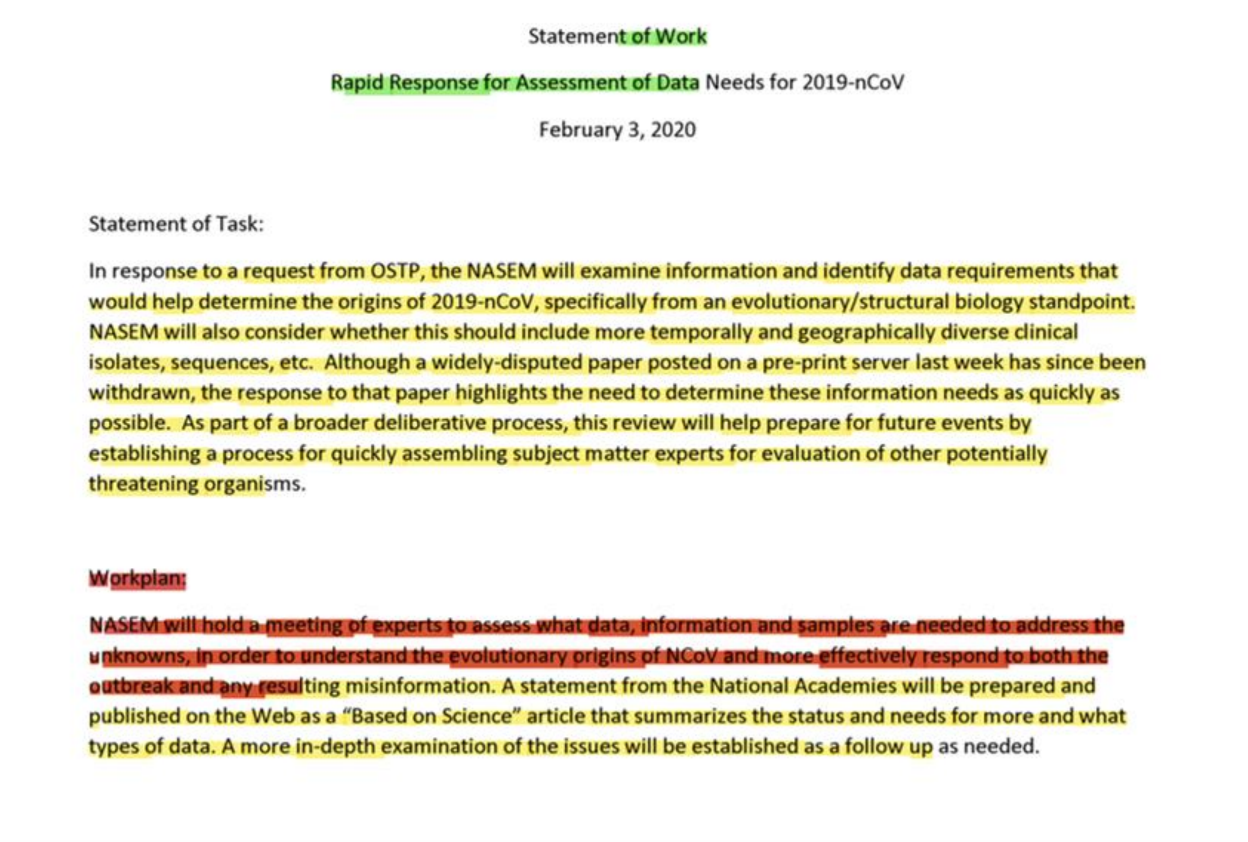
I finally finished going through more than 85,000 pages of FOIA documents related to Ralph Baric & Peter Daszak & the NIH; The most surprising thing I've come across was something I haven't seen discussed by US RTK or anyone else, although given the volume of files to go through that's understandable.

Specifically, based on the 2/17 documents [a 337 page sub-set of Baric emails], US Right-to-Know had published an article about the coordination between Baric, Daszak and others in preparing a document to be published that was written to quash speculation of the rumor that COVID-19 had leaked from a lab at the Wuhan Institute of Virology. The emails also show an earlier letter written along the same lines, that had been prepared by NASEM for the OSTP (The White House's Office of Science & Technology Policy). As I wrote in Part III:

While reading through the correspondence, I noticed Dr. Fauci had been included in an email chain just prior to 2/4, when the group of scientists was discussing the content that should be included within the OSTP letter. This had already been noticed, but since it was the only such appearance of Fauci as a mail recipient, it seems to have been considered simply as a curiosity, showing that he was aware of the general conversation about how the scientific community should respond to growing speculation of gain-of-function studies being the cause of COVID-19.

However, the attachment to that email [see Part I] **was a timeline of speakers for the event and the explanation of its purpose:**

[Per US Right-to-Know's recent FOIA request]



Statement of Work

Rapid Response for Assessment of Data Needs for 2019-nCoV

February 3, 2020

Statement of Task:

In response to a request from OSTP, the NASEM will examine information and identify data requirements that would help determine the origins of 2019-nCoV, specifically from an evolutionary/structural biology standpoint. NASEM will also consider whether this should include more temporally and geographically diverse clinical isolates, sequences, etc. Although a widely-disputed paper posted on a pre-print server last week has since been withdrawn, the response to that paper highlights the need to determine these information needs as quickly as possible. As part of a broader deliberative process, this review will help prepare for future events by establishing a process for quickly assembling subject matter experts for evaluation of other potentially threatening organisms.

Workplan:

NASEM will hold a meeting of experts to assess what data, information and samples are needed to address the unknowns, in order to understand the evolutionary origins of NCoV and more effectively respond to both the outbreak and any resulting misinformation. A statement from the National Academies will be prepared and published on the Web as a "Based on Science" article that summarizes the status and needs for more and what types of data. A more in-depth examination of the issues will be established as a follow up as needed.

Kristian Anderson, Peter Daszak, Robert Baric and others were gung-ho about putting out this statement, and a second one that was ultimately published a few days later, but in the midst of 80K+ emails [whose response chains run backwards] some of the details are out of order, and the connection to a specific meeting was never made by US Right-to-Know, who focused on the backdoor coordination between two of the scientists who would later be implicated by their publicly-available research.

….that Fauci supported efforts to combat 'misinformation' - specifically, inquiries into whether gain-of-function experiments at the Wuhan Institute of Virology. Given that Baric and the WIV had received significant amounts of funding over the previous decade, coordinated by Peter Daszak, from the NIH, it's not terribly surprising that Fauci would've wanted to suppress information that could lead to criticism concerning federal funding. Indeed, that was only one of many gain-of-function projects supported by the NIH.

Fauci's opposition of many of President Trump's positions on various aspects of the pandemic has been characterized as a heroic defense of science against anti-intellectual conspiracy theories, but Fauci's advocacy and efforts to suppress research into COVID's potential lab origins, and to signal solidarity with GOF researchers, came just as President Trump would have begun to hear intelligence reports that considered that to be a plausible line of investigation.

In March 2020, Trump aired his suspicions publicly, almost certainly because he had seen intelligence reports along those lines. Only recently have officials like Matthew Pottinger and David Asher come forward to discuss investigations into China, and as the Dep. National Security Advisor, Pottinger would've seen that intelligence as well as been part of the intended audience for the OSTP memo.

How did this impact research into COVID-19's origins? The highlights in this image show the stunning output from the researchers either present at the meeting or connected to it; by comparison, there were only 2 peer-reviewed articles advocating the possibility of a lab origin before August, out of ***23,000.*** It would've been fairly simple to put that into practice, because the speakers at that meeting were Andrew Pope [NASEM], Kevin Droegemeier [OSTP], Chris Hassell [HHS & P3CO] and Anthony Fauci [NIAID]. Pope was the policy director of the National Academies of Science, Engineering & Medicine, which honors the best American scientists and publishes research. Droegemeier was the presidential science advisor, Hassell was the chief science advisor of the Dept. of Health & Human Services, and Fauci has been the #2 at the NIH, which controls all federal funding of *academic* scientific research. That's a lot of levers that can be pulled to ensure compliance, and it obviously worked:

DRASTIC RESEARCH

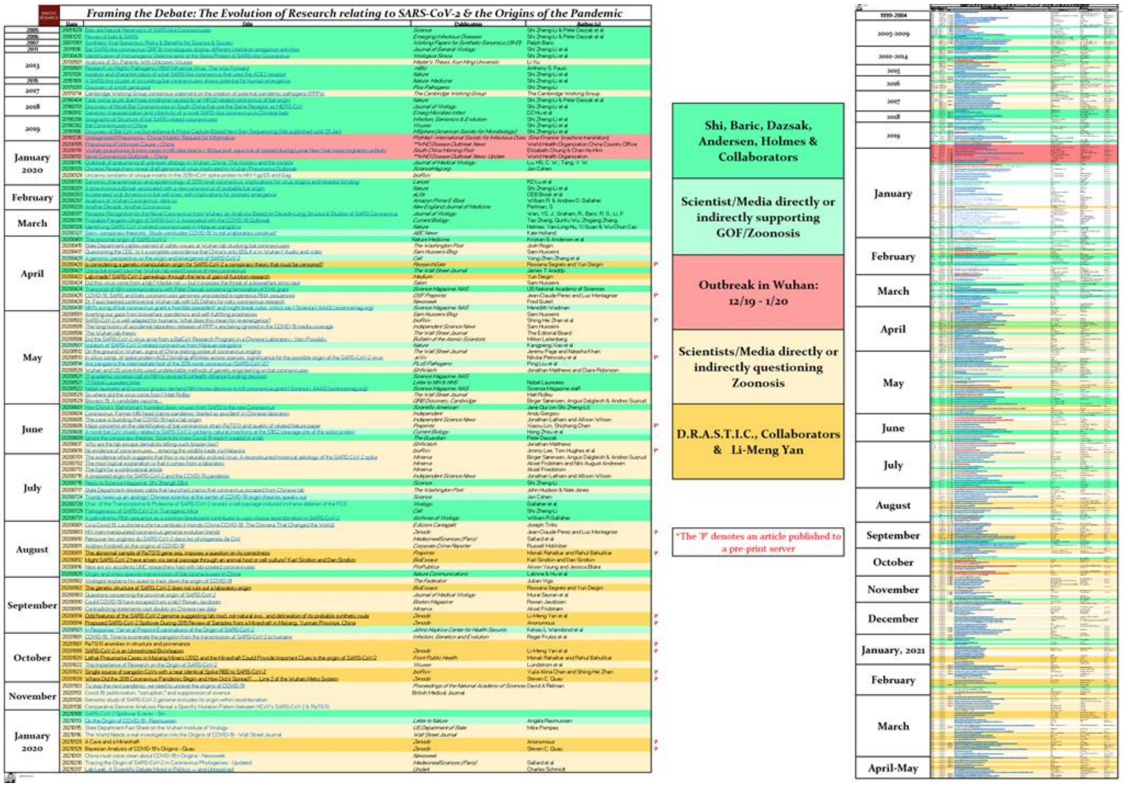
So, Daszak & EH Alliance's response to a global pandemic they've predicted [and exist to prevent] is:
1) No research
2) Coordinating statements to protect against anticipated criticism:

Date	Event	Authors, Orchestrators	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV		
12/30	Auto ProMed warning email sent out		
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server		
12/31	Daszak on phone with WIV gathering intel		
1/1	Huanan Seafood Market closed		
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish		
1/3	China notifies the WHO of a 'viral pneumonia of unknown cause'		
1/3	China's CDC sequences the genome		
1/7	Daszak in possession of 'info to be shared offline with NAS director'	*This has never been publicly addressed	
1/10	Genome shared with Virological.org via E. Holmes		
1/14	1st reported case of Human to Human transmission	*1st suspected in late December	
1/20	1st Shi paper on genome submitted		
1/23	Wuhan lockdown is finally announced		
1/29	Pre-print of potential HIV/COVID-19 link published [retracted days later]		
1/30	WHO intiates 'Public Health Emergency of International Concern'		
1/31	President Trump announces travel ban for travelers from China		
2/1	"Analysis of Wuhan Coronavirus: déjà vu"	Gallaher @ www.Virological.org	Tulane (TU)
2/3	"A pneumonia outbreak associated with a new coronavirus of probable bat origin" RaTG13	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	Fauci, Hassell, Daszak, Baric et al	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/7	NASEM letter sent to OSTP/NSTC	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	"No Credible evidence supporting claims of the laboratory engineering of SARS-CoV-2"	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/16	"The Proximal origin of SARS-CoV-2" - signed by signatories of the *Lancet* letter	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Lancet* letter published	Daszak,	EHA, UNC, Scripps,
2/16 - 2/24	Initial WHO investigation & report [NIH's Clifford Lane (Clinical Dir., NIAID)]		Works for Fauci
2/26	"Escaping Pandora's Box: Another Novel Coronavirus"	Daszak, Laubenberger	EHA, NIH
3/1	"2019-nCoV in context: lessons learned?"	Karesh	EHA
March	Multiple papers published advocating Pangolins as intermediate host	Holmes & Friends in China	Sydney U/China
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	Dir. Francis Ross	NIH - Fauci's boss
4/10	"Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins"	Holmes & Friends in China	
4/27	NIH cuts funding for EHA [restored 3 months later]	Dir. Francis Ross	NIH - Fauci's boss
4/30	NAS decries funding cuts in *Science*	Editors of *Science*	
5/21	Letter from 77 Nobel Prize winners denouncing EHA funding cuts	orchestrated by Daszak - friends in high places	EHA
5/22	Baric issues a correction to a **2015** paper to add the sequence of his chimaeric SARS-like CoV	*Which might have looked like GOF 5 years earlier...	
5/22	Letter from presidents of 31 Academic Societies denouncing EHA funding cuts	orchestrated by Daszak	EHA
July	Daszak applies & is chosen as a member of the WHO investigative team		
July	EHA gets new & improved funding from NIH		
11/17	Shi submits an addendum to her 2/3 paper to clarify RaTG13 provenance	Shi	WIV

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021

@charlesrixey

Here’s the same trend, writ large over 14 months, with 387 news or journal articles discussing aspects of the two origin hypotheses:



The Arc of History Bends towards…..Justice?

The COVID-19 pandemic represents a true paradigm shift in modern history, but its impact can't fully be measured until its origin story is told - largely because the emergence of COVID-19 in Wuhan came just as China has been closing the gap with the US to become the largest economy in the world [now estimated to occur circa 2028]. China's rise means that the United States once again has a near-peer geo-political foil intent on hegemonic control of east Asia and the Pacific

As the accumulation of scientific evidence about COVID-19 grows, the needle has been moving in only 1 direction - towards scientific research in Wuhan - and the global scientific community is in danger of repeating the same mistake twice, by doubling down on trusting them. Regardless of what the origin story ***is***, the the scientific community must decide whether or not it will continue to censor debate in order to protect its cherished heroes. It's likely that Americans would not be happy to discover how their taxes funded and enabled research that ultimately sparked a pandemic, or how Peter Daszak wants to sextuple that total for the *Global Virome Project*.

But, I would argue that staying silent would be far worse - because **if** it ultimately emerges that COVID-19 is the result of science experiments that went wrong, then the Ivory Tower that has been built around scientists will crumble to dust, **just as humanity comes face-to-face with exponential technological and societal upheaval**. COVID-19 is likely the first tremor of the coming biotech revolution, and our loss would be China's gain. Now ***that*** sounds like a Greek tragedy.

Prometheus & Pandora V: Prometheus Shrugged (6/5/21)

Prometheus Shrugged

6/5/2021

New Note: the 6/1 FOIA release of 3,234 pages of Dr. Fauci's emails required a re-write of the article I was about to publish, mostly because the assertions I've made in this series were proven by a key section of the document [and missed, just as in February, by the media]. What follows is 'the preponderance of the evidence.'

The duality of knowledge as gift & curse is the original archetype

Prometheus Shrugged

In its ideal formulation, science is a torch that lights the path of progress, and scientists are the philosopher-kings who carry the torch for humanity as we emerge from the darkness of our ignorance. Plato's ideal *Republic* required leaders who could selflessly carry the torch without becoming enamored by their own superiority, as only men of extreme wisdom and humility could stand so close to the flame without succumbing to the temptation to use it for their own purposes.

The COVID-19 pandemic has illuminated the role of scientists in our society, but what we've learned is that at present, our scientists aren't even close to the philosopher kings society has long held them up to be. Instead, they are more like the 'artists' in Plato's *Allegory of the Cave*, holding up the figures that cast shadows on the cave wall, and assuring us that the shadows are reality. ***The greatest conceit, however, is that many scientists still believe they are on the outside, leading us on behalf of our best interests - when in truth, their greed and dependence on bureaucratic largesse has trapped scientists in the cave with everyone else.*** Throughout the pandemic, scientists have admonished societies across the globe, and they've been struck by the rejection of their mandates. All scientists need to do is take a look behind them to understand our reactions, ***because even we cave dwellers can see that the shadows cast by scientists don't look heroic - they look monstrous.***

Post-Modern Prometheus

In Ayn Rand's most famous novel, *Atlas Shrugged*, industrialists of the world conspire to abandon the world in an effort to **ctrl+alt+del** the system and free its people. The COVID-19 pandemic led to a sort of post-modern, real-world distortion of that story - one in which the scientists leading us through this genesis of the technological revolution abandoned the world ***in an effort to protect themselves - not us***. They retreated to the very pedestal we had raised them up upon. As I wrote in part IV:

> *Against this historic backdrop, it's not surprising that people across the globe have mixed emotions about the public health response where they live. Faith in the abilities of scientific establishments to protect the rest of us has been rocked by a reality tv show in which almost every decision, projection, recommendation and mandate has been ineffectual or worse. The frequency of these errors has led to questioning of everything, even those things scientists got right. My intuition tells me that the reason for such backlash has less to do with the esteem our societies have bestowed on scientists, and more to do with the esteem they have bestowed on themselves.*

It might seem strange or gratuitous to focus on Dr. Anthony Fauci, rather than the host of characters who were more directly tied to the actual research and experiments that are collectively referred to as ***Gain of Function***; after all, Fauci's role within the scientific establishment is largely bureaucratic. The best explanation for why I've chosen him to feature is analogous to the myth of Prometheus: when he learned that Prometheus had stolen fire and given it to mankind, Zeus responded with Pandora - the first and most beautiful woman in the history of mankind. Just as man couldn't resist her beauty, Pandora couldn't resist the temptation to open the 'box' [jar] and unleash all of the troubles that have ***plagued*** mankind ever since. A decade ago, when scientists discovered Pandora's Box, Fauci enabled Pandora as she approached the box; a year ago, after she opened it, Fauci didn't attempt to replace the lid; instead, he decided to simply hide the box. No one knew that Dr. Fauci would soon become one of the most recognizable faces on the planet, but ***he*** knew that he had been a strong proponent of GOF research.

However, this wasn't a victimless crime; no one knew that the Wuhan outbreak was about to kill [at least] 4 million people. Fauci led a small group that coordinated the cover-up & censorship of evidence that COVID-19 may have resulted from experimentation in a Chinese lab, and for a year their efforts were disturbingly successful. It is that group [that I've nicknamed 'the 4 Horsemen'] that convened a series of meetings with prominent scientists in the first few days of February; they entered that fateful stretch as skeptics of the Chinese 'natural origin' claim, but emerged as its strongest supporters.

My guess is that the group took a hard look in the mirror and didn't like what was looking back at them. It seems that their response, rather than further self-reflection, was to just embrace becoming vampires instead.

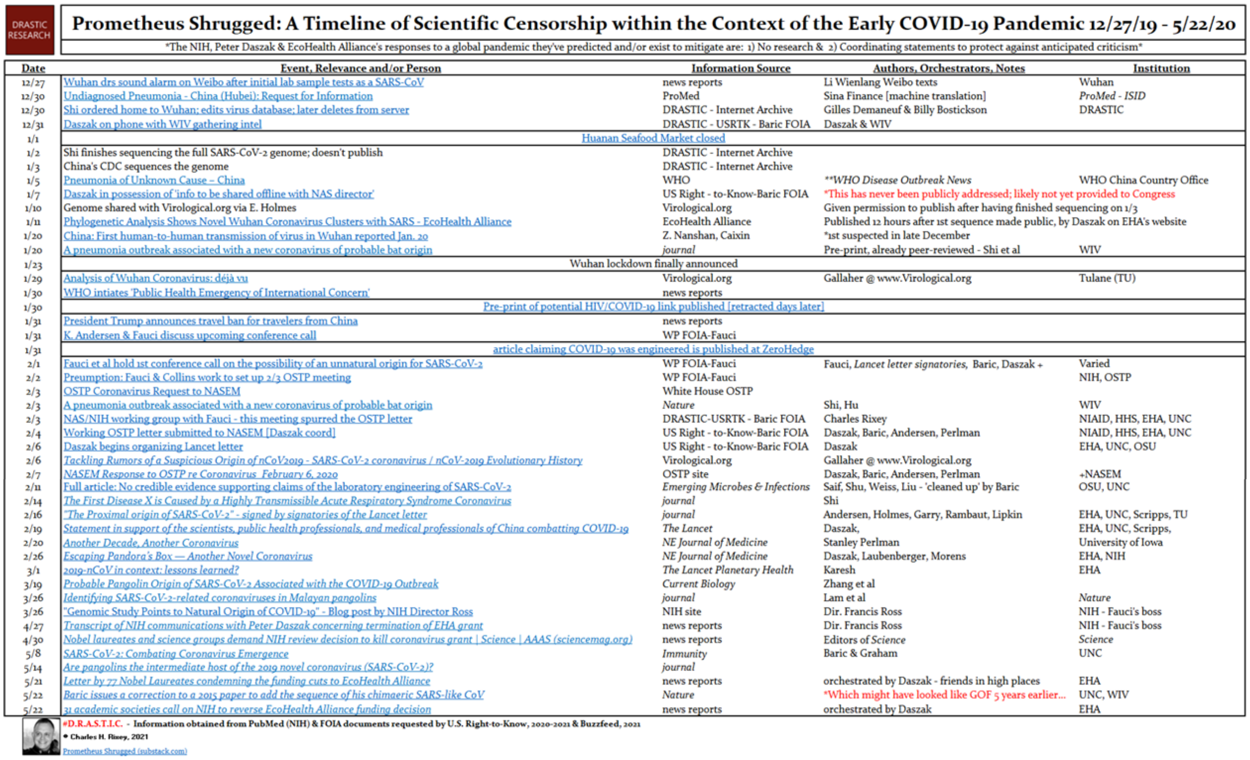
Background, Sources & Purpose

The previous articles in my 'Prometheus & Pandora' series [informally, I call it '***Requiem for a Steam…..ing Pile of BS'***]:

I - *Trust the Scientists - Not the Science?* [Fauci helped framed the debate]
II - *The West must not go gently into a COVID-19 goodnight* [The big picture]*
III - *The Apocryphal Origins of SARS-CoV-2* [How scientists manipulated research]
IV - *Edifice Wrecks* [How much are scientists prepared to lose to protect themselves?]
[*Note - for BLUF, click here]

The lack of understanding surrounding this facet of the origin investigation was shocking to me, but what's become painfully clear is that my idealistic notions of 'investigative journalism' don't bear much resemblance to reality. It's obvious that the sheer volume of information to process is partially to blame, but when the purpose is to uncover the origins of a pandemic that killed 3.5 million people, there is no excuse for anything less than our best efforts.

My primary research interest within the search for the origins of SARS-CoV-2 was previously centered on various threads within China, not here in the US. When the non-profit investigative group US Right-To-Know published a series of documents they'd obtained through FOIA requests made last summer, I read the articles simply because they detailed how Peter Daszak and other scientists conspired to publish an open letter in the *Lancet* journal [note: links to most references discussed in this article can be found in a PDF version of the chronology below] that rejected the possibility of the COVID-19 pandemic having resulted from a leak at one of the higher safety-level laboratories in Wuhan.



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

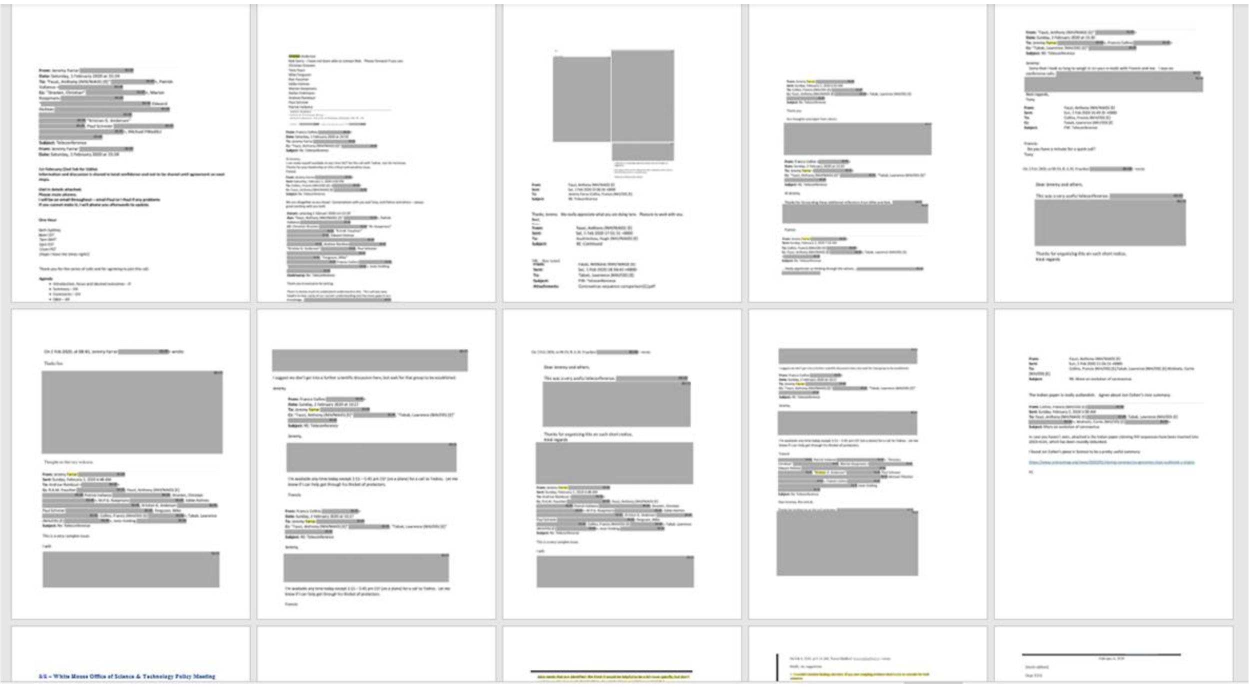
Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories*, Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - **Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021**

• Charles H. Rixey, 2021

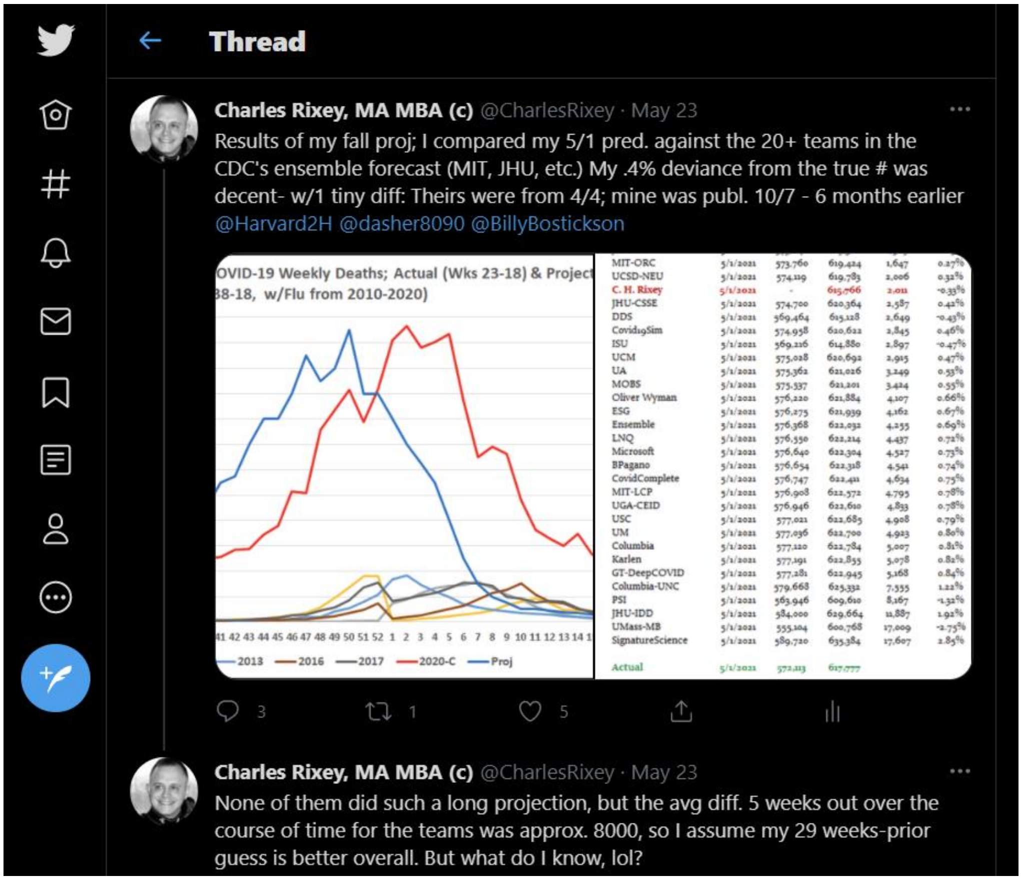
Prometheus Shrugged (substack.com)

At the time of publication, I was still working on cutting & cropping a chronological//subject-organized PDF of several hundred emails drawn from relevant sections of 5 FOIA collections. Once complete, that file will be linked to here.



Specifically, these collections include US RTK's Ralph Baric [x2], Linda Saif and Rita Colwell files [12/1/20 - 2/17/21], as well as Buzzfeed's Anthony Fauci collection from 6/1/21; together they amount to more than 88,000 pages [at least half of which are repetitious].

I decided to go through all of the Baric emails [83K] in February, because it seemed likely that simple searches of the files could miss all sorts of oddities. My instincts turned out to be right, although most of the juiciest excerpts dealt with the 'Red Dawn' cell of expert figures that served as a sounding board for the US government response. Someday, I'll have time to turn towards a full critique of the HHS & CDC actions, but my desire for justice for pandemic victims makes my work with DRASTIC a higher priority. Just know that my track record in analyzing and forecasting the course of the pandemic in the US, as hinted at below, is more a source of anger than pride - largely because the evidence tells us that we ***could've*** done better, yet rarely prioritized people over politics.



Charles Rixey, MA MBA (c) @CharlesRixey · May 23

Results of my fall proj; I compared my 5/1 pred. against the 20+ teams in the CDC's ensemble forecast (MIT, JHU, etc.) My .4% deviance from the true # was decent- w/1 tiny diff: Theirs were from 4/4; mine was publ. 10/7 - 6 months earlier @Harvard2H @dasher8090 @BillyBostickson

MIT-ORC	5/1/2021	573,760	619,424	1,647	0.27%
UCSD-NEU	5/1/2021	574,119	619,783	2,006	0.32%
C. H. Rixey	5/1/2021	-	615,766	2,011	-0.33%
JHU-CSSE	5/1/2021	574,700	620,364	2,587	0.42%
DDS	5/1/2021	569,464	615,128	2,649	-0.43%
Covid19Sim	5/1/2021	574,958	620,622	2,845	0.46%
ISU	5/1/2021	569,216	614,880	2,897	-0.47%
UCM	5/1/2021	575,028	620,692	2,915	0.47%
UA	5/1/2021	575,362	621,026	3,249	0.53%
MOBS	5/1/2021	575,537	621,201	3,424	0.55%
Oliver Wyman	5/1/2021	576,220	621,884	4,107	0.66%
ESG	5/1/2021	576,275	621,939	4,162	0.67%
Ensemble	5/1/2021	576,368	622,032	4,255	0.69%
LNQ	5/1/2021	576,550	622,214	4,437	0.72%
Microsoft	5/1/2021	576,640	622,304	4,527	0.73%
BPagano	5/1/2021	576,654	622,318	4,541	0.74%
CovidComplete	5/1/2021	576,747	622,411	4,634	0.75%
MIT-LCP	5/1/2021	576,908	622,572	4,795	0.78%
UGA-CEID	5/1/2021	576,946	622,610	4,833	0.78%
USC	5/1/2021	577,021	622,685	4,908	0.79%
UM	5/1/2021	577,036	622,700	4,923	0.80%
Columbia	5/1/2021	577,120	622,784	5,007	0.81%
Karlen	5/1/2021	577,191	622,855	5,078	0.82%
GT-DeepCOVID	5/1/2021	577,281	622,945	5,168	0.84%
Columbia-UNC	5/1/2021	579,668	625,332	7,555	1.22%
PSI	5/1/2021	563,946	609,610	8,167	-1.32%
JHU-IDD	5/1/2021	584,000	629,664	11,887	1.92%
UMass-MB	5/1/2021	555,104	600,768	17,009	-2.75%
SignatureScience	5/1/2021	589,720	635,384	17,607	2.85%
Actual	5/1/2021	572,113	617,777		

Charles Rixey, MA MBA (c) @CharlesRixey · May 23

None of them did such a long projection, but the avg diff. 5 weeks out over the course of time for the teams was approx. 8000, so I assume my 29 weeks-prior guess is better overall. But what do I know, lol?

*I just noticed an error in this tweet - the 'actual deaths' line should say 5/1, not 5/14

A Study in Scarlet

What ultimately set me on this collision course with Fauci's record was the first snippet of curious coincidence I found in the Ralph Baric emails - ironically, in the same set of pages that US Right-to-Know had discovered Peter Daszak and other scientists conspiring amongst each other to squash any discussion of 'engineering' within the COVID-origins facet of the pandemic. Having spent my military career in the WMD arena, it was obvious to me that the circumstances surrounding COVID-19's emergence in Wuhan deserved far greater attention, so the collusion of many connected scientists to suppress that discussion was suspect. Then I noticed Dr. Fauci's name popping up, a single time, as a recipient of one of the emails within the chain - just before the collusion conversation.

To: 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; 'andersen@scripps.edu'[andersen@scripps.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'trevor@bedford.io'[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; Gigi Gronvall[ggronvall@jhu.edu]; 'tinglesby@jhu.edu'[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; 'KATHRYBR'[KATHRYBR@dni.gov]; Tony Fauci (afauci@niaid.nih.gov)[afauci@niaid.nih.gov]; Hassell, David (Chris) (OS/ASPR/IO)[David.Hassell@hhs.gov]; 'Mex7@cdc.gov'[Mex7@cdc.gov]; 'rlbull@fbi.gov'[rlbull@fbi.gov]; 'Watson, Ian D. EOP/OSTP'[Ian.D.Watson@ostp.eop.gov]; Kadlec, Robert (OS/ASPR/IO)[Robert.Kadlec@hhs.gov]; 'Conrad, Patricia (NIH/NIAID) [E]'[conradpa@niaid.nih.gov]; Barasch, Kimberly (NIH/NIAID) [C][kimberly.barasch@nih.gov]

The email included attachments outlining the format of a conference to be held that morning, covering "Rapid Response for Assessment of Data Needs for 2019-nCoV." It certainly didn't seem to be related to collusion & cover-ups.

The National Academies of
SCIENCES · ENGINEERING · MEDICINE

Expert Meeting
Rapid Response for Assessment of Data Needs for 2019-nCoV

Agenda

February 3, 2020
2:00 p.m.–3:00 p.m. (ET)

Keck Center, Room 103
500 5th St NW, Washington, DC 20001

Join from PC, Mac, Linux, iOS or Android: https://nasem.zoom.us/
Telephone:
Meeting ID:
International numbers available: https://nasem.zoom.us/

Meeting Objective: *Assess what data, information and samples are needed to understand the evolutionary origins of 2019-nCoV and more effectively respond to the outbreak and resulting misinformation.*

2:00 p.m. **Welcome and Introductions** (*5 mins*)

ANDREW POPE
Director, Board on Health Sciences Policy
National Academies of Sciences, Engineering, and Medicine

2:05 p.m. **Statement of Work** (*10 mins*)

KELVIN DROEGEMEIER
Director
Office of Science and Technology Policy

D. CHRISTIAN ("CHRIS") HASSELL
Senior Science Advisor
U.S. Department of Health and Human Services

2:15 p.m. **Perspective from NIH/NIAID** (*10 mins*)

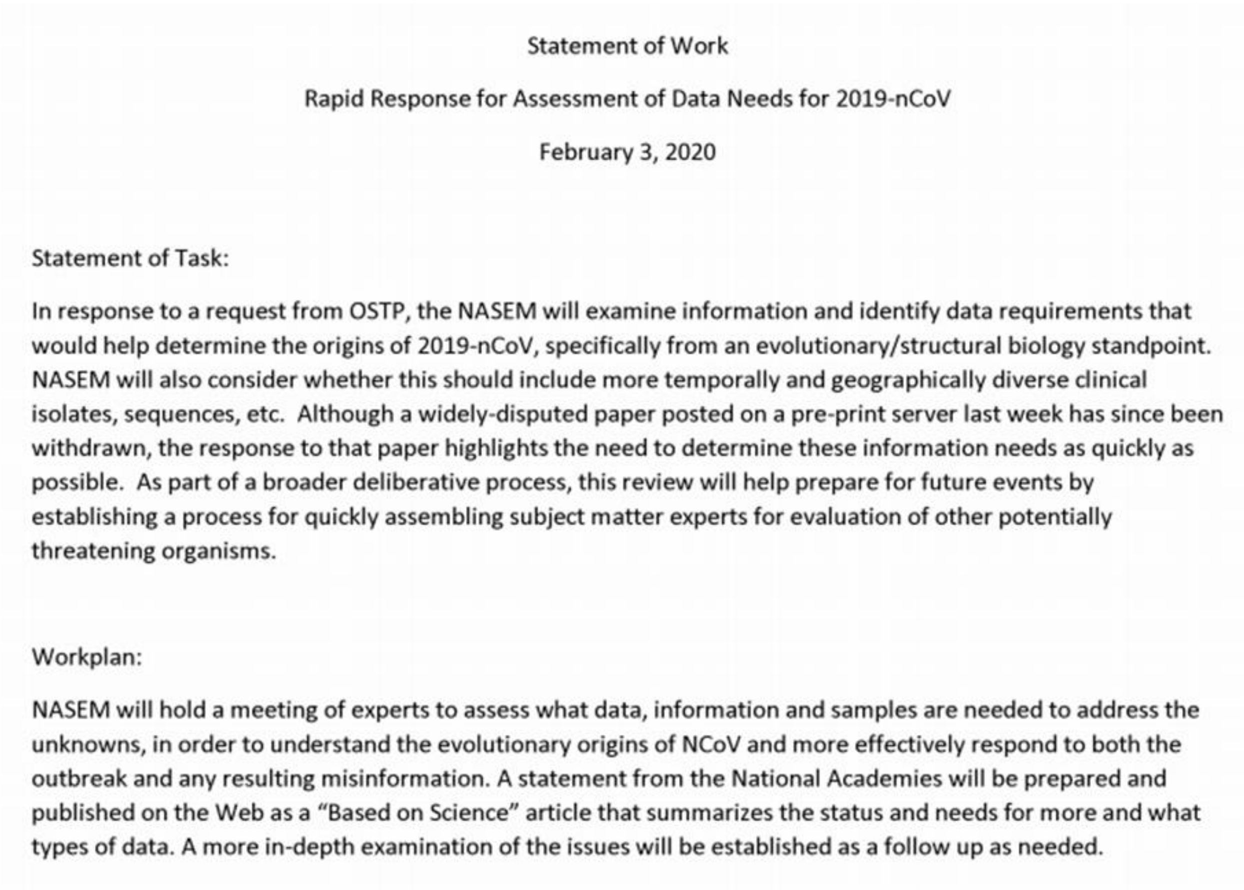
ANTHONY ("TONY") S. FAUCI
Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health

2:25 p.m. **Discussion of Meeting Objective** (*30 mins*)

2:55 p.m. **Determine Next Steps** (*5 mins*)

3:00 p.m. **Adjourn**

Except - one of the topics to be covered was ‘more effectively respond to the outbreak **and resulting information,”** which certainly could be relevant to the email’s other recipients. I became curious as to what Fauci’s ‘perspective’ on that issue was, especially after reading the ‘statement of work’ for the meeting.



Statement of Work

Rapid Response for Assessment of Data Needs for 2019-nCoV

February 3, 2020

Statement of Task:

In response to a request from OSTP, the NASEM will examine information and identify data requirements that would help determine the origins of 2019-nCoV, specifically from an evolutionary/structural biology standpoint. NASEM will also consider whether this should include more temporally and geographically diverse clinical isolates, sequences, etc. Although a widely-disputed paper posted on a pre-print server last week has since been withdrawn, the response to that paper highlights the need to determine these information needs as quickly as possible. As part of a broader deliberative process, this review will help prepare for future events by establishing a process for quickly assembling subject matter experts for evaluation of other potentially threatening organisms.

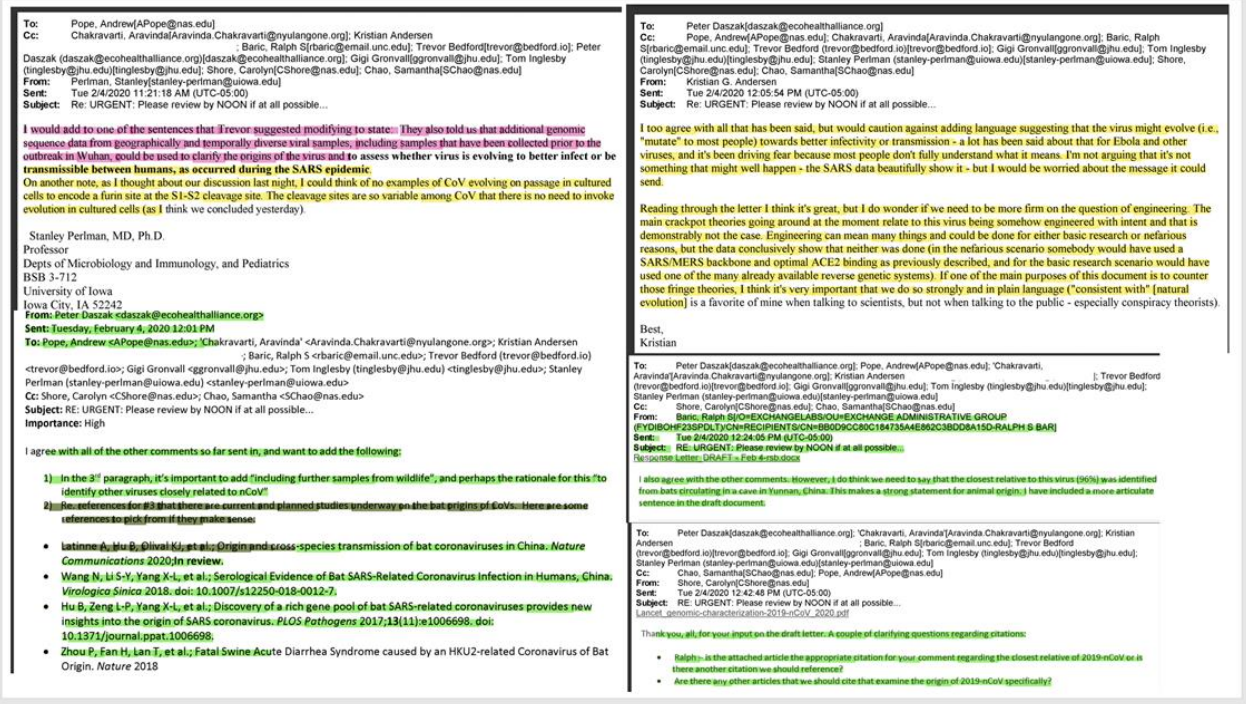
Workplan:

NASEM will hold a meeting of experts to assess what data, information and samples are needed to address the unknowns, in order to understand the evolutionary origins of NCoV and more effectively respond to both the outbreak and any resulting misinformation. A statement from the National Academies will be prepared and published on the Web as a "Based on Science" article that summarizes the status and needs for more and what types of data. A more in-depth examination of the issues will be established as a follow up as needed.

Interesting. Given Fauci's history within the Gain-of-Function debate and his role in steering federal research grants/funding, he certainly had a vested interest in the manner of SARS-CoV-2's emergence. But this also seemed to be his only appearance in any of US RTK's 85,000 pages of documents.

Then I re-read the conversation that followed, and what stood out to me was the incredible ***unanimity*** of opinion regarding COVID's natural origins. How could they have possibly been so certain, when the genome itself had been available for less than two weeks? Other questions emerged, including "why did K. Droegemeier, the president's chief science advisor as the head of the White House's Office of Science & Technology Policy, send a request letter to the National Academies of Sciences, Engineering & Mathematics [NASEM] asking for the meeting to be held, dated the same day as the meeting, in which he was a speaker? It seemed like an unnecessary paper shuffle to justify an emergency hearing **-** unless the point was to make it appear as though he was acting on behalf of the National Security Council and the executive branch at large.

That seemed unlikely, given that President Trump was beginning to receive intelligence of activities at the Wuhan Institute of Virology, which meant that the intelligence community was far less certain about the situation than these scientists, **perhaps the greatest collection of conflicts of interest assembled since the doctors who lobbied against cigarette smoke as a carcinogen for tobacco companies**. And the deeper I dug, the more obvious the hypocrisies became.



To: Pope, Andrew[APope@nas.edu]
Cc: Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Tue 2/4/2020 11:21:18 AM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I would add to one of the sentences that Trevor suggested modifying to state: They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus and **to assess whether virus is evolving to better infect or be transmissible between humans, as occurred during the SARS epidemic**.
On another note, as I thought about our discussion last night, I could think of no examples of CoV evolving on passage in cultured cells to encode a furin site at the S1-S2 cleavage site. The cleavage sites are so variable among CoV that there is no need to invoke evolution in cultured cells (as I think we concluded yesterday).

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, February 4, 2020 12:01 PM
To: Pope, Andrew <APope@nas.edu>; 'Chakravarti, Aravinda' <Aravinda.Chakravarti@nyulangone.org>; Kristian Andersen ; Baric, Ralph S <rbaric@email.unc.edu>; Trevor Bedford (trevor@bedford.io) <trevor@bedford.io>; Gigi Gronvall <ggronvall@jhu.edu>; Tom Inglesby (tinglesby@jhu.edu) <tinglesby@jhu.edu>; Stanley Perlman (stanley-perlman@uiowa.edu) <stanley-perlman@uiowa.edu>
Cc: Shore, Carolyn <CShore@nas.edu>; Chao, Samantha <SChao@nas.edu>
Subject: RE: URGENT: Please review by NOON if at all possible...
Importance: High

I agree with all of the other comments so far sent in, and want to add the following:

1) In the 3rd paragraph, it's important to add "including further samples from wildlife", and perhaps the rationale for this "to identify other viruses closely related to nCoV"
2) Re. references for #3 that there are current and planned studies underway on the bat origins of CoVs. Here are some references to pick from if they make sense:

- Latinne A, Hu B, Olival KJ, et al.; Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications* 2020;**In review.**
- Wang N, Li S-Y, Yang X-L, et al.; Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Virologica Sinica* 2018. doi: 10.1007/s12250-018-0012-7.
- Hu B, Zeng L-P, Yang X-L, et al.; Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLOS Pathogens* 2017;**13**(11):e1006698. doi: 10.1371/journal.ppat.1006698.
- Zhou P, Fan H, Lan T, et al.; Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. *Nature* 2018

To: Peter Daszak[daszak@ecohealthalliance.org]
Cc: Pope, Andrew[APope@nas.edu]; Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Kristian G. Andersen
Sent: Tue 2/4/2020 12:05:54 PM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., "mutate" to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other viruses, and it's been driving fear because most people don't fully understand what it means. I'm not arguing that it's not something that might well happen - the SARS data beautifully show it - but I would be worried about the message it could send.

Reading through the letter I think it's great, but I do wonder if we need to be more firm on the question of engineering. The main crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter those fringe theories, I think it's very important that we do so strongly and in plain language ("consistent with" [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists).

Best,
Kristian

To: Peter Daszak[daszak@ecohealthalliance.org]; Pope, Andrew[APope@nas.edu]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
Sent: Tue 2/4/2020 12:24:05 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Response Letter_DRAFT - Feb 4-rsb.docx

I also agree with the other comments. However, I do think we need to say that the closest relative to this virus (96%) was identified from bats circulating in a cave in Yunnan, China. This makes a strong statement for animal origin. I have included a more articulate sentence in the draft document.

To: Peter Daszak[daszak@ecohealthalliance.org]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Chao, Samantha[SChao@nas.edu]; Pope, Andrew[APope@nas.edu]
From: Shore, Carolyn[CShore@nas.edu]
Sent: Tue 2/4/2020 12:42:48 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Lancet_genomic-characterization-2019-nCoV_2020.pdf

Thank you, all, for your input on the draft letter. A couple of clarifying questions regarding citations:

- Ralph – is the attached article the appropriate citation for your comment regarding the closest relative of 2019-nCoV or is there another citation we should reference?
- Are there any other articles that we should cite that examine the origin of 2019-nCoV specifically?

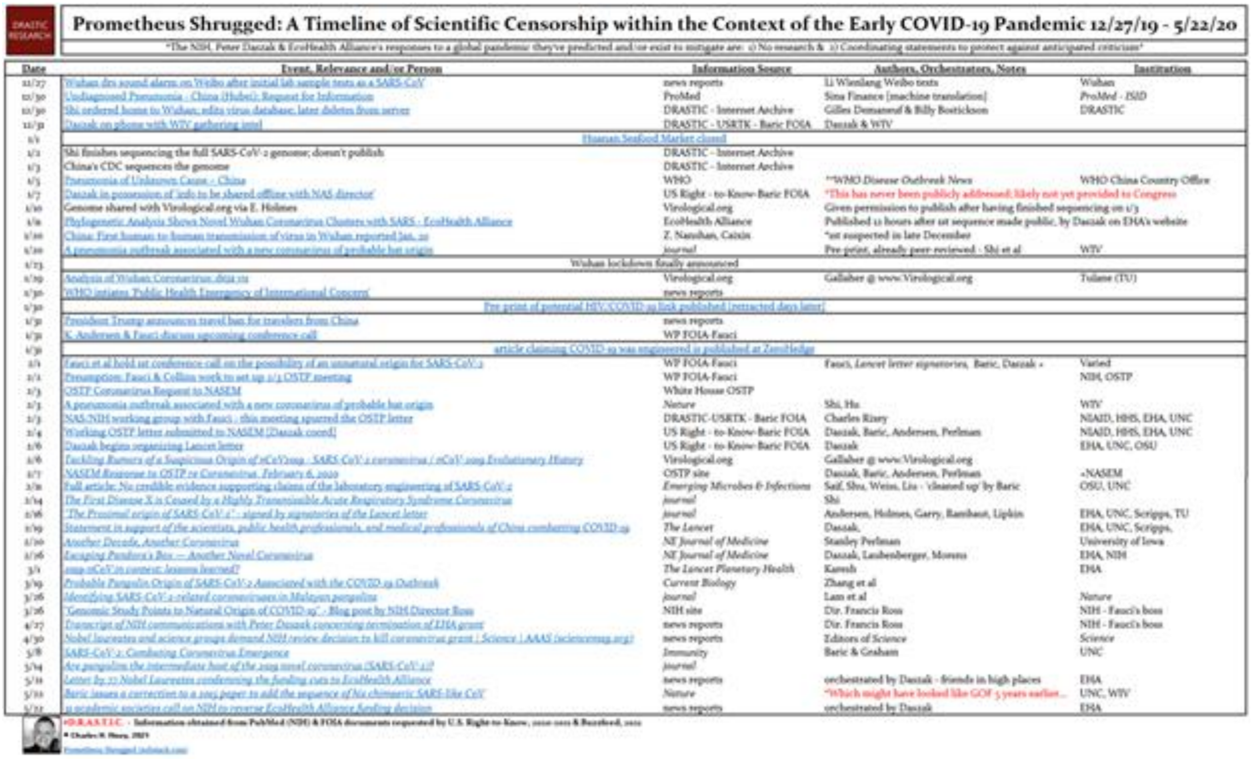
Other details that seemed to have been missed was that the discussions Daszak, Baric and others engaged in as part of writing a response letter to OSTP [again, one of the speakers at the event, guiding the discussion] were distinct, and actually referred to two separate letters. Among the many comments and edits made to the OSTP draft, Daszak had **specifically included precise rejections of a non-natural origin -** but the final version [as with the other sources, linked in the PDF mentioned above] was missing each of those statements, presumably cut by one of the individuals in whose name the document was being produced - the 3 heads of the academies that make up NASEM.

It’s important to point out that the speakers on 2/3 were ***highly*** influential pillars of the American scientific enterprise: the OSTP head advises the president, NASEM [Pope] is at the top of the system that honors career achievements and publishes *Science* and other leading journals, the NIH controls federal research funds [Fauci alone playing a major role in doling out $4 billion in annual grants] and works in concert with the HHS to set priorities, enforce relevant doctrine, and influence national policy for advanced research.

Therefore, when a unanimous endorsement in favor of zoonosis was broadcast in the following weeks by the powers-that-be in the scientific community, it became clear that seriously advocating for a non-natural origin for SARS-CoV-2 was tantamount to career suicide; even the senior scientists whose accomplishments gave them some insulation from retribution [including a Nobel Prize winner in Luc Montagnier] had their pro-lab-leak-hypothesis articles rejected for publication, a further signal that interested scientists could look at what ever they wanted, provided they paid for the experiments themselves and were willing to accept that a pre-print server was the final destination.

My continued research into the breadth of censorship [results shown further below] left me with just a few unknown points, which made it the case far more circumstantial than it should’ve been. It was possible, though highly unlikely, that there ***WAS*** total certainty among the leaders of American scientific institutions, especially since many had been long-time supporters of GOF research. Therefore, it’s been difficult to find evidence that the purpose of their censorship was something other than honest belief in zoonosis, despite the massive conflicts of interest.

Ultimately, the volume of evidence became so strong that I was willing to push forward anyway - which was the goal of my article that this new version has replaced. I uncovered two more letters, a dozen articles and voluminous email traffic that showed **clear, egregious and often anti-scientific** actions taken by the same cabal of connections:



Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

"The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism"

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wenliang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database, later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause - China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 11 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human to human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: deja vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO initiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet* letter signatories, Baric, Daszak +	Varied
2/1	Presumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS-NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV 2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus, February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/18	Full article: *No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2*	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2"* - signed by signatories of the Lancet letter	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of Science	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/21	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

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Prometheus Shrugged (substack.com)

How did this impact research into COVID-19's origins? The highlights in the image below show the stunning output from the researchers either present at the meeting or connected to it; by comparison, there were 0 peer-reviewed articles advocating the possibility of a lab origin before August 12th, out of ***23,000 [in total, there's now been 150,000].*** That's a lot of levers that can be pulled to ensure compliance, and it obviously worked:

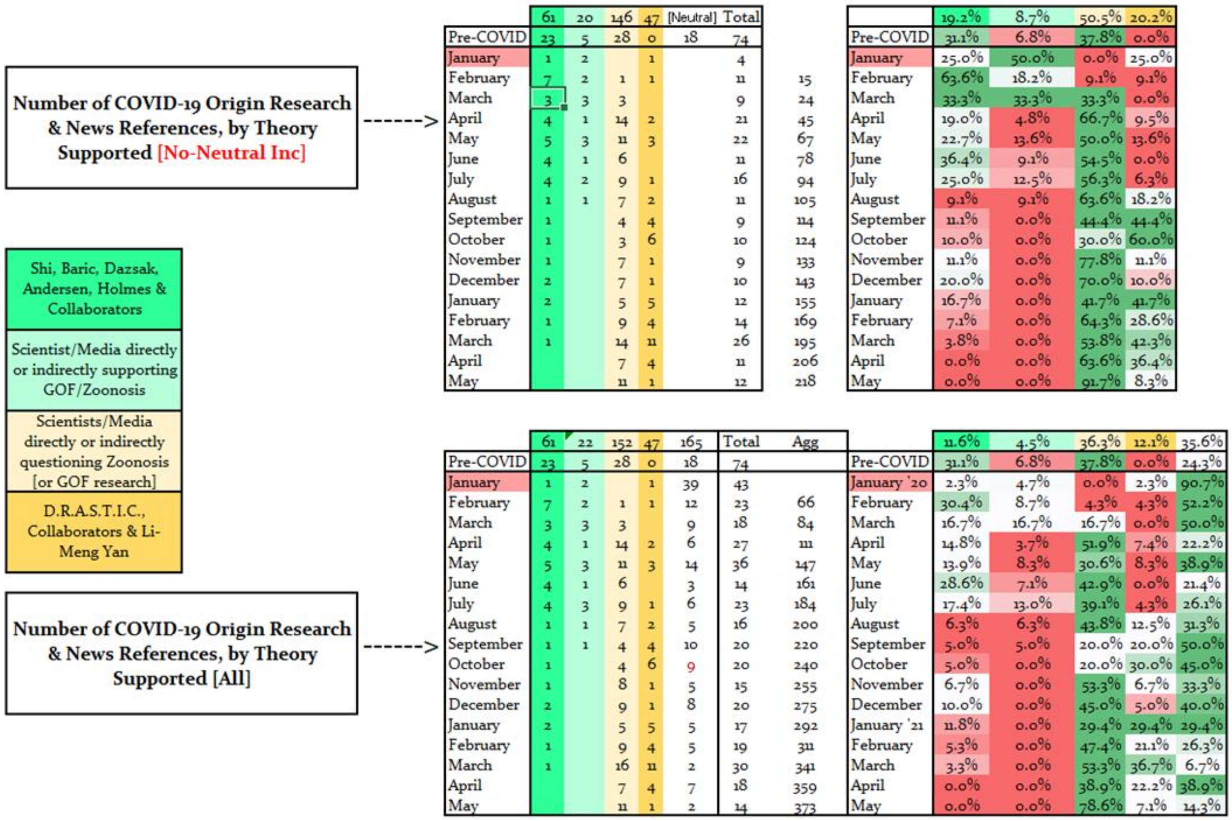
By sorting the full spectrum of research, news and commentary over the last 17 months, the disparity becomes even more apparent:

205 Peer Reviewed Articles......

233 of all other types of publications

The broad spectrum of COVID-19 origin-related published written material, since December, 2019.

Unlike in China, where a vast surveillance state immediately began destroying evidence of all kinds, a vastly smaller and more targeted campaign of censorship was taking place elsewhere - especially in the United States. That last point is crucial, because American scientists and institutions have driven global research for most of the last 100 years - either through innovation, funding or both. The resilience of the scientific establishment has been impressive, given that the tide turned against a natural origin in other written media a year ago:



Number of COVID-19 Origin Research & News References, by Theory Supported [No-Neutral Inc]

	61	20	146	47	[Neutral]	Total	
Pre-COVID	23	5	28	0	18	74	
January	1	2		1		4	
February	7	2	1	1		11	15
March	3	3	3			9	24
April	4	1	14	2		21	45
May	5	3	11	3		22	67
June	4	1	6			11	78
July	4	2	9	1		16	94
August	1	1	7	2		11	105
September	1		4	4		9	114
October	1		3	6		10	124
November	1		7	1		9	133
December	2		7	1		10	143
January	2		5	5		12	155
February	1		9	4		14	169
March	1		14	11		26	195
April			7	4		11	206
May			11	1		12	218

	19.2%	8.7%	50.5%	20.2%
Pre-COVID	31.1%	6.8%	37.8%	0.0%
January	25.0%	50.0%	0.0%	25.0%
February	63.6%	18.2%	9.1%	9.1%
March	33.3%	33.3%	33.3%	0.0%
April	19.0%	4.8%	66.7%	9.5%
May	22.7%	13.6%	50.0%	13.6%
June	36.4%	9.1%	54.5%	0.0%
July	25.0%	12.5%	56.3%	6.3%
August	9.1%	9.1%	63.6%	18.2%
September	11.1%	0.0%	44.4%	44.4%
October	10.0%	0.0%	30.0%	60.0%
November	11.1%	0.0%	77.8%	11.1%
December	20.0%	0.0%	70.0%	10.0%
January	16.7%	0.0%	41.7%	41.7%
February	7.1%	0.0%	64.3%	28.6%
March	3.8%	0.0%	53.8%	42.3%
April	0.0%	0.0%	63.6%	36.4%
May	0.0%	0.0%	91.7%	8.3%

Shi, Baric, Dazsak, Andersen, Holmes & Collaborators

Scientist/Media directly or indirectly supporting GOF/Zoonosis

Scientists/Media directly or indirectly questioning Zoonosis [or GOF research]

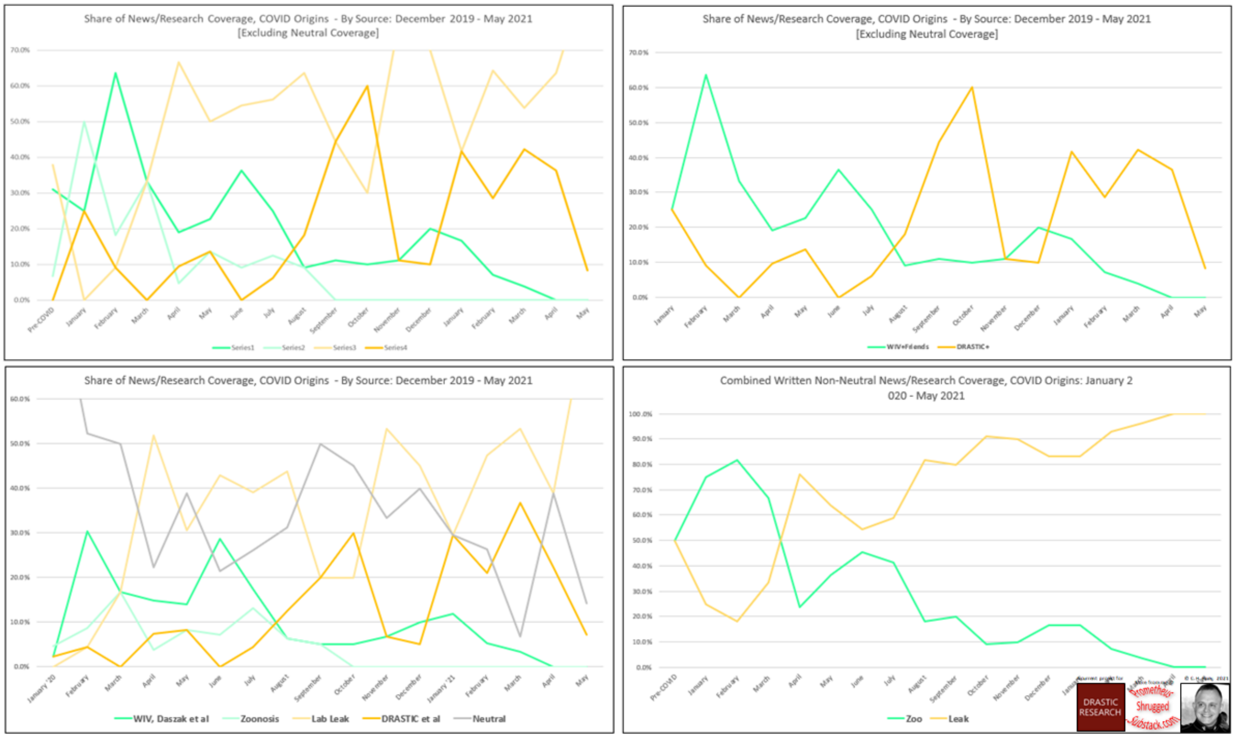
D.R.A.S.T.I.C., Collaborators & Li-Meng Yan

Number of COVID-19 Origin Research & News References, by Theory Supported [All]

	61	22	152	47	165	Total	Agg
Pre-COVID	23	5	28	0	18	74	
January	1	2		1	39	43	
February	7	2	1	1	12	23	66
March	3	3	3		9	18	84
April	4	1	14	2	6	27	111
May	5	3	11	3	14	36	147
June	4	1	6		3	14	161
July	4	3	9	1	6	23	184
August	1	1	7	2	5	16	200
September	1	1	4	4	10	20	220
October	1		4	6	9	20	240
November	1		8	1	5	15	255
December	2		9	1	8	20	275
January	2		5	5	5	17	292
February	1		9	4	5	19	311
March	1		16	11	2	30	341
April			7	4	7	18	359
May			11	1	2	14	373

	11.6%	4.5%	36.3%	12.1%	35.6%
Pre-COVID	31.1%	6.8%	37.8%	0.0%	24.3%
January '20	2.3%	4.7%	0.0%	2.3%	90.7%
February	30.4%	8.7%	4.3%	4.3%	52.2%
March	16.7%	16.7%	16.7%	0.0%	50.0%
April	14.8%	3.7%	51.9%	7.4%	22.2%
May	13.9%	8.3%	30.6%	8.3%	38.9%
June	28.6%	7.1%	42.9%	0.0%	21.4%
July	17.4%	13.0%	39.1%	4.3%	26.1%
August	6.3%	6.3%	43.8%	12.5%	31.3%
September	5.0%	5.0%	20.0%	20.0%	50.0%
October	5.0%	0.0%	20.0%	30.0%	45.0%
November	6.7%	0.0%	53.3%	6.7%	33.3%
December	10.0%	0.0%	45.0%	5.0%	40.0%
January '21	11.8%	0.0%	29.4%	29.4%	29.4%
February	5.3%	0.0%	47.4%	21.1%	26.3%
March	3.3%	0.0%	53.3%	36.7%	6.7%
April	0.0%	0.0%	38.9%	22.2%	38.9%
May	0.0%	0.0%	78.6%	7.1%	14.3%

As my research into COVID-19 has progressed over the last 14 months, the ‘arc of evidence’ has never bent towards the SARS-CoV-2 virus having emerged via random, natural chance. At the same time, the messaging from the leadership of our scientific institutions has remained fairly constant; the unwillingness to adjust to new evidence or allow open debate on lockdowns, various therapeutics and the continued validity of school closures is now questioned even by former supporters of the strategy.



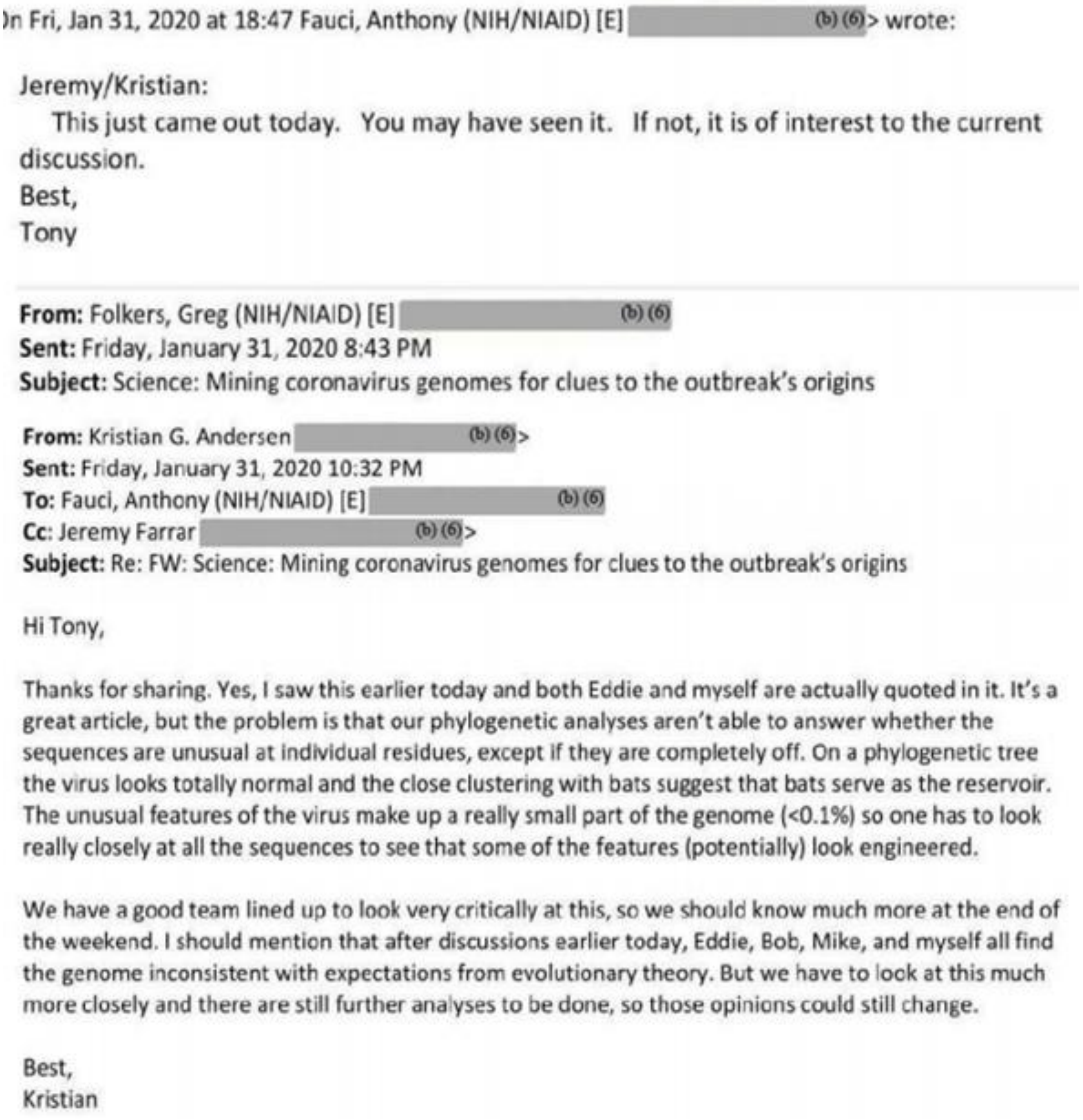
The 1887 novel *A Study in Scarlet* introduced the character of Sherlock Holmes to the world; in it, Holmes famously described his work as the methodical uncovering of a full narrative woven discreetly within the noise of everyday experience. In the midst of grand debates about the perils and future of scientific discovery, I've only grown more convinced that it's the mundane details that really tie things together - despite our reliance on flashy statistics or smoking guns to grab the attention of others. It was the accumulation and careful synthesis of such mundane details that made the value of Dr. Fauci's emails jump out at me on June 1st - and no one has put the puzzle pieces fully together in the interim.

"Trust the Science, Not the Scientists"

My confidence arises from the inertia of the evidence I've compiled; it certainly highlights how dependent people have become on media sources we trust to analyze evidence for us. My guess is that this reliance extends to the media themselves, which should make us wonder what the actual abilities and sources of our ‘fact-checkers’ are. Because a full accounting of the many arguments would take me two more weeks to write, I will conclude with a few short examples of what the Fauci emails actually tell us.

There has been a significant focus on largely irrelevant aspects of his communications last year - I was literally stunned to discover that neither the *Washington Post* nor *Buzzfeed* really touched on any of the controversial findings; both pieces were laudatory, in fact. It makes me wonder why they even bothered to request the FOIA documents at all, and certainly whether they actually read all of it. By June 1st, I’d had plenty of practice in traversing FOIA email documents, and it didn’t hurt that a 1/3 of them [at least] had been read within the Baric files. I’d covered at least 70% of the Fauci files by the time I posted my first commentary later on the 1st, and only yesterday did I see a commentator actually mention a connection with the Baric emails.

1) Knowledge of and credibility given to the possibility of a lab-leak hypothesis.



)n Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] (b) (6)> wrote:

Jeremy/Kristian:
This just came out today. You may have seen it. If not, it is of interest to the current discussion.
Best,
Tony

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)
Sent: Friday, January 31, 2020 8:43 PM
Subject: Science: Mining coronavirus genomes for clues to the outbreak's origins

From: Kristian G. Andersen (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Jeremy Farrar (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

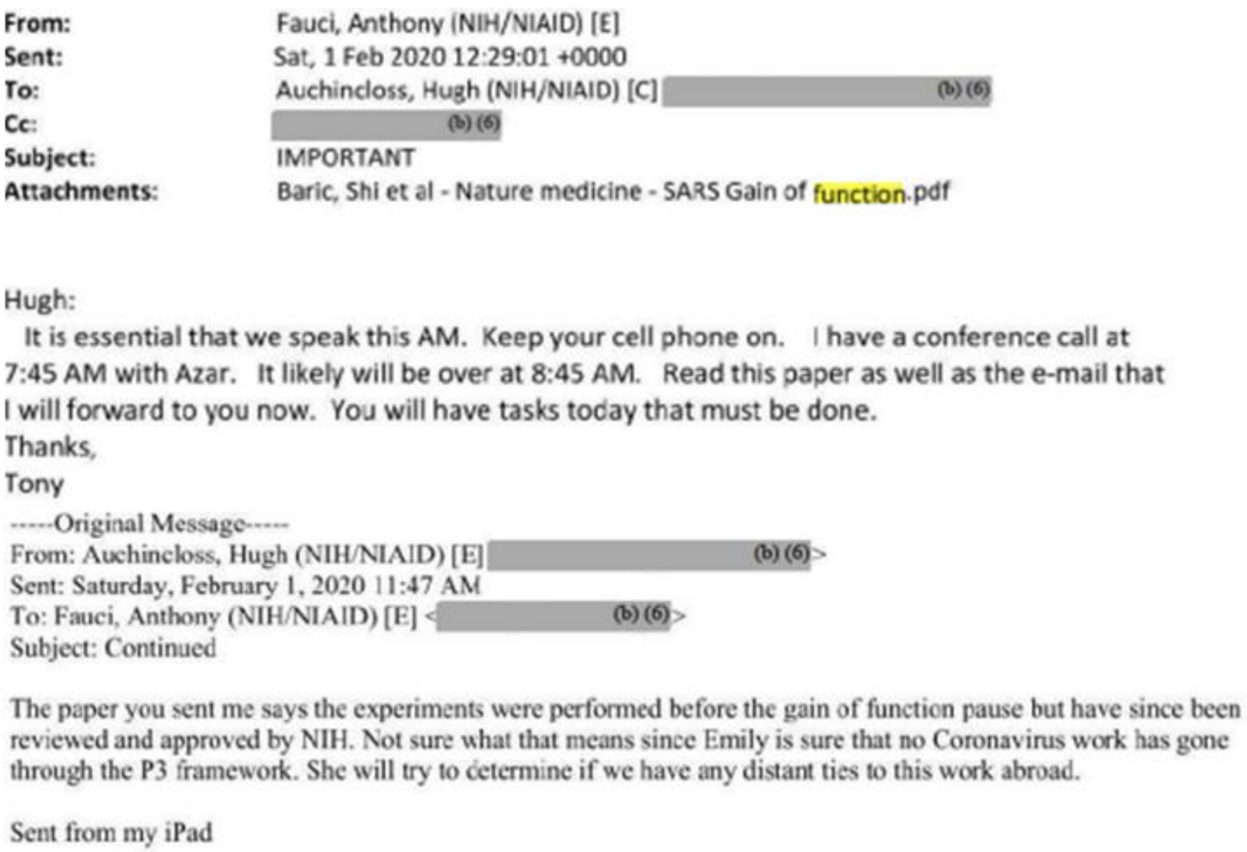
Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

Here, Kristian Andersen admits that he, Eddie Holmes and others harbor serious doubts about a 'natural origin,' even though he publicly rejects it days later, and privately works with Peter Daszak, Baric and others to put together the OSTP letter, the *Lancet* letter and the seminal letter in *Nature* that has earned a place in history. In the last few days, Andersen has come out and publicly explained that he hadn't yet weighed the evidence of the announced closest ancestor virus, RaTG13, which had just been published at that time. However, the pre-print had been available for more than a week, and during the period from 1/31 - 2/4, he spent hours a day communicating with Fauci et al, and specifically two meetings described in the emails, in which the available evidence was mulled over and taken seriously throughout. The literal purpose of both meetings centered on the importance of determining how to approach the topic, and in particular, the OSTP meeting was designed to produce a statement that could be used by the government to signal how scientists should handle the debate [they were supposed to ignore it]. Or are we supposed to believe that Andersen, amongst the likes of Fauci and Francis Collins, was late to the party, had missed the pre-print evidence, but saw enough within the significantly flawed RaTG13 genome to unequivocally conclude that his prior assessment had been wrong? He certainly seemed to take the theory seriously enough to ensure that the OSTP letter left no margin for interpretation - just like everyone else who ‘converted’ between 2/1 & 2/4.

2) They understood what the big picture was:



From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 12:29:01 +0000
To: Auchincloss, Hugh (NIH/NIAID) [C] [redacted] (b) (6)
Cc: [redacted] (b) (6)
Subject: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

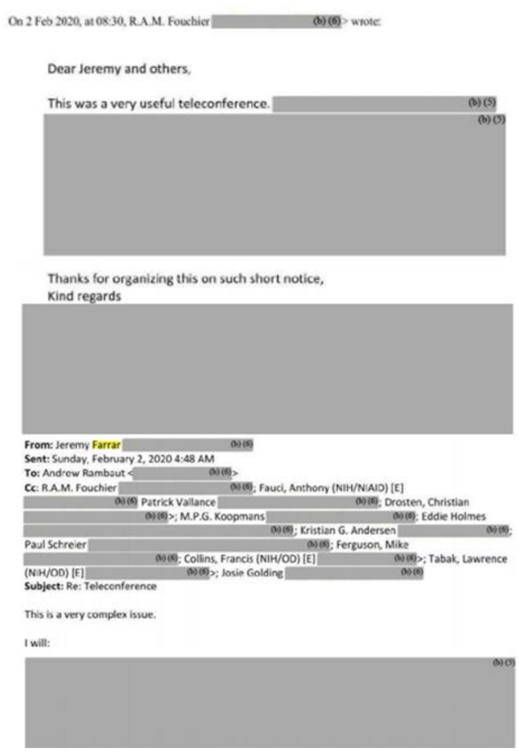
Hugh:
It is essential that we speak this AM. Keep your cell phone on. I have a conference call at 7:45 AM with Azar. It likely will be over at 8:45 AM. Read this paper as well as the e-mail that I will forward to you now. You will have tasks today that must be done.
Thanks,
Tony

-----Original Message-----
From: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6)>
Sent: Saturday, February 1, 2020 11:47 AM
To: Fauci, Anthony (NIH/NIAID) [E] <[redacted] (b) (6)>
Subject: Continued

The paper you sent me says the experiments were performed before the gain of function pause but have since been reviewed and approved by NIH. Not sure what that means since Emily is sure that no Coronavirus work has gone through the P3 framework. She will try to determine if we have any distant ties to this work abroad.

Sent from my iPad

There was no doubt amongst the co-conspirators that Baric's 2015 experiments with Zheng-Li Shi were an important catalyst in the WIV's progression to higher-quality chimaeric CoV production - exactly the skills needed to make a successful 'dual-use' pathogen. Fauci's assistant Auchincloss needed no interpretation before verifying the details of the related grant, or to determine what it was that Fauci needed him to do. Perhaps we should follow the example of his assistant. Given that Fauci testified ***last week*** before Congress that funds hadn't even been provided to the WIV laboratory, or for GOF, what was he concerned about here?



On 2 Feb 2020, at 08:30, R.A.M. Fouchier [redacted] (b) (6)> wrote:

Dear Jeremy and others,

This was a very useful teleconference. [redacted] (b) (5)

[redacted] (b) (5)

Thanks for organizing this on such short notice,
Kind regards

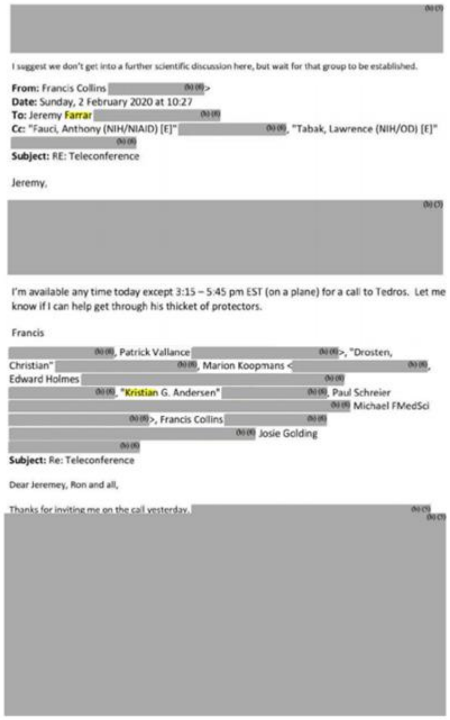
[redacted]

From: Jeremy Farrar [redacted] (b) (6)
Sent: Sunday, February 2, 2020 4:48 AM
To: Andrew Rambaut <[redacted] (b) (6)>
Cc: R.A.M. Fouchier [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6) Patrick Vallance [redacted] (b) (6); Drosten, Christian [redacted] (b) (6)>; M.P.G. Koopmans [redacted] (b) (6); Eddie Holmes [redacted] (b) (6); Kristian G. Andersen [redacted] (b) (6); Paul Schreier [redacted] (b) (6); Ferguson, Mike [redacted] (b) (6); Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>; Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)>; Josie Golding [redacted] (b) (6)
Subject: Re: Teleconference

This is a very complex issue.

I will:

[redacted] (b) (5)



[redacted] (b) (5)

I suggest we don't get into a further scientific discussion here, but wait for that group to be established.

From: Francis Collins [redacted] (b) (6)>
Date: Sunday, 2 February 2020 at 10:27
To: Jeremy Farrar [redacted] (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Subject: RE: Teleconference

Jeremy,

[redacted] (b) (5)

I'm available any time today except 3:15 – 5:45 pm EST (on a plane) for a call to Tedros. Let me know if I can help get through his thicket of protectors.

Francis

[redacted] (b) (6), Patrick Vallance [redacted] (b) (6)>, "Drosten, Christian" [redacted] (b) (6), Marion Koopmans <[redacted] (b) (6), Edward Holmes [redacted] (b) (6) [redacted] (b) (6), "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) Michael FMedSci [redacted] (b) (6)>, Francis Collins [redacted] (b) (6) [redacted] (b) (6) Josie Golding [redacted] (b) (6)
Subject: Re: Teleconference

Dear Jeremey, Ron and all,

Thanks for inviting me on the call yesterday. [redacted] (b) (5)

[redacted] (b) (5)

After the 2/2 meeting, the tone of the participants didn't sound like everyone had become a skeptic of a non-natural origin. It sounded like they **needed to make a decision.**

3) It's important keep glancing at the chronology I posted above, as you read through the various elements and arguments. Almost immediately, the entire group of scientists began furiously publishing articles rejecting the possibility of manipulation. It would've been stunning for the existing or emerging

evidence to have pushed scientists away from a lab-escape scenario, since the biggest revelation after its genome was published for scientists other than Shi to discover was that someone had found a furin cleavage site (FCS) within the genome - which no virologist would've held up at first glance as evidence that it came from nature. In part 2, I embedded a video of a portion of a conference discussing GOF shortly before it went into effect. The FCS featured prominently in those discussions, which isn't surprising when one considers that it is widely used in such research. Therefore, the **fact that ZL-Shi 'skipped' it in her seminal paper, and the notion that the discovery of the FCS apparently didn't make Andersen more suspicious, is insulting.**

4) NASEM wouldn't defend the statements Daszak tried to add to their statement on 2/4. They deleted them because they couldn't substantiate such sweeping statements.

5) It's almost impossible to isolate the number of questions within a blog, so many points must necessarily be left for others to discuss. However, there is still a gold mine of of potential issues within them. One curious appearance was Ron Klain, the current and former chief of staff for now-president Biden. His interest in pandemics is certainly genuine, but having a senior campaign official so actively connected to Dr. Fauci makes one wonder what the scope of interactions were between them, especially during the push for vaccines in the fall, a particular area of expertise and curiosity for Mr. Klain. One could simply point out the sheer volume of redactions, many of which are not likely to buttress the image currently being projected by many journalists.

The Best -Laid Plans of Mice & Men

2 simple observations arise from having researched this alternate, messy view of reality beyond has been force-fed to the public for a year and a half:

1) We [citizens] ***can*** handle the truth. We definitely handle truth better if we're told before everyone is dead - at a minimum, before the annual memorials begin.

2) Science should focus on leadership, not censorship.

Imagine how differently events might have played out had any major figure [not retired] had dared to state the obvious in a way that couldn't be silenced by censorship. Anthony Fauci has led the NIAID since shortly after my 1st birthday - but being in the perfect position and possessing the requisite experience to make bold decisions makes his deliberate actions to suppress research even more offensive.

As this article has sought to reinforce, a lack of context has plagued almost every aspect of this pandemic, but rarely has context been so obscured by those whom we trust the most to provide it - and given my extensive experience learning about the past, I don't feel any need to reference a secondary source in defense of that claim.

It almost doesn't even matter what reasons Fauci had for acting as he did, because impacts speak louder than words. His willingness to prevent broad inquiry into GOF helped enable the Chinese to stall an investigation almost to the point of allowing them to escape further scrutiny once the WHO report was published [just picture the earlier image of peer-reviewed papers for & against the zoonotic hypothesis]. I named my origin reference project "**The arc of inquiry bends towards enlightenment**" because the volume of research in any subject naturally correlates with the tendency for efforts to cluster in the direction that's most promising. The statistics clearly show that zoonosis is not that direction in the COVID-19 origin debate.

Fauci's decision to double down on the same mitigation tactics last winter produced a predictable result [so predictable that I actually ***did*** predict it] - an epidemic curve that tracked very closely to the H1N1 novel pandemic in 2009. In every case, his moves were more safe-sided than the politicians who were actually running for re-election, and they did little to prevent the spread of the disease. Many observers have been asking why the protective measures he advocated for failed so miserably, but I recommend that we shift our perspective; a better question would be to ask ourselves **what** he was so driven to protect [if not the American people] during the twilight of his incredible career, with all worldly accolades already earned, and the ability to speak and have leaders listen.

Whatever that legacy is, it is in the midst of leading our public trust in science over a cliff, in a bus that's already on fire, with no brakes, and with no attempt to change course. Dr. Fauci understands all of this, of course, and continues undeterred.

Therefore, it's important to respond in a blunt manner that he understands:

-We must demand that 'The Proximal Origins of SARS-CoV-2" be immediately retracted by *Nature* - preferably via a written request from Fauci himself.

-A full congressional investigation must be formed, and immediately begin issuing subpoenas and compiling testimony under oath. This includes the leaders of any federal institution that participated in the censorship of lab-leak origin research. For many individuals, the intensity of their efforts is the equivalent of obstructing justice.

Obstructing justice in defense of a potential crime against humanity might be the true legacy of Dr. Fauci. Whatever it is, however, it's obviously not in *our* best interest.

Epilogue

The 21st century has seen the continued acceleration of technological advancement [most effectively predicted by Ray Kurzweil], along with the attendant dichotomy of remarkable progress towards the elimination of global poverty (down 90% in recent decades) and increasing social turmoil sparked [in part] by the disorienting impact of so much rapid change in so many aspects of daily human life.

The COVID-19 pandemic is, in many ways, as much a symptom of humanity's growing pains as it is a consequence of the disease caused by the SARS-CoV-2 virus. Because of the stunning impact COVID-19 has had upon human civilization, superficial analyses of the pandemic's origins are not just unsuitable - they could dangerously obscure the fundamental lessons humanity should be learning from this shared tragedy.

The Best -Laid Plans of Mice & Men

But, I would argue that staying silent would be far worse - *because* ***if*** *it ultimately emerges that COVID-19 is the result of science experiments that went wrong, then the Ivory Tower that has been built around scientists will crumble to dust,* ***just as humanity comes face-to-face with exponential technological and societal upheaval****. COVID-19 is likely the first tremor of the coming biotech revolution, and our loss would be China's gain. Now* ***that*** *sounds like a Greek tragedy.*[I]

References

References

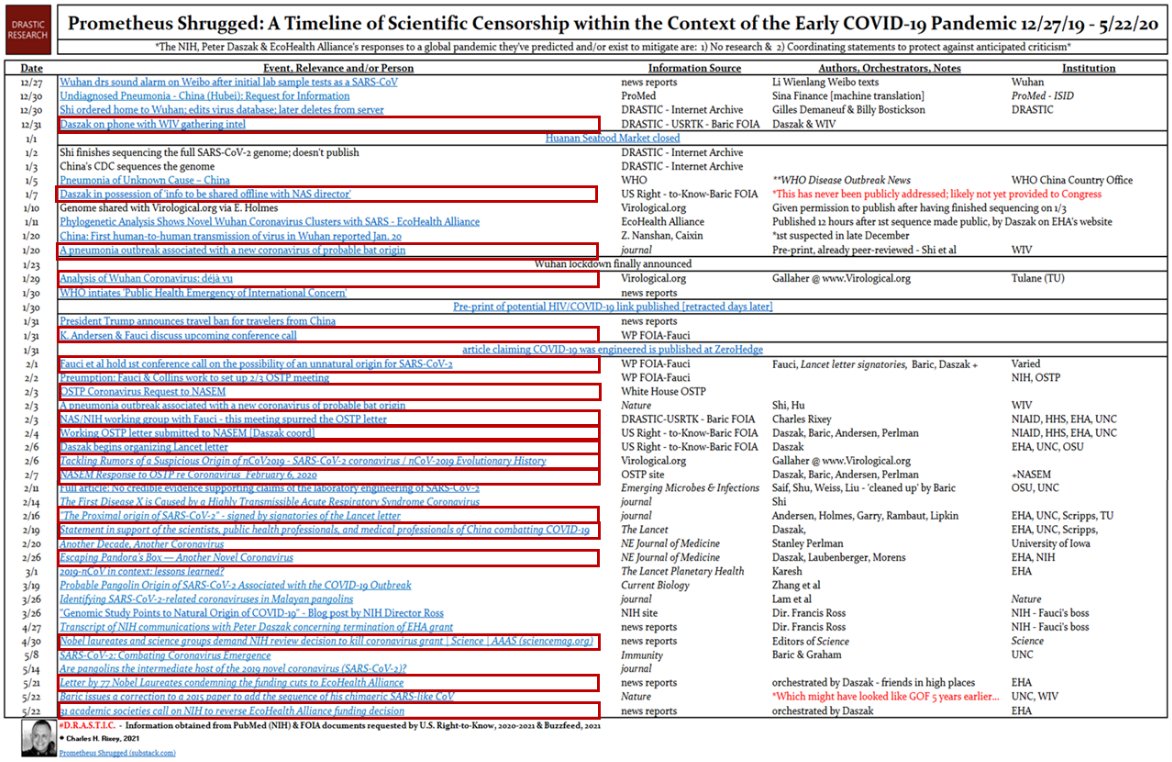
A full list of the 520 COVID-origin sources within my analysis can be found on ResearchGate

Appendix:

This appendix follows Peter Daszak's activities at the start of the pandemic, the 2/1/20 conference call led by Jeremy Farrar & Dr. Fauci, the 2/3 OSTP meeting, the 2/4 deliberations amongst the authors of a NASEM letter meant for the OSTP, the 2/6 – 2/19 work that produced the *Lancet* letter and *The Proximal Origins of SARS-CoV-2*, and other assorted examples of collusion via published material in peer-reviewed journals.

Lastly, I've provided quantitative evidence of the impact of censorship that began as a result of that four day stretch in early February, 2020. I've endeavored to include all of the most relevant pieces I've found that cover some aspect of the origin debate, but my exhaustive efforts can't fully remove subjectivity from my choices of what deserved inclusion in the list. I can, however, say that the peer-reviewed articles accurately depict the proportions of the two main origin theories within the overall 140,890 articles in PubMed's LitCOVID research database.

Documents & Events for which evidence is included herein:



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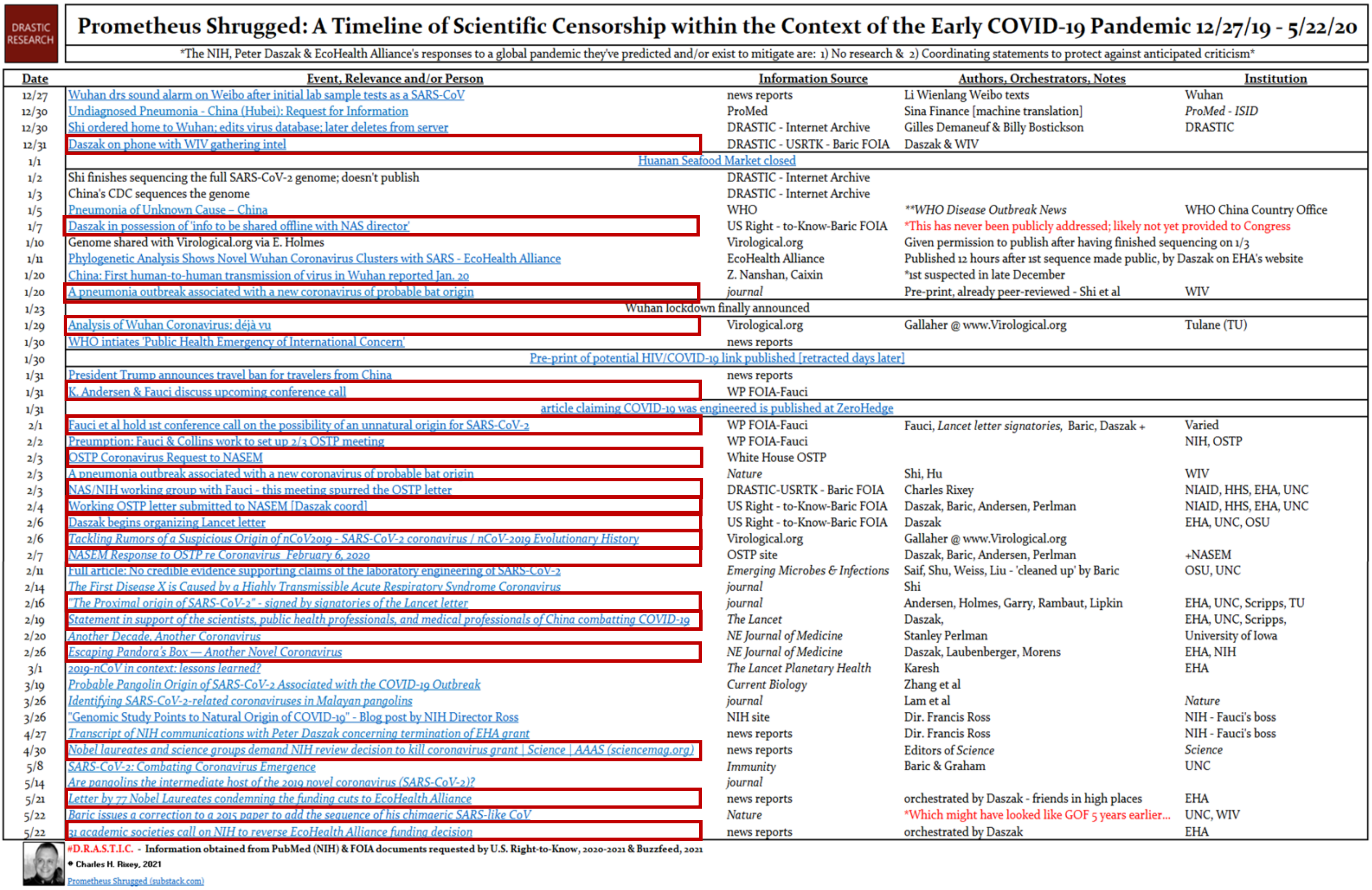

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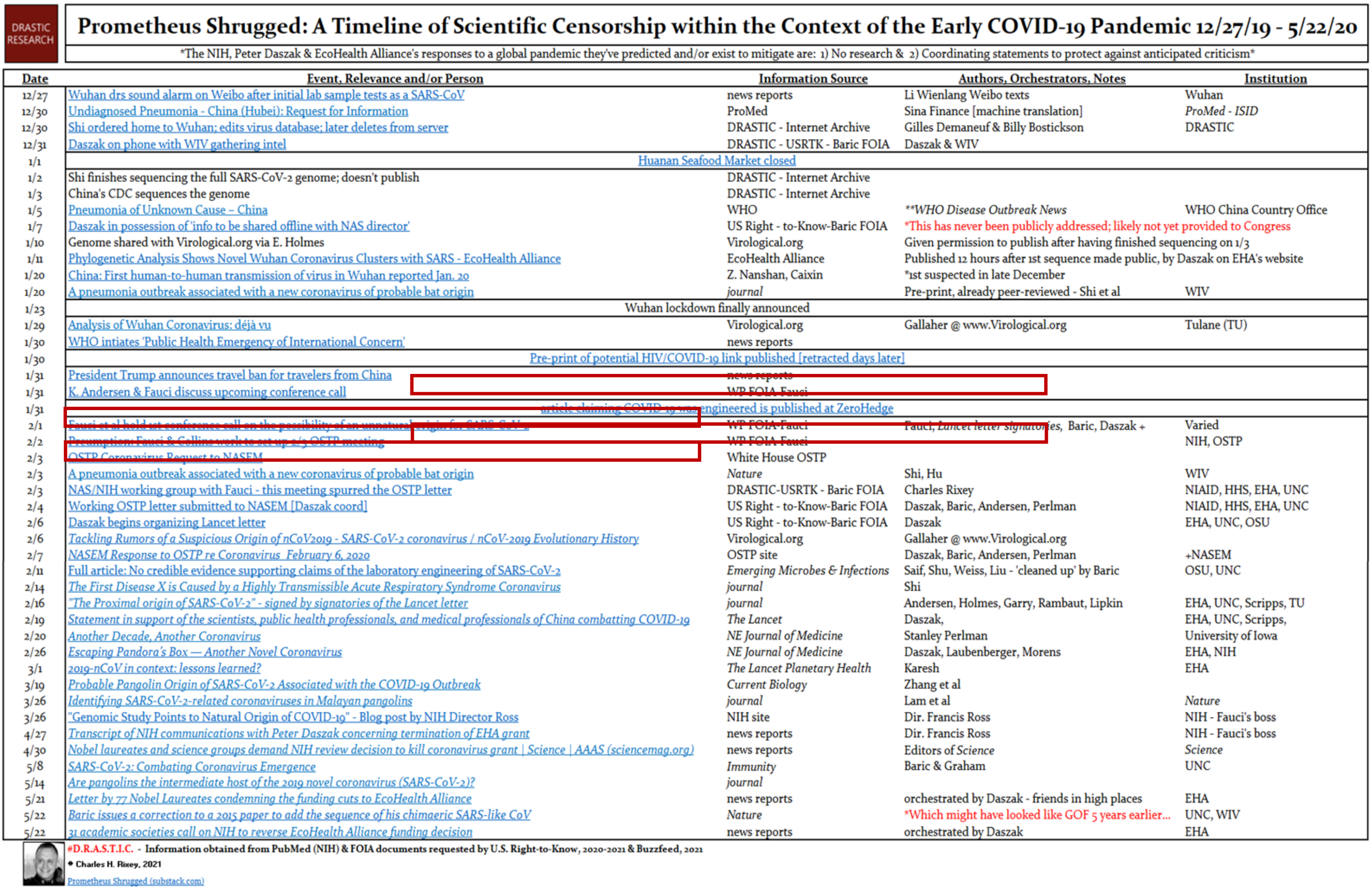

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FOIA Emails: Dr. Fauci's coordination efforts

These document Fauci's interactions with scientists and politicians to weaken the connection between he and the US to gain-of-function research at the Wuhan Institute of Virology

Source: Buzzfeed FOIA documents for Dr. Anthony Fauci

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Tue, 3 Mar 2020 03:26:29 +0000
To: Collins, Francis (NIH/OD) [E];Giroir, Brett (HHS/OASH)
Cc: Steele, Danielle (HHS/IOS);Tabak, Lawrence (NIH/OD) [E]
Subject: RE: SARS CoV-2 in humanized mice

Ditto.

From: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)
Sent: Monday, March 2, 2020 9:32 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] <[redacted] (b) (6)>; Steele, Danielle (HHS/IOS) [redacted] (b) (6); Tabak, Lawrence (NIH/OD) [E] <[redacted] (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Larry has it right. Tony may want to add.

Francis

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Monday, March 2, 2020 8:14 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)>
Cc: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>; Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Steele, Danielle (HHS/IOS) [redacted] (b) (6)
Subject: Re: SARS CoV-2 in humanized mice

Brett,

Tony or Francis may offer additional insight, but the [redacted] (b) (5) [redacted].

I hope this helps.
Larry

From: "Giroir, Brett (HHS/OASH)" <[redacted] (b) (6)>
Date: Monday, March 2, 2020 at 7:25 PM
To: "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)>
Cc: Francis Collins [redacted] (b) (6)>, Anthony Fauci [redacted] (b) (6)>, "Steele, Danielle (HHS/IOS)" [redacted] (b) (6)>, "Giroir, Brett (HHS/OASH)" [redacted] (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Dear Larry,

Thank you for your patience. The question has been raised, [redacted] (b) (5)

I appreciate your willingness to continue to work on this and respond to the questions that I am receiving.

V/r
Brett

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: [redacted] (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Thursday, February 20, 2020 5:29 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)>
Cc: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>; Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6); Steele, Danielle (HHS/IOS) [redacted] (b) (6)>
Subject: Re: SARS CoV-2 in humanized mice

Brett,
I have discussed with both Francis and Tony [redacted] (b) (5)

With regard to your questions:

[redacted] (b) (5)

[redacted] (b) (5)

Hope this is helpful. Please let me know if you require additional information.
Best wishes,
Larry

From: "Giroir, Brett (HHS/OASH)" [redacted] (b) (6)>
Date: Thursday, February 20, 2020 at 12:32 PM
To: "Tabak, Lawrence (NIH/OD) [E]" < [redacted] (b) (6)
Cc: "Steele, Danielle (HHS/IOS)" [redacted] (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Can you give me a quick call?

[redacted] (b) (5)

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: [redacted] (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Thursday, February 20, 2020 12:19 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)>
Cc: Steele, Danielle (HHS/IOS) [redacted] (b) (6)>
Subject: Re: SARS CoV-2 in humanized mice

[redacted] (b) (5)

Thanks
Larry

From: "Giroir, Brett (HHS/OASH)" [redacted] (b) (6)>
Date: Thursday, February 20, 2020 at 12:17 PM
To: "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Cc: "Steele, Danielle (HHS/IOS)" [redacted] (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Larry

[redacted] (b) (5)

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: [redacted] (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Wednesday, February 19, 2020 11:04 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)
Cc: Steele, Danielle (HHS/IOS) [redacted] (b) (6)
Subject: FW: SARS CoV-2 in humanized mice

Brett,

[redacted] (b) (5)

Thanks for your consideration,
Larry

From: "Hasenkrug, Kim (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Wednesday, February 19, 2020 at 5:50 PM

To: "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Subject: SARS CoV-2 in humanized mice

Hi Dr. Tabak, [redacted] (b) (5)

[redacted] (b) (5)

Best regards,

Kim

Kim J Hasenkrug, Ph.D.
Senior Investigator
Chief, Retroviral Immunology Section
Laboratory of Persistent Viral Diseases
Rocky Mountain Laboratories
National Institute of Allergy and Infectious Diseases
National Institutes of Health
903 S. 4th Street
Hamilton, MT 59840
[redacted] (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Mon, 2 Mar 2020 00:48:25 +0000
To: Cassetti, Cristina (NIH/NIAID) [E];Giroir, Brett (HHS/OASH)
Cc: Conrad, Patricia (NIH/NIAID) [E]
Subject: RE: COVID and Chloroquine

Thanks, Cristina

From: Cassetti, Cristina (NIH/NIAID) [E] (b) (6)>
Sent: Sunday, March 1, 2020 7:06 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6) Giroir, Brett (HHS/OASH)
(b) (6)
Cc: Conrad, Patricia (NIH/NIAID) [E] (b) (6)>
Subject: RE: COVID and Chloroquine

Hi,

Sorry for the late response, I just flew back from (b) (6).

NIAD doesn't have ongoing trials with chloroquine and I heard that such trials are being conducted in China.

We are planning to evaluate chloroquine in animal models ASAP. If any therapeutic with a good clinical safety profile (like chloroquine) appears to be effective in vivo against COVID-19, we are planning to quickly add to them to the Remdesivir therapeutic trial as another arm.

Let me know if you have other questions.

Kind regards,

Cristina

Cristina Cassetti, Ph.D.
Deputy Director
Division of Microbiology and Infectious Diseases
National Institute of Allergy and Infectious Diseases, NIH
5601 Fishers Lane, Room 7G51
Rockville, MD 20852
Tel: (b) (6)
(b) (6)

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Saturday, February 29, 2020 8:20 PM

To: Giroir, Brett (HHS/OASH) (b) (6)>
Cc: Cassetti, Cristina (NIH/NIAID) [E] (b) (6)>; Conrad, Patricia (NIH/NIAID) [E] (b) (6)>
Subject: RE: COVID and Chloroquine
Importance: High

Brett:

Thanks for the note. I will run this by the people in our Program and get back to you.

Best,
Tony

Cristina:

Are we or anyone else doing anything with clinical trials and chloroquine for COVID-19? Please respond directly to ADM Giroir.

Thanks,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Giroir, Brett (HHS/OASH) (b) (6)>
Sent: Saturday, February 29, 2020 9:31 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: COVID and Chloroquine

You know the old data and the new data. New in vitro look promising.
Do you have good visibility on the trials being conducted? Or is NIH running any of these?

Your time is precious, so 10 word response sufficient.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 22 Feb 2020 12:06:10 +0000
To: Cassetti, Cristina (NIH/NIAID) [E]
Subject: FW: DEAR TONY: CORONAVIRUS

Please handle.

From: Dr. Michael Jacobs (b) (6)>
Sent: Friday, February 21, 2020 6:14 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Cc: Alexander Tarakhovsky (b) (6); Lockshin, Michael MD (b) (6); Dr. Michael Jacobs (b) (6)>
Subject: DEAR TONY: CORONAVIRUS

dear tony:

i am a cornell medical school cumc (b)(6) graduate. i am associate professor of dermatology at weill-cornell in private practice. (b) (6) alexander tarakhovsky is (b) (6) and a professor at rockefeller university. he is a virologist.

we have been following the corona virus pandemic closely, and a few days ago became alarmed at the news that the chinese government is sterilizing their paper money from hubei province.

we think that there is a possibility that the virus was released from a lab in wuhan, the biotech area of china. we also think that the virus might be complexed with another organism, such as a yeast or fungus, to make it more sticky.

we would like to discuss this with you further. we feel that immediate action must be taken by united states scientists to try to neutralize this threat.

please contact alexander and me at your earliest convenience at above emails or my mobile (b) (6) or office (b) (6) michael lockshin gave me your email.

with kind regards

michael jacobs

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Tue, 5 May 2020 13:00:29 +0000
To: Lipkin, Ian W.
Subject: RE: SARS-CoV-2

Thanks, Ian. I hope that you are well.
Best,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Lipkin, Ian W. (b) (6)
Sent: Tuesday, May 5, 2020 8:39 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: Fwd: SARS-CoV-2

Tony,

(b) (4) This prompted the letter I sent to him last evening to which he responded this morning. I dont expect a response but wanted to keep you updated. We deeply appreciate your efforts in steering and messaging.

All my best,
Ian

Ps. Skoll just invested $5M in piloting the GIDEoN international capacity building and surveillance network that includes Cliff and others in your intramural team.

Begin forwarded message:

From: ZhuChen [redacted] (b) (6)>
Subject: Re:SARS-CoV-2
Date: May 5, 2020 at 8:16:23 AM EDT
To: Lipkin, Ian W. [redacted] (b) (6)>

Dear Ian,
Thank you for your email detailing the [redacted] (b) (4) (b) (4) (b) (4). I shall keep you informed of any progress in the coming weeks.
Best,
Zhu

------------------ Original ------------------
From: "Lipkin, Ian W. [redacted] (b) (6);
Date: Tue, May 5, 2020 06:06 AM
To: "ZhuChen" [redacted] (b) (6)>;
Subject: SARS-CoV-2

Dear Zhu,
The COVID-19 pandemic poses an unprecedented threat not only to global public health but also to economic and political stability. Uncertainty about the origin of COVID-19 pandemic is causing friction worldwide, particularly between China and the United States. There is agreement that the causative agent, SARS-CoV-2 originated in a bat. There is also a high level of confidence that the virus was <u>not</u> deliberately modified in any laboratory. What we do not know is the answers to two questions: (1) whether a precursor virus circulated in the human population before it evolved to become a pandemic virus and (2) whether a precursor virus adapted to humans by first passing through another animal. [redacted] (b) (4)

[redacted] (b) (4)

With great affection,
Ian
W. Ian Lipkin, MD
John Snow Professor of Epidemiology and Director
Center for Infection and Immunity
Mailman School of Public Health

Professor of Pathology and Neurology
College of Physicians & Surgeons
Columbia University
722 West 168th Street, 17th Floor
New York, NY 10032
Voice: [redacted] (b) (6)
Fax: (212) 342-9044
Email: [redacted] (b) (6)

Administrative Coordinator
[redacted] (b) (6)

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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Mon, 20 Apr 2020 01:25:42 +0000
To: bgertz@washingtontimes.com
Cc: Miller, Katie R. EOP/OVP;Short, Marc T. EOP/OVP
Subject: Scientific paper on origin of coronavirus

Bill:

Here are the links to the scientific papers and a commentary about the scientific basis of the origins of SARS-Cov-2.

The proximal origin of SARS-CoV-2. Andersen KG, Rambaut A, Lipkin WI, **Holmes** EC, Garry RF. Nat Med. 2020 Apr;26(4):450-452. doi: 10.1038/s41591-020-0820-9. No abstract available.
A Genomic Perspective on the Origin and Emergence of SARS-CoV-2.Zhang YZ, **Holmes** EC. Cell. 2020 Apr 16;181(2):223-227. doi: 10.1016/j.cell.2020.03.035. Epub 2020 Mar 26.
Also this statement from Eddie Holmes
https://bit.ly/2ym1UGe

Best regards,
Tony
Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

> On Apr 19, 2020, at 2:21 PM, Bill Gertz <bgertz@washingtontimes.com> wrote:
>
> Katie,
>
> Dr. Fauci on Friday said he would share a scientific paper with the press on the origin of the coronavirus. Can you please help me get a copy of that paper? Thanks in advance.
>
> Bill Gertz

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 19 Apr 2020 03:29:42 +0000
To: Peter Daszak
Subject: RE: Thank you for your public comments re COVID-19's origins

Peter:
Many thanks for your kind note.
Best regards,
Tony

From: Peter Daszak [redacted] (b) (6)
Sent: Saturday, April 18, 2020 9:43 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>
Cc: Stemmy, Erik (NIH/NIAID) [E] [redacted] (b) (6)>; Erbelding, Emily (NIH/NIAID) [E] [redacted] (b) (6)>; Aleksei Chmura [redacted] (b) (6)
Subject: Thank you for your public comments re COVID-19's origins
Importance: High

Tony (cc'ing David so that you might pass this on to Tony once he has a spare second)

As the PI of the R01 grant publicly targeted by Fox News reporters at the Presidential press briefing last night, I just wanted to say a personal thankyou on behalf of our staff and collaborators, for publicly standing up and stating that the scientific evidence supports a natural origin for COVID-19 from a bat-to-human spillover, not a lab release from the Wuhan Institute of Virology.

[redacted] (b) (7)(A)

From my perspective, your comments are brave, and coming from your trusted voice, will help dispel the myths being spun around the virus' origins.

Once this pandemic's over I look forward thanking you in person and let you know how important your comments are to us all.

Cheers,

Peter

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 19 Mar 2020 01:59:12 +0000
To: Lerner, Andrea (NIH/NIAID) [E]
Subject: FW: Coronavirus

Please respond to this person.

-----Original Message-----
From: Beth Abramson (b) (6)>
Sent: Wednesday, March 18, 2020 9:58 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject: Coronavirus

Wondering whether it has been considered that only the vulnerable population (those over 60 and/or those with underlying health conditions)be isolated ? I am a (b) (6)psychiatrist and after contemplating this option was wondering if this could still reduce the risk to healthcare Systems with less disruption to our society. I await your response and appreciate all you are doing. Beth Abramson MD (b) (6)

Sent from my iPhone

From: [redacted] (b) (6)
Sent: Sun, 8 Mar 2020 09:23:28 -0400
To: Kristian G. Andersen
Cc: Jeremy Farrar;Collins, Francis (NIH/OD) [E];Robert Garry;Edward Holmes;Andrew Rambaut;Ian Lipkin;Chris Emery
Subject: Re: SARS-CoV-2 article to be published in Nature Medicine

Kristian:
Thanks for your note. Nice job on the paper.
Tony

> On Mar 6, 2020, at 4:23 PM, Kristian G. Andersen [redacted] (b) (6)>wrote:
>
> Dear Jeremy, Tony, and Francis,
>
> Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 'origins' paper. We're happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).
>
> To keep you in the loop, I just wanted to share the accepted version with you, as well as a draft press release. We're still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.
>
> Tony, thank you for your straight talk on CNN last night - it's being noticed.
>
> Best,
> Kristian
>
> ---
>
> **Kristian G. Andersen, PhD**
> Associate Professor, Scripps Research
> Director of Infectious Disease Genomics, Scripps Research Translational Institute
> Director, Center for Viral Systems Biology
>
> **The Scripps Research Institute**
> 10550 North Torrey Pines Road, SGM-300A
> Department of Immunology and Microbial Science
> La Jolla, CA 92037
>
> [redacted] (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 7 Mar 2020 13:23:54 +0000
To: [redacted] (b) (6)
Subject: FW: [redacted] (b) (4)

fyi

From: Lipkin, Ian W. [redacted] (b) (6)>
Sent: Saturday, March 7, 2020 8:20 AM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Subject: [redacted] (b) (4)

Tony,
Happy to connect you with Zhu. [redacted] (b) (4)

(b) (4) [redacted]

(b) (4)

[redacted]

(b) (4)

[redacted]

(b) (4)

[redacted]

(b) (4)

[redacted]

[redacted] (b) (4)

>>>> With best regards,
>>>>
>>>> Zhu
>>>>
>>>>
>>>> 发件人: Lipkin, Ian W. [redacted] (b) (6)
>>>> 发送时间: 2020年2月9日 23:01
>>>> 收件人: Zhu Chen
>>>> 抄送: George Gao; zhangzongwei
>>>> 主题: Re: important info
>>>>
>>>> Zhu,
>>>> Please call me on [redacted] (b) (6)
>>>>
>>>> Ian
>>>>
>>>>
>>>>
>>>> W. Ian Lipkin, MD
>>>> John Snow Professor of Epidemiology and Director
>>>> Center for Infection and Immunity
>>>> Mailman School of Public Health
>>>>
>>>> Professor of Pathology and Neurology
>>>> College of Physicians & Surgeons
>>>> Columbia University
>>>> 722 West 168th Street, 17th Floor
>>>> New York, NY 10032
>>>> Voice: [redacted] (b) (6)
>>>> Fax: (212) 342-9044
>>>> Email: [redacted] (b) (6)

\>>>>
\>>>> Administrative Coordinator
\>>>> (b) (6)
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\>>>>
\>>>> On Feb 9, 2020, at 9:43 AM, ZhuChen (b) (6)> wrote:
\>>>>
\>>>> Dear Ian,
\>>>> I have an important info to be shared with you. According to the latest report from the National Health Commission, the number of confirmed cases of NCP (2019-nCoV pneumonia) in other Provinces than Hubei (Wuhan is the capital city) was decreased from 890/day on Feb 3rd to 509/day on Feb 8th. So it is still possible for this outbreak to be basically contained in China.
\>>>> Therefore, my suggestion is that we support the current public health policies and strategy to concentrate quality medical human resources and other resources to save more life of severe patients, even though the cost is high, very high. And then, we shall continuously analyze the situation for possible adjustment of policies and measures.
\>>>> Best,
\>>>> Zhu
\>>>>
\>>

possible. We (NIAID/ USG) do not expect to be the only source, but will likely be one of the main sources for this research resource based on experience with Zika.

5. If someone wishes to travel to China to work on the live virus, are there any travel restrictions other than the self isolation/quarantine already in place (and of course subject to change over time)?

For that, contacting CDC directly would make sense. If you would like us to inquire, we can. For high consequence viruses, use of proper PPE has been a mitigating factor in quarantine consideration.

Please feel free to contact me if you have additional questions.

Thanks,
Alan

Alan Embry, Ph.D.
Chief, Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases, NIAID, NIH
5601 Fishers Lane, Room 8E31
Rockville, MD 20892
(b) (6)
(b) (6)

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Thursday, February 13, 2020 6:35 PM
To: Fried, Linda P. (b) (6)>; Redfield, Robert R. (CDC/OD) (b) (6)>
Cc: Conrad, Patricia (NIH/NIAID) [E] <(b) (6); Goldman, Lee (b) (6)>; Booth, Jane <(b) (6)>; Katznelson, Ira I. (b) (6)>; Marston, Hilary (NIH/NIAID) [E] (b) (6)>; Embry, Alan (NIH/NIAID) [E] (b) (6); Eisinger, Robert (NIH/NIAID) [E] (b) (6)>
Subject: RE: Institutional request for information

Linda:

There is a “sample sharing” working group involving NIH and CDC. I have copied both Hilary Marston and Alan Embry from NIAID who are involved in this group and will ask them by this e-mail to respond to items #1 through 4. Regarding returning travelers from China (item #5) if in Wuhan (Hubei province) within previous 14 days, they submit to institutional quarantine; if in non-Hubei province part of China, then they face self-isolation.

Hope that this is helpful.

Best regards,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Fried, Linda P. (b) (6)
Sent: Thursday, February 13, 2020 12:45 PM
To: Redfield, Robert R. (CDC/OD) (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Conrad, Patricia (NIH/NIAID) [E] (b) (6); Goldman, Lee (b) (6)>; Booth, Jane (b) (6)>; Katznelson, Ira I. (b) (6)
Subject: Institutional request for information

Dear Drs. Redfield and Fauci,

I am writing on behalf of Columbia University, which has received a request from Dr. Ian Lipkin to transfer live novel coronavirus from Hong Kong to his BSL3 facility at the University. As we evaluate his request, we note that he has approval from a CDC official to import the virus (see attached). However, as we consider the risks and benefits of Dr. Lipkin's proposal, we ask the two of you:

1. Is the CDC or NIH overseeing the distribution of the live virus in the U.S.?
2. Will you be the sole source of distribution in the U.S., or will institutions be permitted to obtain it directly from other sources?
3. If it can be obtained from other sources, what sources will be permitted? For example, the China or Hong Kong CDC or University of Hong Kong?
4. If you are to be the sole source, when would you expect to have a process for considering requests?
5. If someone wishes to travel to China to work on the live virus, are there any travel restrictions other than the self isolation/quarantine already in place (and of course subject to change over time)?

Thank you very much for your help with these important questions as we all try to do our best to contribute solutions to this health crisis.

With best regards,
Linda

From: [redacted] (b) (6)
Sent: Thu, 6 Feb 2020 15:09:43 -0500
To: Folkers, Greg (NIH/NIAID) [E]
Cc: Conrad, Patricia (NIH/NIAID) [E];Eisinger, Robert (NIH/NIAID) [E];Lerner, Andrea (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Subject: Re: ASF --- Morens + Daszak +Taubeneberger paper

I agree. I will not be a co-author

> On Feb 6, 2020, at 1:59 PM, Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)>wrote:
>
> [redacted] (b) (4)
>
> So the question to you – do you want to be part of this? ie be a coauthor
>
> I would vote no – it wud look weird to add you as a coauthor now. Plus, plate too full……
>
>

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 6 Feb 2020 00:00:36 +0000
To: Jeremy Farrar;Collins, Francis (NIH/OD) [E]
Cc: Josie Golding;Tabak, Lawrence (NIH/OD) [E]
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Jeremy:

I left out an important name for the coronavirus evolution working group. Please include her: Pardis Sabeti at the Broad Institute of MIT and Harvard
Thanks,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Wednesday, February 5, 2020 5:25 PM
To: Jeremy Farrar <(b) (6)>; Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Josie Golding <(b) (6)>; Tabak, Lawrence (NIH/OD) [E]
(b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Jeremy:

Thanks for the note. Looks like things are moving along with WHO. I will list below a number of names for potential members of the working group to examine the evolutionary origin of the 2019-nCoV in addition to the individuals who were on the call with us last Saturday:

Harold Varmus – Weill Cornell Medical Center – New York City
Feng Zhang – MIT (CRISPR expert)
Joseph DeRisi - Chan Zuckerberg (CZ) BioHub (he's paying close attention to the Wuhan strain vs other bat viruses and the SARS virus)

Don Ganem - University of California at San Francisco (UCSF) and the CZ BioHub (knows more about hepadnaviruses but an outstanding clinical and basic virologist)
John Coffin - Tufts and National Cancer Institute, NIH (worked out the confusion over the alleged Chronic Fatigue Syndrome retrovirus that proved to be a xenotropic MLV)
Eugene Koonin - NCBI/National Libreary of Medicine, NIH; https://www.ncbi.nlm.nih.gov/research/groups/koonin/)
Wayne Hendrickson – Columbia University and the New York Structural Biology Center
Gary Nabel – Sanofi (Boston)

Best regards,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Jeremy Farrar [redacted] (b) (6)
Sent: Wednesday, February 5, 2020 6:21 AM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6); Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>
Cc: Josie Golding [redacted] (b) (6)
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Francis and Tony

Couple of things:

- I spoke again with WHO this morning. I believe they have listened and acted. Let me know if you agree
    - At the WHO meeting next week they will set up the Group who will "look at the origins and evolution of 2019n-CoV"
    - They have asked for names to sit on that Group – please do send any names

    - We can have a call this week with a core group of that to frame the work of the Group including – if you could join?
    - I think this puts it under the umbrella of WHO, with action this week and into next
    - With names to be put forward into the Group from us and pressure on this group from your and our teams next week.
- The team will update the draft today and I will forward immediately – they will add further comments on the glycans

Does that sound reasonable to you?

Jeremy

From: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, 4 February 2020 at 13:18
To: Francis Collins < [redacted] (b) (6)>, Jeremy Farrar [redacted] (b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

?? [redacted] (b) (4)

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 6:12 AM
To: Jeremy Farrar [redacted] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Yes, [redacted] (b) (4)

Francis

From: Jeremy Farrar [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 6:08 AM
To: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

[redacted] (b) (4)

On 4 Feb 2020, at 10:58, Collins, Francis (NIH/OD) [E] [redacted] (b) (6)> wrote:

Very thoughtful analysis. [redacted] (b) (4) (b) (4)

Francis

From: Jeremy Farrar [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 2:01 AM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Collins, Francis (NIH/OD) [E]
< [redacted] (b) (6)
Subject: FW: Prevalence of infection and stage of the epidemic in Wuhan

Please treat in confidence – a very rough first draft from Eddie and team – they will send on the edited, cleaner version later.

Pushing WHO again today

From: Edward Holmes [redacted] (b) (6)>
Date: Tuesday, 4 February 2020 at 06:33
To: Jeremy Farrar [redacted] (b) (6)>
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Here's our summary so far. Will be edited further.

It's fundamental science and completely neutral as written. Did not mention other anomalies as this will make us look like loons. As it stands it is excellent basic science I think, which is a service in itself.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 13 Feb 2020 22:36:17 +0000
To: Messonnier, Nancy (CDC/DDID/NCIRD/OD)
Subject: RE: NAS

Nancy:

The official USG group will be convened by NAS. Bob Kadlec is the person with direct knowledge of that. In addition, there is an ad hoc group informally led by Jeremy Farrar of Wellcome Trust. This group has about 15 people, all of whom are highly respected scientists, mostly evolutionary biologists who are convening by e-mail and conference calls (I have been on 2 of these calls since Jeremy invited me) to look at all of the bat, pangolin and human coronavirus sequences to try and determine the evolutionary origin. This is not my area of expertise and so I have backed off and am leaving it all to Jeremy.

Best,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Messonnier, Nancy (CDC/DDID/NCIRD/OD) (b) (6)>
Sent: Thursday, February 13, 2020 5:28 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject: RE: NAS

Thanks. Is someone convening them?

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Thursday, February 13, 2020 5:07 PM

To: Messonnier, Nancy (CDC/DDID/NCIRD/OD) [redacted] (b) (6)
Subject: RE: NAS

Nancy:

It is not a report. It is a letter from NAS to OSTP saying that it is important to bring together a group of experts to study the evolutionary origin the COVID19. I am attaching it here. I have no idea if it has been widely distributed and so please keep it internal.

Best,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Messonnier, Nancy (CDC/DDID/NCIRD/OD) [redacted] (b) (6)
Sent: Thursday, February 13, 2020 1:31 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Subject: NAS

Either you or Bob Kadlec made reference to a NAS report on the origins of SARS – COV2. (b) (5) [redacted]

Thanks.
Nancy

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 9 Feb 2020 23:54:27 +0000
To: [redacted] (b) (6)
Subject: FW: WHO advance team on coronavirus on way to China - Tedros tweet

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Grigsby, Garrett (HHS/OS/OGA) <[redacted] (b) (6)>
Sent: Sunday, February 9, 2020 6:35 PM
To: Fauci, Anthony (NIH/NIAID) [E] <[redacted] (b) (6); Harrison, Brian (HHS/IOS) [redacted] (b) (6)
Cc: Kerr, Lawrence (HHS/OS/OGA) <[redacted] (b) (6); Elvander, Erika (OS/OGA) [redacted] (b) (6)>; Zebley, Kyle (HHS/OS/OGA) [redacted] (b) (6) Redfield, Robert R. (CDC/OD) [redacted] (b) (6); Kadlec, Robert (OS/ASPR/IO) <[redacted] (b) (6); Abram, Anna (FDA/OC) <[redacted] (b) (6)>; Bright, Rick (OS/ASPR/BARDA) [redacted] (b) (6)>
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

Dr F,

[redacted] (b) (5)

From: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>
Sent: Sunday, February 9, 2020 6:24 PM
To: Grigsby, Garrett (HHS/OS/OGA) [redacted] (b) (6)>; Harrison, Brian (HHS/IOS) [redacted] (b) (6)>

Cc: Kerr, Lawrence (HHS/OS/OGA) <[redacted] (b) (6)>; Elvander, Erika (OS/OGA) [redacted] (b) (6); Zebley, Kyle (HHS/OS/OGA) <[redacted] (b) (6)>; Redfield, Robert R. (CDC/OD) [redacted] (b) (6)>; Kadlec, Robert (OS/ASPR/IO) [redacted] (b) (6)>; Abram, Anna (FDA/OC) [redacted] (b) (6)>; Bright, Rick (OS/ASPR/BARDA) [redacted] (b) (6)
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

[redacted] (b) (5)

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Grigsby, Garrett (HHS/OS/OGA) <[redacted] (b) (6)
Sent: Sunday, February 9, 2020 6:03 PM
To: Harrison, Brian (HHS/IOS) [redacted] (b) (6)
Cc: Kerr, Lawrence (HHS/OS/OGA) [redacted] (b) (6); Elvander, Erika (OS/OGA) <[redacted] (b) (6); Zebley, Kyle (HHS/OS/OGA) [redacted] (b) (6)>; Redfield, Robert R. (CDC/OD) [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] <[redacted] (b) (6)>; Kadlec, Robert (OS/ASPR/IO) [redacted] (b) (6)>; Abram, Anna (FDA/OC) [redacted] (b) (6)>; Bright, Rick (OS/ASPR/BARDA) <[redacted] (b) (6)
Subject: FW: WHO advance team on coronavirus on way to China - Tedros tweet

Brian – more clarity from "the horse's mouth" on this advance trip…see below.

From: Grigsby, Garrett (HHS/OS/OGA)
Sent: Sunday, February 9, 2020 6:01 PM
To: SCHWARTLANDER, Bernhard F. [redacted] (b) (6)
Cc: SIMONSON, Stewart [redacted] (b) (6)>
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

Many thanks, Bernard! I know I'll be asked, so I will pass your email up the chain…

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 18:02:22 +0000
To: Billet, Courtney (NIH/NIAID) [E]
Subject: RE: Seeking comment on Indian paper about new Coronavirus

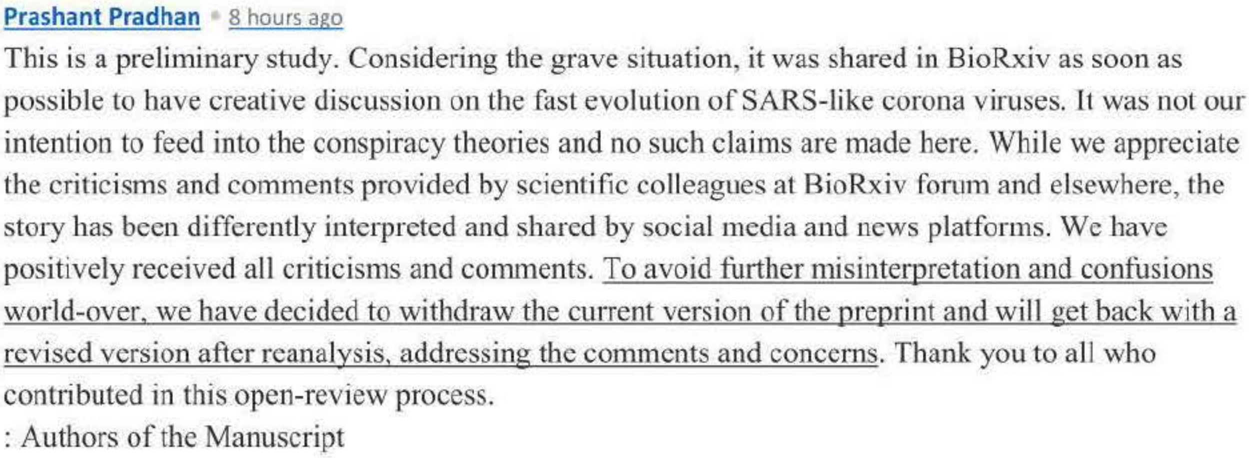
Geeeez

From: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Sunday, February 2, 2020 12:53 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)>; Conrad, Patricia (NIH/NIAID) [E] [redacted] (b) (6)>; Stover, Kathy (NIH/NIAID) [E] [redacted] (b) (6)>; Routh, Jennifer (NIH/NIAID) [E] [redacted] (b) (6)>
Subject: Fwd: Seeking comment on Indian paper about new Coronavirus

FYI re the paper from the Indian researchers.
Talk about trying to put the genie back in the bottle! Yeesh.

From: "Mascola, John (NIH/VRC) [E]" < [redacted] (b) (6)
Date: Sunday, February 2, 2020 at 10:39:42 AM
To: "Routh, Jennifer (NIH/NIAID) [E]" [redacted] (b) (6)>, "Graham, Barney (NIH/VRC) [E]" [redacted] (b) (6) "Hiatt, Nissa (NIH/VRC) [C]" [redacted] (b) (6)>
Cc: "Marston, Hilary (NIH/NIAID) [E]" < [redacted] (b) (6)>, "Billet, Courtney (NIH/NIAID) [E]" [redacted] (b) (6)>, "Stover, Kathy (NIH/NIAID) [E]" [redacted] (b) (6)>
Subject: RE: Seeking comment on Indian paper about new Coronavirus

Also note the following from the author on the BioRxiv comment section:



Prashant Pradhan • 8 hours ago

This is a preliminary study. Considering the grave situation, it was shared in BioRxiv as soon as possible to have creative discussion on the fast evolution of SARS-like corona viruses. It was not our intention to feed into the conspiracy theories and no such claims are made here. While we appreciate the criticisms and comments provided by scientific colleagues at BioRxiv forum and elsewhere, the story has been differently interpreted and shared by social media and news platforms. We have positively received all criticisms and comments. To avoid further misinterpretation and confusions world-over, we have decided to withdraw the current version of the preprint and will get back with a revised version after reanalysis, addressing the comments and concerns. Thank you to all who contributed in this open-review process.
: Authors of the Manuscript

From: Routh, Jennifer (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Sunday, February 2, 2020 10:35 AM
To: Graham, Barney (NIH/VRC) [E] [redacted] (b) (6); Hiatt, Nissa (NIH/VRC) [C] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Mascola, John (NIH/VRC) [E] [redacted] (b) (6)>; Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6)>; Stover, Kathy (NIH/NIAID) [E] < [redacted] (b) (6)
Subject: RE: Seeking comment on Indian paper about new Coronavirus

Hi Barney –

We consulted with HHS and ASF. OCGR is going to send a note to the reporter to decline, noting that the paper is not peer-reviewed. Please let us know if you receive similar requests.

Thanks,
Jen

Jennifer Routh [E]
News and Science Writing Branch
Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases (NIAID)
NIH/HHS
31 Center Drive Room 7A17C
Bethesda, MD 20892
Direct: [redacted] (b) (6)
[redacted] (b) (6)

From: Graham, Barney (NIH/VRC) [E] [redacted] (b) (6)
Sent: Saturday, February 1, 2020 2:11 PM
To: Hiatt, Nissa (NIH/VRC) [C] [redacted] (b) (6)>; Routh, Jennifer (NIH/NIAID) [E] [redacted] (b) (6)>
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)>; Mascola, John (NIH/VRC) [E] [redacted] (b) (6)
Subject: FW: Seeking comment on Indian paper about new Coronavirus

Hi Nissa and Jen,

This is one we don't want to answer without high-level input, but wanted you to know about the rising controversy.

BG

From: Issam AHMED <Issam.AHMED@afp.com>
Sent: Friday, January 31, 2020 5:27 PM
To: Graham, Barney (NIH/VRC) [E] [redacted] (b) (6)
Subject: Seeking comment on Indian paper about new Coronavirus

Dear Dr Graham,

I'm a science journalist with news agency Agence France-Presse writing with a request -- apologies for reaching out on a Friday evening! I was told by a contact you may be willing to give an opinion on this paper that has just gone live https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1.full.pdf it suggests the new Coronavirus has four inserts similar to HIV-1 and this is not a coincidence.

Thanks you very much, if you are able.

Issam Ahmed

Issam AHMED
Health, Science and Environment Correspondent
1500 K St. NW - 20005 Washington
Tel: (202) 414-0521

June 24, 2020
Virus death toll nears half a million as cases surge in US, Latin America

Join us on:

afp.com

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 16:49:35 +0000
To: Collins, Francis (NIH/OD) [E]
Cc: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: Teleconference

Francis:
Do you have a minute for a quick call?
Tony

From: Jeremy Farrar [redacted] (b) (6)
Sent: Sunday, February 2, 2020 11:28 AM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6); Collins, Francis (NIH/OD) [E] [redacted] (b) (6)
Cc: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)>
Subject: Re: Teleconference

Tedros and Bernhard have apparently gone into conclave....they need to decide today in my view. If they do prevaricate, I would appreciate a call with you later tonight or tomorrow to think how we might take forward.

Meanwhile....

https://www.zerohedge.com/geopolitical/coronavirus-contains-hiv-insertions-stoking-fears-over-artificially-created-bioweapon

---

From: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6)>
Date: Sunday, 2 February 2020 at 15:30
To: Jeremy Farrar [redacted] (b) (6)>, Francis Collins [redacted] (b) (6)>
Cc: "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Subject: RE: Teleconference

Jeremy:
Sorry that I took so long to weigh in on your e-mails with Francis and me. I was on conference calls. [redacted] (b) (5) (b) (5)

Best regards,
Tony

From: Jeremy Farrar [redacted] (b) (6)>
Sent: Sunday, February 2, 2020 7:13 AM

To: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Tabak, Lawrence (NIH/OD) [E]
< [redacted] (b) (6)
Subject: Re: Teleconference

....Really appreciate us thinking through the options... [redacted] (b) (5)

From: Francis Collins < [redacted] (b) (6)>
Date: Sunday, 2 February 2020 at 12:03
To: Jeremy Farrar < [redacted] (b) (6)>
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), "Tabak, Lawrence (NIH/OD) [E]"
[redacted] (b) (6)
Subject: RE: Teleconference

Hi Jeremy,

Thanks for forwarding these additional reflections from Mike and Bob. [redacted] (b) (5)
(b) (5) [redacted]

Francis

From: Jeremy Farrar [redacted] (b) (6)
Sent: Sunday, February 2, 2020 6:53 AM
To: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Tabak, Lawrence (NIH/OD) [E]
[redacted] (b) (6)
Subject: Re: Teleconference

Thank you

See thoughts overnight from others.

[redacted] (b) (5)

Jeremy

[redacted]

(b) (5)

From: Francis Collins [redacted] (b) (6)>
Date: Sunday, 2 February 2020 at 10:27
To: Jeremy Farrar [redacted] (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Subject: RE: Teleconference

Jeremy,

[redacted] (b) (5)

I'm available any time today except 3:15 – 5:45 pm EST (on a plane) for a call to Tedros. Let me know if I can help get through his thicket of protectors.

Francis

From: Jeremy Farrar [redacted] (b) (6)
Sent: Sunday, February 2, 2020 4:48 AM
To: Andrew Rambaut < [redacted] (b) (6)>
Cc: R.A.M. Fouchier [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6) Patrick Vallance [redacted] (b) (6); Drosten, Christian [redacted] (b) (6)>; M.P.G. Koopmans [redacted] (b) (6); Eddie Holmes [redacted] (b) (6); Kristian G. Andersen [redacted] (b) (6); Paul Schreier [redacted] (b) (6); Ferguson, Mike [redacted] (b) (6); Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>; Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)>; Josie Golding [redacted] (b) (6)
Subject: Re: Teleconference

This is a very complex issue.

I will:

[redacted] (b) (5)

[redacted] (b) (5)

I suggest we don't get into a further scientific discussion here, but wait for that group to be established.

Jeremy

From: '[redacted] (b) (6)
Date: Sunday, 2 February 2020 at 09:38
To: Jeremy Farrar <[redacted] (b) (6)>
Cc: [redacted] (b) (6)>, "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), Patrick Vallance [redacted] (b) (6)>, "Drosten, Christian" [redacted] (b) (6), Marion Koopmans <[redacted] (b) (6), Edward Holmes [redacted] (b) (6) [redacted] (b) (6), "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) Michael FMedSci [redacted] (b) (6)>, Francis Collins [redacted] (b) (6) [redacted] (b) (6) Josie Golding [redacted] (b) (6)
Subject: Re: Teleconference

Dear Jeremey, Ron and all,

Thanks for inviting me on the call yesterday. [redacted] (b) (5)

[redacted] (b) (5)

[redacted] (b) (5)

Best,
Andrew

On 2 Feb 2020, at 08:40, Jeremy Farrar [redacted] (b) (6)> wrote:

Thanks Ron

[redacted] (b) (5)

Thoughts on that very welcome.

On 2 Feb 2020, at 08:30, R.A.M. Fouchier [redacted] (b) (6)> wrote:

Dear Jeremy and others,

This was a very useful teleconference. [redacted] (b) (5)

[redacted] (b) (5)

Thanks for organizing this on such short notice,
Kind regards

Ron

Ron's notes:

(b) (5)

[redacted]

(b) (5)

[redacted]

[redacted] (b) (5)

Van: Jeremy Farrar [redacted] (b) (6)
Datum: zaterdag 1 februari 2020 om 21:59
Aan: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6)>, Patrick Vallance [redacted] (b) (6)
CC: Christian Drosten [redacted] (b) (6) "M. Koopmans" [redacted] (b) (6), "R.A.M. Fouchier" [redacted] (b) (6), Edward Holmes [redacted] (b) (6) [redacted] (b) (6), Andrew Rambaut [redacted] (b) (6) "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) [redacted] (b) (6), "Ferguson, Mike" [redacted] (b) (6) Francis Collins [redacted] (b) (6), '[redacted] (b) (6)>, Josie Golding [redacted] (b) (6)
Onderwerp: Re: Teleconference

Thank you to everyone for joining.

There is clearly much to understand understand in this. This call was very helpful to hear some of our current understanding and the many gaps in our knowledge. [redacted] (b) (5)

[redacted] (b) (5)

[redacted] (b) (5)

I hope that is a reasonable approach, please send any thoughts or suggestions.

Once again, thank you for making time over a weekend and for such an informed discussion on a complex issue.

Thank you and best wishes Jeremy

From: Jeremy Farrar [redacted] (b) (6)
Date: Saturday, 1 February 2020 at 15:34
To: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6)>, Patrick Vallance < [redacted] (b) (6)
Cc: "Drosten, Christian" [redacted] (b) (6)>, Marion Koopmans [redacted] (b) (6) " [redacted] (b) (6) Edward Holmes [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) [redacted] (b) (6)>, Michael FMedSci [redacted] (b) (6)
Subject: Teleconference

1st February (2nd Feb for Eddie)
Information and discussion is shared in total confidence and not to be shared until agreement on next steps.

Dial in details attached.
Please mute phones.
I will be on email throughout – email Paul or I Paul if any problems
If you cannot make it, I will phone you afterwards to update.

One Hour

6am Sydney
8pm CET
7pm GMT
2pm EST
11am PST
(Hope I have the times right!)

Thank you for the series of calls and for agreeing to join this call.

Agenda

- Introduction, focus and desired outcomes - JF
- Summary – KA
- Comments – EH
- Q&A – All
- Summary and next steps - JF

Kristian Anderson
Bob Garry - I have not been able to contact Bob. Please forward if you can.
Christian Drosten
Tony Fauci
Mike Ferguson
Ron Fouchier
Eddie Holmes
Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance

Andrew Rambaut
Institute for Evolutionary Biology
Ashworth Laboratories, University of Edinburgh, Edinburgh, EH9 3FL, UK

contact – [redacted] (b) (6) | http://tree.bio.ed.ac.uk | tel [redacted] (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 11:26:13 +0000
To: Collins, Francis (NIH/OD) [E];Tabak, Lawrence (NIH/OD) [E];Wolinetz, Carrie (NIH/OD) [E]
Subject: RE: More on evolution of coronavirus

The Indian paper is really outlandish. Agree about Jon Cohen's nice summary.

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Sunday, February 2, 2020 5:58 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E] (b) (6)>; Wolinetz, Carrie (NIH/OD) [E] (b) (6)>
Subject: More on evolution of coronavirus

In case you haven't seen, attached is the Indian paper claiming HIV sequences have been inserted into 2019-nCoV, which has been roundly debunked.

I found Jon Cohen's piece in Science to be a pretty useful summary:

https://www.sciencemag.org/news/2020/01/mining-coronavirus-genomes-clues-outbreak-s-origins

FC

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 22:06:26 +0000
To: Jeremy Farrar;Collins, Francis (NIH/OD) [E]
Subject: RE: Teleconference

Thanks, Jeremy. We really appreciate what you are doing here. Pleasure to work with you.
Best,
Tony

From: Jeremy Farrar (b) (6)>
Sent: Saturday, February 1, 2020 4:00 PM
To: Collins, Francis (NIH/OD) [E] <(b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: Re: Teleconference

We are altogether as you know! Conversations with you and Tony, and Patrick and others – always great working with you both

---

From: Francis Collins (b) (6)>
Date: Saturday, 1 February 2020 at 20:50
To: Jeremy Farrar (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)
Subject: Re: Teleconference

Hi Jeremy,
I can make myself available at any time 24/7 for the call with Tedros. Just let me know.
Thanks for your leadership on this critical and sensitive issue.
Francis

Sent from my iPhone

> On Feb 1, 2020, at 3:07 PM, Jeremy Farrar (b) (6)> wrote:
>
> I have rejoined so a line is open if any help to rejoin.
>
> ---
>
> **From:** Jeremy Farrar (b) (6)>
> **Date:** Saturday, 1 February 2020 at 19:56
> **To:** "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), Francis Collins (b) (6)>, Michael FMedSci (b) (6), Patrick Vallance (b) (6)
> **Subject:** Re: Teleconference

Can I suggest we shut down the call and then redial in?

Just for 5-10mins?

From: Marion Koopmans [redacted] (b) (6)
Date: Saturday, 1 February 2020 at 19:43
To: Jeremy Farrar [redacted] (b) (6)>
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6)>, Patrick Vallance [redacted] (b) (6) "Drosten, Christian" [redacted] (b) (6) [redacted] (b) (6)>, Edward Holmes [redacted] (b) (6), [redacted] (b) (6) [redacted] (b) (6)>, "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) < [redacted] (b) (6) Michael FMedSci [redacted] (b) (6) Francis Collins [redacted] (b) (6)>
Subject: Re: Teleconference

[redacted] (b) (5)

On 1 Feb 2020, at 19:12, Jeremy Farrar [redacted] (b) (6)> wrote:

Kristen and Eddie have shared this and will talk through it on the call. Thank you.

Hope it will help frame the discussions.

From: Jeremy Farrar [redacted] (b) (6)>
Date: Saturday, 1 February 2020 at 15:34

1st February (2nd Feb for Eddie)
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Dial in details attached.
Please mute phones.
I will be on email throughout – email Paul or I Paul if any problems
If you cannot make it, I will phone you afterwards to update.

One Hour

6am Sydney
8pm CET
7pm GMT
2pm EST
11am PST
(Hope I have the times right!)

Thank you for the series of calls and for agreeing to join this call.

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- Introduction, focus and desired outcomes - JF
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Kristian Anderson
Bob Garry - I have not been able to contact Bob. Please forward if you can.
Christian Drosten
Tony Fauci
Mike Ferguson
Ron Fouchier
Eddie Holmes
Marion Koopmans
Stefan Pohlmann
Andrew Rambaut

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 20:03:12 +0000
To: Jeremy Farrar
Subject: RE: Teleconference

Yes

From: Jeremy Farrar [redacted] (b) (6)
Sent: Saturday, February 1, 2020 2:56 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Collins, Francis (NIH/OD) [E] [redacted] (b) (6); Ferguson, Mike [redacted] (b) (6); Patrick Vallance [redacted] (b) (6)
Subject: Re: Teleconference

Can I suggest we shut down the call and then redial in?

Just for 5-10mins?

From: Marion Koopmans [redacted] (b) (6)
Date: Saturday, 1 February 2020 at 19:43
To: Jeremy Farrar [redacted] (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), Patrick Vallance [redacted] (b) (6)>, "Drosten, Christian" [redacted] (b) (6)>, [redacted] (b) (6) Edward Holmes [redacted] (b) (6)>, [redacted] (b) (6) "Kristian G. Andersen" [redacted] (b) (6), Paul Schreier [redacted] (b) (6) Michael FMedSci [redacted] (b) (6)>, Francis Collins [redacted] (b) (6)>
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Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance

<Coronavirus sequence comparison[1].pdf>

[redacted] (b) (6), "NIAID NEWS (NIH/NIAID)" <NIAIDNEWS@niaid.nih.gov>
Subject: FW: coronavirus speaking opportunity

Obviously given the current environment (not to mention some of the names involved in the event), I want to make sure I'm in lockstep with you all from square one. How would you like me to proceed with the request below? The event is open to the public / press.

From: Chertow, Daniel (NIH/CC/CCMD) [E] [redacted] (b) (6)>
Sent: Thursday, January 30, 2020 6:16 PM
To: Cohen, Justin (NIH/CC/OD) [E] [redacted] (b) (6)>; Freimuth, Molly (NIH/CC/OC) [E]
[redacted] (b) (6)>
Cc: Suffredini, Anthony (NIH/CC/CCMD) [E] [redacted] (b) (6)>; Masur, Henry (NIH/CC/CCMD) [E]
[redacted] (b) (6)
Subject: FW: Hudson Institute speaking request

Dear Justin,

I am checking back in with you regarding the below invitation to speak.

I would like to participate in this if possible.

Please confirm that you have received my email.

Thank you.

Sincerely,

Dan

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Thursday, January 30, 2020 at 6:09 PM
To: "Chertow, Daniel (NIH/CC/CCMD) [E]" [redacted] (b) (6)>
Subject: Re: Hudson Institute speaking request

Dear Dan,
Sorry, we have changed something slightly. Instead of taking questions directly from the audience, we will obtain questions from the audience via email while the first part of the event occurs, curate them, and then have them available for Senator Lieberman to ask them of the speakers.
Asha

Asha M. George, DrPH
Executive Director

BIPARTISAN COMMISSION ON BIODEFENSE

202.974.2416

biodefensecommission.org

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Beyond the blueprint

From: Asha M. George <asha.george@biodefensecommission.org>
Sent: Thursday, January 30, 2020 6:02 PM
To: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)
Subject: Re: Hudson Institute speaking request

Dear Dan,
Here are some more specifics regarding the event we will holding at Hudson Institute on novel coronavirus. The meeting will be on February 10th, from 2:00 - 3:30 pm in the Stern Conference Center at Hudson Institute, which is located at 1201 Pennsylvania Avenue, NW, 4th floor, Washington, DC 20004.

We also have the executive conference room reserved from 1:30 pm on. Please plan to arrive around then, so that you can talk with Senator Lieberman and the other speakers before the event starts at 2:00 pm. Just ask the receptionist to direct you where to go.

Here are the speakers:

- Former Senator Joe Lieberman, co-chair, Bipartisan Commission on Biodefense
- Dr. Julie Gerberding, Executive Vice President & Chief Patient Officer, Strategic Communications, Global Public Policy and Population Health, Merck; former Director, Centers for Disease Control and Prevention
- Dr. Billy Karesh, ex officio, Bipartisan Commission on Biodefense; Executive VP, EcoHealth Alliance
- The Honorable Tim Morrison, Senior Fellow, Hudson Institute; former Deputy Assistant to President Trump for National Security; former Special Assistant to the President and Senior Director for Weapons of Mass Destruction and Biodefense
- Mr. Eric Brown, Senior Fellow, Hudson Institute

- Dr. Daniel S. Chertow (CAPT - US Public Health Service), Head, Emerging Pathogens Section, Critical Care Medicine Department, Clinical Center & Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health *(invited)*

The setting will be relatively informal. Scooter Libby will first introduce Senator Lieberman. Then Senator Lieberman will make a short opening statement, and look to Billy to set the stage and talk about the zoonotic nature of the disease, associated disease management considerations, etc., in about 5 minutes. The Senator will then ask each of the other speakers to say a few words from their perspectives. After that, Senator Lieberman will ask some questions of the group, allowing you all to answer and converse. All of this should take about 45 minutes. Then we will allow the audience to ask questions.

We are planning for Senator Lieberman to moderate the discussion and take questions from the audience, but if for some reason he cannot do so, then Billy Karesh will.

I hope you will be able to make it, Dan. Let me know if you have any questions (and if you will be able to make it, of course) and I look forward to seeing you on February 10th.

Asha

Asha M. George, DrPH
Executive Director

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Beyond the blueprint

From: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)>
Sent: Tuesday, January 28, 2020 7:18 PM
To: Asha M. George <asha.george@biodefensecommission.org>
Subject: Re: Hudson Institute speaking request

Dear Asha,

Given that this is a public/press event, I will require additional clearance from my organization in order to participate.

I will reach out to them now and get back to you.

Thank you.

Dan

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Tuesday, January 28, 2020 at 7:15 PM
To: "Chertow, Daniel (NIH/CC/CCMD) [E]" (b) (6)>
Subject: Re: Hudson Institute speaking request

Dear Dan,
Thank you! The meeting will be held on February 10th. We are still trying to nail down a time with Senator Lieberman and Governor Ridge, so I will get back to you about that as soon as possible, hopefully tomorrow.

The meeting will be open to the public and to the press, but Hudson Institute is a think tank, so it's never a negative or rowdy crowd.

Asha

Asha M. George, DrPH
Executive Director

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Beyond the blueprint

From: Chertow, Daniel (NIH/CC/CCMD) [E] [redacted] (b) (6)
Sent: Tuesday, January 28, 2020 5:53 PM
To: Asha M. George <asha.george@biodefensecommission.org>
Subject: Re: Hudson Institute speaking request

Dear Asha,

I am available Feb 10th or 13th and would be happy to present to the group.

Please clarify who will be in attendance and if the event is open or closed to press/public as this would require additional clearance on my end.

Thank you.

Sincerely,

Dan

Daniel S. Chertow, MD, MPH, FCCM, FIDSA
CAPT, United States Public Health Service
Head, Emerging Pathogens Section
Critical Care Medicine Department, NIH Clinical Center &
Laboratory of Immunoregulation, NIAID

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Monday, January 27, 2020 at 6:09 PM

To: "Chertow, Daniel (NIH/CC/CCMD) [E]" <(b) (6)
Subject: Hudson Institute speaking request

Dear Dr. Chertow,
I am the Executive Director of the Bipartisan Commission on Biodefense, co-chaired by former Senator Joe Lieberman and Governor Tom Ridge. Our fiscal sponsor is Hudson Institute, one of the think tanks here in DC. Hudson Institute's chair of the board of trustees (Sarah May Stern) has asked Hudson Institute to run a 90 minute meeting on the novel coronavirus situation. Hudson has asked us to help them pull a brief meeting together in short order.

Considering your experience on the ground dealing with other outbreaks, Hudson Institute invites you to speak at this event. In addition to one of Hudson Institute's China experts, we are also seeing whether Senator Lieberman and Governor Ridge are available to speak.

Here are the dates they are a looking at: February 6, February 10, and February 13. Could you let me know if you are available and if so, when on those dates?

Thank you for your consideration, Dan. I look forward to hearing from you soon.

Asha

Asha M. George, DrPH
Executive Director

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Beyond the blueprint

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:43:31 +0000
To: Kristian G. Andersen
Subject: RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

From: Kristian G. Andersen [redacted] (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Jeremy Farrar [redacted] (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)> wrote:

> Jeremy/Kristian:
> This just came out today. You may have seen it. If not, it is of interest to the current discussion.
> Best,
> Tony
>
> ---
>
> **From:** Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)
> **Sent:** Friday, January 31, 2020 8:43 PM
> **Subject:** Science: Mining coronavirus genomes for clues to the outbreak's origins


As part of a long-running effort to see what viruses bats harbor, researchers in China collect one from a cave in Guandong.
EcoHealth Alliance

Mining coronavirus genomes for clues to the outbreak's origins

By Jon CohenJan. 31, 2020 , 6:20 PM

attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct ...

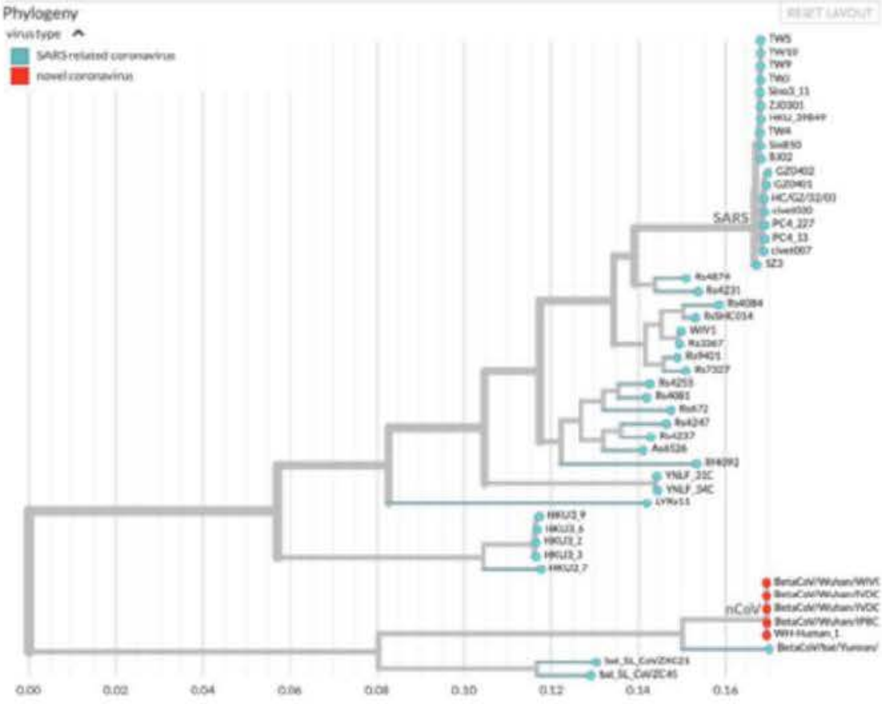
That string of apparent gibberish is anything but: It's a snippet of a DNA sequence from the viral pathogen, dubbed 2019 novel coronavirus (2019-nCoV), that is overwhelming China and frightening the entire world. Scientists are publicly sharing an ever-growing number of full sequences of the virus from patients—53 at last count in the Global Initiative on Sharing All Influenza Data database. These viral genomes are being intensely studied to try to understand the origin of 2019-nCoV and how it fits on the family tree of related viruses found in bats and other species. They have also given glimpses into what this newly discovered virus physically looks like, how it's changing, and how it might be stopped.

"One of the biggest takeaway messages [from the viral sequences] is that there was a single introduction into humans and then human-to-human spread," says Trevor Bedford, a bioinformatics specialist at the University of Washington, Seattle. The role of Huanan Seafood Wholesale Market in Wuhan, China, in spreading 2019-nCoV remains murky, though such sequencing, combined with sampling the market's environment for the presence of the virus, is clarifying that it indeed had an important early role in amplifying the outbreak. The viral sequences, most researchers say, also knock down the idea the pathogen came from a virology institute in Wuhan.

In all, 2019-nCoV has nearly 29,000 nucleotides bases that hold the genetic instruction book to produce the virus. Although it's one of the many viruses whose genes are in the form of RNA, scientists convert the viral genome into DNA, with bases known in shorthand as A, T, C, and G, to make it easier to study. Many analyses of 2019-nCoV's sequences have already appeared on virological.org, nextstrain.org, preprint servers like bioRxiv, and even in peer-reviewed journals. The sharing of the sequences by Chinese researchers allowed public health labs around the world to develop their own diagnostics for the virus, which now has been found in 18 other countries. (*Science*'s news stories on the outbreak can be found here.)

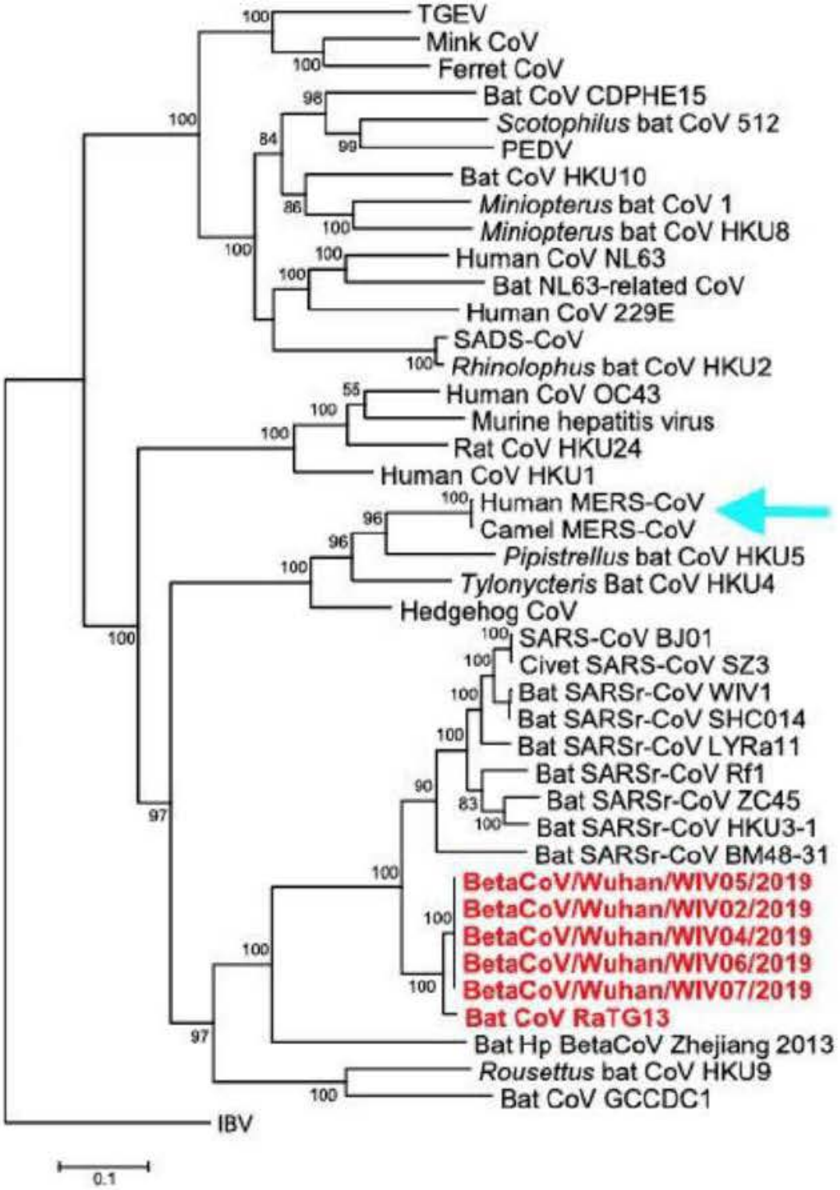
When the first 2019-nCoV sequence became available, researchers placed it on a family tree of known coronaviruses—which are abundant and infect many species—and found that it was most closely related to relatives found in bats. A team led by Shi Zheng-Li, a coronavirus specialist at the Wuhan Institute of Virology, reported on 23 January on bioRxiv that 2019-nCoV's sequence was 96.2% similar to a bat virus and had 79.5% similarity to the coronavirus that causes severe acute respiratory syndrome (SARS), a disease whose initial outbreak was also in China more than 15 years ago. But the SARS coronavirus has a similarly close relationship to bat viruses, and sequence data make a powerful case that it jumped into people from a coronavirus in civets that differed from human SARS viruses by as few as 10 nucleotides. That's one reason why many scientists suspect there's an "intermediary" host species—or several—between bats and 2019-nCoV.

According to Bedford's analysis, the bat coronavirus sequence that Shi Zheng-Li's team highlighted, dubbed RaTG13, differs from 2019-nCoV by nearly 1100 nucleotides. On nextstrain.org, a site he co-founded, Bedford has created coronavirus family trees (example below) that include bat, civet, SARS, and 2019-nCoV sequences. (The trees are interactive—by dragging a computer mouse over them, it's easy to see the differences and similarities between the sequences.)



Bedford's analyses of RaTG13 and 2019-nCoV suggest that the two viruses shared a common ancestor 25 to 65 years ago, an estimate he arrived at by combining the difference in nucleotides between the viruses with the presumed rates of mutation in other coronaviruses. So it likely took decades for RaTG13-like viruses to mutate into 2019-nCoV.

Middle East respiratory syndrome (MERS), another human disease caused by a coronavirus, similarly has a link to bat viruses. But studies have built a compelling case it jumped to humans from camels. And the phylogenetic tree from Shi's bioRxiv paper (below) makes the camel-MERS link easy to see.



The longer a virus circulates in a human populations, the more time it has to develop mutations that differentiate strains in infected people, and given that the 2019-nCoV sequences analyzed to date differ from each other by seven nucleotides at most, this suggests it jumped into humans very recently. But it remains a mystery which animal spread the virus to humans. "There's a very large gray area between viruses detected in bats and the virus now isolated in humans," says Vincent Munster, a virologist at the U.S. National Institute of Allergy and Infectious Diseases who studies coronaviruses in bats, camels, and others species.

Strong evidence suggests the marketplace played an early role in spreading 2019-nCoV, but whether it was the origin of the outbreak remains uncertain. Many of the initially confirmed 2019-nCoV cases—27 of the first 41 in one report, 26 of 47 in another—were connected to the Wuhan market, but up to 45%, including the earliest handful, were not. This raises the possibility that the initial jump into people happened elsewhere.

According to Xinhua, the state-run news agency, "environmental sampling" of the Wuhan seafood market has found evidence of 2019-nCoV. Of the 585 samples tested, 33 were positive for 2019-nCoV and all were in the huge market's western portion, which is where wildlife were sold. "The positive tests from the wet market are hugely important," says Edward Holmes, an evolutionary biologist at the University of Sydney who collaborated with the first group to publicly release a 2019-nCoV sequence. "Such a high rate of positive tests would strongly imply that animals in the market played a key role in the emergence of the virus."

Yet there have been no preprints or official scientific reports on the sampling, so it's not clear which, if any, animals tested positive. "Until you consistently isolate the virus out of a single species, it's really, really difficult to try and determine what the natural host is," says Kristian Andersen, an evolutionary biologist at Scripps Research.

One possible explanation for the confusion about where the virus first entered humans is if there was a batch of recently infected animals sold at different marketplaces. Or an infected animal trader could have transmitted the virus to different people at different markets. Or, Bedford suggests, those early cases could have been infected by viruses that didn't easily transmit and sputtered out. "It would be hugely helpful to have just a sequence or two from the marketplace [environmental sampling] that could illuminate how many zoonoses occurred and when they occurred," Bedford says.

A research group sent fecal and other bodily samples from bats they trapped in caves to the Wuhan Institute of Virology to search for coronaviruses.

EcoHealth Alliance

In the absence of clear conclusions about the outbreak's origin, theories thrive, and some have been scientifically shaky. A sequence analysis led by Wei Ji of Peking University and published online by the *Journal of Medical Virology* received substantial press coverage when it suggested that "snake is the most probable wildlife animal reservoir for the 2019-nCoV." Sequence specialists, however, pilloried it.

Conspiracy theories also abound. A CBC News report about the Canadian government deporting Chinese scientists who worked in a Winnipeg lab that studies dangerous pathogens was distorted on social media to suggest that they were spies who had smuggled out coronaviruses. The Wuhan Institute of Virology, which is the premier lab in China that studies bat and human coronaviruses, has also come under fire. "Experts debunk fringe theory linking China's coronavirus to weapons research," read a headline on a story in *The Washington Post* that focused on the facility.

Concerns about the institute predate this outbreak. *Nature* ran a story in 2017 about it building a new biosafety level 4 lab and included molecular biologist Richard Ebright of Rutgers University, Piscataway, expressing concerns about accidental infections, which he noted repeatedly happened with lab workers handling SARS in Beijing. Ebright, who has a long history of raising red flags about studies with dangerous pathogens, also in 2015 criticized an experiment in which modifications were made to a SARS-like virus circulating in Chinese bats to see whether it had the potential to cause disease in humans. Earlier this week, Ebright questioned the accuracy of Bedford's calculation that there are at least 25 years of evolutionary distance between RaTG13—the virus held in the Wuhan virology institute—and 2019-nCoV, arguing that the mutation rate may have been different as it passed through different hosts before humans. Ebright tells *Science*Insider that the 2019-nCoV data are "consistent with entry into the human population as a natural accident."

Shi did not reply to emails from *Science*, but her longtime collaborator, disease ecologist Peter Daszak of the EcoHealth Alliance, dismissed Ebright's conjecture. "Every time there's an emerging disease, a new virus, the same story comes out: This is a spillover or the release of an agent or a bioengineered virus," Daszak says. "It's just a shame. It seems humans can't resist controversy and these myths, yet it's staring us right in the face. There's this incredible diversity of viruses in wildlife and we've just scratched the surface. Within that diversity, there will be some that can infect people and within that group will be some that cause illness."

A team of researchers from the Wuhan Institute of Virology and the EcoHealth Alliance have trapped bats in caves all over China, like this one in Guangdong, to sample them for coronaviruses.
EcoHealth Alliance

Daszak and Shi's group have for 8 years been trapping bats in caves around China to sample their feces and blood for viruses. He says they have sampled more than 10,000 bats and 2000 other species. They have found some 500 novel coronaviruses, about 50 of which fall relatively close to the SARS virus on the family tree, including RaTG13—it was fished out of a bat fecal sample they collected in 2013 from a cave in Moglang in Yunnan province. "We cannot assume that just because this virus from Yunnan has high sequence identity with the new one that that's the origin," Daszak says, noting that only a tiny fraction of coronaviruses that infect bats have been discovered. "I expect that once we've sampled and sampled and sampled across southern China and central China that we're going to find many other viruses and some of them will be closer [to 2019-nCoV]."

It's not just a "curious interest" to figure out what sparked the current outbreak, Daszak says. "If we don't find the origin, it could still be a raging infection at a farm somewhere, and once this outbreak dies, there could be a continued spillover that's really hard to stop. But the jury is still out on what the real origins of this are."

Posted in:

- Asia/Pacific

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:34:43 +0000
To: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: Teleconference
Attachments: Coronavirus sequence comparison[1].pdf

FYI

From: Jeremy Farrar [redacted] (b) (6)>
Sent: Saturday, February 1, 2020 1:13 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>; Patrick Vallance [redacted] (b) (6)
[redacted]
Cc: Drosten, Christian [redacted] (b) (6); Marion Koopmans
[redacted] (b) (6)|>; R.A.M. Fouchier [redacted] (b) (6); Edward Holmes
[redacted] (b) (6) Andrew Rambaut [redacted] (b) (6)
Kristian G. Andersen [redacted] (b) (6); Paul Schreier [redacted] (b) (6);
[redacted] (b) (6); Ferguson, Mike [redacted] (b) (6); Collins, Francis (NIH/OD) [E]
[redacted] (b) (6)
Subject: Re: Teleconference

Kristen and Eddie have shared this and will talk through it on the call. Thank you.

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From: Jeremy Farrar [redacted] (b) (6)
Date: Saturday, 1 February 2020 at 15:34

1st February (2nd Feb for Eddie)
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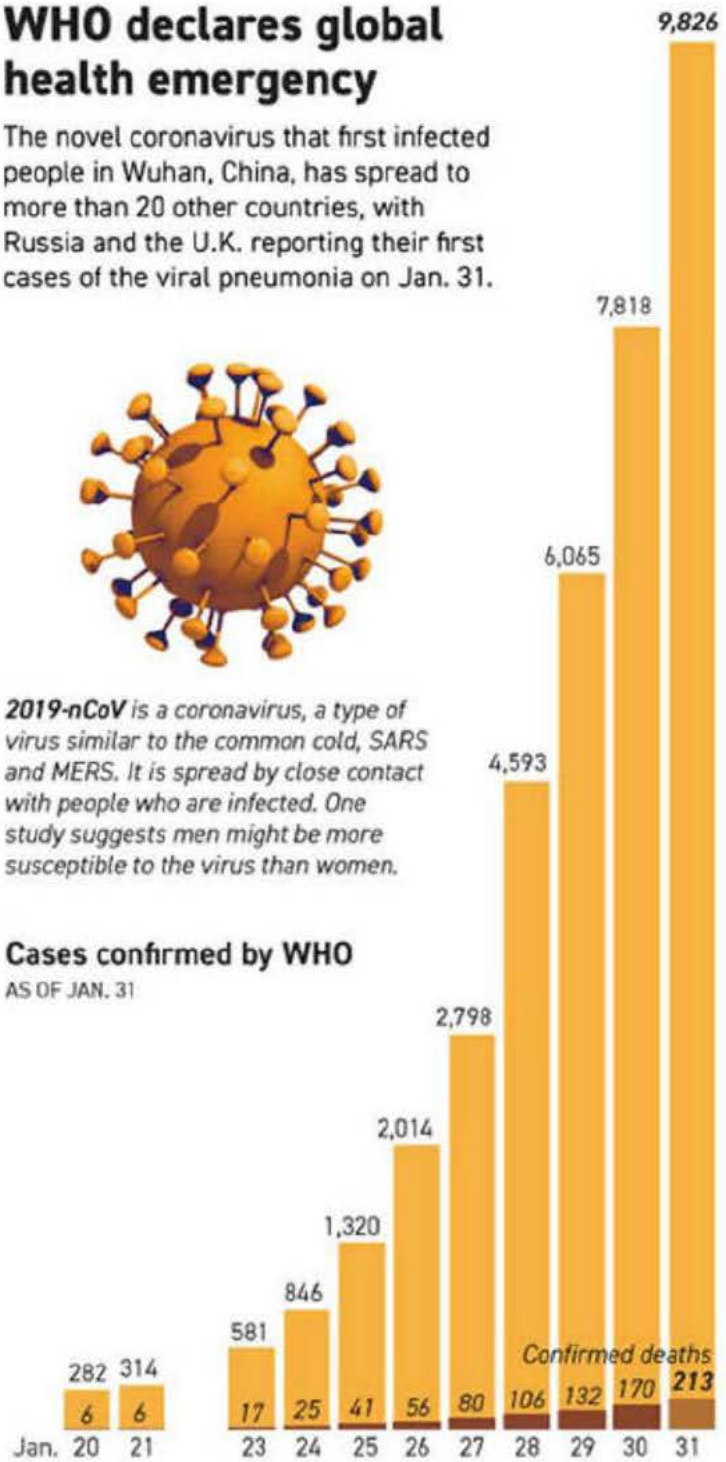


WHO declares global health emergency

The novel coronavirus that first infected people in Wuhan, China, has spread to more than 20 other countries, with Russia and the U.K. reporting their first cases of the viral pneumonia on Jan. 31.

***2019-nCoV** is a coronavirus, a type of virus similar to the common cold, SARS and MERS. It is spread by close contact with people who are infected. One study suggests men might be more susceptible to the virus than women.*

Cases confirmed by WHO

AS OF JAN. 31

Sources: WHO, South China Morning Post, news reports

By Patterson Clark, POLITICO Pro DataPoint

Patterson Clark/POLITICO Pro DataPoint

"There is a compelling reason that the American people want us to consider this and so we're going to have to figure this one out and balance both of those issues," Hahn said, referring to safety and affordability.

The FDA for years has mostly stayed out of the debate around drug prices; the agency doesn't regulate the cost of medicines or health insurance coverage. But Hahn talked up FDA's role in getting prices down by approving more generics, acknowledging that "the American people are expecting us to do more." Trump has touted the FDA's record on boosting competition via generic approvals.

As FDA works on finalizing the importation rule, Hahn said the agency will be open to addressing criticism that states can't save money bringing in drugs from Canada if the pathway is too burdensome. But he stressed safety is tantamount. "Our primary concern is the protection of the drug supply," he said.

Hahn said he has also talked with CMS Administrator Seema Verma about addressing costs of new brand-name products that are approved with limited data sets, similar to the way CMS decides to cover some medical devices. That approach — known as coverage with evidence development — lets CMS cover a new product on the condition that manufacturers keep providing data.

FDA has not done that, but new medicines are increasingly being approved on smaller clinical trials without hard data on clinical benefits — and can come with six-figure price tags.

As an academic, Hahn had co-written an editorial suggesting that payments for newly approved radiation oncology devices could be linked to older products until enough evidence builds up to show that the new products are superior. Only then would manufacturers have more pricing leeway.

"It's a CMS call about coverage with evidence development, but I do think in this world where we are concerned, and rightfully so, about the cost of medicine and health et cetera, that we should be looking at all avenues to approach that," he told POLITICO.

Over the last few years, some critics have said the FDA is overcorrecting and moving too quickly to approve drugs without adequate evidence. But Hahn did not indicate he would put the brakes on.

"At the end of the day there is this balance between the gold standard and being efficient and getting things in people's hands I'm totally confident in the agency's ability to do that."

Hahn must balance all that while leading the FDA's response to the Wuhan crisis, which has heightened some lawmakers' concern about U.S. reliance on Chinese drug manufacturing after incidents of contamination with carcinogens.

"We have to be concerned about the supply chain to make sure that we have enough of what we need if there are any potential outbreaks here," Rep. Susan Brooks (R-Ind.) said after a closed-door briefing Thursday for Energy and Commerce committee members with top health officials. The fact that China manufactures much of the protective medical gear used in U.S. hospitals and clinics "should cause us to be reexamining what we're doing in China versus what should be brought back to this country." she said.

Outside of the coronavirus, a host of thorny regulatory issues await Hahn. Industry and lawmakers have pressed for a clear FDA framework on selling cannabidiol, the popular hemp and marijuana byproduct decriminalized by the 2018 farm bill — and since sold as medicine, dietary supplements and infused in food, cosmetics and skincare products.

"You cannot walk down the street without seeing the products" but there is a dearth of solid data on how safe and effective CBD actually is, said Hahn.

Those CBD challenges have fueled larger discussions about how to better regulate the vast dietary supplement market, where manufacturers often push legal boundaries by making unverified claims about how herbal or homeopathic products can help people.

"It will be something else next," said Hahn. We don't want to overstep our bounds but we want to make sure that safe and effective products are in the hands of people."

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 17:51:31 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: RE: Continued

OK. Stay tuned.

-----Original Message-----
From: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)>
Sent: Saturday, February 1, 2020 11:47 AM
To: Fauci, Anthony (NIH/NIAID) [E] <(b) (6)>
Subject: Continued

The paper you sent me says the experiments were performed before the gain of function pause but have since been reviewed and approved by NIH. Not sure what that means since Emily is sure that no Coronavirus work has gone through the P3 framework. She will try to determine if we have any distant ties to this work abroad.

Sent from my iPad

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 13:19:06 +0000
To: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

Here it is

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 12:29:01 +0000
To: Auchincloss, Hugh (NIH/NIAID) [C] [redacted] (b) (6)
Cc: [redacted] (b) (6)
Subject: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

Hugh:

It is essential that we speak this AM. Keep your cell phone on. I have a conference call at 7:45 AM with Azar. It likely will be over at 8:45 AM. Read this paper as well as the e-mail that I will forward to you now. You will have tasks today that must be done.

Thanks,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: [redacted] (b) (6)
FAX: (301) 496-4409
E-mail: [redacted] (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 02:48:59 +0000
To: Kadlec, Robert (OS/ASPR/IO)
Cc: (b) (6)
Subject: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Bob:

This just came out today. Gives a balanced view.

Best,
Tony

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)>
Sent: Friday, January 31, 2020 8:43 PM
Subject: Science: Mining coronavirus genomes for clues to the outbreak's origins

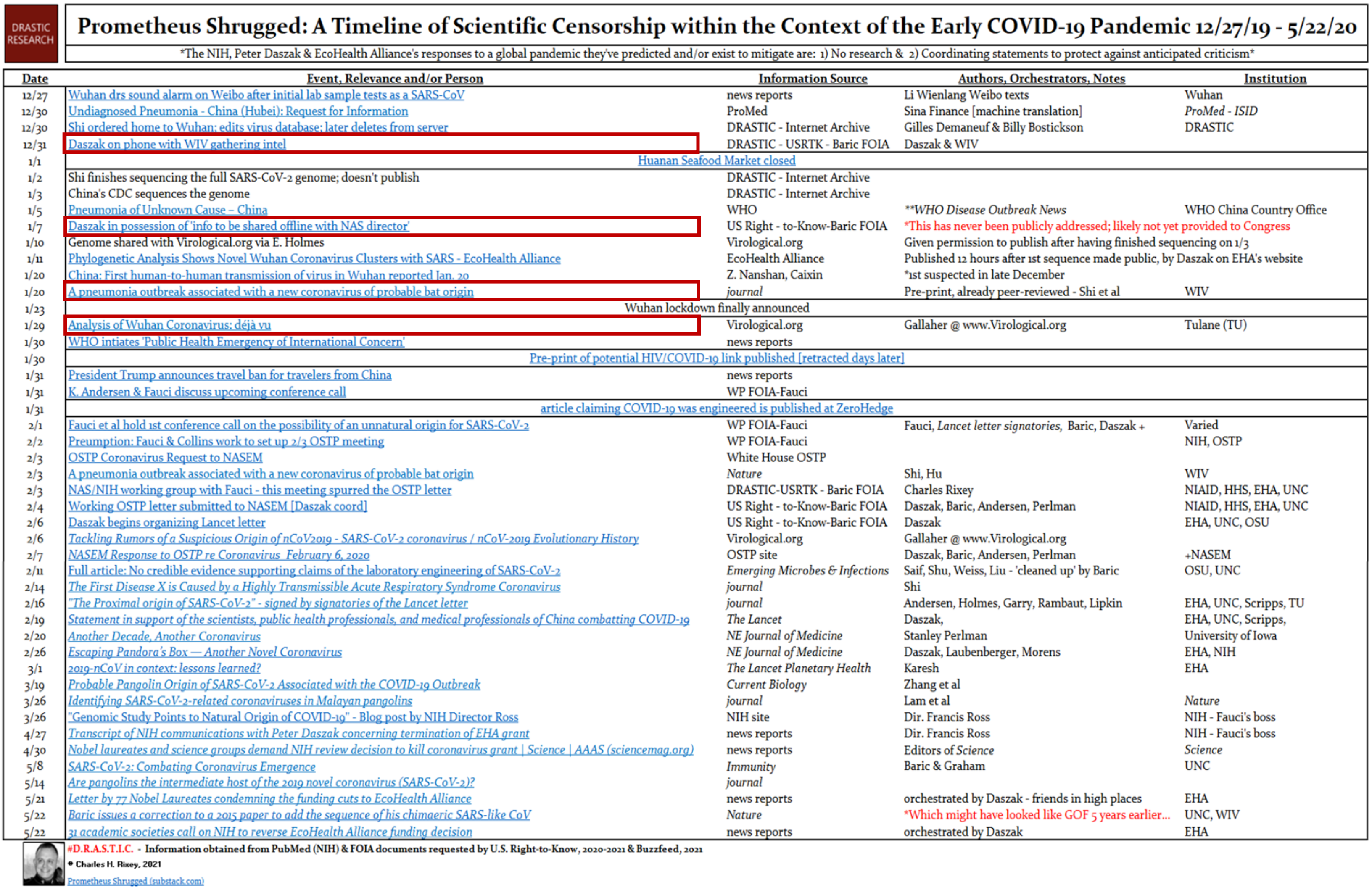
As part of a long-running effort to see what viruses bats harbor, researchers in China collect one from a cave in Guandong.
EcoHealth Alliance

Mining coronavirus genomes for clues to the outbreak's origins

By Jon CohenJan. 31, 2020 , 6:20 PM

attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct ...

That string of apparent gibberish is anything but: It's a snippet of a DNA sequence from the viral pathogen, dubbed 2019 novel coronavirus (2019-nCoV), that is overwhelming China and frightening the entire world. Scientists are publicly sharing an ever-growing number of full sequences of the virus from patients—53 at last count in the Global Initiative on Sharing All Influenza Data database. These viral genomes are being intensely studied to try to understand the origin of 2019-nCoV and how it fits on the family tree of related viruses found in bats and other species. They have also given glimpses into what this newly discovered virus physically looks like, how it's changing, and how it might be stopped.



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

• Charles H. Rixey, 2021

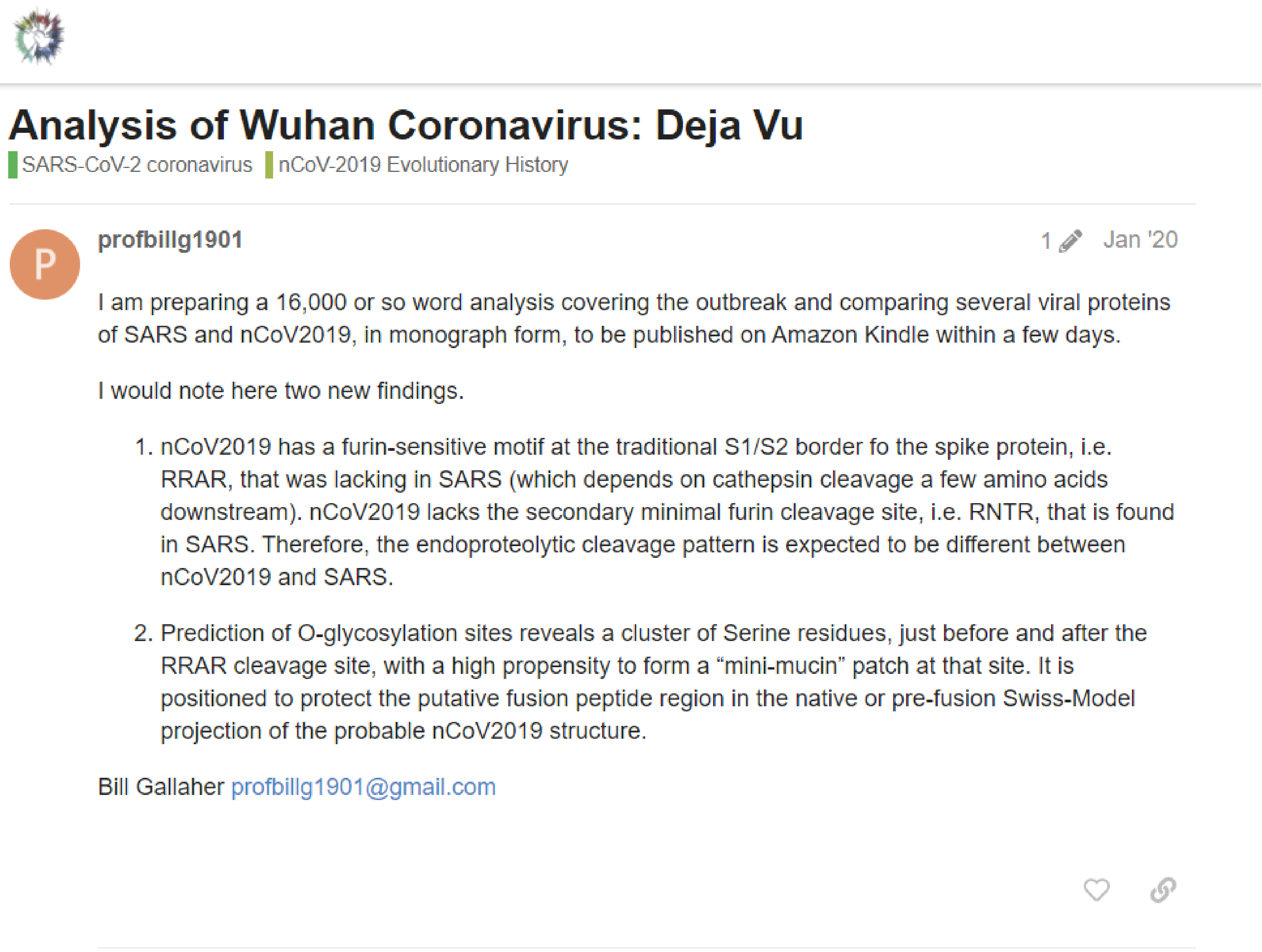
Prometheus Shrugged (substack.com)

FOIA Emails: Peter Daszak during the early outbreak

These highlight Daszak's activities from the earliest days of the pandemic, starting on 12/31/19

Source: US Right-to-Know FOIA documents for Ralph Baric; Volumes I, II & XI

1st Mention of the SARS-CoV-2 FCS: 1/29/20
virological.org – W. Gallaher



Analysis of Wuhan Coronavirus: Deja Vu

SARS-CoV-2 coronavirus | nCoV-2019 Evolutionary History

profbillg1901 1 ✎ Jan '20

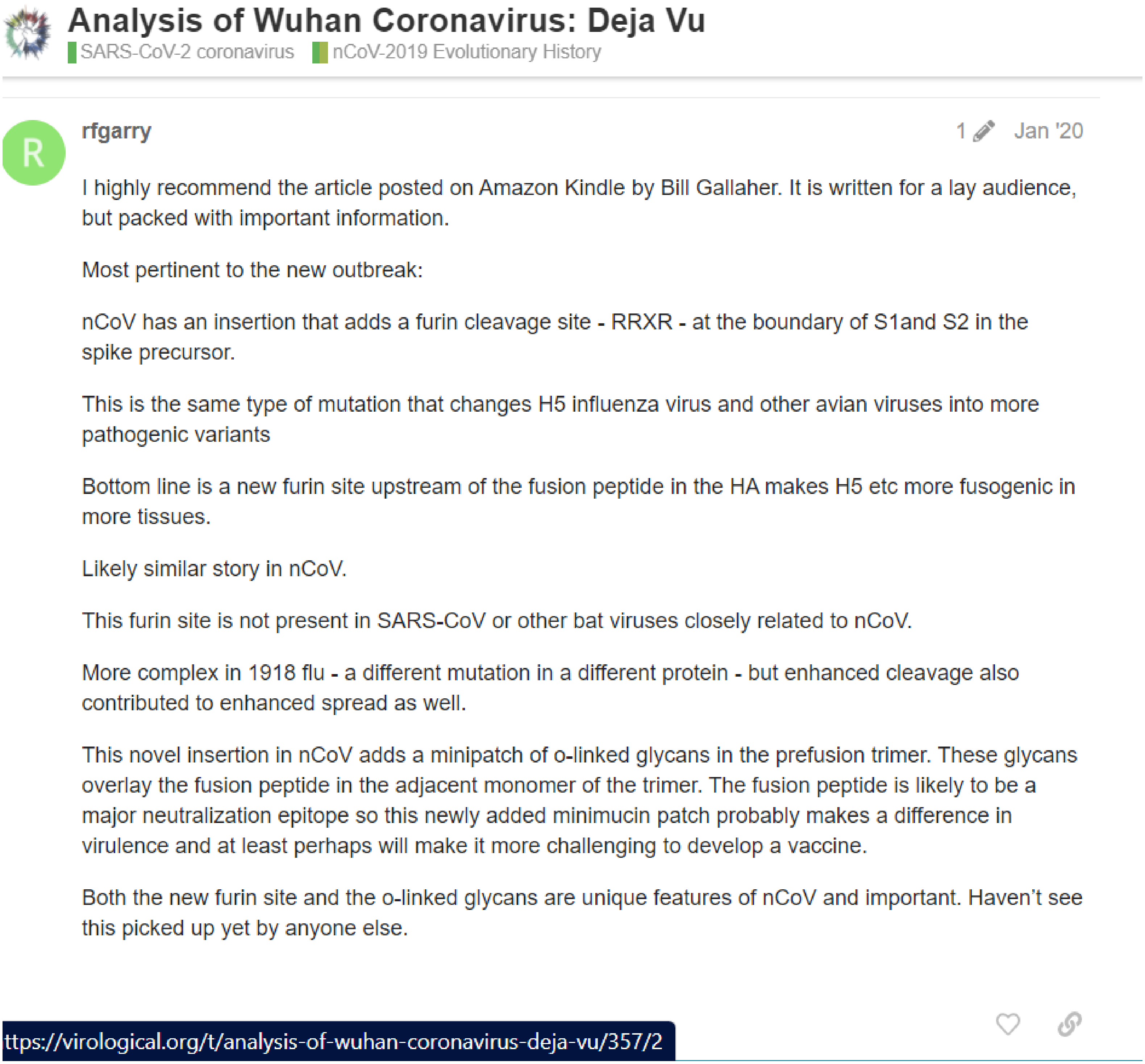
I am preparing a 16,000 or so word analysis covering the outbreak and comparing several viral proteins of SARS and nCoV2019, in monograph form, to be published on Amazon Kindle within a few days.

I would note here two new findings.

1. nCoV2019 has a furin-sensitive motif at the traditional S1/S2 border fo the spike protein, i.e. RRAR, that was lacking in SARS (which depends on cathepsin cleavage a few amino acids downstream). nCoV2019 lacks the secondary minimal furin cleavage site, i.e. RNTR, that is found in SARS. Therefore, the endoproteolytic cleavage pattern is expected to be different between nCoV2019 and SARS.
2. Prediction of O-glycosylation sites reveals a cluster of Serine residues, just before and after the RRAR cleavage site, with a high propensity to form a "mini-mucin" patch at that site. It is positioned to protect the putative fusion peptide region in the native or pre-fusion Swiss-Model projection of the probable nCoV2019 structure.

Bill Gallaher profbillg1901@gmail.com

1st mention of the SARS-CoV-2 FCS – 1/31/20
Garry response to Gallaher



Analysis of Wuhan Coronavirus: Deja Vu

rfgarry 1 Jan '20

I highly recommend the article posted on Amazon Kindle by Bill Gallaher. It is written for a lay audience, but packed with important information.

Most pertinent to the new outbreak:

nCoV has an insertion that adds a furin cleavage site - RRXR - at the boundary of S1and S2 in the spike precursor.

This is the same type of mutation that changes H5 influenza virus and other avian viruses into more pathogenic variants

Bottom line is a new furin site upstream of the fusion peptide in the HA makes H5 etc more fusogenic in more tissues.

Likely similar story in nCoV.

This furin site is not present in SARS-CoV or other bat viruses closely related to nCoV.

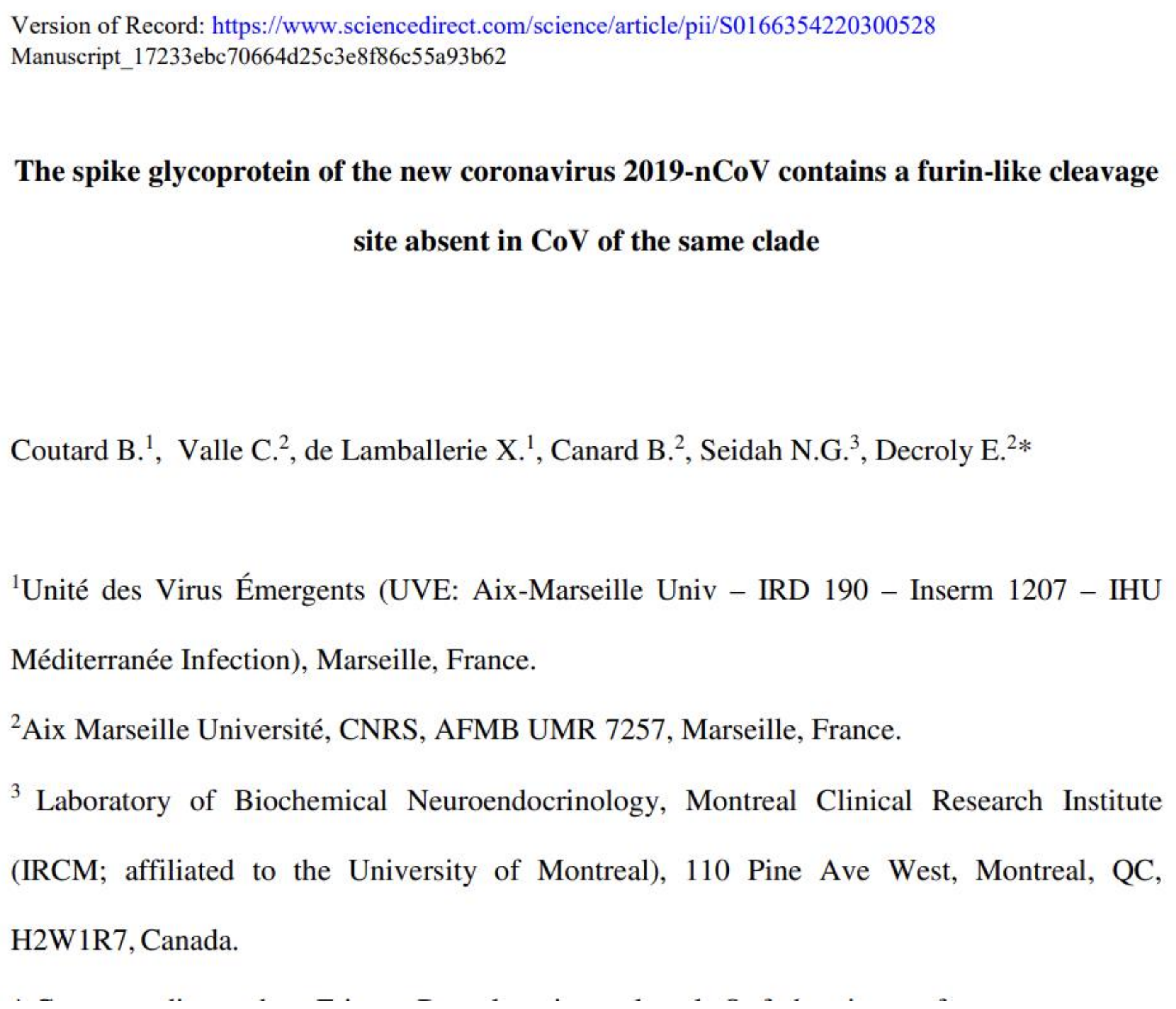
More complex in 1918 flu - a different mutation in a different protein - but enhanced cleavage also contributed to enhanced spread as well.

This novel insertion in nCoV adds a minipatch of o-linked glycans in the prefusion trimer. These glycans overlay the fusion peptide in the adjacent monomer of the trimer. The fusion peptide is likely to be a major neutralization epitope so this newly added minimucin patch probably makes a difference in virulence and at least perhaps will make it more challenging to develop a vaccine.

Both the new furin site and the o-linked glycans are unique features of nCoV and important. Haven't see this picked up yet by anyone else.

ttps://virological.org/t/analysis-of-wuhan-coronavirus-deja-vu/357/2

1st mention of the SARS-CoV-2 FCS – 1/31/20
Garry response to Gallaher



Version of Record: https://www.sciencedirect.com/science/article/pii/S0166354220300528
Manuscript_17233ebc70664d25c3e8f86c55a93b62

The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade

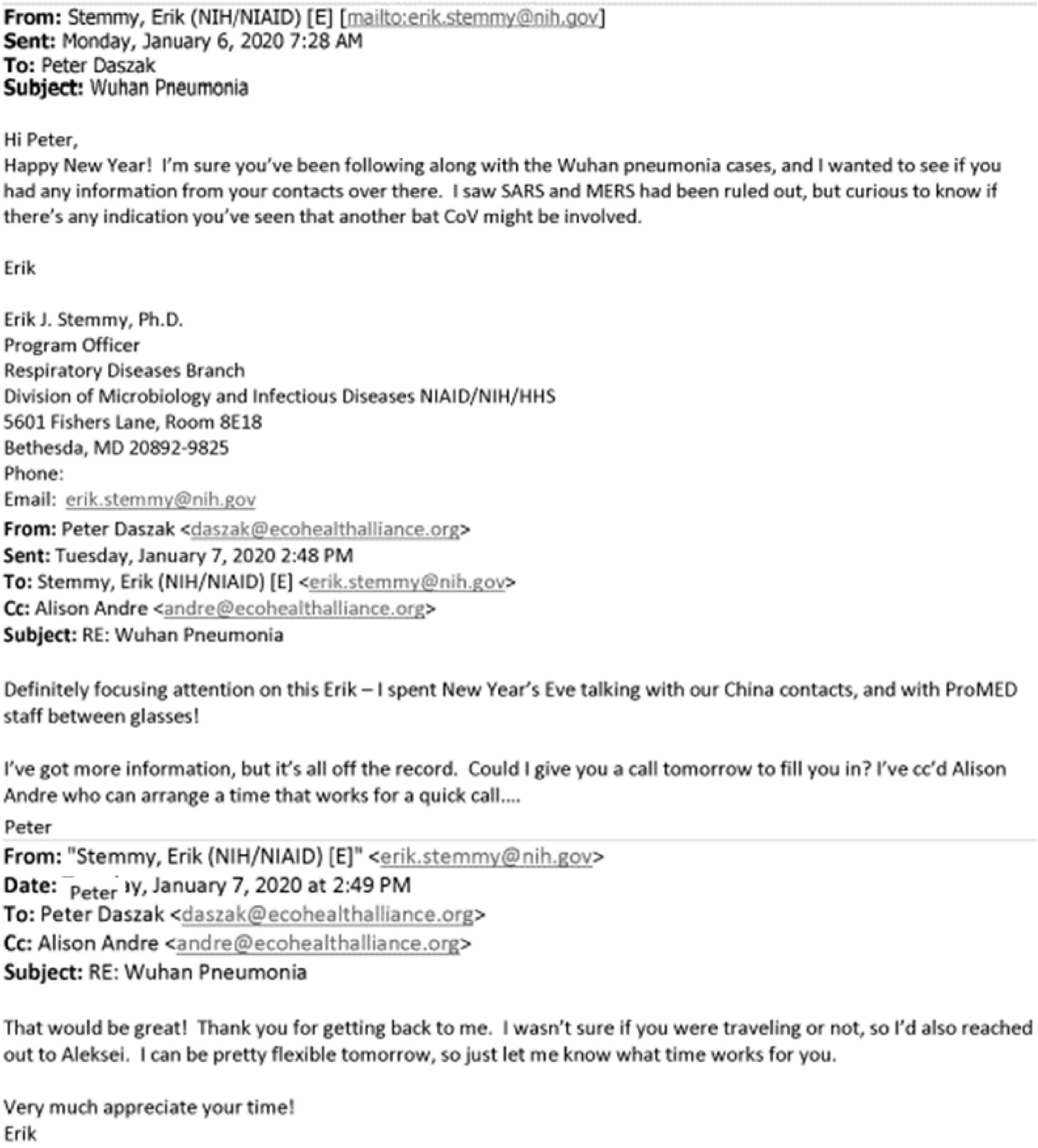
Coutard B.[1], Valle C.[2], de Lamballerie X.[1], Canard B.[2], Seidah N.G.[3], Decroly E.[2]*

[1]Unité des Virus Émergents (UVE: Aix-Marseille Univ – IRD 190 – Inserm 1207 – IHU Méditerranée Infection), Marseille, France.

[2]Aix Marseille Université, CNRS, AFMB UMR 7257, Marseille, France.

[3] Laboratory of Biochemical Neuroendocrinology, Montreal Clinical Research Institute (IRCM; affiliated to the University of Montreal), 110 Pine Ave West, Montreal, QC, H2W1R7, Canada.

Erik Stemmy [NIH] reaches out to Daszak – 1/6/20



From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Monday, January 6, 2020 7:28 AM
To: Peter Daszak
Subject: Wuhan Pneumonia

Hi Peter,
Happy New Year! I'm sure you've been following along with the Wuhan pneumonia cases, and I wanted to see if you had any information from your contacts over there. I saw SARS and MERS had been ruled out, but curious to know if there's any indication you've seen that another bat CoV might be involved.

Erik

Erik J. Stemmy, Ph.D.
Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases NIAID/NIH/HHS
5601 Fishers Lane, Room 8E18
Bethesda, MD 20892-9825
Phone:
Email: erik.stemmy@nih.gov

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 2:48 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

Definitely focusing attention on this Erik – I spent New Year's Eve talking with our China contacts, and with ProMED staff between glasses!

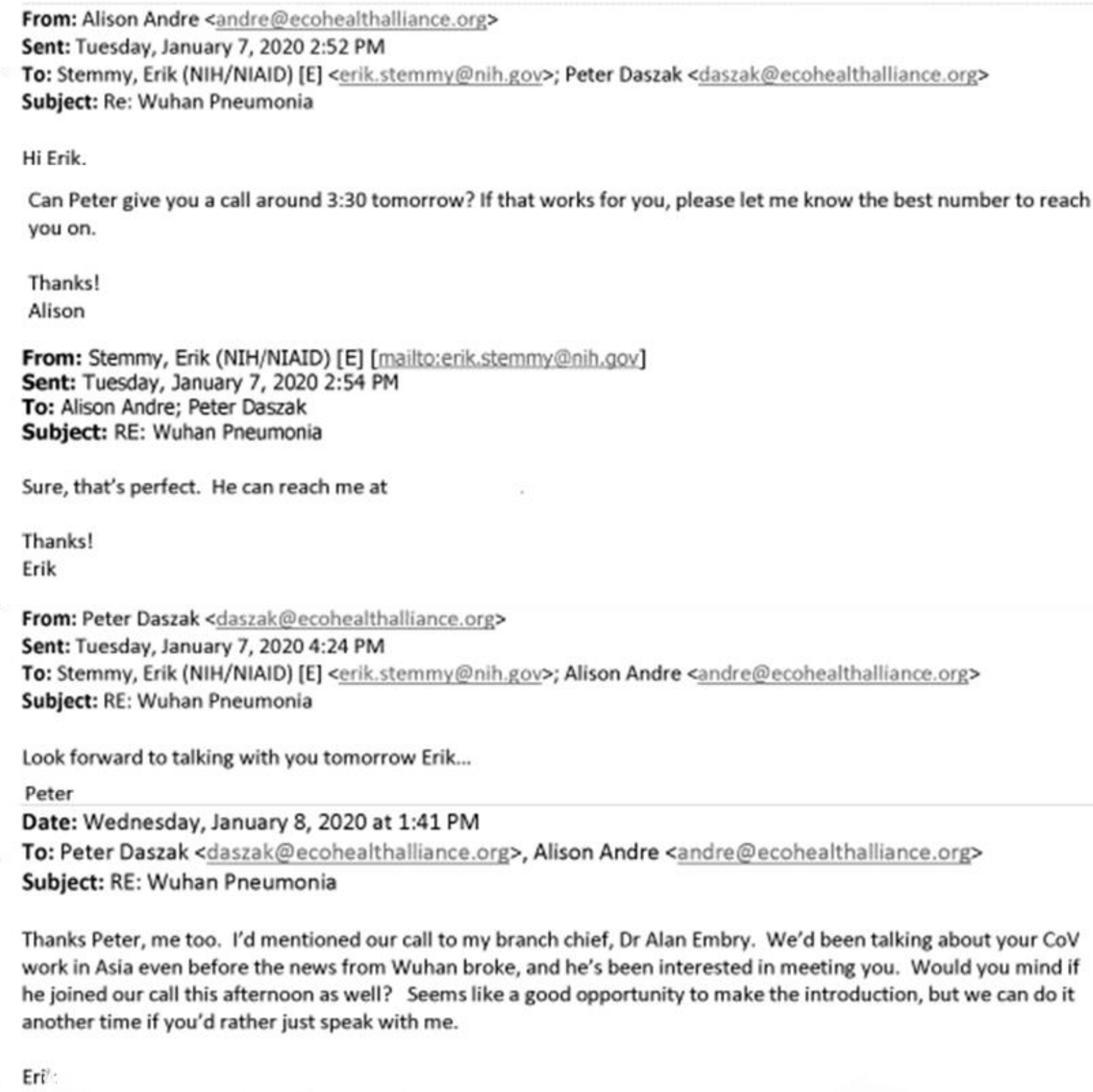
I've got more information, but it's all off the record. Could I give you a call tomorrow to fill you in? I've cc'd Alison Andre who can arrange a time that works for a quick call....

Peter

From: "Stemmy, Erik (NIH/NIAID) [E]" <erik.stemmy@nih.gov>
Date: Peter ay, January 7, 2020 at 2:49 PM
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

That would be great! Thank you for getting back to me. I wasn't sure if you were traveling or not, so I'd also reached out to Aleksei. I can be pretty flexible tomorrow, so just let me know what time works for you.

Very much appreciate your time!
Erik



From: Alison Andre <andre@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 2:52 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: Wuhan Pneumonia

Hi Erik.

Can Peter give you a call around 3:30 tomorrow? If that works for you, please let me know the best number to reach you on.

Thanks!
Alison

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Tuesday, January 7, 2020 2:54 PM
To: Alison Andre; Peter Daszak
Subject: RE: Wuhan Pneumonia

Sure, that's perfect. He can reach me at

Thanks!
Erik

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 4:24 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

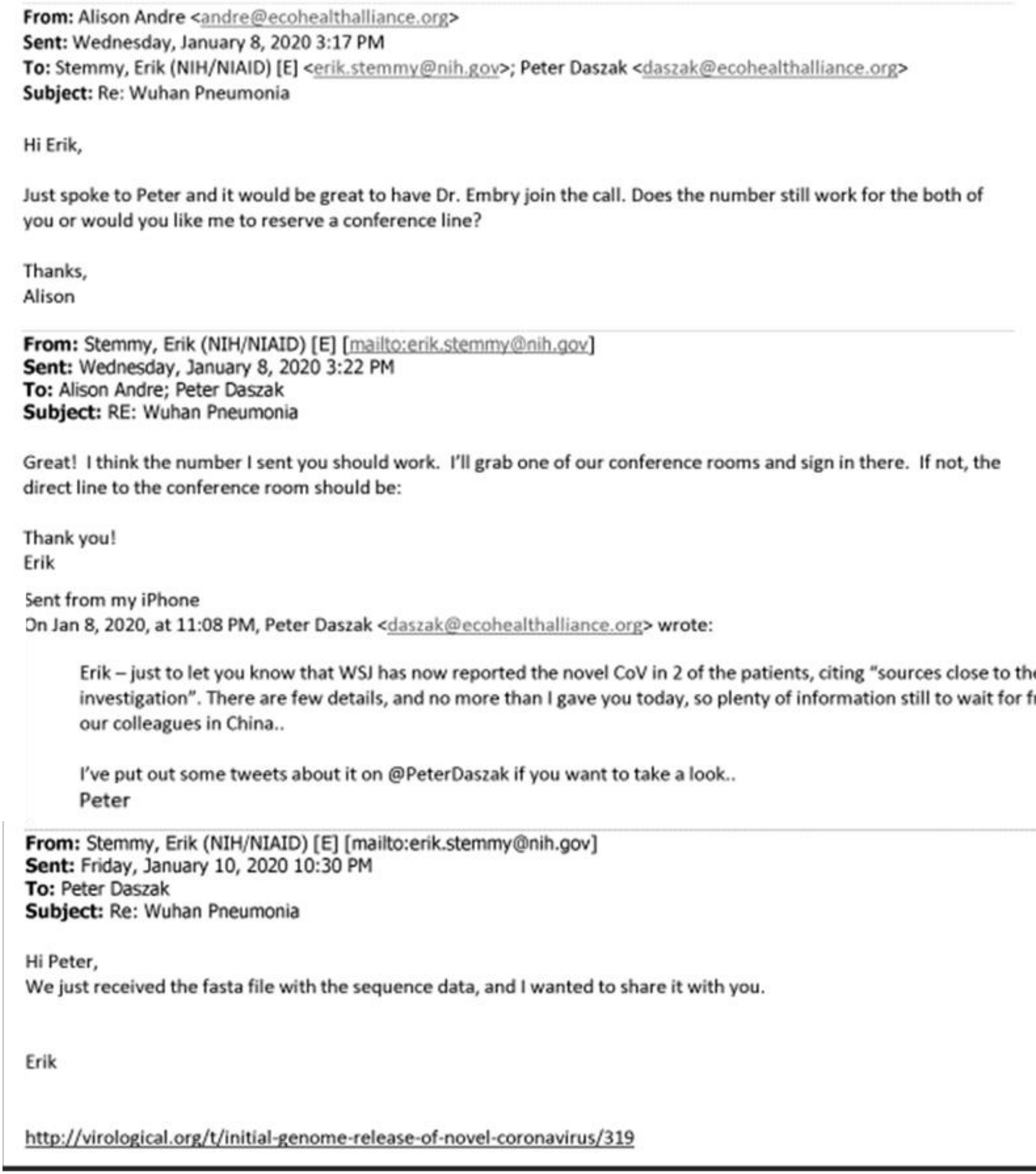
Look forward to talking with you tomorrow Erik...

Peter

Date: Wednesday, January 8, 2020 at 1:41 PM
To: Peter Daszak <daszak@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

Thanks Peter, me too. I'd mentioned our call to my branch chief, Dr Alan Embry. We'd been talking about your CoV work in Asia even before the news from Wuhan broke, and he's been interested in meeting you. Would you mind if he joined our call this afternoon as well? Seems like a good opportunity to make the introduction, but we can do it another time if you'd rather just speak with me.

Erik



From: Alison Andre <andre@ecohealthalliance.org>
Sent: Wednesday, January 8, 2020 3:17 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: Wuhan Pneumonia

Hi Erik,

Just spoke to Peter and it would be great to have Dr. Embry join the call. Does the number still work for the both of you or would you like me to reserve a conference line?

Thanks,
Alison

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Wednesday, January 8, 2020 3:22 PM
To: Alison Andre; Peter Daszak
Subject: RE: Wuhan Pneumonia

Great! I think the number I sent you should work. I'll grab one of our conference rooms and sign in there. If not, the direct line to the conference room should be:

Thank you!
Erik

Sent from my iPhone
On Jan 8, 2020, at 11:08 PM, Peter Daszak <daszak@ecohealthalliance.org> wrote:

> Erik – just to let you know that WSJ has now reported the novel CoV in 2 of the patients, citing "sources close to th investigation". There are few details, and no more than I gave you today, so plenty of information still to wait for fr our colleagues in China..
>
> I've put out some tweets about it on @PeterDaszak if you want to take a look..
> Peter

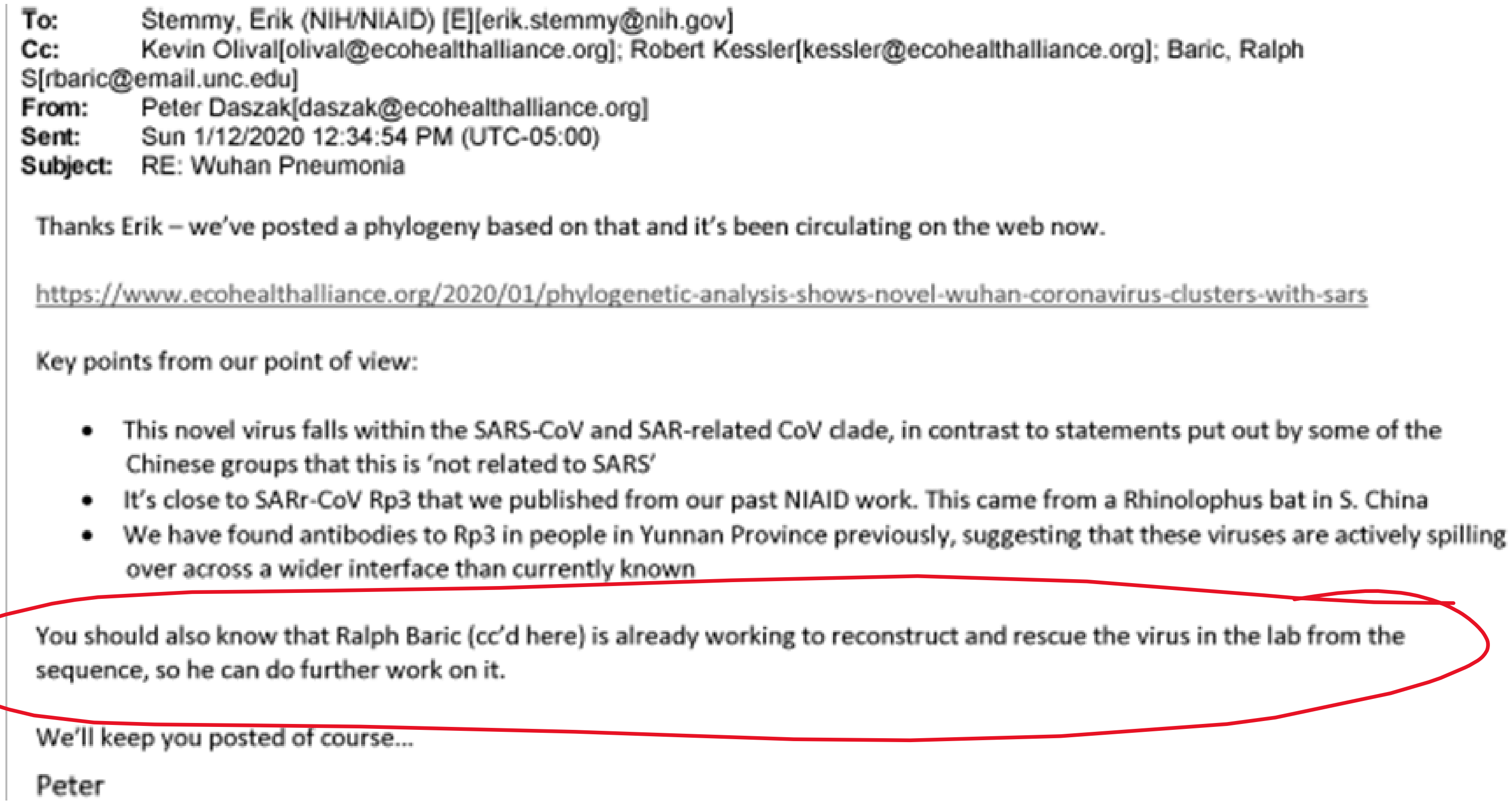
From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Friday, January 10, 2020 10:30 PM
To: Peter Daszak
Subject: Re: Wuhan Pneumonia

Hi Peter,
We just received the fasta file with the sequence data, and I wanted to share it with you.

Erik

http://virological.org/t/initial-genome-release-of-novel-coronavirus/319

Baric already reconstructing for experiments – 1/12/20



To: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Cc: Kevin Olival[olival@ecohealthalliance.org]; Robert Kessler[kessler@ecohealthalliance.org]; Baric, Ralph S[rbaric@email.unc.edu]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Sun 1/12/2020 12:34:54 PM (UTC-05:00)
Subject: RE: Wuhan Pneumonia

Thanks Erik – we've posted a phylogeny based on that and it's been circulating on the web now.

https://www.ecohealthalliance.org/2020/01/phylogenetic-analysis-shows-novel-wuhan-coronavirus-clusters-with-sars

Key points from our point of view:

- This novel virus falls within the SARS-CoV and SAR-related CoV clade, in contrast to statements put out by some of the Chinese groups that this is 'not related to SARS'
- It's close to SARr-CoV Rp3 that we published from our past NIAID work. This came from a Rhinolophus bat in S. China
- We have found antibodies to Rp3 in people in Yunnan Province previously, suggesting that these viruses are actively spilling over across a wider interface than currently known

You should also know that Ralph Baric (cc'd here) is already working to reconstruct and rescue the virus in the lab from the sequence, so he can do further work on it.

We'll keep you posted of course...

Peter

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; 'adolfo.garcia-sastre@mssm.edu'[adolfo.garcia-sastre@mssm.edu]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S. (apekosz@jhsph.edu)[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schult Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'[david_topham@urmc.rochester.edu]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; lsauer2@jhmi.edu[lsauer2@jhmi.edu]
Cc: Ryan Camping[ryan.camping@mssm.edu]; Melissa Uccellini[melissa.uccellini@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Collins, Erin-Joi[emcneal@emory.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]
From: Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]
Sent: Mon 1/13/2020 1:52:50 PM (UTC-05:00)
Subject: RE: Wuhan Pneumonia response

Wuhan Pneumonia response
Tue, Jan 14, 2020 10:00 AM - 11:00 AM (EST)

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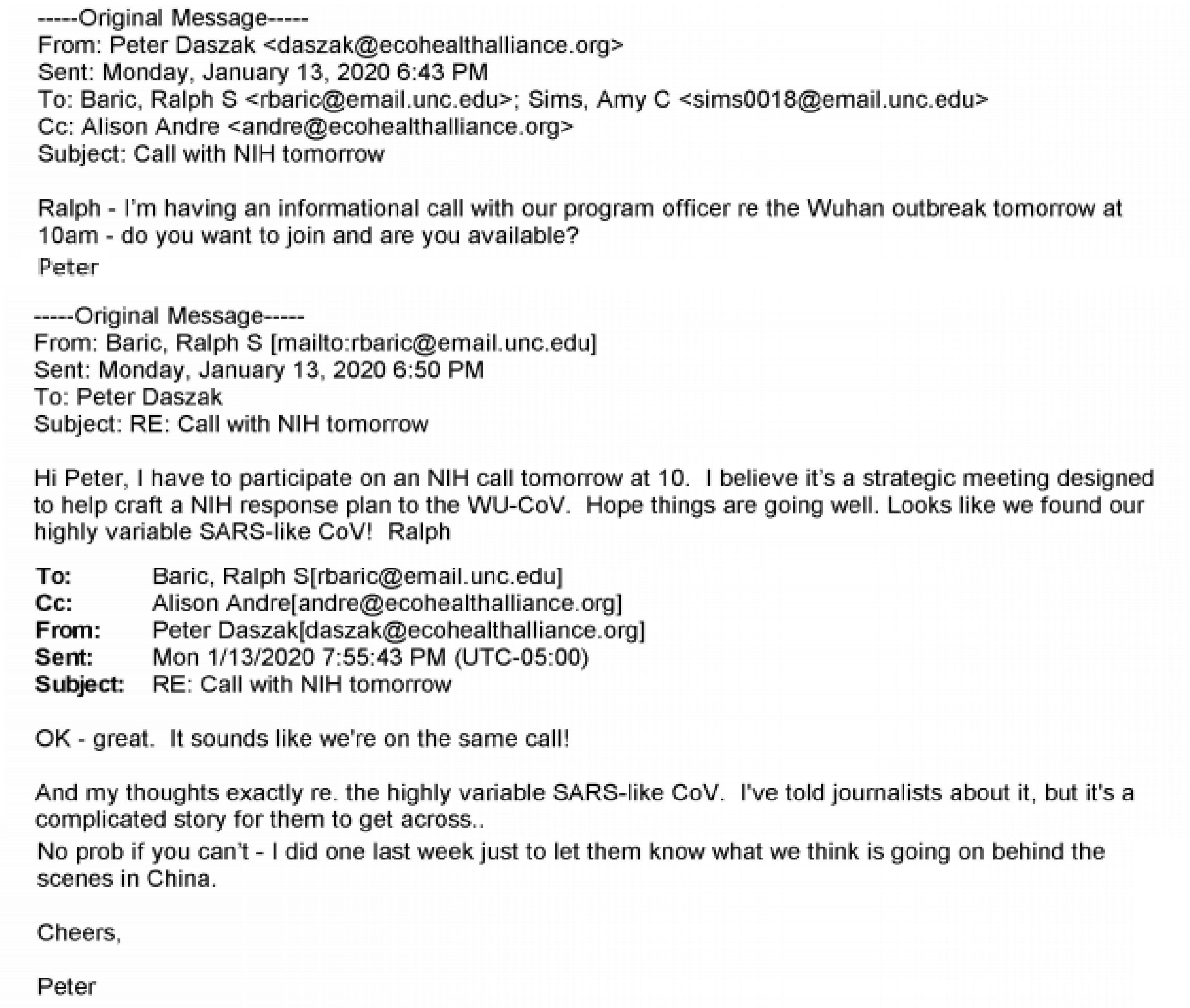

-----Original Message-----
From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, January 13, 2020 6:43 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Sims, Amy C <sims0018@email.unc.edu>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: Call with NIH tomorrow

Ralph - I'm having an informational call with our program officer re the Wuhan outbreak tomorrow at 10am - do you want to join and are you available?
Peter

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Subject: RE: Call with NIH tomorrow

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To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Alison Andre[andre@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Mon 1/13/2020 7:55:43 PM (UTC-05:00)
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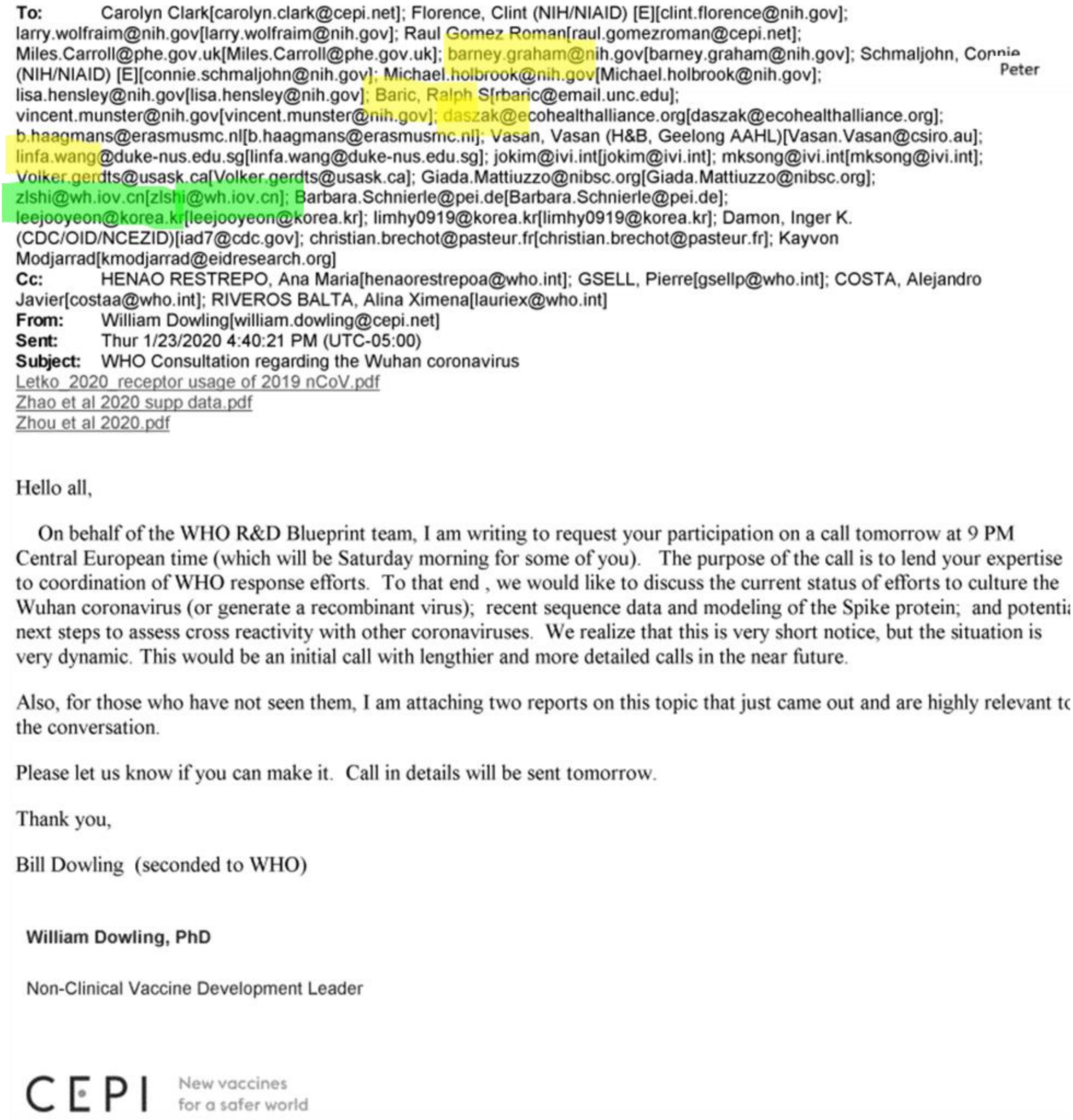
Cheers,

Peter



To: Carolyn Clark[carolyn.clark@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; Raul Gomez Roman[raul.gomezroman@cepi.net]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; barney.graham@nih.gov[barney.graham@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot@pasteur.fr[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]

Peter

Cc: HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]

From: William Dowling[william.dowling@cepi.net]

Sent: Thur 1/23/2020 4:40:21 PM (UTC-05:00)

Subject: WHO Consultation regarding the Wuhan coronavirus

Letko_2020_receptor usage of 2019 nCoV.pdf

Zhao et al 2020 supp data.pdf

Zhou et al 2020.pdf

Hello all,

On behalf of the WHO R&D Blueprint team, I am writing to request your participation on a call tomorrow at 9 PM Central European time (which will be Saturday morning for some of you). The purpose of the call is to lend your expertise to coordination of WHO response efforts. To that end , we would like to discuss the current status of efforts to culture the Wuhan coronavirus (or generate a recombinant virus); recent sequence data and modeling of the Spike protein; and potenti next steps to assess cross reactivity with other coronaviruses. We realize that this is very short notice, but the situation is very dynamic. This would be an initial call with lengthier and more detailed calls in the near future.

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Thank you,

Bill Dowling (seconded to WHO)

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; adolfo.garcia-sastre@mssm.edu; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. (apekosz@jhsph.edu) <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@STJUDE.ORG>; david_topham@urmc.rochester.edu; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>
Cc: ryan.camping@mssm.edu; Melissa Uccellini <melissa.uccellini@mssm.edu>; McKenzie, Pamela <Pamela.McKenzie@STJUDE.ORG>; Neu, Donna <Donna_Neu@URMC.Rochester.edu>; Kathryn Shaw-Saliba <kshaw15@jhu.edu>; Collins, Erin-Joi <emcneal@emory.edu>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Lampley, Rebecca (NIH/VRC) [F] <rebecca.lampley@nih.gov>
Subject: Wuhan Pneumonia response - setting up a call
Importance: High

Hi all,

As you all have heard, China is reporting a novel coronavirus is causing viral pneumonia in Wuhan. While we have very little information at this point, NIAID leadership would like to begin thinking about how we would perform a research response should the outbreak continue and we get access to samples. We would like to hear what you think would be important research directions to pursue to start as well as the capabilities your groups may have given what is known at the moment. We can also discuss potential resources needed from NIAID by your groups so that we can prepare on this end to help you all if needed.

We will look to add some additional coronavirus experts to the call, and if there's anyone I haven't copied here from CEIRS that you think should be involved, please let me know. We need to move quickly, so the goal is to have a call next week at the time when most people are available.

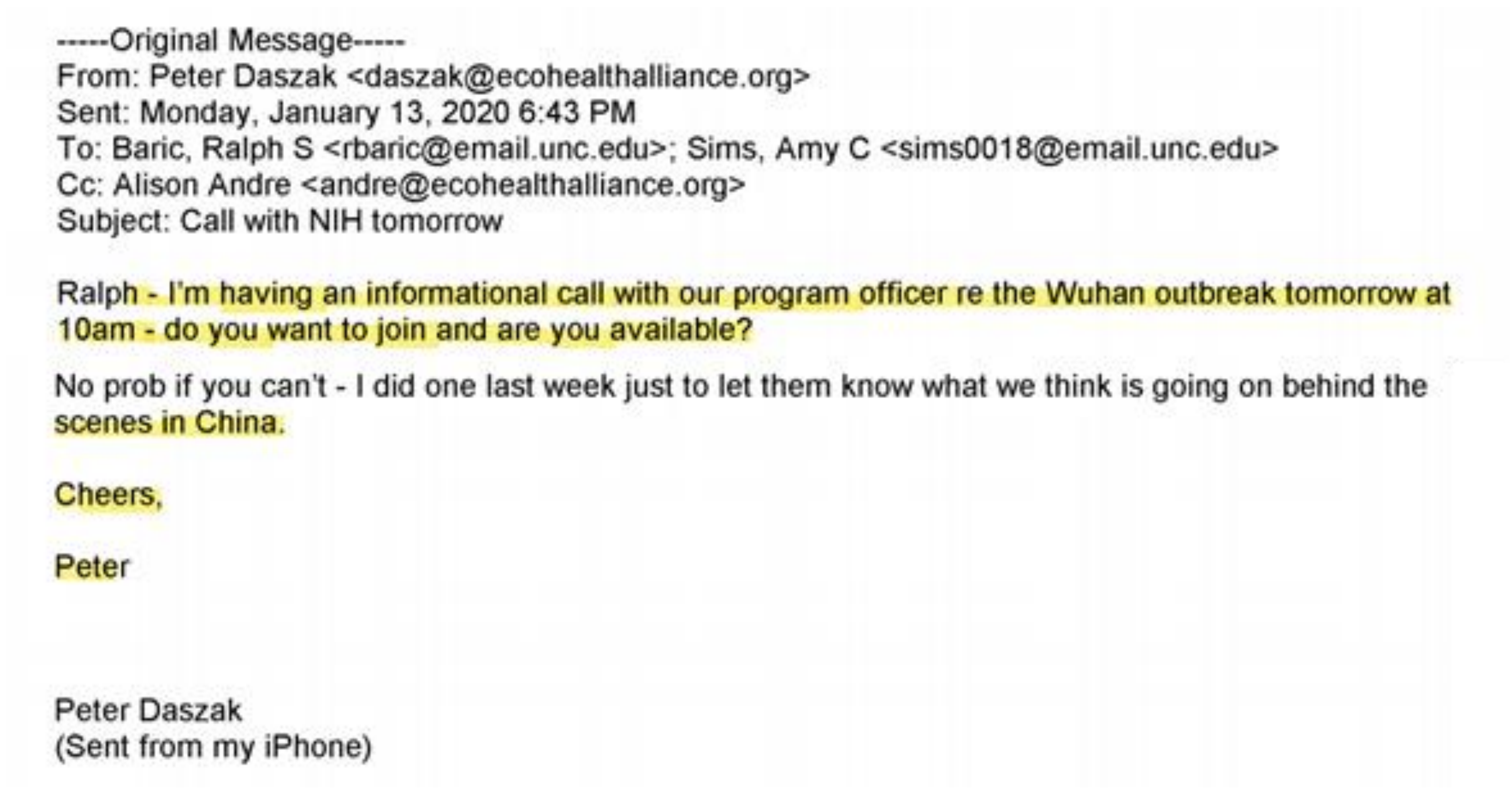
Below is a doodle poll to find a time. Please fill out by the **end of the day tomorrow** so we can schedule a time accordingly.

I know it is already such a busy time – but I'm hopeful since we know the drill for these sorts of things that preparing now will help us.

Thank you all, and looking forward to getting your feedback and input.

Marciela

(Coordinators – this is FYI only and for scheduling, you don't have to be on the call)



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From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, January 13, 2020 6:43 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Sims, Amy C <sims0018@email.unc.edu>
Cc: Alison Andre <andre@ecohealthalliance.org>
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Cheers,

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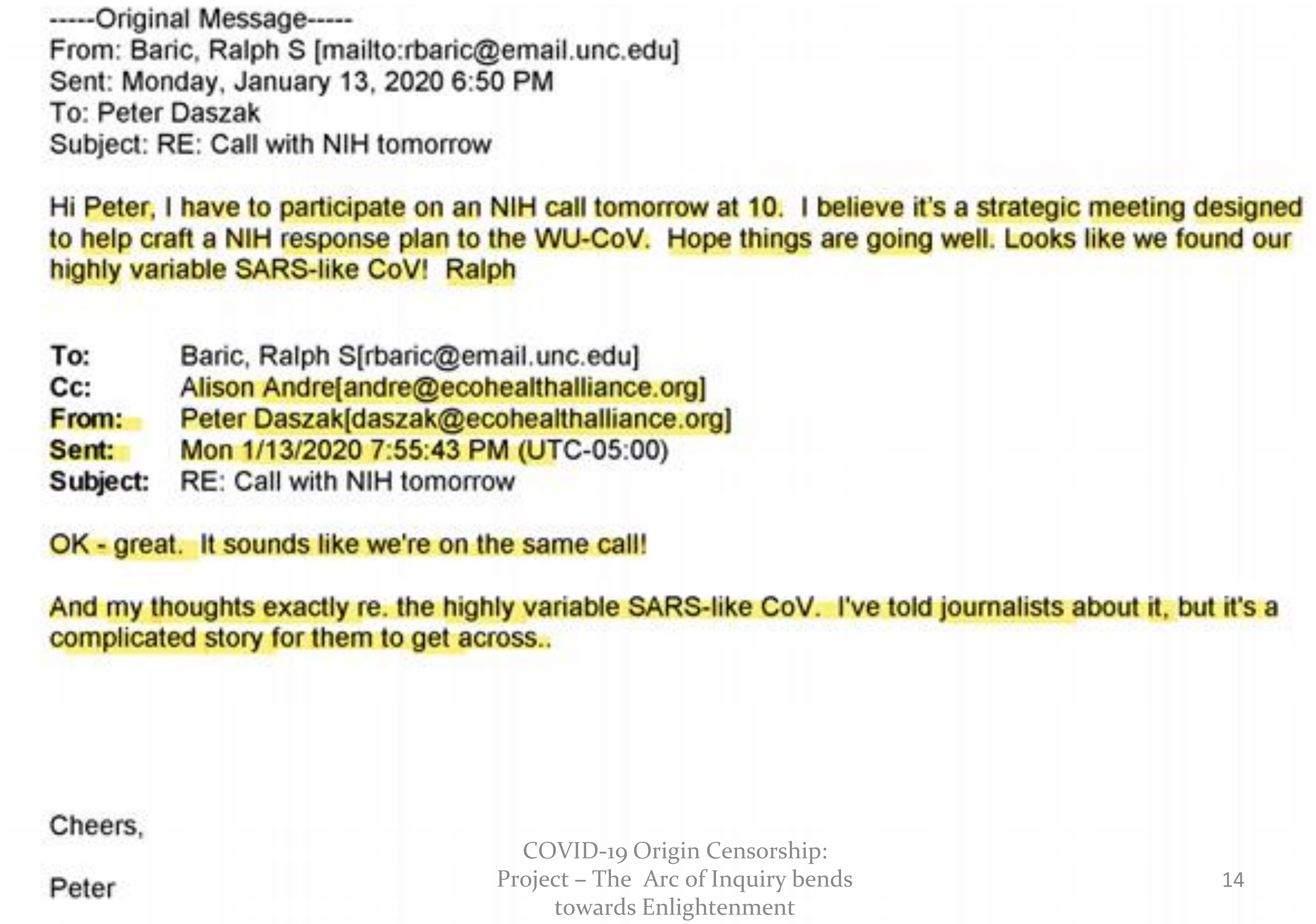
Peter Daszak
(Sent from my iPhone)



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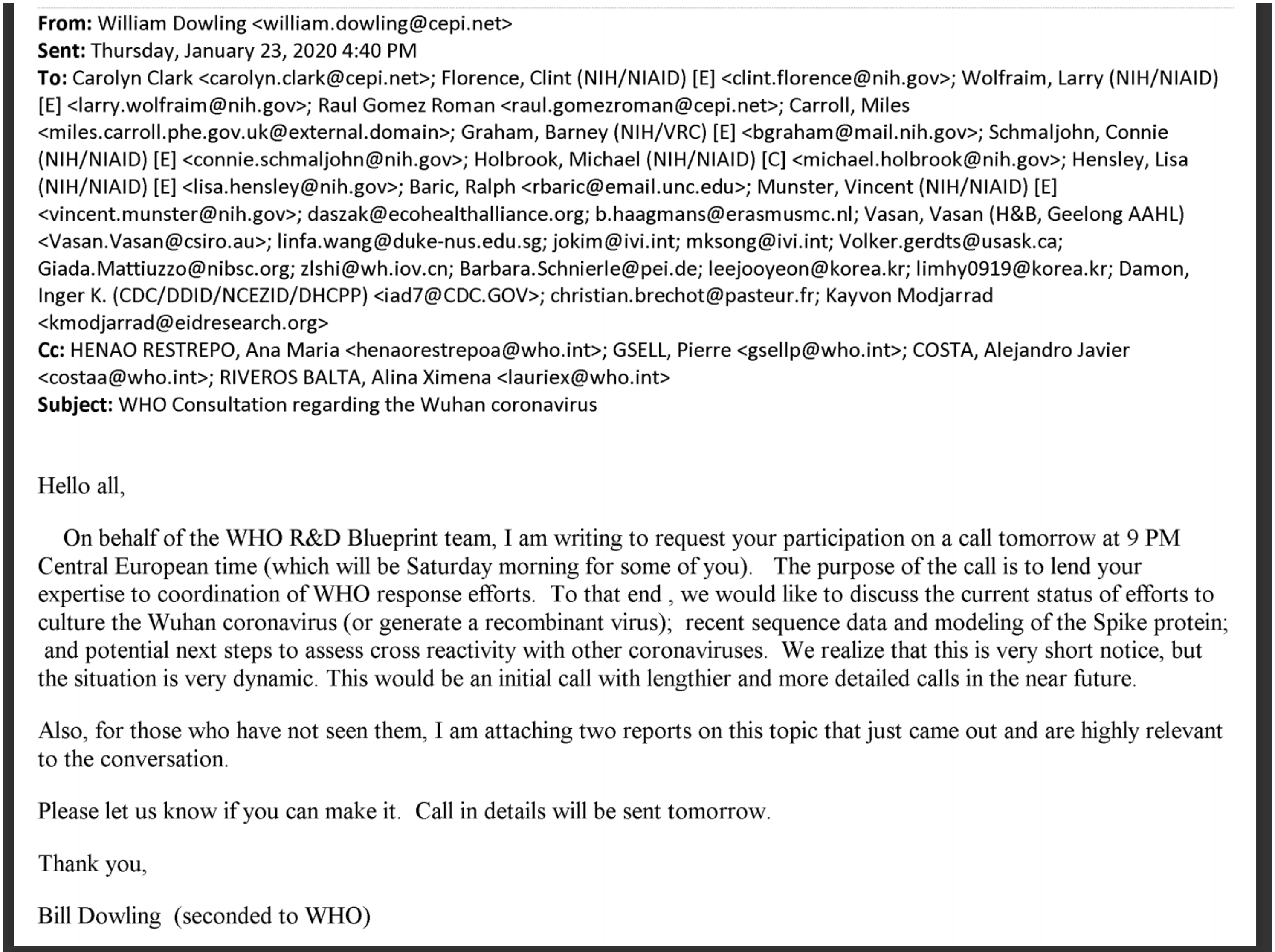

From: William Dowling <william.dowling@cepi.net>
Sent: Thursday, January 23, 2020 4:40 PM
To: Carolyn Clark <carolyn.clark@cepi.net>; Florence, Clint (NIH/NIAID) [E] <clint.florence@nih.gov>; Wolfraim, Larry (NIH/NIAID) [E] <larry.wolfraim@nih.gov>; Raul Gomez Roman <raul.gomezroman@cepi.net>; Carroll, Miles <miles.carroll.phe.gov.uk@external.domain>; Graham, Barney (NIH/VRC) [E] <bgraham@mail.nih.gov>; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Holbrook, Michael (NIH/NIAID) [C] <michael.holbrook@nih.gov>; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; Baric, Ralph <rbaric@email.unc.edu>; Munster, Vincent (NIH/NIAID) [E] <vincent.munster@nih.gov>; daszak@ecohealthalliance.org; b.haagmans@erasmusmc.nl; Vasan, Vasan (H&B, Geelong AAHL) <Vasan.Vasan@csiro.au>; linfa.wang@duke-nus.edu.sg; jokim@ivi.int; mksong@ivi.int; Volker.gerdts@usask.ca; Giada.Mattiuzzo@nibsc.org; zlshi@wh.iov.cn; Barbara.Schnierle@pei.de; leejooyeon@korea.kr; limhy0919@korea.kr; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP) <iad7@CDC.GOV>; christian.brechot@pasteur.fr; Kayvon Modjarrad <kmodjarrad@eidresearch.org>
Cc: HENAO RESTREPO, Ana Maria <henaorestrepoa@who.int>; GSELL, Pierre <gsellp@who.int>; COSTA, Alejandro Javier <costaa@who.int>; RIVEROS BALTA, Alina Ximena <lauriex@who.int>
Subject: WHO Consultation regarding the Wuhan coronavirus

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Thank you,

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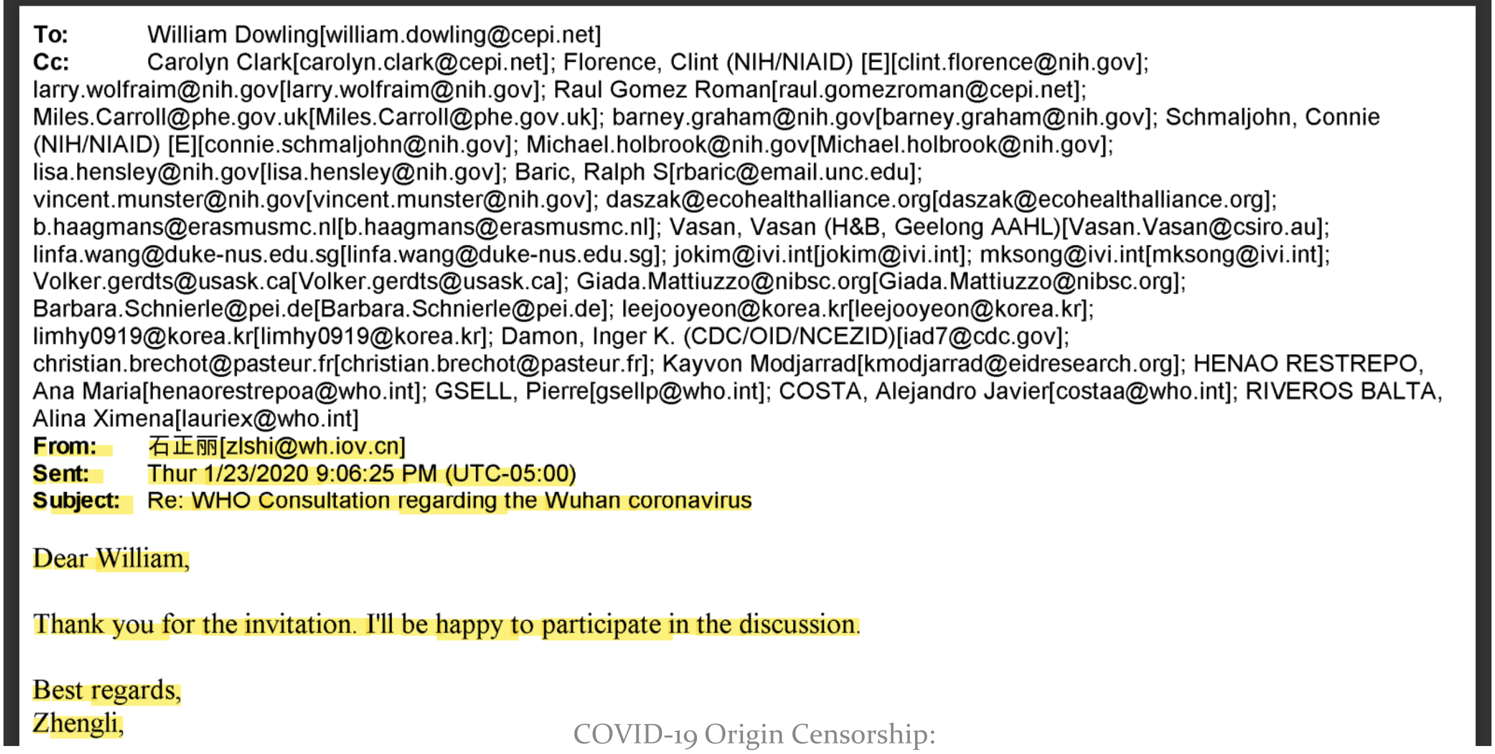
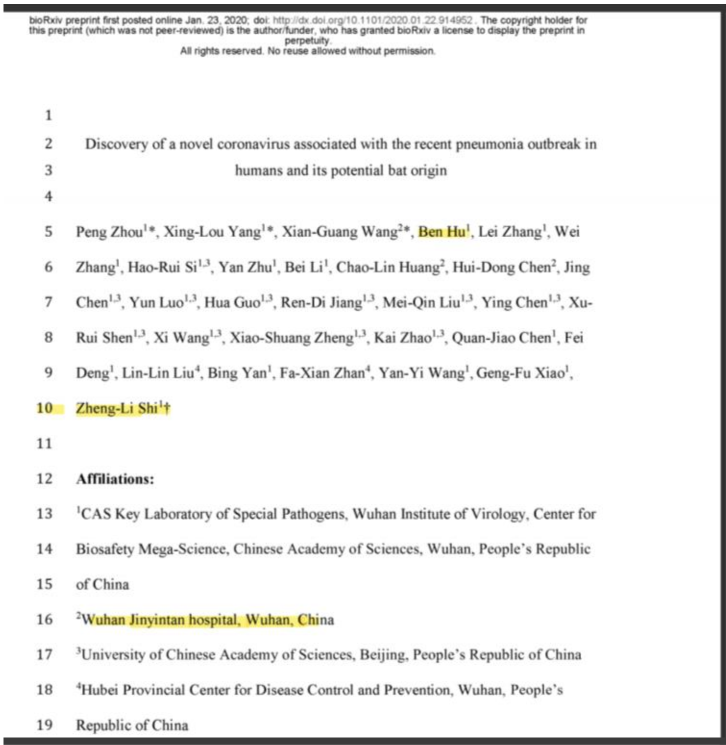


To: William Dowling[william.dowling@cepi.net]
Cc: Carolyn Clark[carolyn.clark@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; Raul Gomez Roman[raul.gomezroman@cepi.net]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; barney.graham@nih.gov[barney.graham@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot@pasteur.fr[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]
From: 石正丽[zlshi@wh.iov.cn]
Sent: Thur 1/23/2020 9:06:25 PM (UTC-05:00)
Subject: Re: WHO Consultation regarding the Wuhan coronavirus

Dear William,

Thank you for the invitation. I'll be happy to participate in the discussion.

Best regards,
Zhengli,



Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin

Peng Zhou[1]*, Xing-Lou Yang[1]*, Xian-Guang Wang[2]*, Ben Hu[1], Lei Zhang[1], Wei Zhang[1], Hao-Rui Si[1,3], Yan Zhu[1], Bei Li[1], Chao-Lin Huang[2], Hui-Dong Chen[2], Jing Chen[1,3], Yun Luo[1,3], Hua Guo[1,3], Ren-Di Jiang[1,3], Mei-Qin Liu[1,3], Ying Chen[1,3], Xu-Rui Shen[1,3], Xi Wang[1,3], Xiao-Shuang Zheng[1,3], Kai Zhao[1,3], Quan-Jiao Chen[1], Fei Deng[1], Lin-Lin Liu[4], Bing Yan[1], Fa-Xian Zhan[4], Yan-Yi Wang[1], Geng-Fu Xiao[1], Zheng-Li Shi[1]†

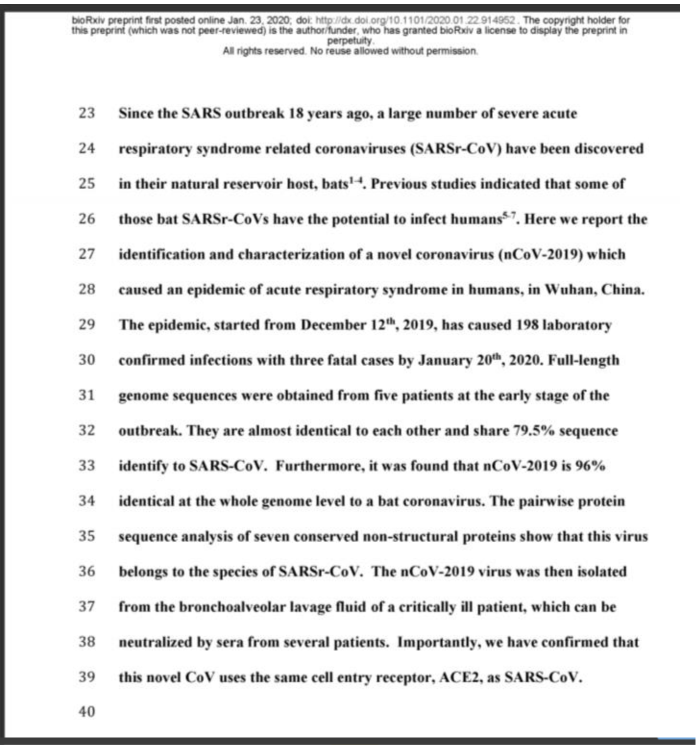
Affiliations:

[1]CAS Key Laboratory of Special Pathogens, Wuhan Institute of Virology, Center for Biosafety Mega-Science, Chinese Academy of Sciences, Wuhan, People's Republic of China

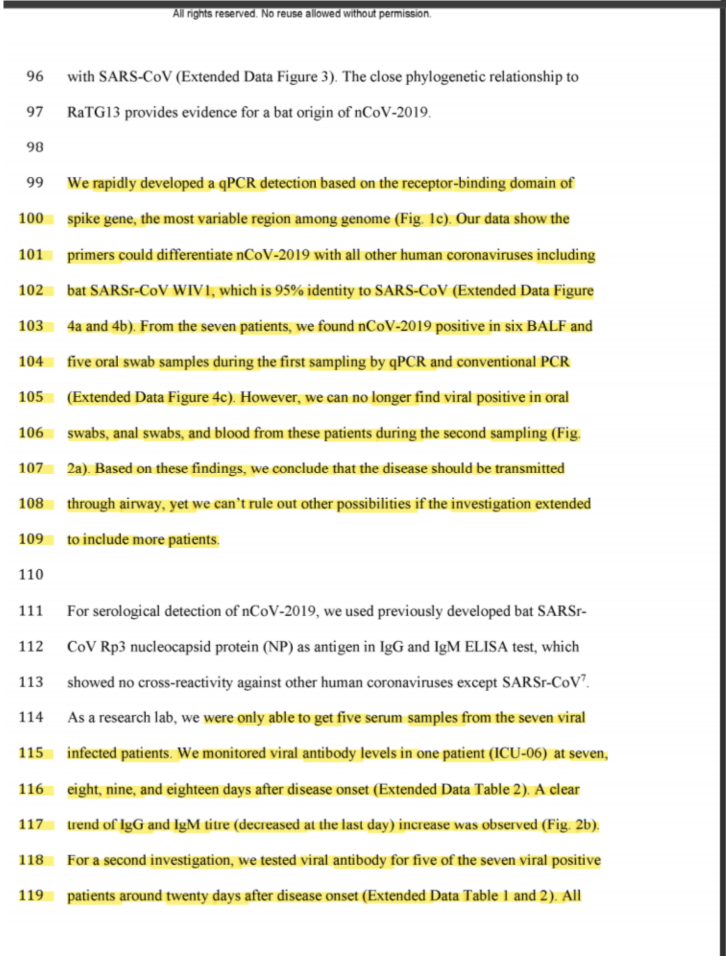
[2]Wuhan Jinyintan hospital, Wuhan, China

[3]University of Chinese Academy of Sciences, Beijing, People's Republic of China

[4]Hubei Provincial Center for Disease Control and Prevention, Wuhan, People's Republic of China



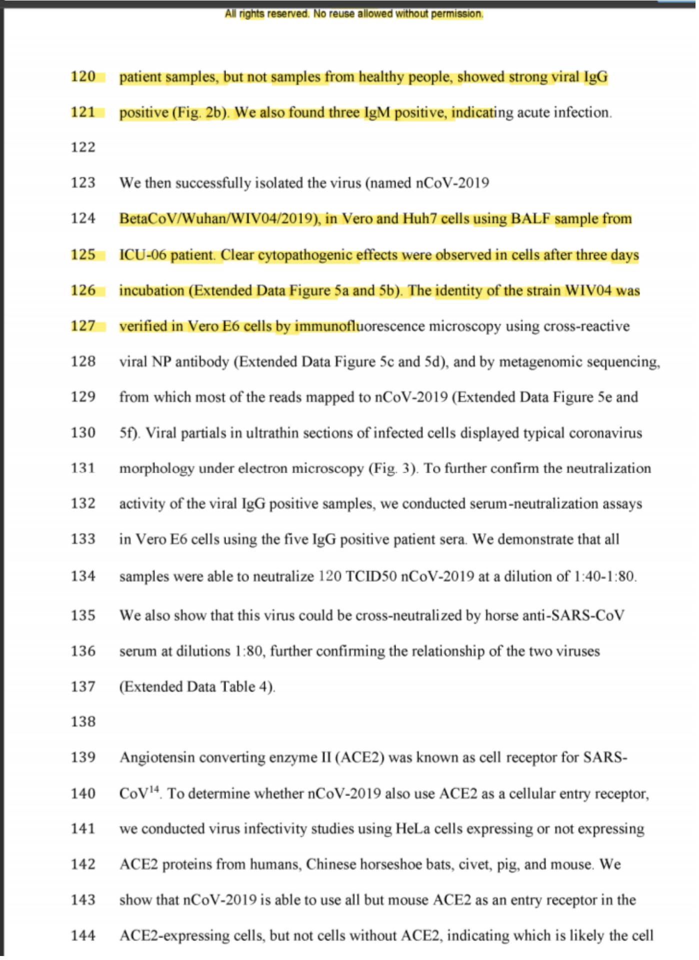
Since the SARS outbreak 18 years ago, a large number of severe acute respiratory syndrome related coronaviruses (SARSr-CoV) have been discovered in their natural reservoir host, bats[1-4]. Previous studies indicated that some of those bat SARSr-CoVs have the potential to infect humans[5-7]. Here we report the identification and characterization of a novel coronavirus (nCoV-2019) which caused an epidemic of acute respiratory syndrome in humans, in Wuhan, China. The epidemic, started from December 12th, 2019, has caused 198 laboratory confirmed infections with three fatal cases by January 20th, 2020. Full-length genome sequences were obtained from five patients at the early stage of the outbreak. They are almost identical to each other and share 79.5% sequence identify to SARS-CoV. Furthermore, it was found that nCoV-2019 is 96% identical at the whole genome level to a bat coronavirus. The pairwise protein sequence analysis of seven conserved non-structural proteins show that this virus belongs to the species of SARSr-CoV. The nCoV-2019 virus was then isolated from the bronchoalveolar lavage fluid of a critically ill patient, which can be neutralized by sera from several patients. Importantly, we have confirmed that this novel CoV uses the same cell entry receptor, ACE2, as SARS-CoV.



with SARS-CoV (Extended Data Figure 3). The close phylogenetic relationship to RaTG13 provides evidence for a bat origin of nCoV-2019.

We rapidly developed a qPCR detection based on the receptor-binding domain of spike gene, the most variable region among genome (Fig. 1c). Our data show the primers could differentiate nCoV-2019 with all other human coronaviruses including bat SARSr-CoV WIV1, which is 95% identity to SARS-CoV (Extended Data Figure 4a and 4b). From the seven patients, we found nCoV-2019 positive in six BALF and five oral swab samples during the first sampling by qPCR and conventional PCR (Extended Data Figure 4c). However, we can no longer find viral positive in oral swabs, anal swabs, and blood from these patients during the second sampling (Fig. 2a). Based on these findings, we conclude that the disease should be transmitted through airway, yet we can't rule out other possibilities if the investigation extended to include more patients.

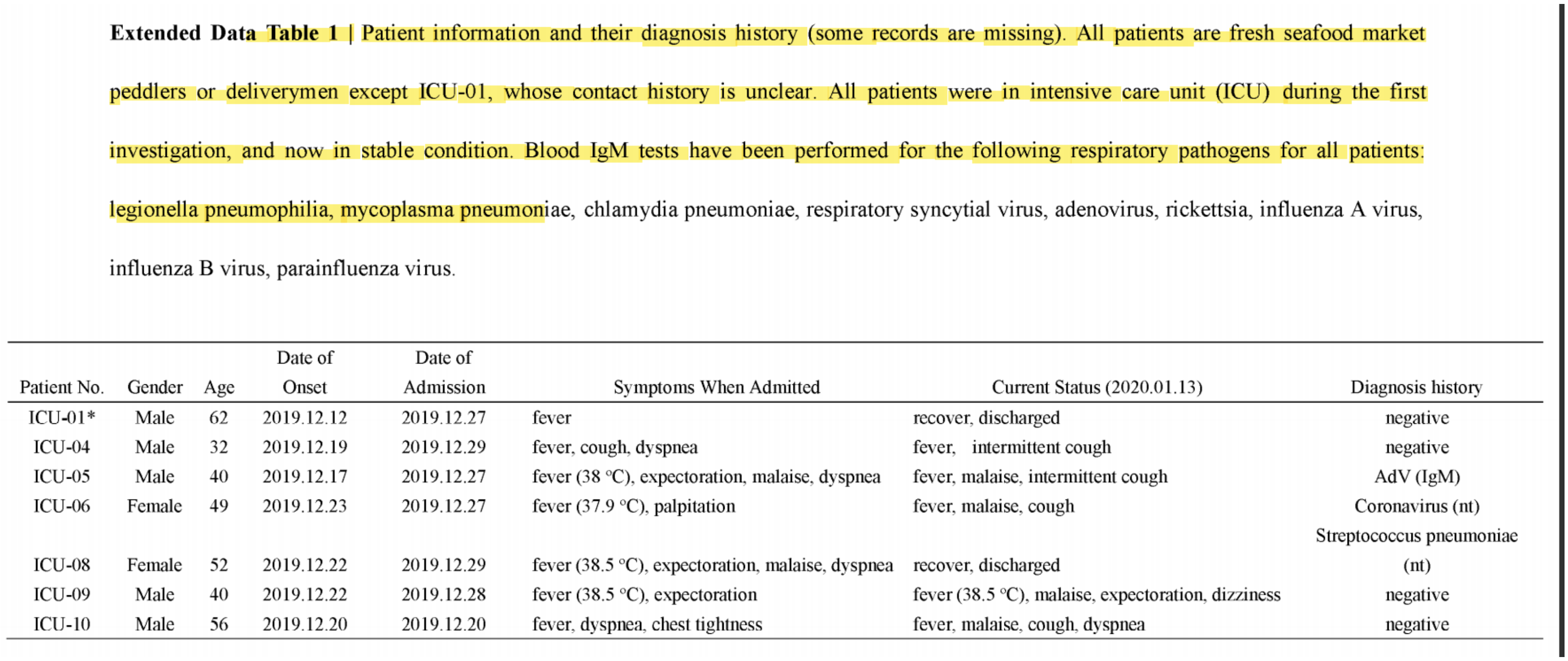
For serological detection of nCoV-2019, we used previously developed bat SARSr-CoV Rp3 nucleocapsid protein (NP) as antigen in IgG and IgM ELISA test, which showed no cross-reactivity against other human coronaviruses except SARSr-CoV[7]. As a research lab, we were only able to get five serum samples from the seven viral infected patients. We monitored viral antibody levels in one patient (ICU-06) at seven, eight, nine, and eighteen days after disease onset (Extended Data Table 2). A clear trend of IgG and IgM titre (decreased at the last day) increase was observed (Fig. 2b). For a second investigation, we tested viral antibody for five of the seven viral positive patients around twenty days after disease onset (Extended Data Table 1 and 2). All



patient samples, but not samples from healthy people, showed strong viral IgG positive (Fig. 2b). We also found three IgM positive, indicating acute infection.

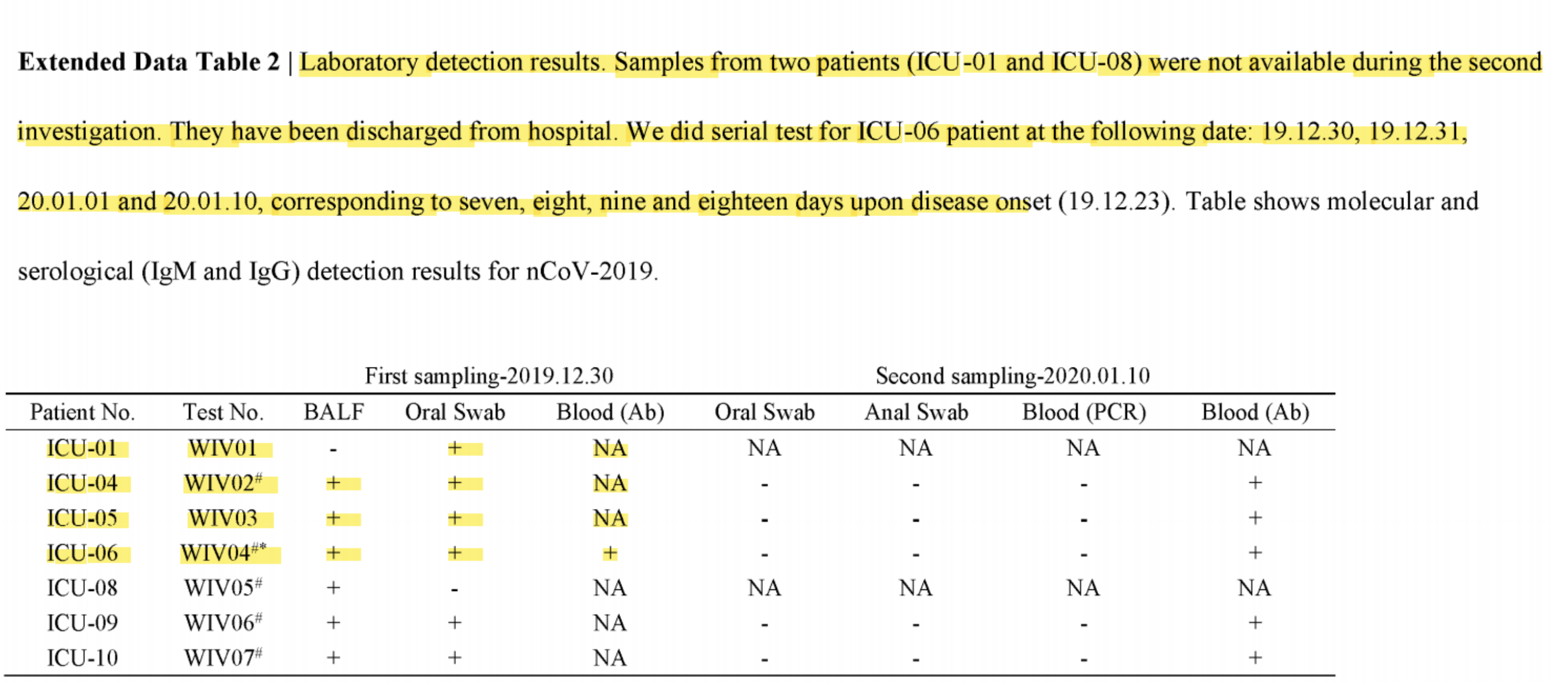
We then successfully isolated the virus (named nCoV-2019 BetaCoV/Wuhan/WIV04/2019), in Vero and Huh7 cells using BALF sample from ICU-06 patient. Clear cytopathogenic effects were observed in cells after three days incubation (Extended Data Figure 5a and 5b). The identity of the strain WIV04 was verified in Vero E6 cells by immunofluorescence microscopy using cross-reactive viral NP antibody (Extended Data Figure 5c and 5d), and by metagenomic sequencing, from which most of the reads mapped to nCoV-2019 (Extended Data Figure 5e and 5f). Viral partials in ultrathin sections of infected cells displayed typical coronavirus morphology under electron microscopy (Fig. 3). To further confirm the neutralization activity of the viral IgG positive samples, we conducted serum-neutralization assays in Vero E6 cells using the five IgG positive patient sera. We demonstrate that all samples were able to neutralize 120 TCID50 nCoV-2019 at a dilution of 1:40-1:80. We also show that this virus could be cross-neutralized by horse anti-SARS-CoV serum at dilutions 1:80, further confirming the relationship of the two viruses (Extended Data Table 4).

Angiotensin converting enzyme II (ACE2) was known as cell receptor for SARS-CoV[14]. To determine whether nCoV-2019 also use ACE2 as a cellular entry receptor, we conducted virus infectivity studies using HeLa cells expressing or not expressing ACE2 proteins from humans, Chinese horseshoe bats, civet, pig, and mouse. We show that nCoV-2019 is able to use all but mouse ACE2 as an entry receptor in the ACE2-expressing cells, but not cells without ACE2, indicating which is likely the cell



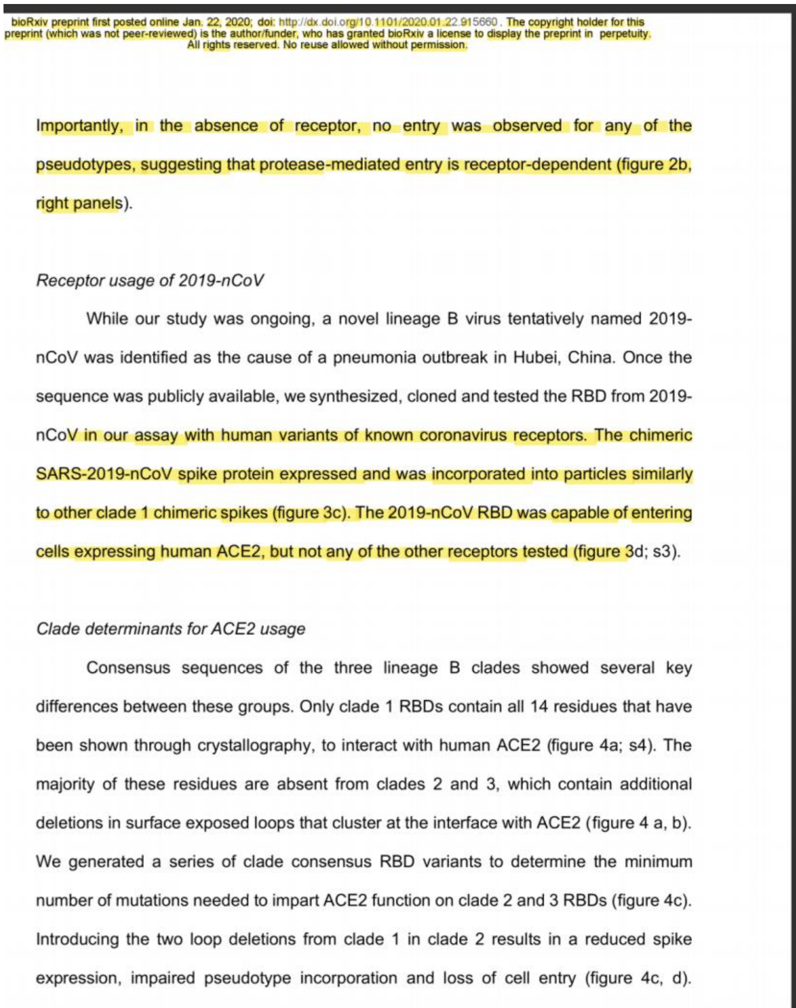
Extended Data Table 1 | Patient information and their diagnosis history (some records are missing). All patients are fresh seafood market peddlers or deliverymen except ICU-01, whose contact history is unclear. All patients were in intensive care unit (ICU) during the first investigation, and now in stable condition. Blood IgM tests have been performed for the following respiratory pathogens for all patients: legionella pneumophilia, mycoplasma pneumoniae, chlamydia pneumoniae, respiratory syncytial virus, adenovirus, rickettsia, influenza A virus, influenza B virus, parainfluenza virus.

Patient No.	Gender	Age	Date of Onset	Date of Admission	Symptoms When Admitted	Current Status (2020.01.13)	Diagnosis history
ICU-01*	Male	62	2019.12.12	2019.12.27	fever	recover, discharged	negative
ICU-04	Male	32	2019.12.19	2019.12.29	fever, cough, dyspnea	fever, intermittent cough	negative
ICU-05	Male	40	2019.12.17	2019.12.27	fever (38 °C), expectoration, malaise, dyspnea	fever, malaise, intermittent cough	AdV (IgM)
ICU-06	Female	49	2019.12.23	2019.12.27	fever (37.9 °C), palpitation	fever, malaise, cough	Coronavirus (nt)
ICU-08	Female	52	2019.12.22	2019.12.29	fever (38.5 °C), expectoration, malaise, dyspnea	recover, discharged	Streptococcus pneumoniae (nt)
ICU-09	Male	40	2019.12.22	2019.12.28	fever (38.5 °C), expectoration	fever (38.5 °C), malaise, expectoration, dizziness	negative
ICU-10	Male	56	2019.12.20	2019.12.20	fever, dyspnea, chest tightness	fever, malaise, cough, dyspnea	negative



Extended Data Table 2 | Laboratory detection results. Samples from two patients (ICU-01 and ICU-08) were not available during the second investigation. They have been discharged from hospital. We did serial test for ICU-06 patient at the following date: 19.12.30, 19.12.31, 20.01.01 and 20.01.10, corresponding to seven, eight, nine and eighteen days upon disease onset (19.12.23). Table shows molecular and serological (IgM and IgG) detection results for nCoV-2019.

		First sampling-2019.12.30			Second sampling-2020.01.10			
Patient No.	Test No.	BALF	Oral Swab	Blood (Ab)	Oral Swab	Anal Swab	Blood (PCR)	Blood (Ab)
ICU-01	WIV01	-	+	NA	NA	NA	NA	NA
ICU-04	WIV02$^{\#}$	+	+	NA	-	-	-	+
ICU-05	WIV03	+	+	NA	-	-	-	+
ICU-06	WIV04$^{\#*}$	+	+	+	-	-	-	+
ICU-08	WIV05$^{\#}$	+	-	NA	NA	NA	NA	NA
ICU-09	WIV06$^{\#}$	+	+	NA	-	-	-	+
ICU-10	WIV07$^{\#}$	+	+	NA	-	-	-	+



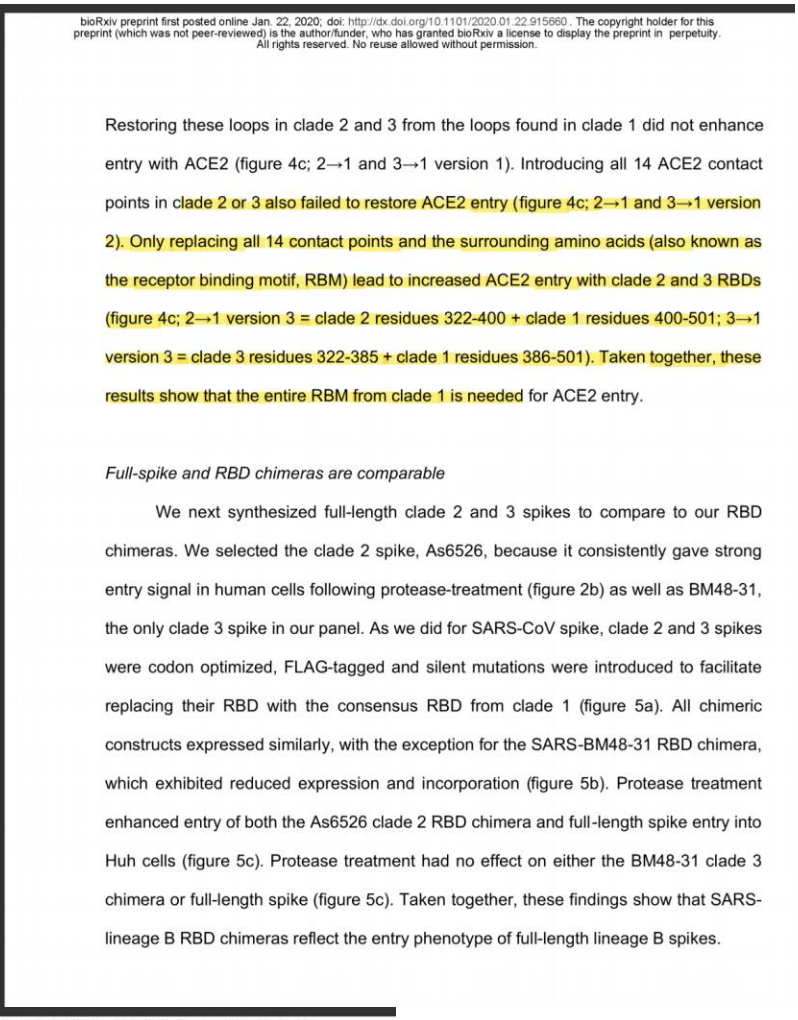
Importantly, in the absence of receptor, no entry was observed for any of the pseudotypes, suggesting that protease-mediated entry is receptor-dependent (figure 2b, right panels).

Receptor usage of 2019-nCoV

While our study was ongoing, a novel lineage B virus tentatively named 2019-nCoV was identified as the cause of a pneumonia outbreak in Hubei, China. Once the sequence was publicly available, we synthesized, cloned and tested the RBD from 2019-nCoV in our assay with human variants of known coronavirus receptors. The chimeric SARS-2019-nCoV spike protein expressed and was incorporated into particles similarly to other clade 1 chimeric spikes (figure 3c). The 2019-nCoV RBD was capable of entering cells expressing human ACE2, but not any of the other receptors tested (figure 3d; s3).

Clade determinants for ACE2 usage

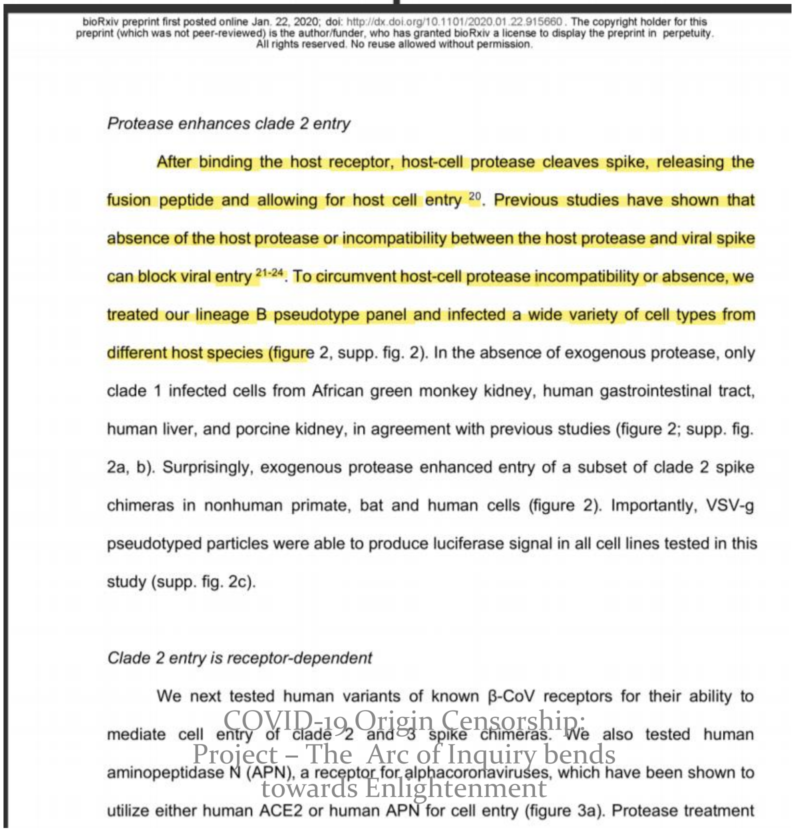
Consensus sequences of the three lineage B clades showed several key differences between these groups. Only clade 1 RBDs contain all 14 residues that have been shown through crystallography, to interact with human ACE2 (figure 4a; s4). The majority of these residues are absent from clades 2 and 3, which contain additional deletions in surface exposed loops that cluster at the interface with ACE2 (figure 4 a, b). We generated a series of clade consensus RBD variants to determine the minimum number of mutations needed to impart ACE2 function on clade 2 and 3 RBDs (figure 4c). Introducing the two loop deletions from clade 1 in clade 2 results in a reduced spike expression, impaired pseudotype incorporation and loss of cell entry (figure 4c, d).



Restoring these loops in clade 2 and 3 from the loops found in clade 1 did not enhance entry with ACE2 (figure 4c; 2→1 and 3→1 version 1). Introducing all 14 ACE2 contact points in clade 2 or 3 also failed to restore ACE2 entry (figure 4c; 2→1 and 3→1 version 2). Only replacing all 14 contact points and the surrounding amino acids (also known as the receptor binding motif, RBM) lead to increased ACE2 entry with clade 2 and 3 RBDs (figure 4c; 2→1 version 3 = clade 2 residues 322-400 + clade 1 residues 400-501; 3→1 version 3 = clade 3 residues 322-385 + clade 1 residues 386-501). Taken together, these results show that the entire RBM from clade 1 is needed for ACE2 entry.

Full-spike and RBD chimeras are comparable

We next synthesized full-length clade 2 and 3 spikes to compare to our RBD chimeras. We selected the clade 2 spike, As6526, because it consistently gave strong entry signal in human cells following protease-treatment (figure 2b) as well as BM48-31, the only clade 3 spike in our panel. As we did for SARS-CoV spike, clade 2 and 3 spikes were codon optimized, FLAG-tagged and silent mutations were introduced to facilitate replacing their RBD with the consensus RBD from clade 1 (figure 5a). All chimeric constructs expressed similarly, with the exception for the SARS-BM48-31 RBD chimera, which exhibited reduced expression and incorporation (figure 5b). Protease treatment enhanced entry of both the As6526 clade 2 RBD chimera and full-length spike entry into Huh cells (figure 5c). Protease treatment had no effect on either the BM48-31 clade 3 chimera or full-length spike (figure 5c). Taken together, these findings show that SARS-lineage B RBD chimeras reflect the entry phenotype of full-length lineage B spikes.



Protease enhances clade 2 entry

After binding the host receptor, host-cell protease cleaves spike, releasing the fusion peptide and allowing for host cell entry [20]. Previous studies have shown that absence of the host protease or incompatibility between the host protease and viral spike can block viral entry [21-24]. To circumvent host-cell protease incompatibility or absence, we treated our lineage B pseudotype panel and infected a wide variety of cell types from different host species (figure 2, supp. fig. 2). In the absence of exogenous protease, only clade 1 infected cells from African green monkey kidney, human gastrointestinal tract, human liver, and porcine kidney, in agreement with previous studies (figure 2; supp. fig. 2a, b). Surprisingly, exogenous protease enhanced entry of a subset of clade 2 spike chimeras in nonhuman primate, bat and human cells (figure 2). Importantly, VSV-g pseudotyped particles were able to produce luciferase signal in all cell lines tested in this study (supp. fig. 2c).

Clade 2 entry is receptor-dependent

We next tested human variants of known β-CoV receptors for their ability to mediate cell entry of clade 2 and 3 spike chimeras. We also tested human aminopeptidase N (APN), a receptor for alphacoronaviruses, which have been shown to utilize either human ACE2 or human APN for cell entry (figure 3a). Protease treatment

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Accelerated Article Preview

A pneumonia outbreak associated with a new coronavirus of probable bat origin

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Open access

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A pneumonia outbreak associated with a new coronavirus of probable bat origin

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Since the SARS outbreak 18 years ago, a large number of severe acute respiratory syndrome-related coronaviruses (SARSr-CoV) have been discovered in their natural reservoir host, bats[1-4]. Previous studies indicated that some of those bat SARSr-CoVs have the potential to infect humans[5-7]. Here we report the identification and characterization of a novel coronavirus (2019-nCoV) which caused an epidemic of acute respiratory syndrome in humans in Wuhan, China. The epidemic, which started from 12 December 2019, has caused 2,050 laboratory-confirmed infections with 56 fatal cases by 26 January 2020. Full-length genome sequences were obtained from five patients at the early stage of the outbreak. They are almost identical to each other and share 79.5% sequence identify to SARS-CoV. Furthermore, it was found that 2019-nCoV is 96% identical at the whole genome level to a bat coronavirus. The pairwise protein sequence analysis of seven conserved non-structural proteins show that this virus belongs to the species of SARSr-CoV. The 2019-nCoV virus was then isolated from the bronchoalveolar lavage fluid of a critically ill patient, which can be neutralized by sera from several patients. Importantly, we have confirmed that this novel CoV uses the same cell entry receptor, ACE2, as SARS-CoV.

Coronavirus has caused two large-scale pandemic in the last two decades, SARS and MERS (Middle East respiratory syndrome)[1-9]. It was generally believed that SARSr-CoV, mainly found in bats, might cause future disease outbreak[10,11]. Here we report on a series of unidentified pneumonia disease outbreaks in Wuhan, Hubei province, central China. Started from a local seafood market, the outbreak has grown substantial to infect 2050 people in China with 56 deaths and to infect 35 people in 11 other countries up to January 26, 2020[12]. Typical clinical symptoms of these patients are fever, dry cough, dyspnea, headache, and pneumonia. Disease onset may result in progressive respiratory failure due to alveolar damage (as observed by transverse chest CT images) and even death. The disease was determined as viral induced pneumonia by clinicians according to clinical symptoms and other criteria including body temperature rising, lymphocytes and white blood cells decreasing (sometimes normal for the later), new pulmonary infiltrates on chest radiography, and no obvious improvement upon three days antibiotics treatment. It appears most of the early cases had contact history with the original seafood market, but the disease progressed to human-to-human transmission now.

Samples from seven patients with severe pneumonia (six are sea - food market sellers or delivers), who were enrolled in intensive unit cares at the beginning of the outbreak, were sent to WIV laboratory for pathogen diagnosis (Extended Data Table 1). As a CoV lab, we first used pan-CoV PCR primers to test these samples[13], considering the outbreak happened in winter and in a market, same environment as SARS. We found five PCR positive. A sample (WIV04) collected from bronchoalveolar lavage fluid (BALF) was analysed by metagenomics analysis using next-generation sequencing (NGS) to identify potential etiological agents. Of the 10,038,758 total reads, or 1582 total reads obtained after human genome filtering, 1378 (87.1%) matched sequences of SARSr-CoV (Fig. 1a). By *de novo* assembly and targeted PCR, we obtained a 29,891-bp CoV genome that shared 79.5% sequence identity to SARS-CoV BJ01 (GenBank accession number AY278488.2). High genome coverage was obtained by remapping the total reads to this genome (Extended Data Figure 1). This sequence has been submitted to GISAID (accession no. EPI_ISL_402124). Following the name by WHO, we tentatively call it novel coronavirus 2019 (2019-nCoV). Four more full-length genome sequences of 2019-nCoV (WIV02, WIV05, WIV06, and WIV07) (GISAID accession nos. EPI_ISL_402127-402130) that were above 99.9% identical to each other were subsequently obtained from other four patients using NGS and PCR (Extended Data Table 2).

The virus genome consists of six major open reading frames (ORFs) common to coronaviruses and a number of other accessory genes (Fig. 1b). Further analysis indicates that some of the 2019-nCoV genes shared less than 80% nt sequence identity to SARS-CoV. However, the seven conserved replicase domains in ORF1ab that were used for

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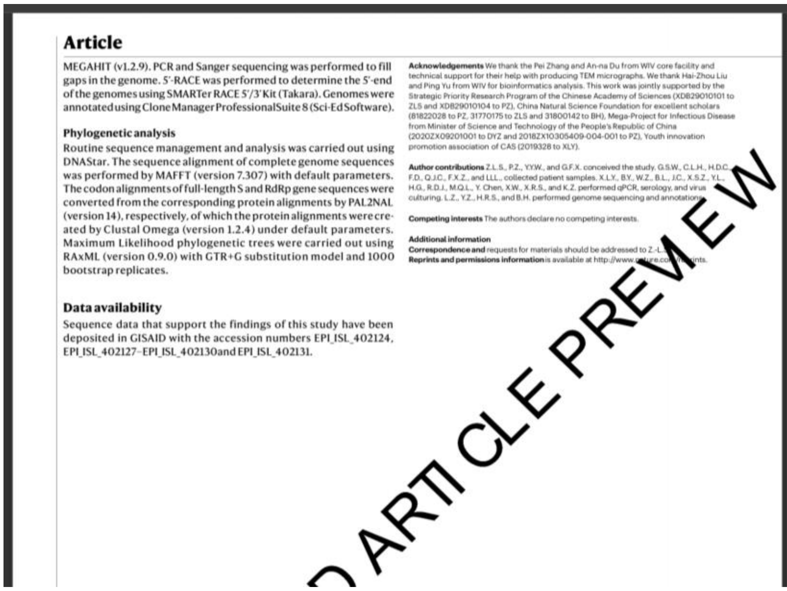

MEGAHIT (v1.2.9). PCR and Sanger sequencing was performed to fill gaps in the genome. 5′-RACE was performed to determine the 5′-end of the genomes using SMARTer RACE 5′/3′ Kit (Takara). Genomes were annotated using Clone Manager Professional Suite 8 (Sci-Ed Software).

Phylogenetic analysis

Routine sequence management and analysis was carried out using DNAStar. The sequence alignment of complete genome sequences was performed by MAFFT (version 7.307) with default parameters. The codon alignments of full-length S and RdRp gene sequences were converted from the corresponding protein alignments by PAL2NAL (version 14), respectively, of which the protein alignments were created by Clustal Omega (version 1.2.4) under default parameters. Maximum Likelihood phylogenetic trees were carried out using RAxML (version 0.9.0) with GTR+G substitution model and 1000 bootstrap replicates.

Data availability

Sequence data that support the findings of this study have been deposited in GISAID with the accession numbers EPI_ISL_402124, EPI_ISL_402127–EPI_ISL_402130 and EPI_ISL_402131.

Acknowledgements We thank the Pei Zhang and An-na Du from WIV core facility and technical support for their help with producing TEM micrographs. We thank Hai-Zhou Liu and Ping Yu from WIV for bioinformatics analysis. This work was jointly supported by the Strategic Priority Research Program of the Chinese Academy of Sciences (XDB29010101 to ZLS and XDB29010104 to PZ), China Natural Science Foundation for excellent scholars (81822028 to PZ, 31770175 to ZLS and 31800142 to BH), Mega-Project for Infectious Disease from Minister of Science and Technology of the People's Republic of China (2020ZX09201001 to DYZ and 2018ZX10305409-004-001 to PZ), Youth innovation promotion association of CAS (2019328 to XLY).

Author contributions Z.L.S., P.Z., Y.Y.W., and G.F.X. conceived the study. G.S.W., C.L.H., H.D.C., F.D., Q.J.C., F.X.Z., and L.L.L., collected patient samples. X.L.Y., B.Y., W.Z., B.L., J.C., X.S.Z., Y.L., H.G., R.D.J., M.Q.L., Y. Chen, X.W., X.R.S., and K.Z. performed qPCR, serology, and virus culturing. L.Z., Y.Z., H.R.S., and B.H. performed genome sequencing and annotations.

Competing interests The authors declare no competing interests.

Additional information
Correspondence and requests for materials should be addressed to Z.-L.S.
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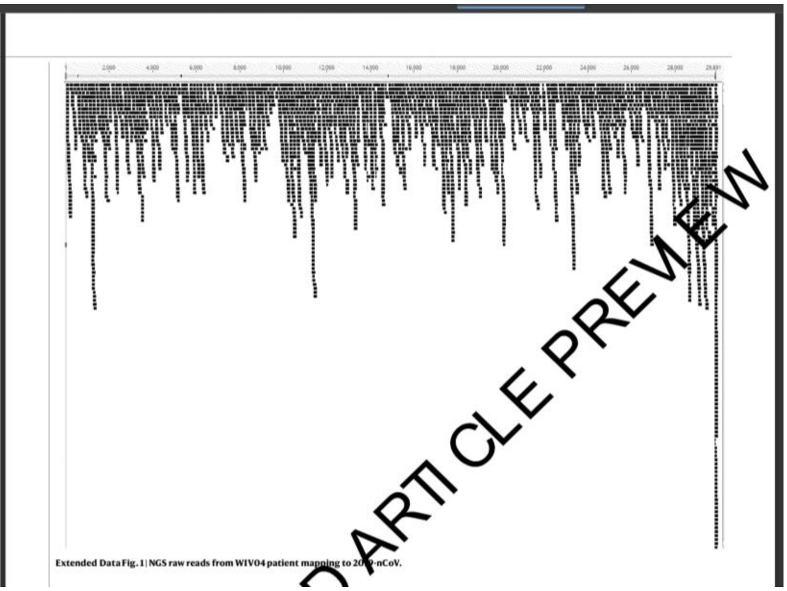

Extended Data Fig. 1 | NGS raw reads from WIV04 patient mapping to 2019-nCoV.

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2019-nCoV sampled from nine patients who were among the early cases of this severe infection are almost genetically identical, which suggests very recent emergence of this virus in

from a bat reservoir, although it remains unclear if a currently unknown animal species acted as an intermediate host between bats and humans.

for 2494 laboratory-confirmed cases of infection and 858 fatalities since September, 2012, including 38 deaths following a single introduction into South Korea.[8,9]

In late December, 2019, several patients with viral pneumonia were found to be epidemiologically associated with the Huanan seafood market in Wuhan, in the Hubei province of China, where a number of non-aquatic animals such as birds and rabbits were also on sale before the outbreak. A novel, human-infecting coronavirus,[10,11] provisionally named 2019 novel coronavirus (2019-nCoV), was identified with use of next-generation sequencing. As of Jan 28, 2020, China has reported more than 5900 confirmed and more than 90 00 suspected cases of 2019-nCoV infection across 33 Chinese provinces or municipalities, with 106 fatalities. In addition, 2019-nCoV has now been reported in Thailand, Japan, South Korea, Malaysia, Singapore, and the USA. Infections in medical workers and family clusters were also reported and human-to-human transmission has been confirmed.[12] Most of the infected patients had a high fever and some had dyspnoea, with chest radiographs revealing invasive lesions in both lungs.[12,13]

We report the epidemiological data of nine inpatients, from at least three hospitals in Wuhan, who were diagnosed with viral pneumonia of unidentified cause. Using next-generation sequencing of bronchoalveolar lavage fluid samples and cultured isolates from these patients, 2019-nCoV was found. We describe the genomic characterisation of ten genomes of this novel virus, providing important information on the origins and cell receptor binding of the virus.

Methods

Patients and samples

Nine patients with viral pneumonia and negative for common respiratory pathogens, who presented to at least three hospitals in Wuhan, were included in this study. Eight of the patients had visited the Huanan seafood market before the onset of illness, and one patient (WH04) did not visit the market but stayed in a hotel near the market between Dec 23 and Dec 27, 2019 (table). Five of the patients (WH19001, WH19002, WH19004, WH19008, and YS8011) had samples collected by the Chinese Center for Disease Control and Prevention (CDC) which were tested for 18 viruses and four bacteria using the RespiFinderSmart22 Kit (PathoFinder, Maastricht, Netherlands) on the LightCycler 480 Real-Time PCR system (Roche, Rotkreuz, Switzerland). Presence of SARS-CoV and MERS-CoV was tested using a previously reported method.[14] All five CD C samples were negative for all common respiratory pathogens screened for. Four of the patients (WH01, WH02, WH03, and WH04) had samples collected by BGI (Beijing, China), and were tested for fiveviruses and one bacterium using the RespiPathogen 6 Kit (Jiangsu Macro & Micro Test, Nantong, China) on the Applied Biosystems ABI 7500 Real-Time PCR system (ThermoFisher Scientific, Foster City, CA, USA). All four samples were negative for the targeted respiratory pathogens.

Virus isolation

Special-pathogen-free human airway epithelial (HAE) cells were used for virus isolation. Briefly,bronchoalveolar lavage fluids or throat swabs from the patients were inoculated into the HAE cells through the apical surfaces. HAE cells were maintained in an air–liquid interface incubated at 37°C. The cells were monitored daily for cytopathic effects by light microscopy and the cell supernatants were collected for use in quantitative RT-PCR assays. After three passages, apical samples were collected for sequencing.

BGI sequencing strategy

All collected samples were sent to BGI for sequencing. 140 μL bronchoalveolar lavage fluid samples (WH01 to WH04) were reserved for RNA extraction using the QIAamp Viral RNA Mini Kit (52904; Qiagen, Heiden, Germany), according to the manufacturer's recommendations. A probe-captured technique was used to remove human nucleic acid. The remaining RNA was

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Dalian, China) and chemically competent *Escherichia coli* (DH5α cells; TaKaRa), according to the manufacturer's instructions. PCR products were sequenced with use of M13 forward and reverse primers.

Virus genome analysis and annotation

Reference virus genomes were obtained from GenBank using Blastn with 2019-nCoV as a query. The open reading frames of the verified genome sequences were predicted using Geneious (version 11.1.5) and annotated using the Conserved Domain Database.[19] Pairwise sequence identities were also calculated using Geneious. Potential genetic recombination was investigated using SimPlot software (version 3.5.1)[20] and phylogenetic analysis.

Phylogenetic analysis

Sequence alignment of 2019-nCoV with reference sequences was done with Mafft software (version 7.450).[21] Phylogenetic analyses of the complete genome and major coding regions were done with RAxML software (version 8.2.9)[22] with 1000 bootstrap replicates, employing the general time reversible nucleotide substitution model.

Development of molecular diagnostics for 2019-nCoV

On the basis of the genome sequences obtained, a real-time PCR detection assay was developed. PCR primers and probes were designed using Applied Biosystems Primer Express Software (ThermoFisher Scientific, Foster City, CA, USA) on the basis of our sequenced virus genomes. The specific primers and probe set (labelled with the reporter 6-carboxyfluorescein [FAM] and the quencher Black Hole Quencher 1 [BHQ1]) for *orf1a* were as follows: forward primer 5′-AGAAGATTGGTTAGATGATGATAGT-3′; reverse primer 5′-TTCCATCTCTAATTGAGGTTGAACC-3′; and probe 5′-FAM-TCCTCACTGCCGTCTTGTTGACCA-BHQ1-3′. The human *GAPDH* gene was used as an internal control (forward primer 5′-TCAAGAAGGTGGTGAAGCAGG-3′; reverse primer 5′-CAGCGTCAAAGGTGGAGGAGT-3′; probe 5′-VIC-CCTCAAGGGCATCCTGGGCTACACT-BHQ1-3′). Primers and probes were synthesised by BGI (Beijing, China). RT-PCR was done with an Applied Biosystems 7300 Real-Time PCR System (ThermoScientific), with 30 μL reaction volumes consisting of 14 μL of diluted RNA, 15 μL of 2X Taqman One-Step RT-PCR Master Mix Reagents (4309169; Applied Biosystems,

GFG and WS had access to all the data in the study, and GFG, WS, WT, WC, and GW were responsible for the decision to submit for publication.

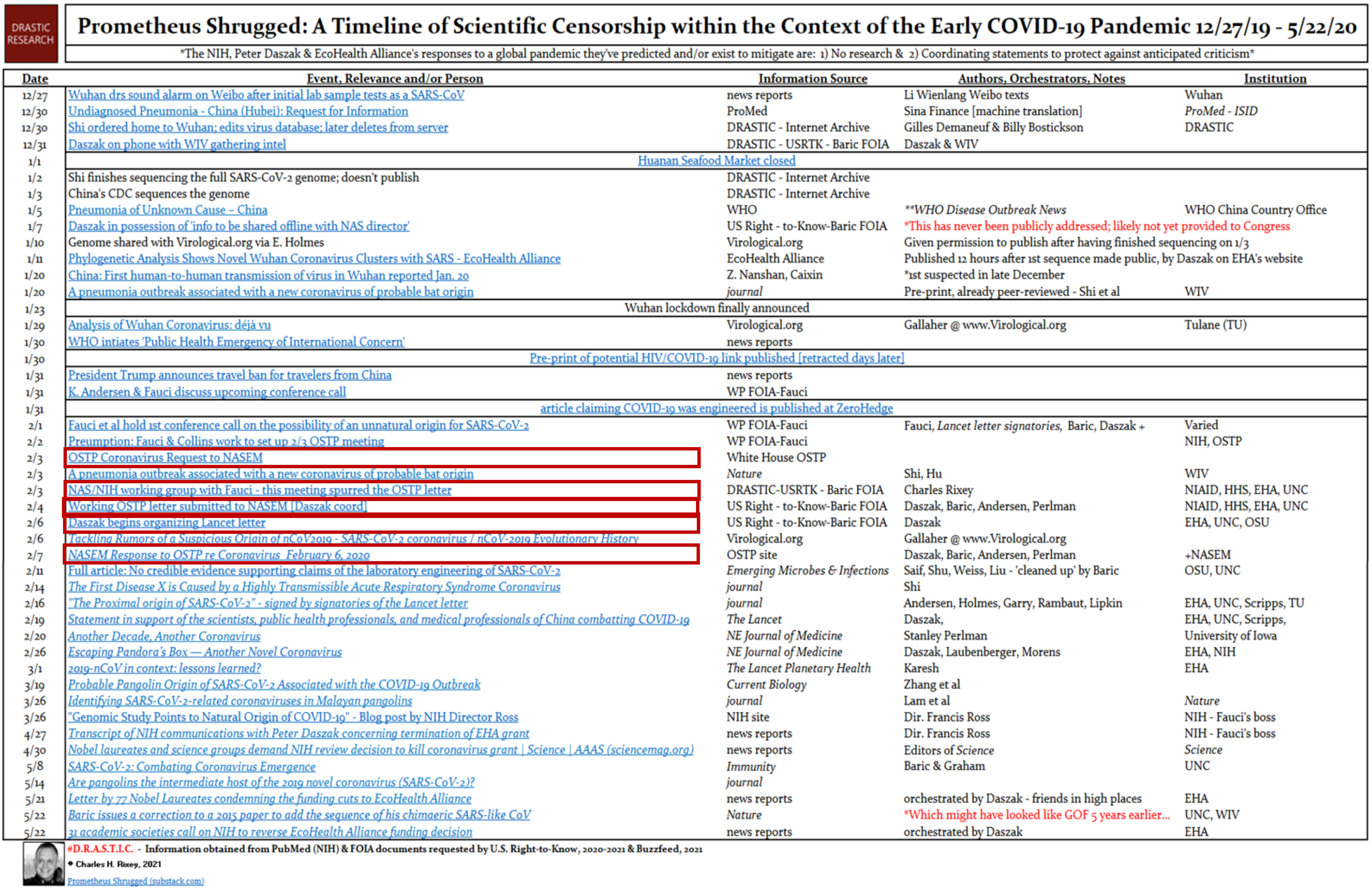
Results

From the nine patients' samples analysed, eight complete and two partial genome sequences of 2019-nCoV were obtained. These data have been deposited in the China National Microbiological Data Center (accession number NMDC10013002 and genome accession numbers NMDC60013002-01 to NMDC60013002-10) and the data from BGI have been deposited in the China National GeneBank (accession numbers CNA0007332–35).

Based on these genomes, we developed a real-time PCR assay and tested the original clinical samples from the BGI (WH01, WH02, WH03, and WH04) again to determine their threshold cycle (Ct) values (table). The remaining samples were tested by a different real-time PCR assay developed by the Chinese CDC, with Ct values ranging from 22·85 to 32·41 (table). These results confirmed the presence of 2019-nCoV in the patients.

Bronchoalveolar lavage fluid samples or cultured viruses of nine patients were used for next-generation sequencing. After removing host (human) reads, de novo assembly was done and the contigs obtained used as queries to search the non-redundant protein database. Some contigs identified in all the samples were closely related to the bat SARS-like betacoronavirus bat-SL-CoVZC45 betacoronavirus.[23] Bat-SL-CoVZC45 was then used as the reference genome and reads from each pool were mapped to it, generating consensus sequences corresponding to all the pools. These consensus sequences were then used as new reference genomes. Eight complete genomes and two partial genomes (from samples WH19002 and WH02; table) were obtained. The de novo assembly of the clean reads from all the pools did not identify any other long contigs that corresponded to other viruses at high abundance.

The eight complete genomes were nearly identical across the whole genome, with sequence identity above 99·98%, indicative of a very recent emergence into the human population (figure 1A). The largest nucleotide difference was four mutations. Notably, the sequence identity between the two virus genomes from the same patient (WH19001, from bronchoalveolar lavage fluid, and WH19005, from cell culture) was more than 99·99%,



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier…	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

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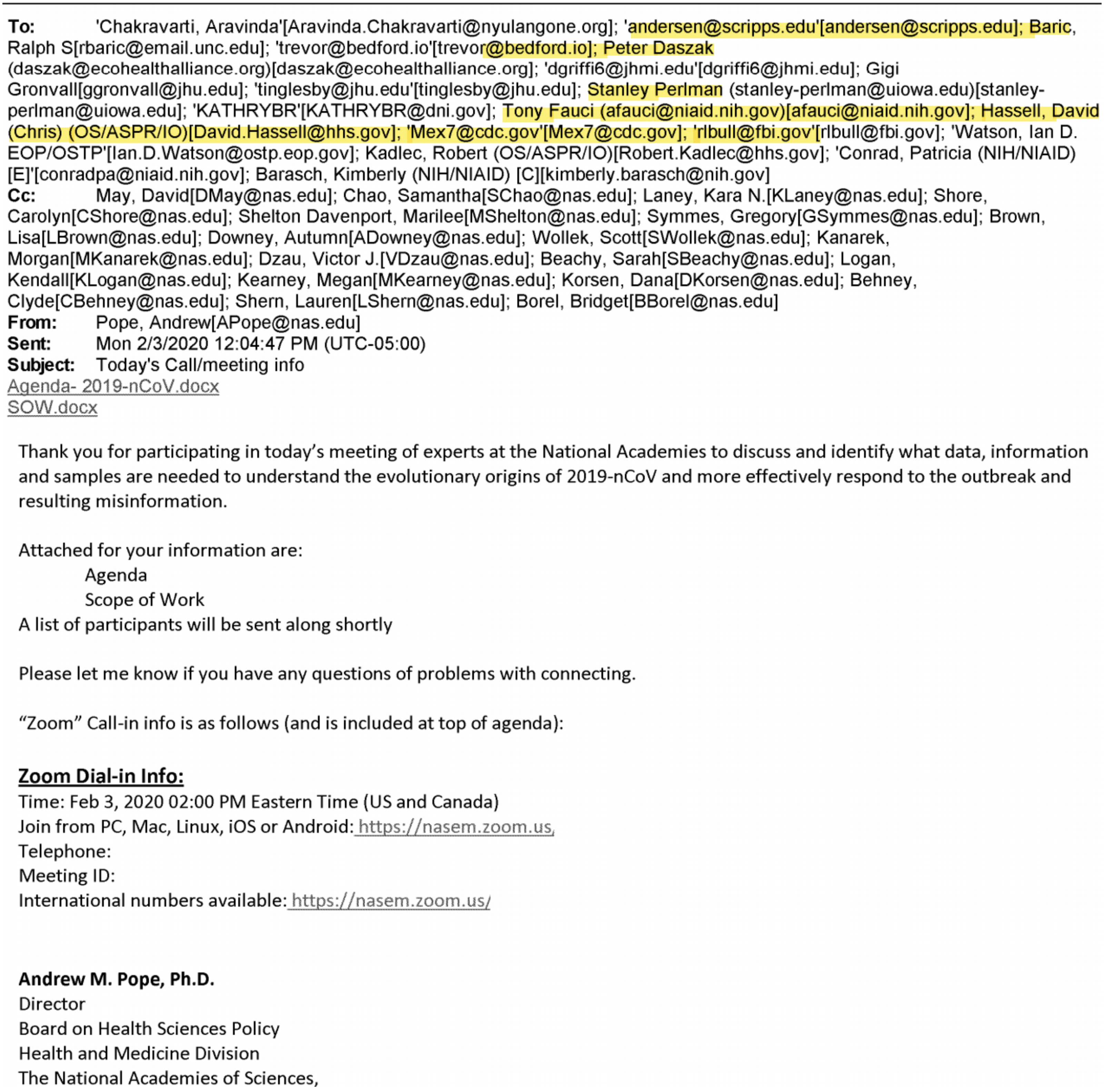
Prometheus Shrugged (substack.com)

FOIA Emails: 2/3/20
OSTP – NIH – NASEM meeting

These emails capture the discussion of scientists working to craft a suitable letter for the White House's Office of Science & Technology Policy (OSTP), following a meeting on 2/3.

Source: US Right-to-Know FOIA documents for Ralph Baric, Vol. I & XI



To: 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; 'andersen@scripps.edu'[andersen@scripps.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'trevor@bedford.io'[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; Gigi Gronvall[ggronvall@jhu.edu]; 'tinglesby@jhu.edu'[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; 'KATHRYBR'[KATHRYBR@dni.gov]; Tony Fauci (afauci@niaid.nih.gov)[afauci@niaid.nih.gov]; Hassell, David (Chris) (OS/ASPR/IO)[David.Hassell@hhs.gov]; 'Mex7@cdc.gov'[Mex7@cdc.gov]; 'rlbull@fbi.gov'[rlbull@fbi.gov]; 'Watson, Ian D. EOP/OSTP'[Ian.D.Watson@ostp.eop.gov]; Kadlec, Robert (OS/ASPR/IO)[Robert.Kadlec@hhs.gov]; 'Conrad, Patricia (NIH/NIAID) [E]'[conradpa@niaid.nih.gov]; Barasch, Kimberly (NIH/NIAID) [C][kimberly.barasch@nih.gov]
Cc: May, David[DMay@nas.edu]; Chao, Samantha[SChao@nas.edu]; Laney, Kara N.[KLaney@nas.edu]; Shore, Carolyn[CShore@nas.edu]; Shelton Davenport, Marilee[MShelton@nas.edu]; Symmes, Gregory[GSymmes@nas.edu]; Brown, Lisa[LBrown@nas.edu]; Downey, Autumn[ADowney@nas.edu]; Wollek, Scott[SWollek@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; Dzau, Victor J.[VDzau@nas.edu]; Beachy, Sarah[SBeachy@nas.edu]; Logan, Kendall[KLogan@nas.edu]; Kearney, Megan[MKearney@nas.edu]; Korsen, Dana[DKorsen@nas.edu]; Behney, Clyde[CBehney@nas.edu]; Shern, Lauren[LShern@nas.edu]; Borel, Bridget[BBorel@nas.edu]
From: Pope, Andrew[APope@nas.edu]
Sent: Mon 2/3/2020 12:04:47 PM (UTC-05:00)
Subject: Today's Call/meeting info
Agenda- 2019-nCoV.docx
SOW.docx

Thank you for participating in today's meeting of experts at the National Academies to discuss and identify what data, information and samples are needed to understand the evolutionary origins of 2019-nCoV and more effectively respond to the outbreak and resulting misinformation.

Attached for your information are:
- Agenda
- Scope of Work

A list of participants will be sent along shortly

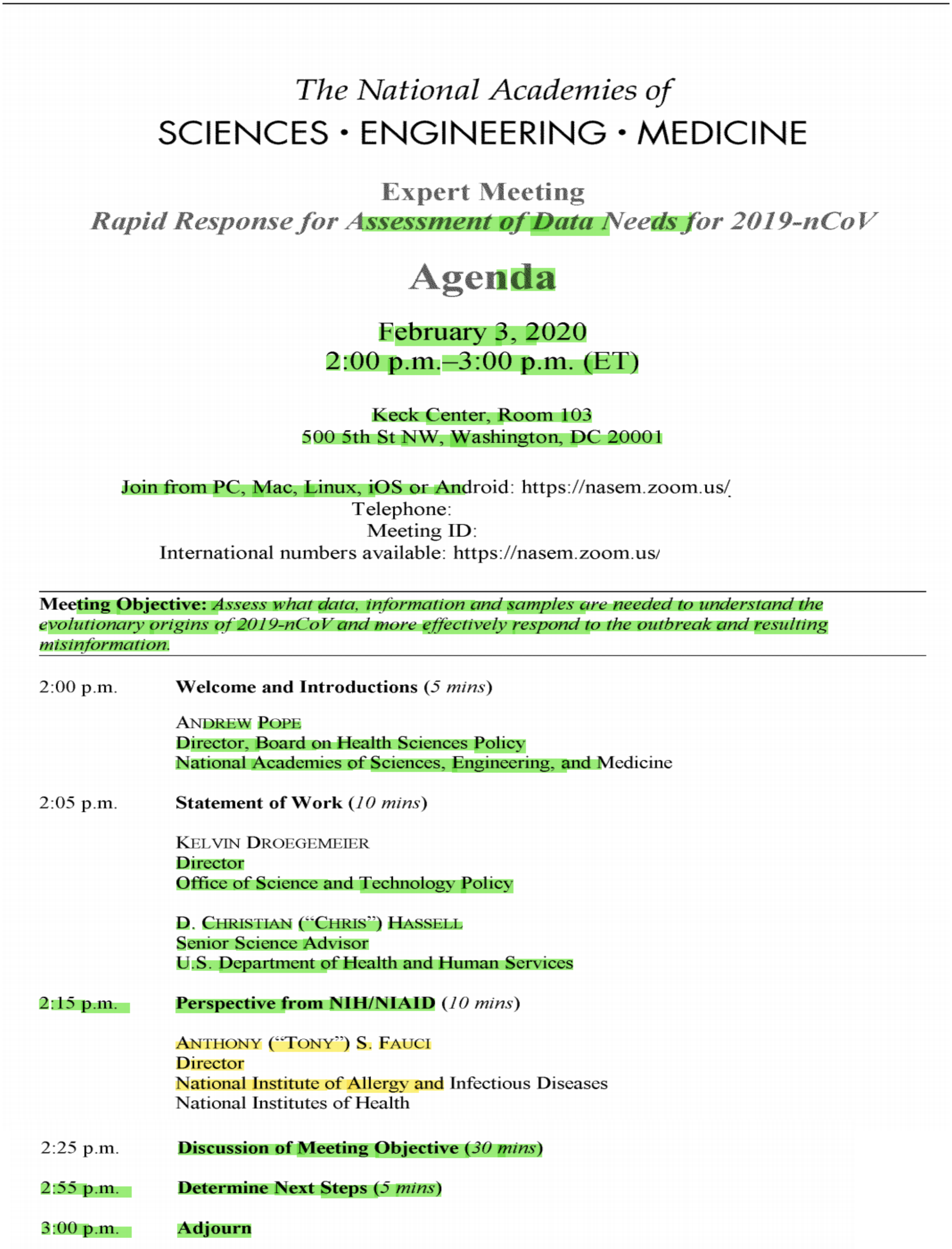
Please let me know if you have any questions of problems with connecting.

"Zoom" Call-in info is as follows (and is included at top of agenda):

Zoom Dial-in Info:
Time: Feb 3, 2020 02:00 PM Eastern Time (US and Canada)
Join from PC, Mac, Linux, iOS or Android: https://nasem.zoom.us,
Telephone:
Meeting ID:
International numbers available: https://nasem.zoom.us/

Andrew M. Pope, Ph.D.
Director
Board on Health Sciences Policy
Health and Medicine Division
The National Academies of Sciences,

COVID-19 Origin Censorship: Project – The Arc of Inquiry bends towards Enlightenment



The National Academies of
SCIENCES • ENGINEERING • MEDICINE

Expert Meeting
Rapid Response for Assessment of Data Needs for 2019-nCoV

Agenda

February 3, 2020
2:00 p.m.–3:00 p.m. (ET)

Keck Center, Room 103
500 5th St NW, Washington, DC 20001

Join from PC, Mac, Linux, iOS or Android: https://nasem.zoom.us/
Telephone:
Meeting ID:
International numbers available: https://nasem.zoom.us/

Meeting Objective: *Assess what data, information and samples are needed to understand the evolutionary origins of 2019-nCoV and more effectively respond to the outbreak and resulting misinformation.*

2:00 p.m. **Welcome and Introductions** (*5 mins*)

ANDREW POPE
Director, Board on Health Sciences Policy
National Academies of Sciences, Engineering, and Medicine

2:05 p.m. **Statement of Work** (*10 mins*)

KELVIN DROEGEMEIER
Director
Office of Science and Technology Policy

D. CHRISTIAN ("CHRIS") HASSELL
Senior Science Advisor
U.S. Department of Health and Human Services

2:15 p.m. **Perspective from NIH/NIAID** (*10 mins*)

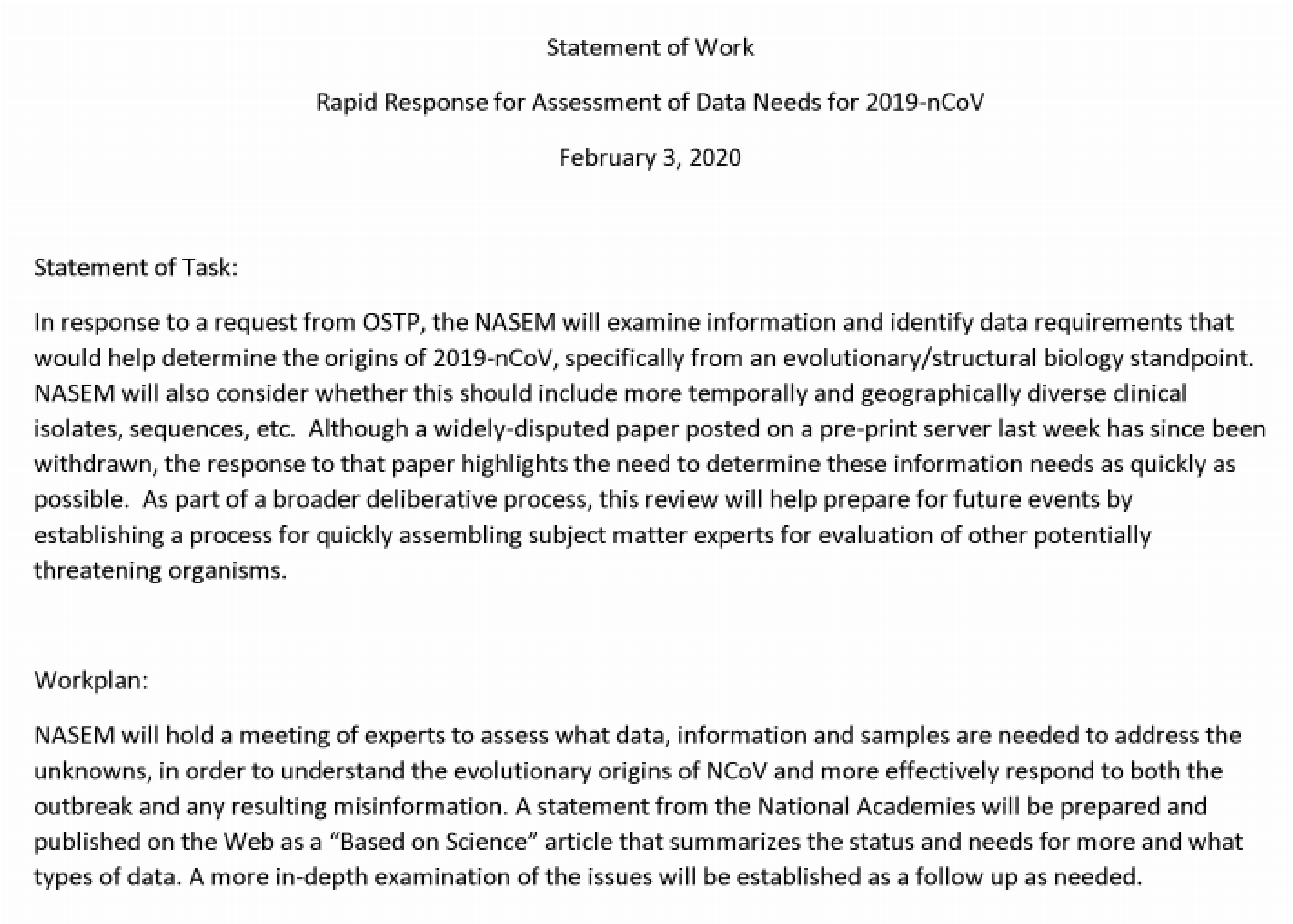
ANTHONY ("TONY") S. FAUCI
Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health

2:25 p.m. **Discussion of Meeting Objective** (*30 mins*)

2:55 p.m. **Determine Next Steps** (*5 mins*)

3:00 p.m. **Adjourn**

COVID-19 Origin Censorship:
Project – The Arc of Inquiry bends
towards Enlightenment



Statement of Work

Rapid Response for Assessment of Data Needs for 2019-nCoV

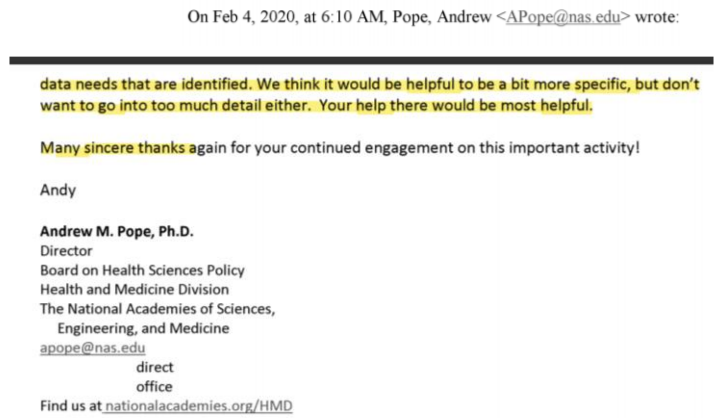
February 3, 2020

Statement of Task:

In response to a request from OSTP, the NASEM will examine information and identify data requirements that would help determine the origins of 2019-nCoV, specifically from an evolutionary/structural biology standpoint. NASEM will also consider whether this should include more temporally and geographically diverse clinical isolates, sequences, etc. Although a widely-disputed paper posted on a pre-print server last week has since been withdrawn, the response to that paper highlights the need to determine these information needs as quickly as possible. As part of a broader deliberative process, this review will help prepare for future events by establishing a process for quickly assembling subject matter experts for evaluation of other potentially threatening organisms.

Workplan:

NASEM will hold a meeting of experts to assess what data, information and samples are needed to address the unknowns, in order to understand the evolutionary origins of NCoV and more effectively respond to both the outbreak and any resulting misinformation. A statement from the National Academies will be prepared and published on the Web as a "Based on Science" article that summarizes the status and needs for more and what types of data. A more in-depth examination of the issues will be established as a follow up as needed.



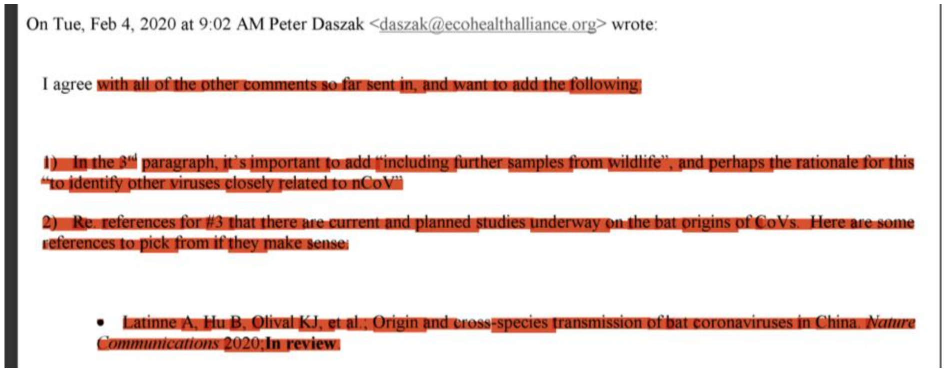
On Feb 4, 2020, at 6:10 AM, Pope, Andrew <APope@nas.edu> wrote:

data needs that are identified. We think it would be helpful to be a bit more specific, but don't want to go into too much detail either. Your help there would be most helpful.

Many sincere thanks again for your continued engagement on this important activity!

Andy

Andrew M. Pope, Ph.D.
Director
Board on Health Sciences Policy
Health and Medicine Division
The National Academies of Sciences,
Engineering, and Medicine
apope@nas.edu
direct
office
Find us at nationalacademies.org/HMD



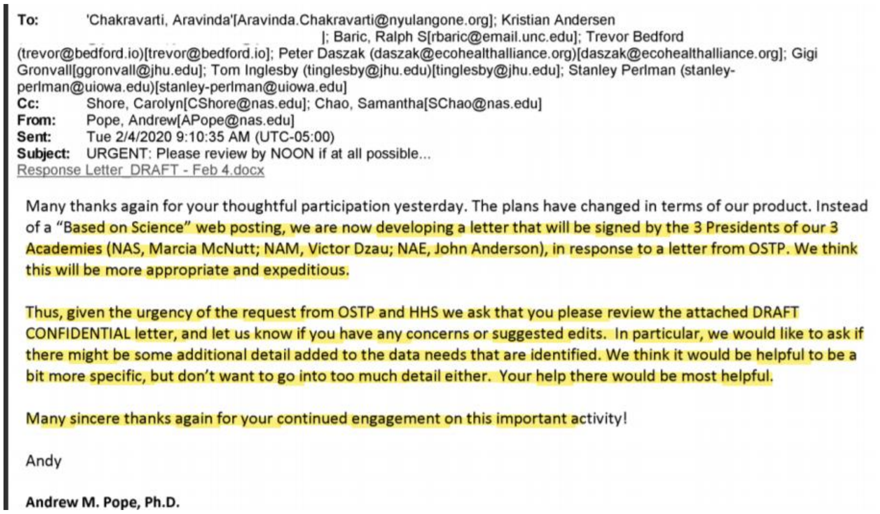
On Tue, Feb 4, 2020 at 9:02 AM Peter Daszak <daszak@ecohealthalliance.org> wrote:

I agree with all of the other comments so far sent in, and want to add the following:

1) In the 3rd paragraph, it's important to add "including further samples from wildlife", and perhaps the rationale for this "to identify other viruses closely related to nCoV"

2) Re. references for #3 that there are current and planned studies underway on the bat origins of CoVs. Here are some references to pick from if they make sense:

- Latinne A, Hu B, Olival KJ, et al.; Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications* 2020;**In review**.



To: 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Pope, Andrew[APope@nas.edu]
Sent: Tue 2/4/2020 9:10:35 AM (UTC-05:00)
Subject: URGENT: Please review by NOON if at all possible...
Response Letter_DRAFT - Feb 4.docx

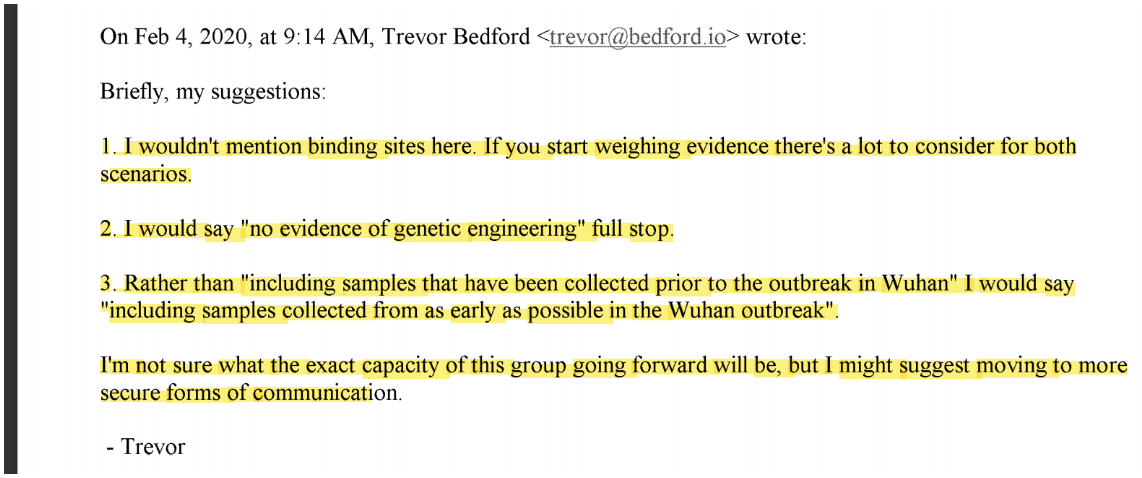
Many thanks again for your thoughtful participation yesterday. The plans have changed in terms of our product. Instead of a "Based on Science" web posting, we are now developing a letter that will be signed by the 3 Presidents of our 3 Academies (NAS, Marcia McNutt; NAM, Victor Dzau; NAE, John Anderson), in response to a letter from OSTP. We think this will be more appropriate and expeditious.

Thus, given the urgency of the request from OSTP and HHS we ask that you please review the attached DRAFT CONFIDENTIAL letter, and let us know if you have any concerns or suggested edits. In particular, we would like to ask if there might be some additional detail added to the data needs that are identified. We think it would be helpful to be a bit more specific, but don't want to go into too much detail either. Your help there would be most helpful.

Many sincere thanks again for your continued engagement on this important activity!

Andy

Andrew M. Pope, Ph.D.



On Feb 4, 2020, at 9:14 AM, Trevor Bedford <trevor@bedford.io> wrote:

Briefly, my suggestions:

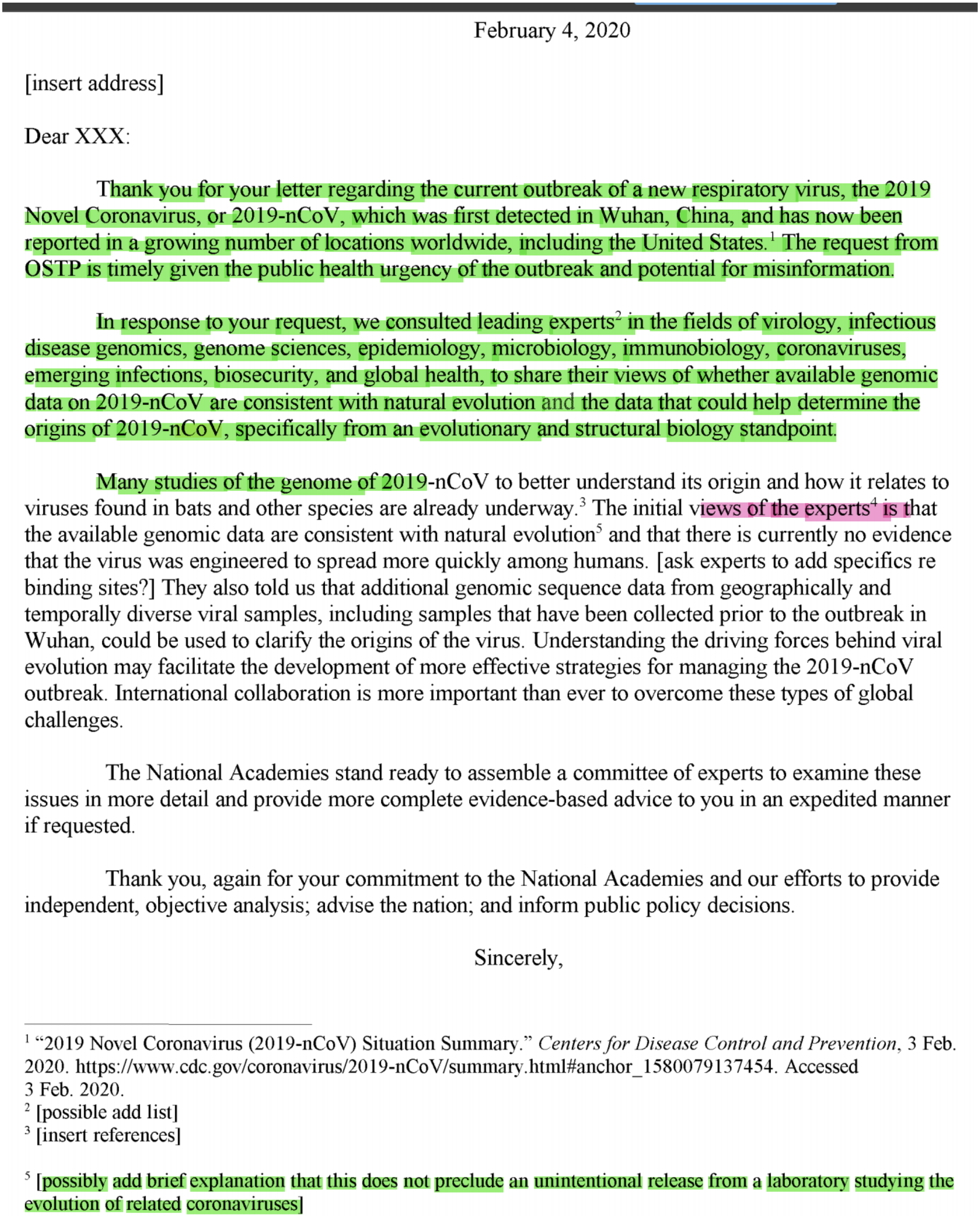
1. I wouldn't mention binding sites here. If you start weighing evidence there's a lot to consider for both scenarios.

2. I would say "no evidence of genetic engineering" full stop.

3. Rather than "including samples that have been collected prior to the outbreak in Wuhan" I would say "including samples collected from as early as possible in the Wuhan outbreak".

I'm not sure what the exact capacity of this group going forward will be, but I might suggest moving to more secure forms of communication.

- Trevor



February 4, 2020

[insert address]

Dear XXX:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the public health urgency of the outbreak and potential for misinformation.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health, to share their views of whether available genomic data on 2019-nCoV are consistent with natural evolution and the data that could help determine the origins of 2019-nCoV, specifically from an evolutionary and structural biology standpoint.

Many studies of the genome of 2019-nCoV to better understand its origin and how it relates to viruses found in bats and other species are already underway.[3] The initial views of the experts[4] is that the available genomic data are consistent with natural evolution[5] and that there is currently no evidence that the virus was engineered to spread more quickly among humans. [ask experts to add specifics re binding sites?] They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus. Understanding the driving forces behind viral evolution may facilitate the development of more effective strategies for managing the 2019-nCoV outbreak. International collaboration is more important than ever to overcome these types of global challenges.

The National Academies stand ready to assemble a committee of experts to examine these issues in more detail and provide more complete evidence-based advice to you in an expedited manner if requested.

Thank you, again for your commitment to the National Academies and our efforts to provide independent, objective analysis; advise the nation; and inform public policy decisions.

Sincerely,

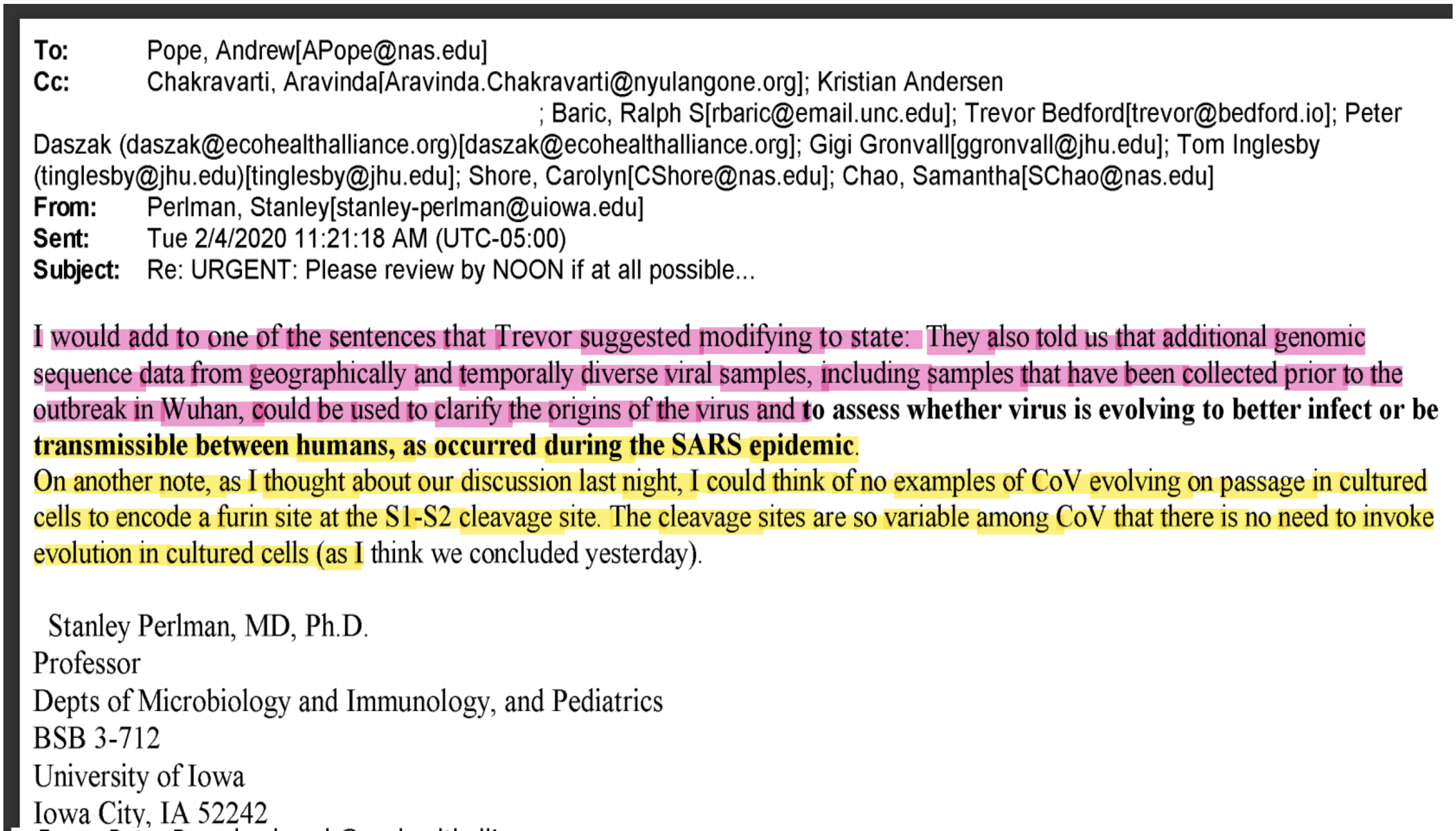
---

[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] [possible add list]

[3] [insert references]

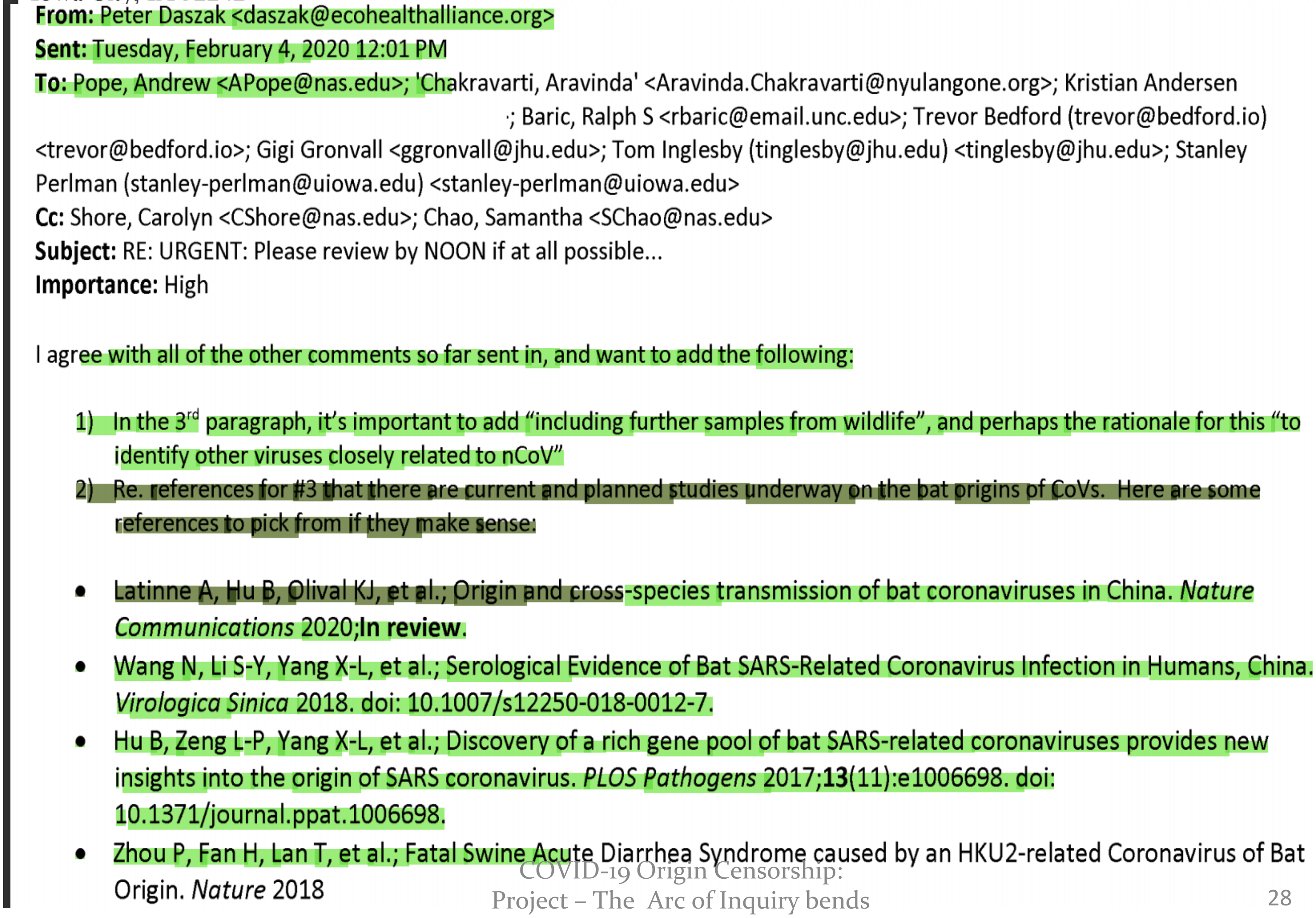
[5] [possibly add brief explanation that this does not preclude an unintentional release from a laboratory studying the evolution of related coronaviruses]



To: Pope, Andrew[APope@nas.edu]
Cc: Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen ; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Tue 2/4/2020 11:21:18 AM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I would add to one of the sentences that Trevor suggested modifying to state: They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus and **to assess whether virus is evolving to better infect or be transmissible between humans, as occurred during the SARS epidemic**.
On another note, as I thought about our discussion last night, I could think of no examples of CoV evolving on passage in cultured cells to encode a furin site at the S1-S2 cleavage site. The cleavage sites are so variable among CoV that there is no need to invoke evolution in cultured cells (as I think we concluded yesterday).

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

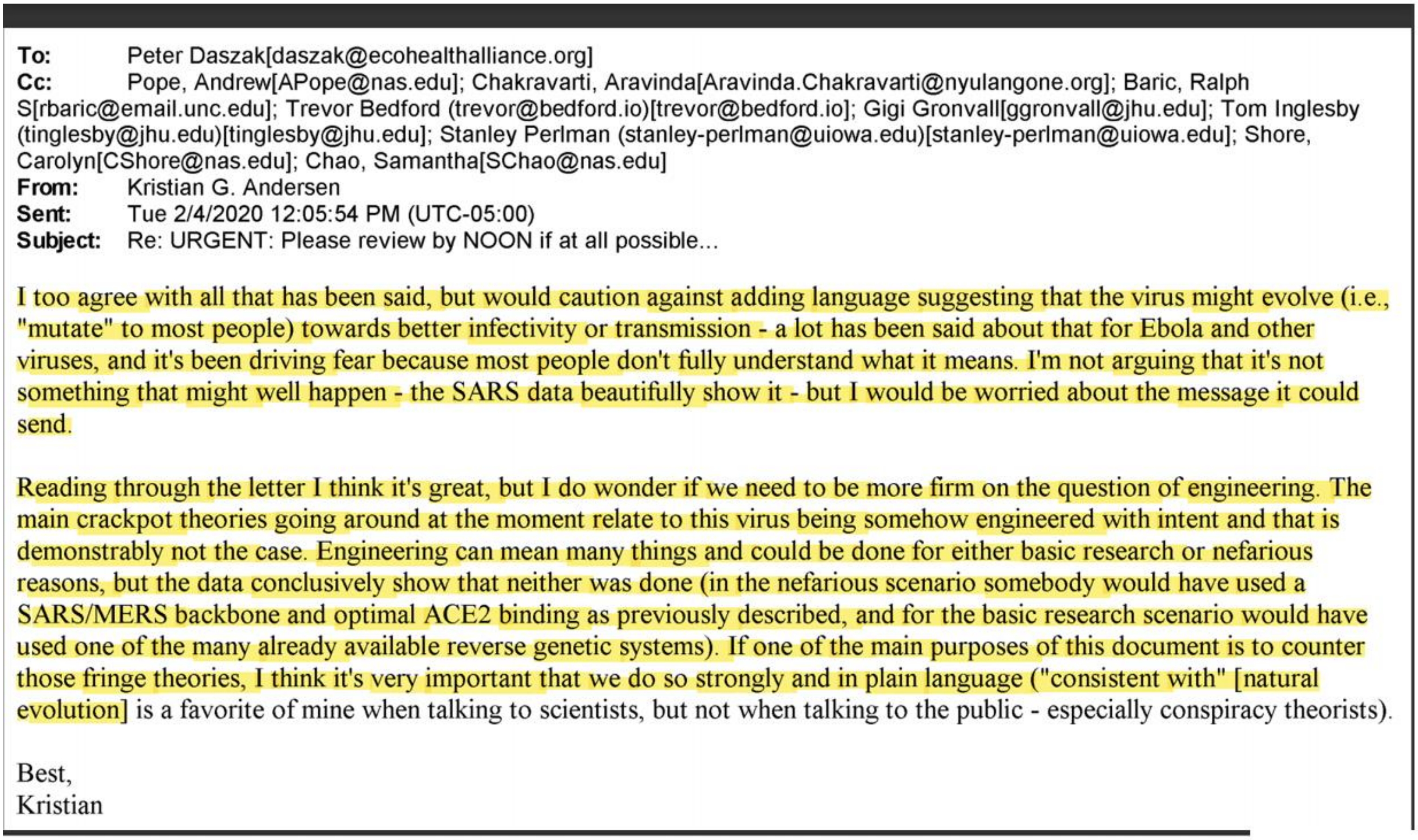


From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, February 4, 2020 12:01 PM
To: Pope, Andrew <APope@nas.edu>; 'Chakravarti, Aravinda' <Aravinda.Chakravarti@nyulangone.org>; Kristian Andersen ; Baric, Ralph S <rbaric@email.unc.edu>; Trevor Bedford (trevor@bedford.io) <trevor@bedford.io>; Gigi Gronvall <ggronvall@jhu.edu>; Tom Inglesby (tinglesby@jhu.edu) <tinglesby@jhu.edu>; Stanley Perlman (stanley-perlman@uiowa.edu) <stanley-perlman@uiowa.edu>
Cc: Shore, Carolyn <CShore@nas.edu>; Chao, Samantha <SChao@nas.edu>
Subject: RE: URGENT: Please review by NOON if at all possible...
Importance: High

I agree with all of the other comments so far sent in, and want to add the following:

1) In the 3rd paragraph, it's important to add "including further samples from wildlife", and perhaps the rationale for this "to identify other viruses closely related to nCoV"
2) Re. references for #3 that there are current and planned studies underway on the bat origins of CoVs. Here are some references to pick from if they make sense:

- Latinne A, Hu B, Olival KJ, et al.; Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications* 2020;**In review**.
- Wang N, Li S-Y, Yang X-L, et al.; Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Virologica Sinica* 2018. doi: 10.1007/s12250-018-0012-7.
- Hu B, Zeng L-P, Yang X-L, et al.; Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLOS Pathogens* 2017;**13**(11):e1006698. doi: 10.1371/journal.ppat.1006698.
- Zhou P, Fan H, Lan T, et al.; Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. *Nature* 2018

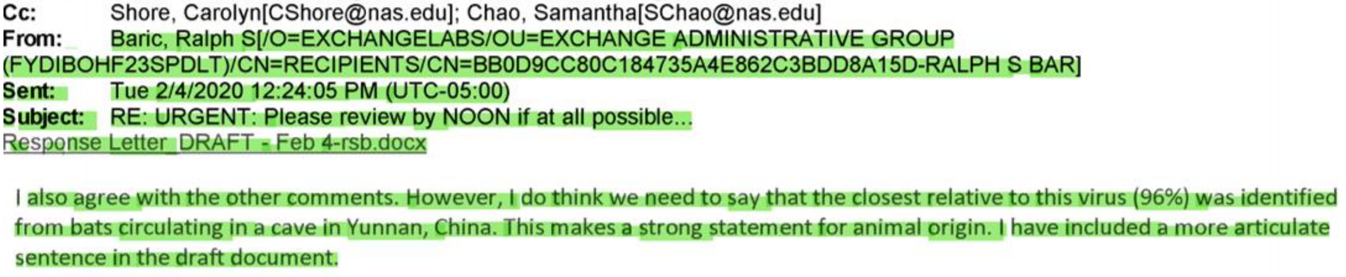


To: Peter Daszak[daszak@ecohealthalliance.org]
Cc: Pope, Andrew[APope@nas.edu]; Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Kristian G. Andersen
Sent: Tue 2/4/2020 12:05:54 PM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., "mutate" to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other viruses, and it's been driving fear because most people don't fully understand what it means. I'm not arguing that it's not something that might well happen - the SARS data beautifully show it - but I would be worried about the message it could send.

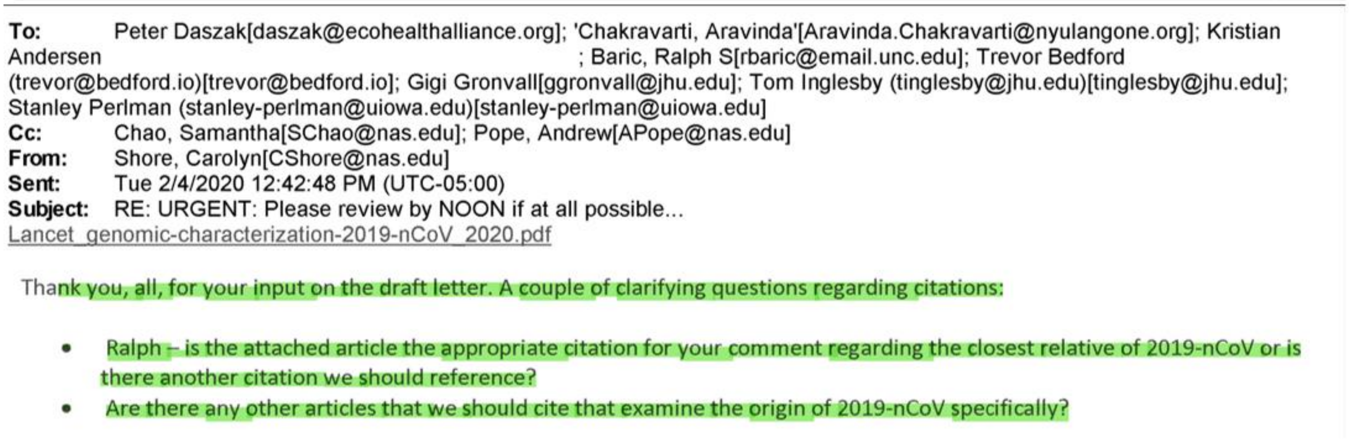
Reading through the letter I think it's great, but I do wonder if we need to be more firm on the question of engineering. The main crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter those fringe theories, I think it's very important that we do so strongly and in plain language ("consistent with" [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists).

Best,
Kristian



To: Peter Daszak[daszak@ecohealthalliance.org]; Pope, Andrew[APope@nas.edu]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen [redacted]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
Sent: Tue 2/4/2020 12:24:05 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Response Letter_DRAFT - Feb 4-rsb.docx

I also agree with the other comments. However, I do think we need to say that the closest relative to this virus (96%) was identified from bats circulating in a cave in Yunnan, China. This makes a strong statement for animal origin. I have included a more articulate sentence in the draft document.



To: Peter Daszak[daszak@ecohealthalliance.org]; 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen [redacted]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Chao, Samantha[SChao@nas.edu]; Pope, Andrew[APope@nas.edu]
From: Shore, Carolyn[CShore@nas.edu]
Sent: Tue 2/4/2020 12:42:48 PM (UTC-05:00)
Subject: RE: URGENT: Please review by NOON if at all possible...
Lancet_genomic-characterization-2019-nCoV_2020.pdf

Thank you, all, for your input on the draft letter. A couple of clarifying questions regarding citations:

- Ralph – is the attached article the appropriate citation for your comment regarding the closest relative of 2019-nCoV or is there another citation we should reference?
- Are there any other articles that we should cite that examine the origin of 2019-nCoV specifically?

CONFIDENTIAL DRAFT

February 4, 2020

[insert address]

Dear XXX:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the public health urgency of the outbreak and potential for misinformation.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health, to share their views of whether available genomic data on 2019-nCoV are consistent with natural evolution and the data that could help determine the origins of 2019-nCoV, specifically from an evolutionary and structural biology standpoint.

Many studies of the genome of 2019-nCoV to better understand its origin and how it relates to viruses found in bats and other species are already underway.[3] The initial views of the experts[4] is that the available genomic data are consistent with natural evolution[5] and that there is currently no evidence that the virus was engineered to spread more quickly among humans. [ask experts to add specifics re binding sites?] They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus. Understanding the driving forces behind viral evolution may facilitate the development of more effective strategies for managing the 2019-nCoV outbreak. International collaboration is more important than ever to overcome these types of global challenges.

The National Academies stand ready to assemble a committee of experts to examine these issues in more detail and provide more complete evidence-based advice to you in an expedited manner if requested.

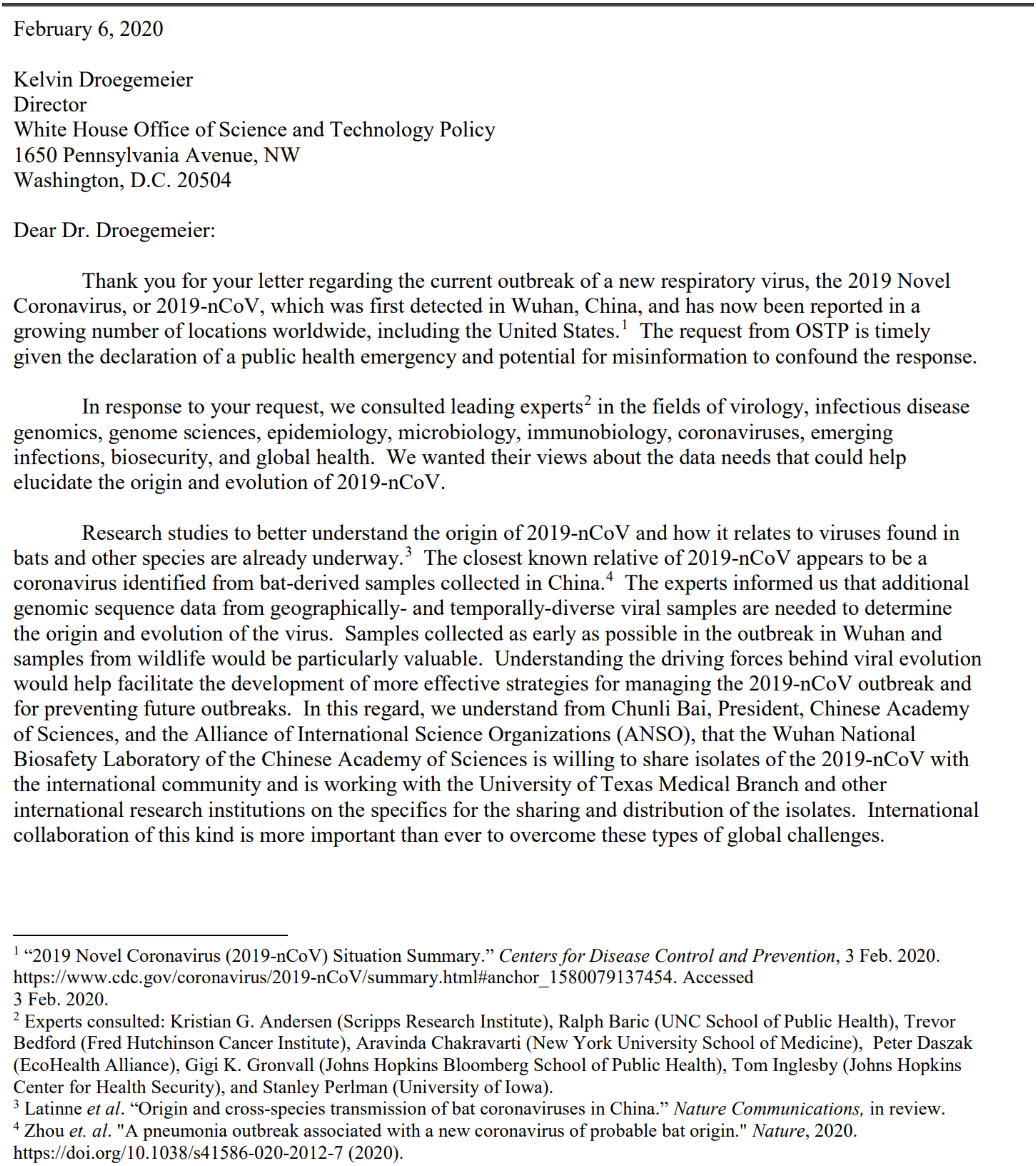
Thank you, again for your commitment to the National Academies and our efforts to provide independent, objective analysis; advise the nation; and inform public policy decisions.

Sincerely,

---

[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] [possible add list]



February 6, 2020

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy
1650 Pennsylvania Avenue, NW
Washington, D.C. 20504

Dear Dr. Droegemeier:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the declaration of a public health emergency and potential for misinformation to confound the response.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health. We wanted their views about the data needs that could help elucidate the origin and evolution of 2019-nCoV.

Research studies to better understand the origin of 2019-nCoV and how it relates to viruses found in bats and other species are already underway.[3] The closest known relative of 2019-nCoV appears to be a coronavirus identified from bat-derived samples collected in China.[4] The experts informed us that additional genomic sequence data from geographically- and temporally-diverse viral samples are needed to determine the origin and evolution of the virus. Samples collected as early as possible in the outbreak in Wuhan and samples from wildlife would be particularly valuable. Understanding the driving forces behind viral evolution would help facilitate the development of more effective strategies for managing the 2019-nCoV outbreak and for preventing future outbreaks. In this regard, we understand from Chunli Bai, President, Chinese Academy of Sciences, and the Alliance of International Science Organizations (ANSO), that the Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences is willing to share isolates of the 2019-nCoV with the international community and is working with the University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. International collaboration of this kind is more important than ever to overcome these types of global challenges.

---

[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] Experts consulted: Kristian G. Andersen (Scripps Research Institute), Ralph Baric (UNC School of Public Health), Trevor Bedford (Fred Hutchinson Cancer Institute), Aravinda Chakravarti (New York University School of Medicine), Peter Daszak (EcoHealth Alliance), Gigi K. Gronvall (Johns Hopkins Bloomberg School of Public Health), Tom Inglesby (Johns Hopkins Center for Health Security), and Stanley Perlman (University of Iowa).

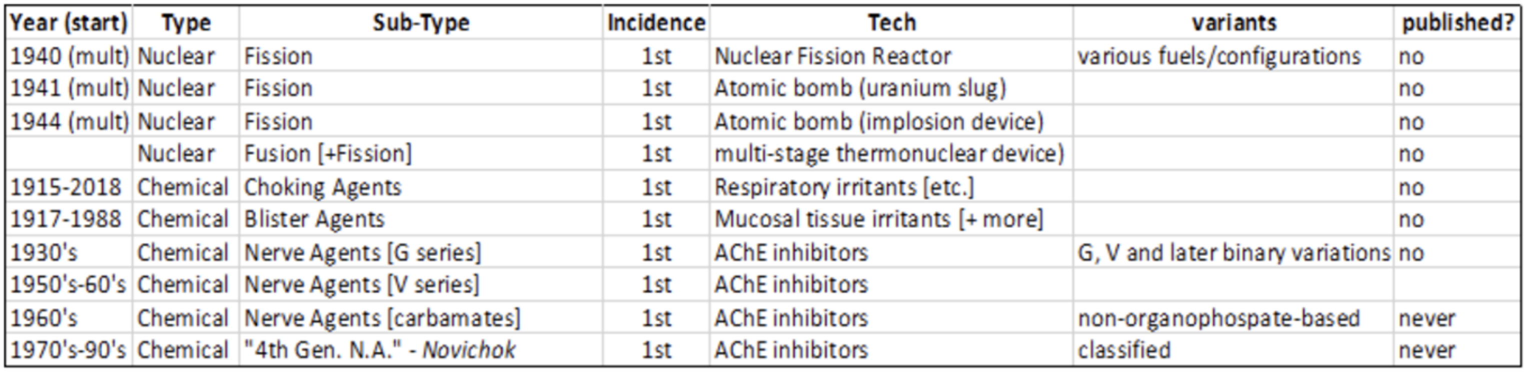
[3] Latinne *et al*. "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications,* in review.

[4] Zhou *et. al*. "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 2020. https://doi.org/10.1038/s41586-020-2012-7 (2020).

Argument #3:

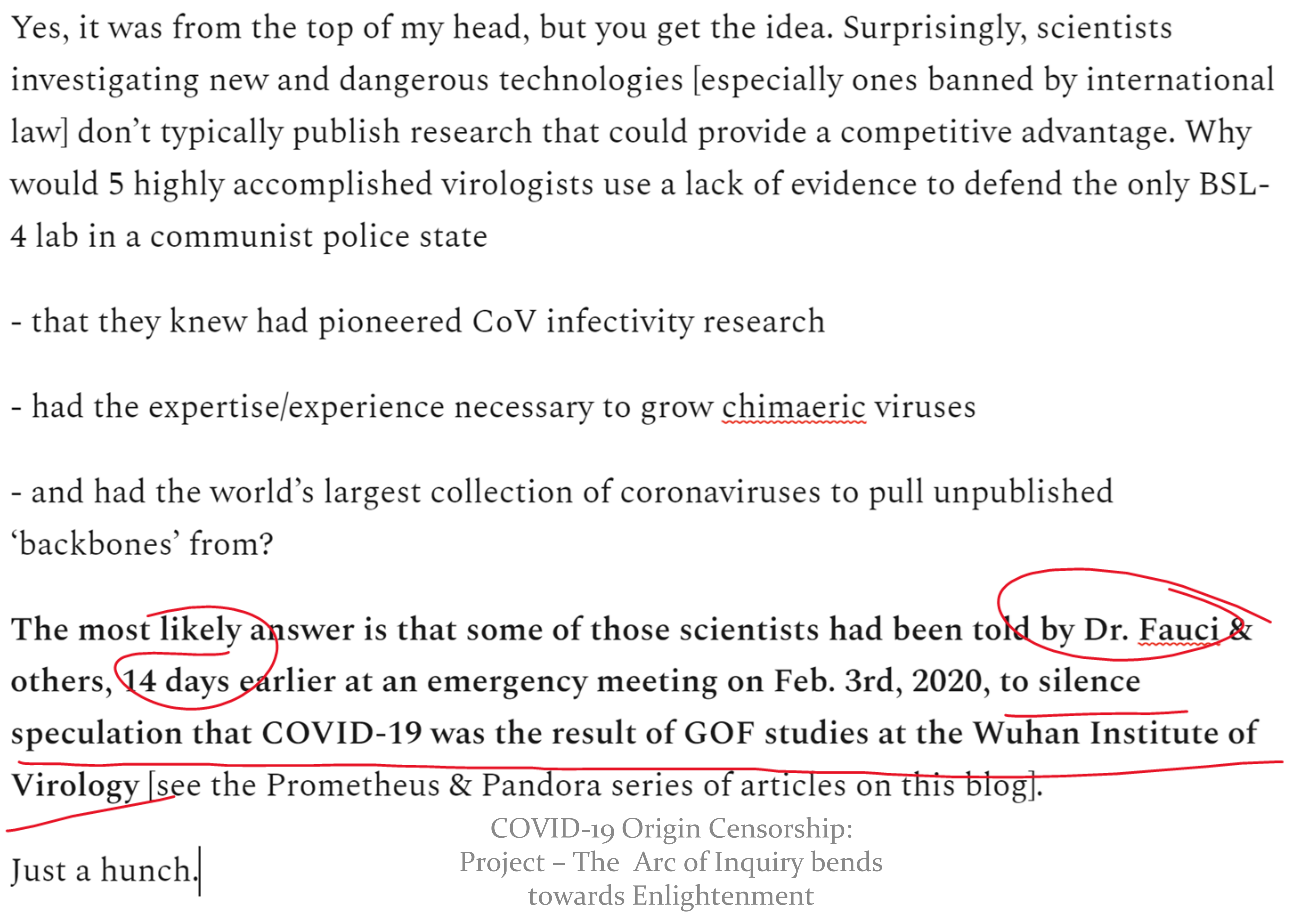
3. There's no evidence of any previously-used backbone [base for genetic engineering].

By far, this was the most ridiculous assertion. It was so obvious that I'm still surprised it was added at all - much less that no journal editor or reader publicly wrote to point it out. I went back to other examples of scientists developing new dangerous technologies, and I didn't see any evidence them publicizing their research beforehand.



Year (start)	Type	Sub-Type	Incidence	Tech	variants	published?
1940 (mult)	Nuclear	Fission	1st	Nuclear Fission Reactor	various fuels/configurations	no
1941 (mult)	Nuclear	Fission	1st	Atomic bomb (uranium slug)		no
1944 (mult)	Nuclear	Fission	1st	Atomic bomb (implosion device)		no
	Nuclear	Fusion [+Fission]	1st	multi-stage thermonuclear device)		no
1915-2018	Chemical	Choking Agents	1st	Respiratory irritants [etc.]		no
1917-1988	Chemical	Blister Agents	1st	Mucosal tissue irritants [+ more]		no
1930's	Chemical	Nerve Agents [G series]	1st	AChE inhibitors	G, V and later binary variations	no
1950's-60's	Chemical	Nerve Agents [V series]	1st	AChE inhibitors		
1960's	Chemical	Nerve Agents [carbamates]	1st	AChE inhibitors	non-organophospate-based	never
1970's-90's	Chemical	"4th Gen. N.A." - *Novichok*	1st	AChE inhibitors	classified	never

Yes, it was from the top of my head, but you get the idea. Surprisingly, scientists



Yes, it was from the top of my head, but you get the idea. Surprisingly, scientists investigating new and dangerous technologies [especially ones banned by international law] don't typically publish research that could provide a competitive advantage. Why would 5 highly accomplished virologists use a lack of evidence to defend the only BSL-4 lab in a communist police state

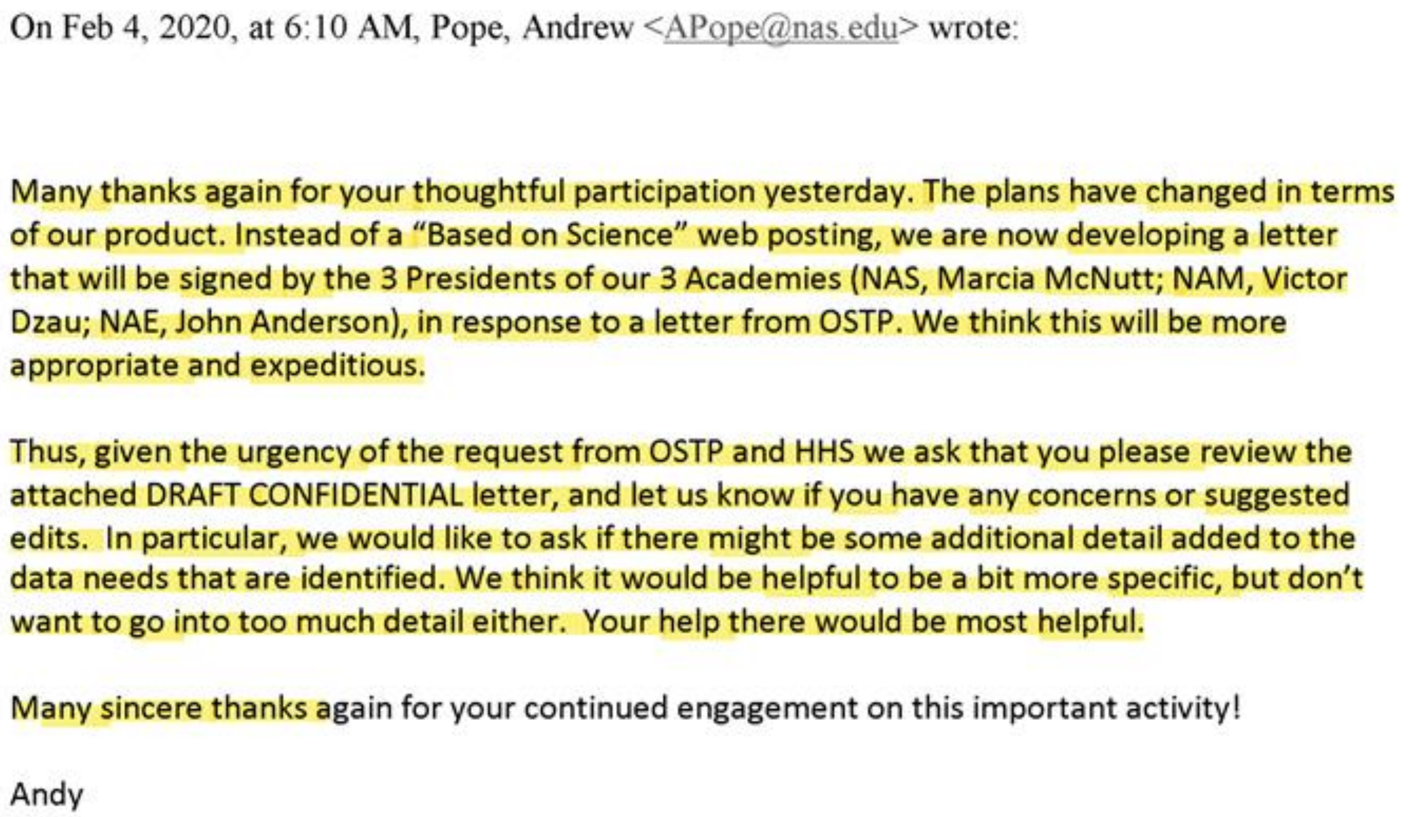
- that they knew had pioneered CoV infectivity research

- had the expertise/experience necessary to grow chimaeric viruses

- and had the world's largest collection of coronaviruses to pull unpublished 'backbones' from?

The most likely answer is that some of those scientists had been told by Dr. Fauci & others, 14 days earlier at an emergency meeting on Feb. 3rd, 2020, to silence speculation that COVID-19 was the result of GOF studies at the Wuhan Institute of Virology [see the Prometheus & Pandora series of articles on this blog].

Just a hunch.



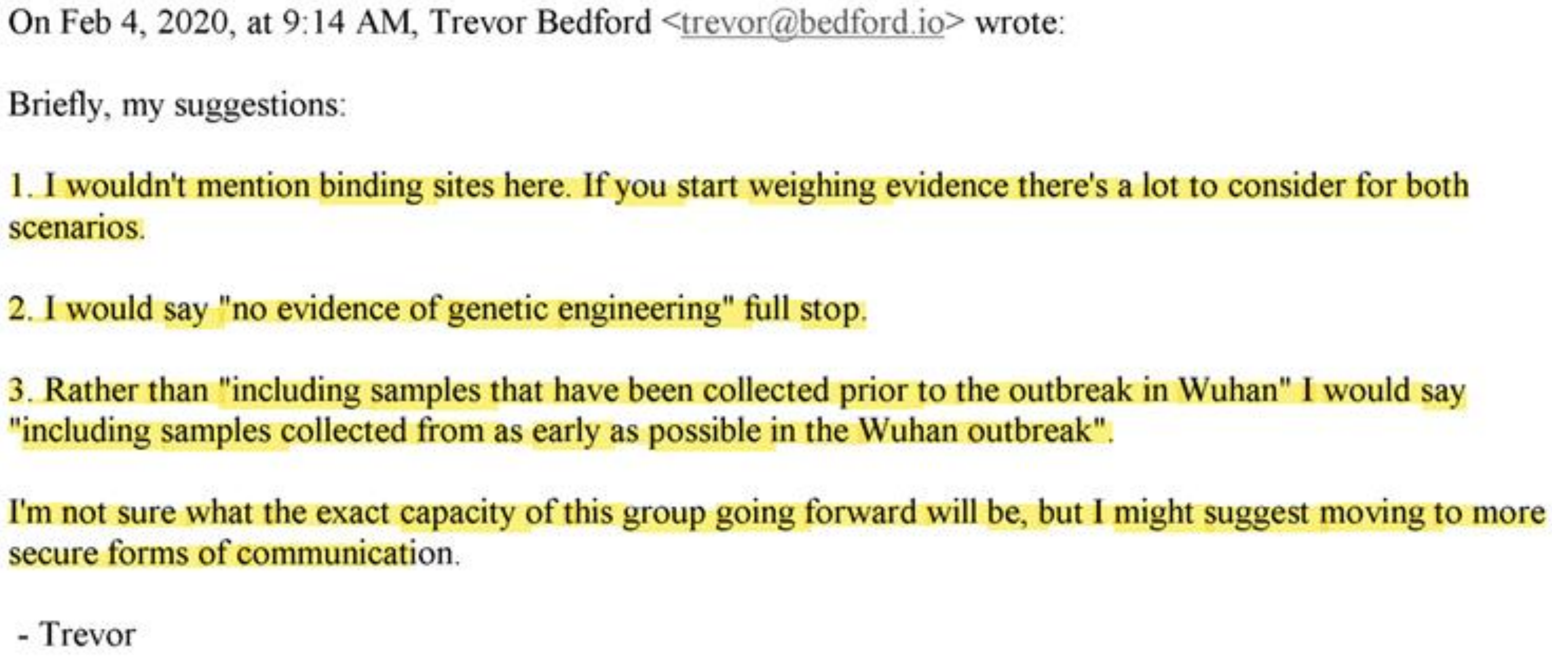
On Feb 4, 2020, at 6:10 AM, Pope, Andrew <APope@nas.edu> wrote:

Many thanks again for your thoughtful participation yesterday. The plans have changed in terms of our product. Instead of a “Based on Science” web posting, we are now developing a letter that will be signed by the 3 Presidents of our 3 Academies (NAS, Marcia McNutt; NAM, Victor Dzau; NAE, John Anderson), in response to a letter from OSTP. We think this will be more appropriate and expeditious.

Thus, given the urgency of the request from OSTP and HHS we ask that you please review the attached DRAFT CONFIDENTIAL letter, and let us know if you have any concerns or suggested edits. In particular, we would like to ask if there might be some additional detail added to the data needs that are identified. We think it would be helpful to be a bit more specific, but don’t want to go into too much detail either. Your help there would be most helpful.

Many sincere thanks again for your continued engagement on this important activity!

Andy



On Feb 4, 2020, at 9:14 AM, Trevor Bedford <trevor@bedford.io> wrote:

Briefly, my suggestions:

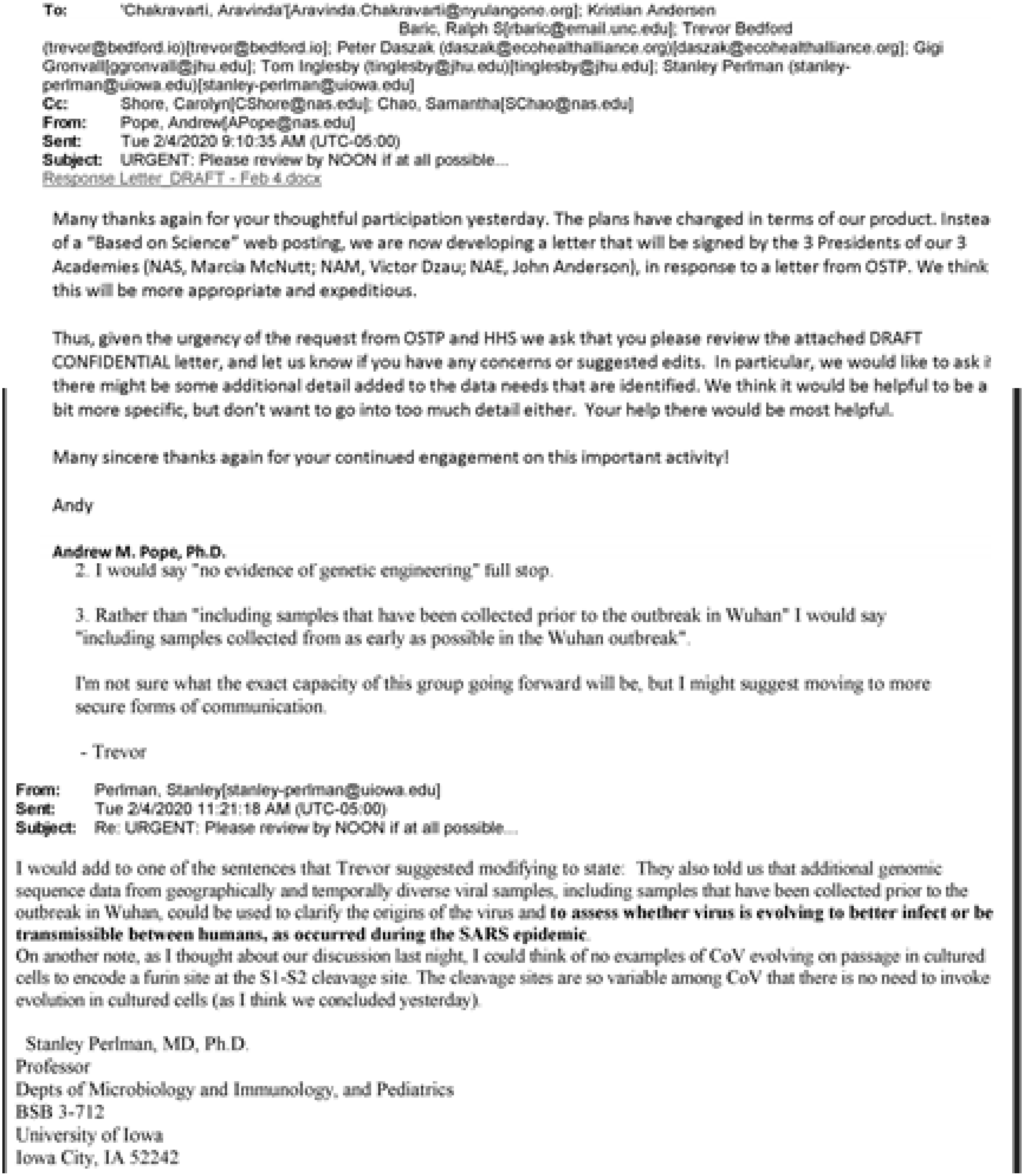
1. I wouldn't mention binding sites here. If you start weighing evidence there's a lot to consider for both scenarios.

2. I would say "no evidence of genetic engineering" full stop.

3. Rather than "including samples that have been collected prior to the outbreak in Wuhan" I would say "including samples collected from as early as possible in the Wuhan outbreak".

I'm not sure what the exact capacity of this group going forward will be, but I might suggest moving to more secure forms of communication.

- Trevor



To: 'Chakravarti, Aravinda'[Aravinda.Chakravarti@nyulangone.org]; Kristian Andersen
Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford
(trevor@bedford.io)[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Pope, Andrew[APope@nas.edu]
Sent: Tue 2/4/2020 9:10:35 AM (UTC-05:00)
Subject: URGENT: Please review by NOON if at all possible...
Response Letter_DRAFT - Feb 4.docx

Many thanks again for your thoughtful participation yesterday. The plans have changed in terms of our product. Instea of a "Based on Science" web posting, we are now developing a letter that will be signed by the 3 Presidents of our 3 Academies (NAS, Marcia McNutt; NAM, Victor Dzau; NAE, John Anderson), in response to a letter from OSTP. We think this will be more appropriate and expeditious.

Thus, given the urgency of the request from OSTP and HHS we ask that you please review the attached DRAFT CONFIDENTIAL letter, and let us know if you have any concerns or suggested edits. In particular, we would like to ask i there might be some additional detail added to the data needs that are identified. We think it would be helpful to be a bit more specific, but don't want to go into too much detail either. Your help there would be most helpful.

Many sincere thanks again for your continued engagement on this important activity!

Andy

Andrew M. Pope, Ph.D.

2. I would say "no evidence of genetic engineering" full stop.

3. Rather than "including samples that have been collected prior to the outbreak in Wuhan" I would say "including samples collected from as early as possible in the Wuhan outbreak".

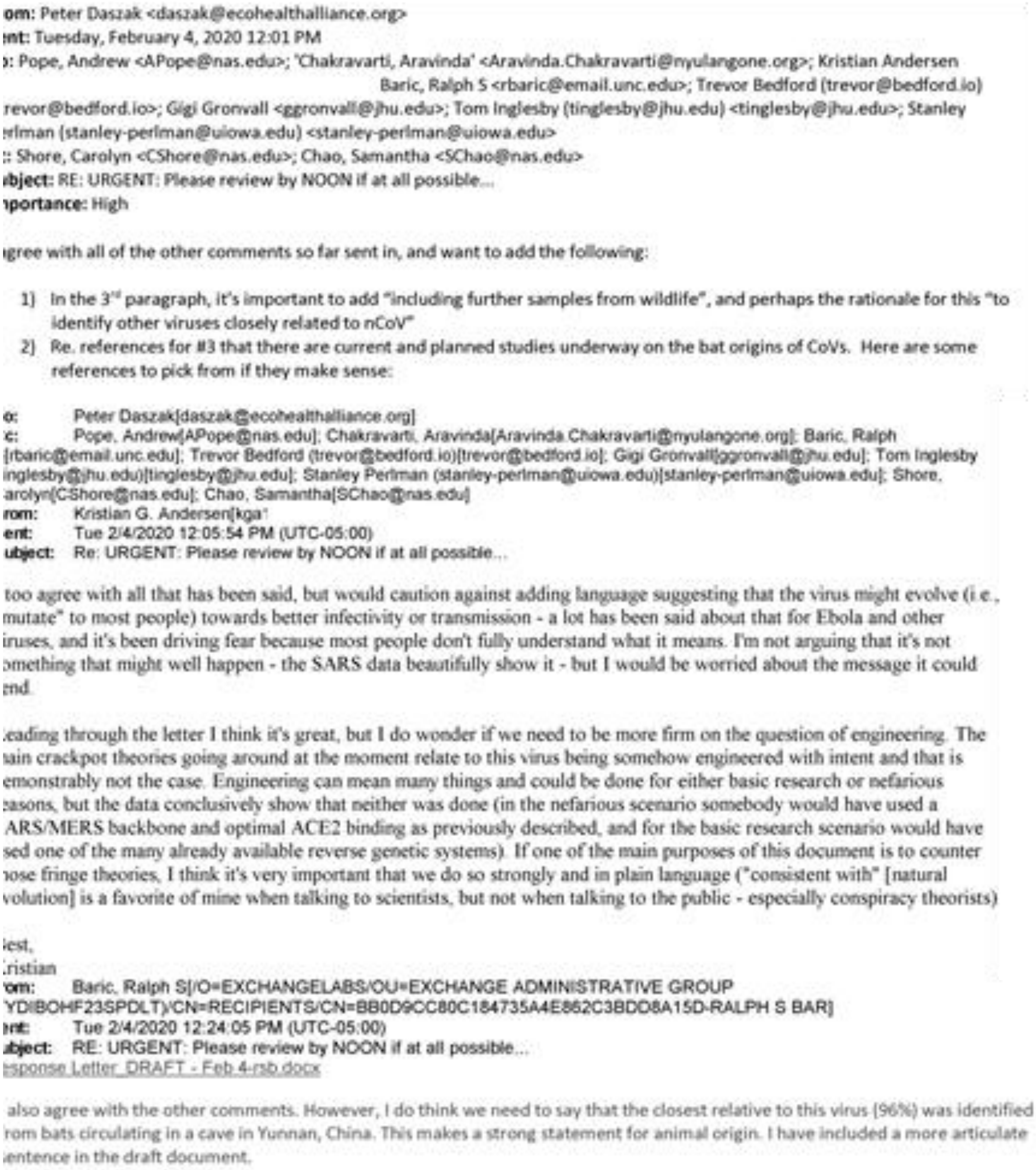
I'm not sure what the exact capacity of this group going forward will be, but I might suggest moving to more secure forms of communication.

\- Trevor

From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Tue 2/4/2020 11:21:18 AM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I would add to one of the sentences that Trevor suggested modifying to state: They also told us that additional genomic sequence data from geographically and temporally diverse viral samples, including samples that have been collected prior to the outbreak in Wuhan, could be used to clarify the origins of the virus and **to assess whether virus is evolving to better infect or be transmissible between humans, as occurred during the SARS epidemic**.
On another note, as I thought about our discussion last night, I could think of no examples of CoV evolving on passage in cultured cells to encode a furin site at the S1-S2 cleavage site. The cleavage sites are so variable among CoV that there is no need to invoke evolution in cultured cells (as I think we concluded yesterday).

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242



om: Peter Daszak <daszak@ecohealthalliance.org>
ent: Tuesday, February 4, 2020 12:01 PM
): Pope, Andrew <APope@nas.edu>; 'Chakravarti, Aravinda' <Aravinda.Chakravarti@nyulangone.org>; Kristian Andersen
Baric, Ralph S <rbaric@email.unc.edu>; Trevor Bedford (trevor@bedford.io)
revor@bedford.io>; Gigi Gronvall <ggronvall@jhu.edu>; Tom Inglesby (tinglesby@jhu.edu) <tinglesby@jhu.edu>; Stanley
erlman (stanley-perlman@uiowa.edu) <stanley-perlman@uiowa.edu>
:: Shore, Carolyn <CShore@nas.edu>; Chao, Samantha <SChao@nas.edu>
ıbject: RE: URGENT: Please review by NOON if at all possible...
nportance: High

ıgree with all of the other comments so far sent in, and want to add the following:

1) In the 3rd paragraph, it's important to add "including further samples from wildlife", and perhaps the rationale for this "to identify other viruses closely related to nCoV"
2) Re. references for #3 that there are current and planned studies underway on the bat origins of CoVs. Here are some references to pick from if they make sense:

o: Peter Daszak[daszak@ecohealthalliance.org]
c: Pope, Andrew[APope@nas.edu]; Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Baric, Ralph
[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby
inglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; Shore,
arolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
rom: Kristian G. Andersen[kga
ent: Tue 2/4/2020 12:05:54 PM (UTC-05:00)
ubject: Re: URGENT: Please review by NOON if at all possible...

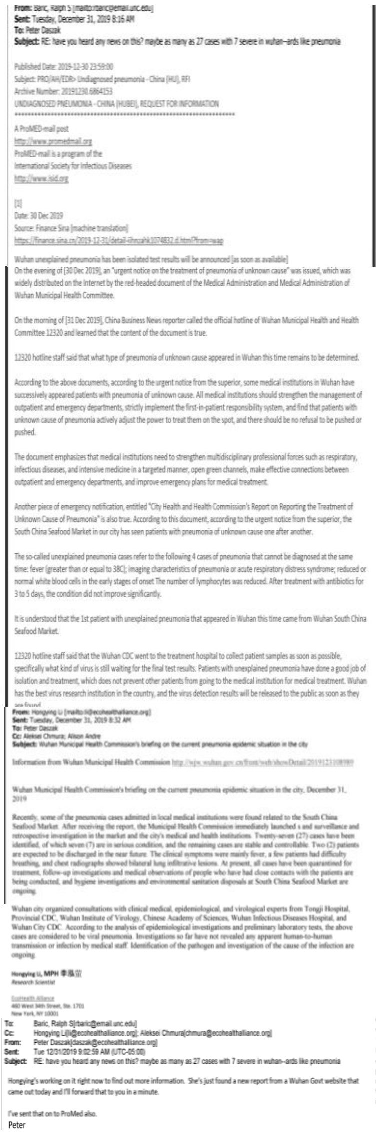
too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., mutate" to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other iruses, and it's been driving fear because most people don't fully understand what it means. I'm not arguing that it's not omething that might well happen - the SARS data beautifully show it - but I would be worried about the message it could end.

eading through the letter I think it's great, but I do wonder if we need to be more firm on the question of engineering. The ıain crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is emonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious easons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a ARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have sed one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter ıose fringe theories, I think it's very important that we do so strongly and in plain language ("consistent with" [natural volution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists)

est,
ristian

om: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP
YDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
ent: Tue 2/4/2020 12:24:05 PM (UTC-05:00)
ıbject: RE: URGENT: Please review by NOON if at all possible...
esponse Letter_DRAFT - Feb 4-rsb.docx

also agree with the other comments. However, I do think we need to say that the closest relative to this virus (96%) was identified rom bats circulating in a cave in Yunnan, China. This makes a strong statement for animal origin. I have included a more articulate entence in the draft document.



From: Baric, Ralph S [mailto:rbaric@email.unc.edu]
Sent: Tuesday, December 31, 2019 8:16 AM
To: Peter Daszak
Subject: RE: have you heard any news on this? maybe as many as 27 cases with 7 severe in wuhan--ards like pneumonia

Published Date: 2019-12-30 23:59:00
Subject: PRO/AH/EDR> Undiagnosed pneumonia - China (HU), RFI
Archive Number: 20191230.6864153
UNDIAGNOSED PNEUMONIA - CHINA (HUBEI), REQUEST FOR INFORMATION
****
A ProMED-mail post
http://www.promedmail.org
ProMED-mail is a program of the
International Society for Infectious Diseases
http://www.isid.org

[1]
Date: 30 Dec 2019
Source: Finance Sina [machine translation]
https://finance.sina.cn/2019-12-31/detail-iihnzahk1074832.d.html?from=wap

Wuhan unexplained pneumonia has been isolated test results will be announced [as soon as available]
On the evening of [30 Dec 2019], an "urgent notice on the treatment of pneumonia of unknown cause" was issued, which was widely distributed on the Internet by the red-headed document of the Medical Administration and Medical Administration of Wuhan Municipal Health Committee.

On the morning of [31 Dec 2019], China Business News reporter called the official hotline of Wuhan Municipal Health and Health Committee 12320 and learned that the content of the document is true.

12320 hotline staff said that what type of pneumonia of unknown cause appeared in Wuhan this time remains to be determined.

According to the above documents, according to the urgent notice from the superior, some medical institutions in Wuhan have successively appeared patients with pneumonia of unknown cause. All medical institutions should strengthen the management of outpatient and emergency departments, strictly implement the first-in-patient responsibility system, and find that patients with unknown cause of pneumonia actively adjust the power to treat them on the spot, and there should be no refusal to be pushed or pushed.

The document emphasizes that medical institutions need to strengthen multidisciplinary professional forces such as respiratory, infectious diseases, and intensive medicine in a targeted manner, open green channels, make effective connections between outpatient and emergency departments, and improve emergency plans for medical treatment.

Another piece of emergency notification, entitled "City Health and Health Commission's Report on Reporting the Treatment of Unknown Cause of Pneumonia" is also true. According to this document, according to the urgent notice from the superior, the South China Seafood Market in our city has seen patients with pneumonia of unknown cause one after another.

The so-called unexplained pneumonia cases refer to the following 4 cases of pneumonia that cannot be diagnosed at the same time: fever (greater than or equal to 38C); imaging characteristics of pneumonia or acute respiratory distress syndrome; reduced or normal white blood cells in the early stages of onset The number of lymphocytes was reduced. After treatment with antibiotics for 3 to 5 days, the condition did not improve significantly.

It is understood that the 1st patient with unexplained pneumonia that appeared in Wuhan this time came from Wuhan South China Seafood Market.

12320 hotline staff said that the Wuhan CDC went to the treatment hospital to collect patient samples as soon as possible, specifically what kind of virus is still waiting for the final test results. Patients with unexplained pneumonia have done a good job of isolation and treatment, which does not prevent other patients from going to the medical institution for medical treatment. Wuhan has the best virus research institution in the country, and the virus detection results will be released to the public as soon as they are found.

From: Hongying Li [mailto:li@ecohealthalliance.org]
Sent: Tuesday, December 31, 2019 8:32 AM
To: Peter Daszak
Cc: Aleksei Chmura; Alison Andre
Subject: Wuhan Municipal Health Commission's briefing on the current pneumonia epidemic situation in the city

Information from Wuhan Municipal Health Commission http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989

Wuhan Municipal Health Commission's briefing on the current pneumonia epidemic situation in the city, December 31, 2019

Recently, some of the pneumonia cases admitted in local medical institutions were found related to the South China Seafood Market. After receiving the report, the Municipal Health Commission immediately launched s and surveillance and retrospective investigation in the market and the city's medical and health institutions. Twenty-seven (27) cases have been identified, of which seven (7) are in serious condition, and the remaining cases are stable and controllable. Two (2) patients are expected to be discharged in the near future. The clinical symptoms were mainly fever, a few patients had difficulty breathing, and chest radiographs showed bilateral lung infiltrative lesions. At present, all cases have been quarantined for treatment, follow-up investigations and medical observations of people who have had close contacts with the patients are being conducted, and hygiene investigations and environmental sanitation disposals at South China Seafood Market are ongoing.

Wuhan city organized consultations with clinical medical, epidemiological, and virological experts from Tongji Hospital, Provincial CDC, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan Infectious Diseases Hospital, and Wuhan City CDC. According to the analysis of epidemiological investigations and preliminary laboratory tests, the above cases are considered to be viral pneumonia. Investigations so far have not revealed any apparent human-to-human transmission or infection by medical staff. Identification of the pathogen and investigation of the cause of the infection are ongoing.

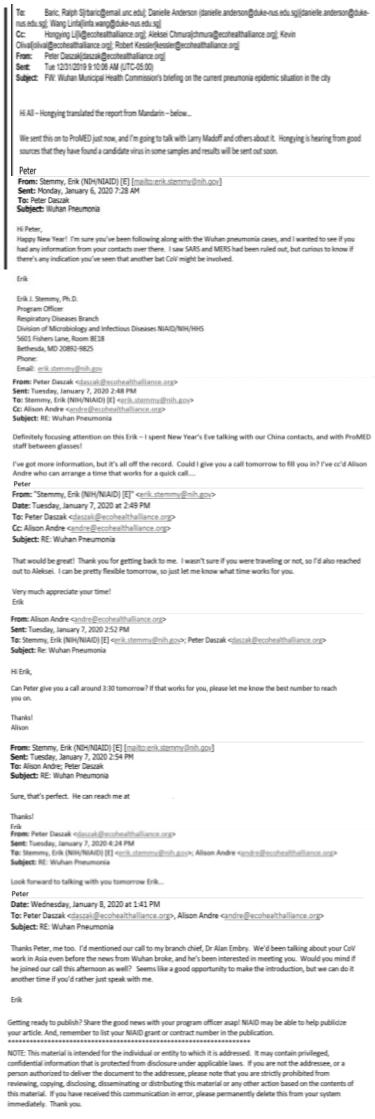
Hongying Li, MPH 李泓萤
Research Scientist

EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Hongying Li[li@ecohealthalliance.org]; Aleksei Chmura[chmura@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Tue 12/31/2019 9:02:59 AM (UTC-05:00)
Subject: RE: have you heard any news on this? maybe as many as 27 cases with 7 severe in wuhan--ards like pneumonia

Hongying's working on it right now to find out more information. She's just found a new report from a Wuhan Govt website that came out today and I'll forward that to you in a minute.

I've sent that on to ProMed also.
Peter



To: Baric, Ralph S[rbaric@email.unc.edu]; Danielle Anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Wang Linfa[linfa.wang@duke-nus.edu.sg]
Cc: Hongying Li[li@ecohealthalliance.org]; Aleksei Chmura[chmura@ecohealthalliance.org]; Kevin Olival[olival@ecohealthalliance.org]; Robert Kessler[kessler@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Tue 12/31/2019 9:10:06 AM (UTC-05:00)
Subject: FW: Wuhan Municipal Health Commission's briefing on the current pneumonia epidemic situation in the city

Hi All – Hongying translated the report from Mandarin – below…

We sent this on to ProMED just now, and I'm going to talk with Larry Madoff and others about it. Hongying is hearing from good sources that they have found a candidate virus in some samples and results will be sent out soon.

Peter

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Monday, January 6, 2020 7:28 AM
To: Peter Daszak
Subject: Wuhan Pneumonia

Hi Peter,
Happy New Year! I'm sure you've been following along with the Wuhan pneumonia cases, and I wanted to see if you had any information from your contacts over there. I saw SARS and MERS had been ruled out, but curious to know if there's any indication you've seen that another bat CoV might be involved.

Erik

Erik J. Stemmy, Ph.D.
Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases NIAID/NIH/HHS
5601 Fishers Lane, Room 8E18
Bethesda, MD 20892-9825
Phone:
Email: erik.stemmy@nih.gov

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 2:48 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

Definitely focusing attention on this Erik – I spent New Year's Eve talking with our China contacts, and with ProMED staff between glasses!

I've got more information, but it's all off the record. Could I give you a call tomorrow to fill you in? I've cc'd Alison Andre who can arrange a time that works for a quick call….
Peter

From: "Stemmy, Erik (NIH/NIAID) [E]" <erik.stemmy@nih.gov>
Date: Tuesday, January 7, 2020 at 2:49 PM
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

That would be great! Thank you for getting back to me. I wasn't sure if you were traveling or not, so I'd also reached out to Aleksei. I can be pretty flexible tomorrow, so just let me know what time works for you.

Very much appreciate your time!
Erik

From: Alison Andre <andre@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 2:52 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: Wuhan Pneumonia

Hi Erik,

Can Peter give you a call around 3:30 tomorrow? If that works for you, please let me know the best number to reach you on.

Thanks!
Alison

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Tuesday, January 7, 2020 2:54 PM
To: Alison Andre; Peter Daszak
Subject: RE: Wuhan Pneumonia

Sure, that's perfect. He can reach me at

Thanks!
Erik

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, January 7, 2020 4:24 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

Look forward to talking with you tomorrow Erik…
Peter

Date: Wednesday, January 8, 2020 at 1:41 PM
To: Peter Daszak <daszak@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan Pneumonia

Thanks Peter, me too. I'd mentioned our call to my branch chief, Dr Alan Embry. We'd been talking about your CoV work in Asia even before the news from Wuhan broke, and he's been interested in meeting you. Would you mind if he joined our call this afternoon as well? Seems like a good opportunity to make the introduction, but we can do it another time if you'd rather just speak with me.

Erik

Getting ready to publish? Share the good news with your program officer asap! NIAID may be able to help publicize your article. And, remember to list your NIAID grant or contract number in the publication.
****
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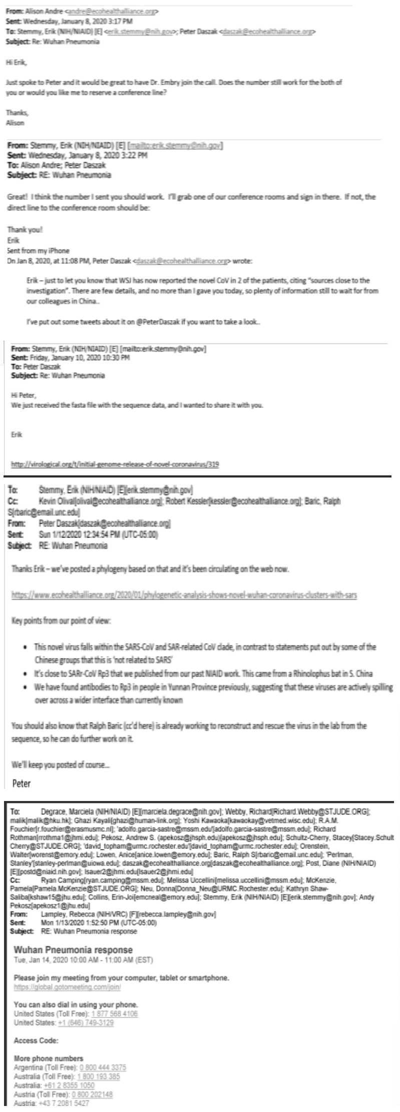

From: Alison Andre <andre@ecohealthalliance.org>
Sent: Wednesday, January 8, 2020 3:17 PM
To: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: Wuhan Pneumonia

Hi Erik,

Just spoke to Peter and it would be great to have Dr. Embry join the call. Does the number still work for the both of you or would you like me to reserve a conference line?

Thanks,
Alison

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Wednesday, January 8, 2020 3:22 PM
To: Alison Andre; Peter Daszak
Subject: RE: Wuhan Pneumonia

Great! I think the number I sent you should work. I'll grab one of our conference rooms and sign in there. If not, the direct line to the conference room should be:

Thank you!
Erik
Sent from my iPhone
On Jan 8, 2020, at 11:08 PM, Peter Daszak <daszak@ecohealthalliance.org> wrote:

> Erik – just to let you know that WSJ has now reported the novel CoV in 2 of the patients, citing "sources close to the investigation". There are few details, and no more than I gave you today, so plenty of information still to wait for from our colleagues in China..
>
> I've put out some tweets about it on @PeterDaszak if you want to take a look..

From: Stemmy, Erik (NIH/NIAID) [E] [mailto:erik.stemmy@nih.gov]
Sent: Friday, January 10, 2020 10:30 PM
To: Peter Daszak
Subject: Re: Wuhan Pneumonia

Hi Peter,
We just received the fasta file with the sequence data, and I wanted to share it with you.

Erik

http://virological.org/t/initial-genome-release-of-novel-coronavirus/319

To: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Cc: Kevin Olival[olival@ecohealthalliance.org]; Robert Kessler[kessler@ecohealthalliance.org]; Baric, Ralph S[rbaric@email.unc.edu]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Sun 1/12/2020 12:34:54 PM (UTC-05:00)
Subject: RE: Wuhan Pneumonia

Thanks Erik – we've posted a phylogeny based on that and it's been circulating on the web now.

https://www.ecohealthalliance.org/2020/01/phylogenetic-analysis-shows-novel-wuhan-coronavirus-clusters-with-sars

Key points from our point of view:

- This novel virus falls within the SARS-CoV and SAR-related CoV clade, in contrast to statements put out by some of the Chinese groups that this is 'not related to SARS'
- It's close to SARr-CoV Rp3 that we published from our past NIAID work. This came from a Rhinolophus bat in S. China
- We have found antibodies to Rp3 in people in Yunnan Province previously, suggesting that these viruses are actively spilling over across a wider interface than currently known

You should also know that Ralph Baric (cc'd here) is already working to reconstruct and rescue the virus in the lab from the sequence, so he can do further work on it.

We'll keep you posted of course…

Peter

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; 'adolfo.garcia-sastre@mssm.edu'[adolfo.garcia-sastre@mssm.edu]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S. (apekosz@jhsph.edu)[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schult Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'[david_topham@urmc.rochester.edu]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; lsauer2@jhmi.edu[lsauer2@jhmi.edu]
Cc: Ryan Camping[ryan.camping@mssm.edu]; Melissa Uccellini[melissa.uccellini@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Collins, Erin-Joi[emcneal@emory.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]
From: Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]
Sent: Mon 1/13/2020 1:52:50 PM (UTC-05:00)
Subject: RE: Wuhan Pneumonia response

Wuhan Pneumonia response
Tue, Jan 14, 2020 10:00 AM - 11:00 AM (EST)

Please join my meeting from your computer, tablet or smartphone.
https://global.gotomeeting.com/join/

You can also dial in using your phone.
United States (Toll Free): 1 877 568 4106
United States: +1 (646) 749-3129

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More phone numbers
Argentina (Toll Free): 0 800 444 3375
Australia (Toll Free): 1 800 193 385
Australia: +61 2 8355 1050
Austria (Toll Free): 0 800 202148
Austria: +43 7 2081 5427

Peter

To: Carolyn Clark[carolyn.clark@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; Raul Gomez Roman[raul.gomezroman@cepi.net]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; barney.graham@nih.gov[barney.graham@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot@pasteur.fr[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]
Cc: HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]
From: William Dowling[william.dowling@cepi.net]
Sent: Thur 1/23/2020 4:40:21 PM (UTC-05:00)
Subject: WHO Consultation regarding the Wuhan coronavirus
Letko_2020_receptor usage of 2019 nCoV.pdf
Zhao et al 2020 supp data.pdf
Zhou et al 2020.pdf

Hello all,

On behalf of the WHO R&D Blueprint team, I am writing to request your participation on a call tomorrow at 9 PM Central European time (which will be Saturday morning for some of you). The purpose of the call is to lend your expertise to coordination of WHO response efforts. To that end , we would like to discuss the current status of efforts to culture the Wuhan coronavirus (or generate a recombinant virus); recent sequence data and modeling of the Spike protein; and potential next steps to assess cross reactivity with other coronaviruses. We realize that this is very short notice, but the situation is very dynamic. This would be an initial call with lengthier and more detailed calls in the near future.

Also, for those who have not seen them, I am attaching two reports on this topic that just came out and are highly relevant to the conversation.

Please let us know if you can make it. Call in details will be sent tomorrow.

Thank you,

Bill Dowling (seconded to WHO)

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

-----Original Message-----
From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, January 13, 2020 6:43 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Sims, Amy C <sims0018@email.unc.edu>
Cc: Alison Andre <andre@ecohealthalliance.org>
Subject: Call with NIH tomorrow

Ralph - I'm having an informational call with our program officer re the Wuhan outbreak tomorrow at 10am - do you want to join and are you available?
Peter

-----Original Message-----
From: Baric, Ralph S [mailto:rbaric@email.unc.edu]
Sent: Monday, January 13, 2020 6:50 PM
To: Peter Daszak
Subject: RE: Call with NIH tomorrow

Hi Peter, I have to participate on an NIH call tomorrow at 10. I believe it's a strategic meeting designed to help craft a NIH response plan to the WU-CoV. Hope things are going well. Looks like we found our highly variable SARS-like CoV! Ralph

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Alison Andre[andre@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Mon 1/13/2020 7:55:43 PM (UTC-05:00)
Subject: RE: Call with NIH tomorrow

OK - great. It sounds like we're on the same call!

And my thoughts exactly re. the highly variable SARS-like CoV. I've told journalists about it, but it's a complicated story for them to get across..
No prob if you can't - I did one last week just to let them know what we think is going on behind the scenes in China.

Cheers,

Peter

February 6, 2020

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy
1650 Pennsylvania Avenue, NW
Washington, D.C. 20504

Dear Dr. Droegemeier:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the declaration of a public health emergency and potential for misinformation to confound the response.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health. We wanted their views about the data needs that could help elucidate the origin and evolution of 2019-nCoV.

Research studies to better understand the origin of 2019-nCoV and how it relates to viruses found in bats and other species are already underway.[3] The closest known relative of 2019-nCoV appears to be a coronavirus identified from bat-derived samples collected in China.[4] The experts informed us that additional genomic sequence data from geographically- and temporally-diverse viral samples are needed to determine the origin and evolution of the virus. Samples collected as early as possible in the outbreak in Wuhan and samples from wildlife would be particularly valuable. Understanding the driving forces behind viral evolution would help facilitate the development of more effective strategies for managing the 2019-nCoV outbreak and for preventing future outbreaks. In this regard, we understand from Chunli Bai, President, Chinese Academy of Sciences, and the Alliance of International Science Organizations (ANSO), that the Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences is willing to share isolates of the 2019-nCoV with the international community and is working with the University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. International collaboration of this kind is more important than ever to overcome these types of global challenges.

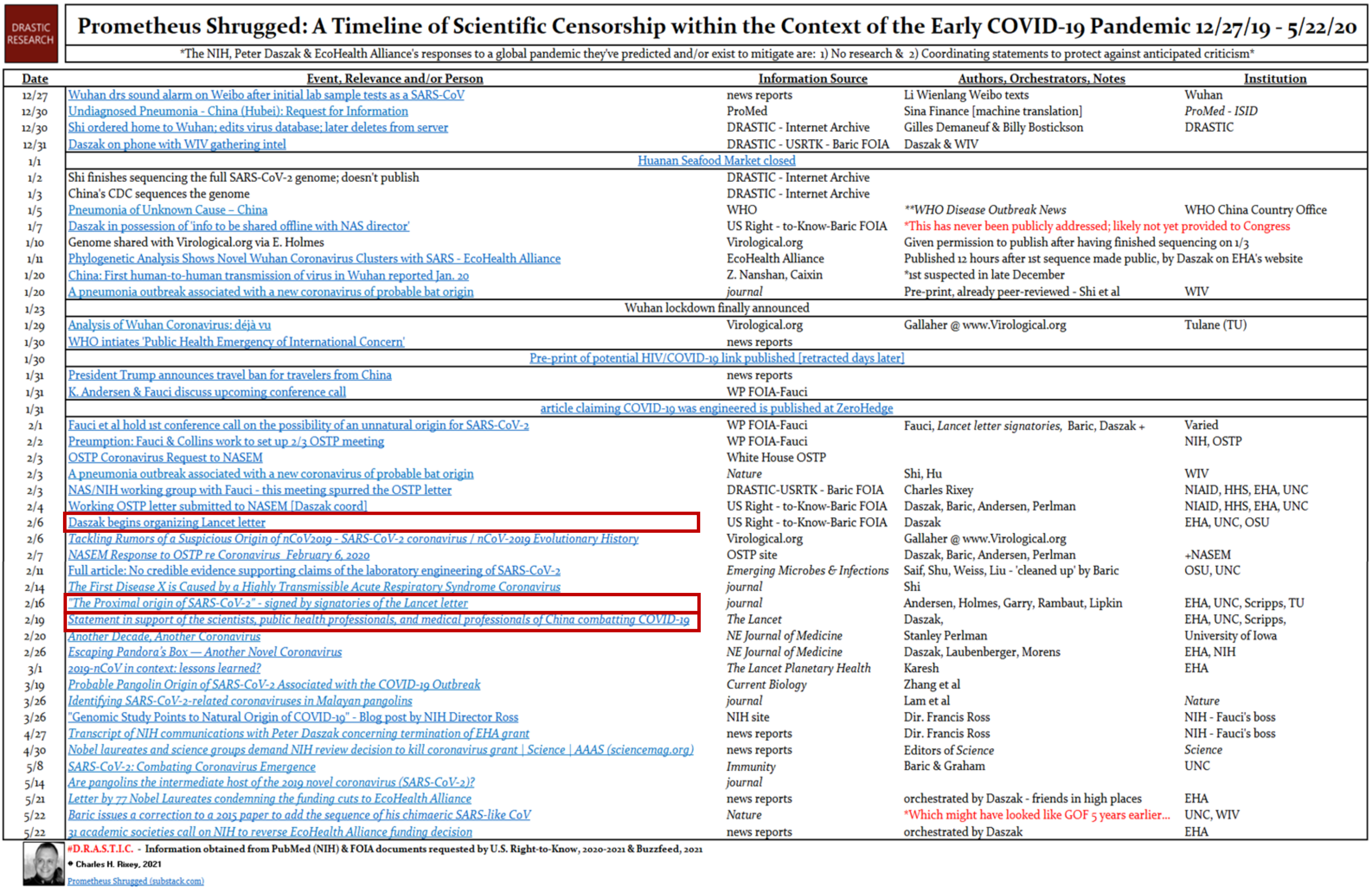
---

[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] Experts consulted: Kristian G. Andersen (Scripps Research Institute), Ralph Baric (UNC School of Public Health), Trevor Bedford (Fred Hutchinson Cancer Institute), Aravinda Chakravarti (New York University School of Medicine), Peter Daszak (EcoHealth Alliance), Gigi K. Gronvall (Johns Hopkins Bloomberg School of Public Health), Tom Inglesby (Johns Hopkins Center for Health Security), and Stanley Perlman (University of Iowa).

[3] Latinne *et al.* "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications*, in review.

[4] Zhou *et. al.* "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 2020. https://doi.org/10.1038/s41586-020-2012-7 (2020).


DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

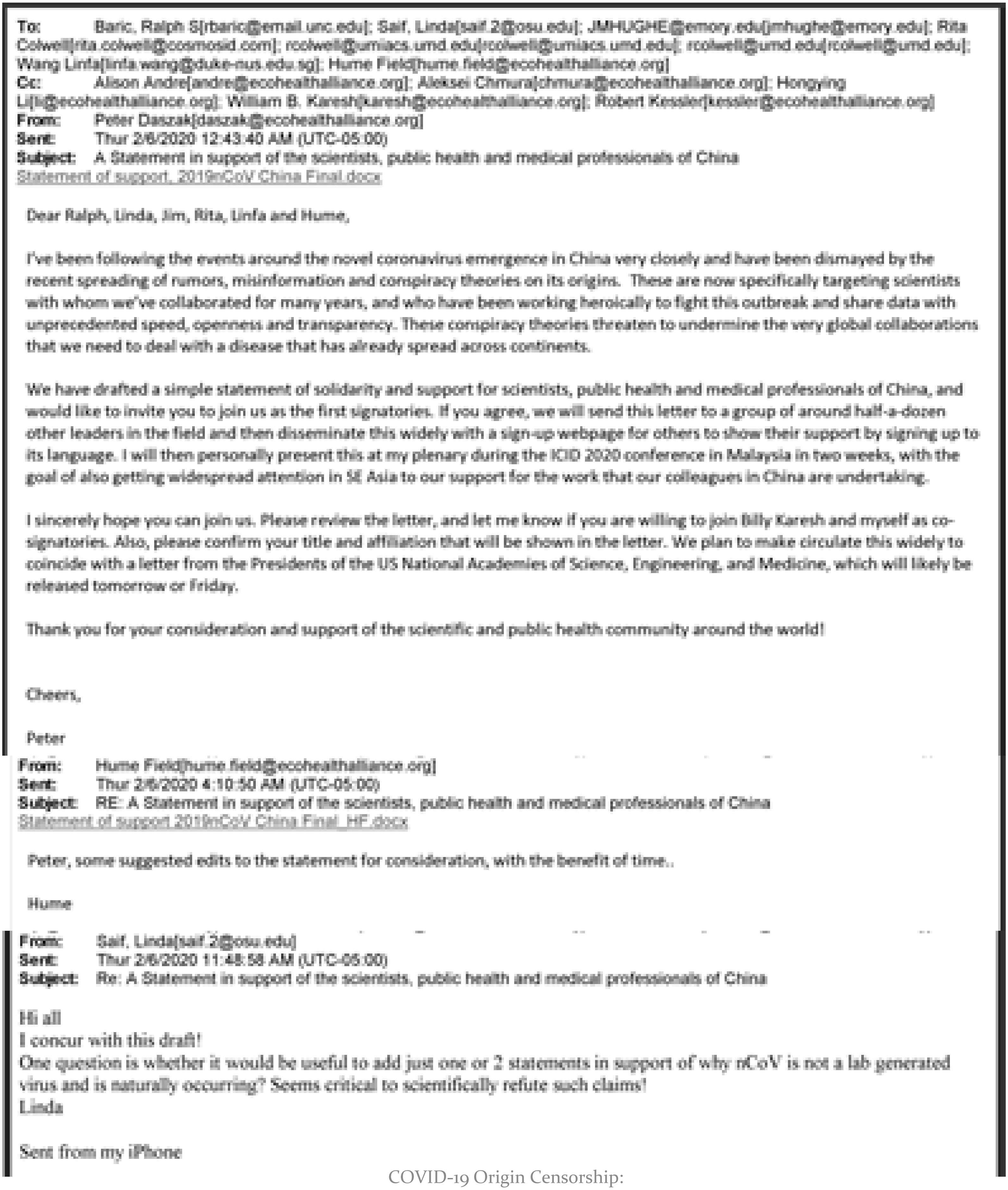
• Charles H. Rixey, 2021

Prometheus Shrugged (substack.com)

Colwell, Linda Saif & Ralph Baric

These highlight further coordination, this time in support of the *Lancet* letter, as Peter Daszak worked to gather signatures from scientists not involved with the 2/3 meeting.

Source: US Right-to-Know FOIA documents for Linda Saif & Rita Colwell



To: Baric, Ralph S[rbaric@email.unc.edu]; Saif, Linda[saif.2@osu.edu]; JMHUGHE@emory.edu[jmhughe@emory.edu]; Rita Colwell[rita.colwell@cosmosid.com]; rcolwell@umiacs.umd.edu[rcolwell@umiacs.umd.edu]; rcolwell@umd.edu[rcolwell@umd.edu]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Hume Field[hume.field@ecohealthalliance.org]
Cc: Alison Andre[andre@ecohealthalliance.org]; Aleksei Chmura[chmura@ecohealthalliance.org]; Hongying Li[li@ecohealthalliance.org]; William B. Karesh[karesh@ecohealthalliance.org]; Robert Kessler[kessler@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Thur 2/6/2020 12:43:40 AM (UTC-05:00)
Subject: A Statement in support of the scientists, public health and medical professionals of China
Statement of support, 2019nCoV China Final.docx

Dear Ralph, Linda, Jim, Rita, Linfa and Hume,

I've been following the events around the novel coronavirus emergence in China very closely and have been dismayed by the recent spreading of rumors, misinformation and conspiracy theories on its origins. These are now specifically targeting scientists with whom we've collaborated for many years, and who have been working heroically to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents.

We have drafted a simple statement of solidarity and support for scientists, public health and medical professionals of China, and would like to invite you to join us as the first signatories. If you agree, we will send this letter to a group of around half-a-dozen other leaders in the field and then disseminate this widely with a sign-up webpage for others to show their support by signing up to its language. I will then personally present this at my plenary during the ICID 2020 conference in Malaysia in two weeks, with the goal of also getting widespread attention in SE Asia to our support for the work that our colleagues in China are undertaking.

I sincerely hope you can join us. Please review the letter, and let me know if you are willing to join Billy Karesh and myself as co-signatories. Also, please confirm your title and affiliation that will be shown in the letter. We plan to make circulate this widely to coincide with a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, which will likely be released tomorrow or Friday.

Thank you for your consideration and support of the scientific and public health community around the world!

Cheers,

Peter

From: Hume Field[hume.field@ecohealthalliance.org]
Sent: Thur 2/6/2020 4:10:50 AM (UTC-05:00)
Subject: RE: A Statement in support of the scientists, public health and medical professionals of China
Statement of support 2019nCoV China Final_HF.docx

Peter, some suggested edits to the statement for consideration, with the benefit of time..

Hume

From: Saif, Linda[saif.2@osu.edu]
Sent: Thur 2/6/2020 11:48:58 AM (UTC-05:00)
Subject: Re: A Statement in support of the scientists, public health and medical professionals of China

Hi all
I concur with this draft!
One question is whether it would be useful to add just one or 2 statements in support of why nCoV is not a lab generated virus and is naturally occurring? Seems critical to scientifically refute such claims!
Linda

Sent from my iPhone

Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

We, the undersigned, are scientists who have followed the emergence of 2019-nCoV, and are deeply concerned about its global impact on people's health and well-being. We have watched as the scientists, public health and medical professionals of China have worked heroically to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. We sign this statement in solidarity with all scientists, public health, and medical professionals in China who continue to save lives and protect *global* health during the challenge of this novel coronavirus outbreak. We want you to know that we are all in this together, with you in front of us on the battlefield against the novel coronavirus.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientific evidence overwhelmingly suggests that this virus originated in wildlife, as have so many other emerging diseases (*1-4*). This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent (INSERT REF). Conspiracy theories will do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We need to prioritize scientific evidence and unity over misinformation and conjecture now. We want you all to know that **we stand with you**, the science and health professionals of China, in your fight against this virus.

We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

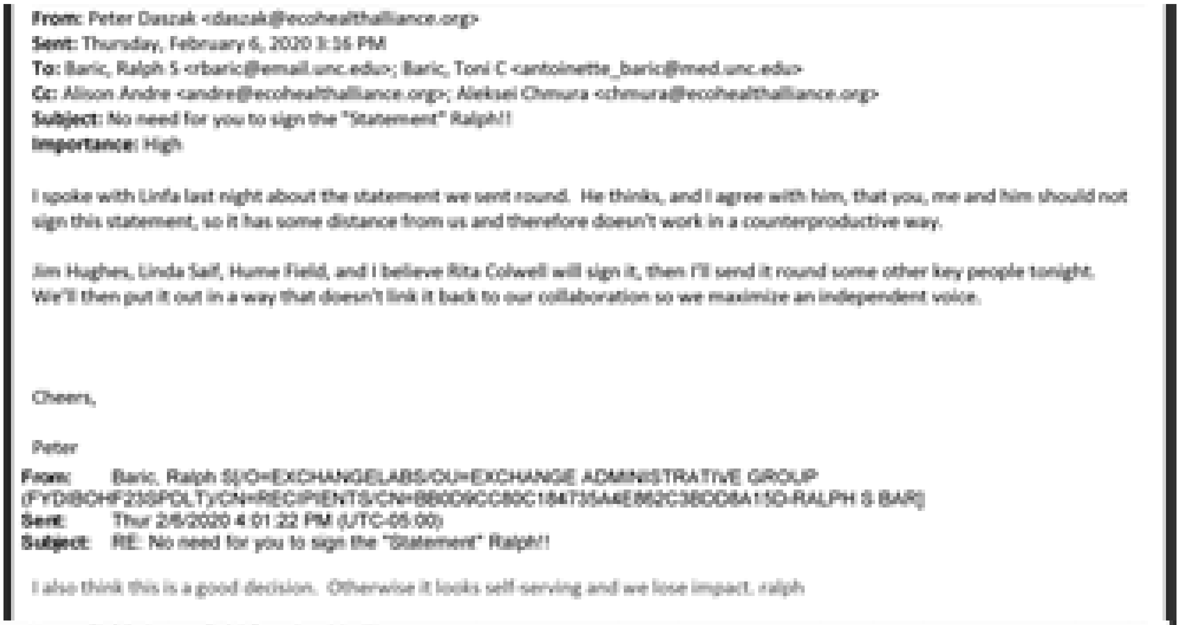
Please add your name in an act of support by going to [INSERT LINK HERE].

Signatories

Dr. Peter Daszak, President, EcoHealth Alliance
Dr. Jim Hughes, Professor Emeritus, Emory University
Dr. Rita Colwell, former Director of National Science Foundation
Dr. Ralph Baric, Professor, The University of North Carolina, Chapel Hill
Dr. Linda Saif, Distinguished University Professor, The Ohio State University
Dr. Billy Karesh, Executive Vice President, EcoHealth Alliance
Dr. Linfa Wang, Professor, Duke-NUS Medical School
Dr. Hume Field, Honorary Professor, The University of Queensland

References

1. P. Zhou *et al.*, A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, (2020).
2. R. Lu *et al.*, Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, (2020).
3. N. Zhu *et al.*, A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*, (2020).
4. L. Ren *et al.*, Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. *Chin Med J. Epub ahead of print*, (2020).



From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Thursday, February 6, 2020 3:16 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>
Cc: Alison Andre <andre@ecohealthalliance.org>; Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: No need for you to sign the "Statement" Ralph!!
Importance: High

I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that you, me and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way.

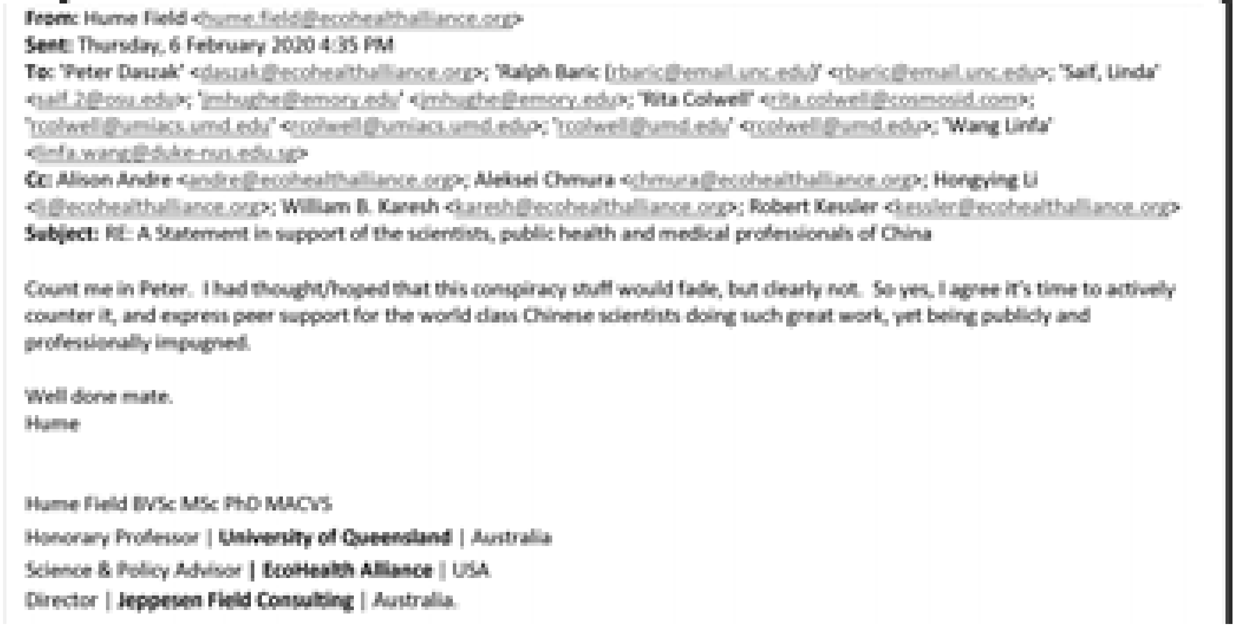
Jim Hughes, Linda Saif, Hume Field, and I believe Rita Colwell will sign it, then I'll send it round some other key people tonight. We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.

Cheers,

Peter

From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC85C184735A4E862C38DD8A15D-RALPH S BAR]
Sent: Thur 2/6/2020 4:01:22 PM (UTC-05:00)
Subject: RE: No need for you to sign the "Statement" Ralph!!

I also think this is a good decision. Otherwise it looks self-serving and we lose impact. ralph

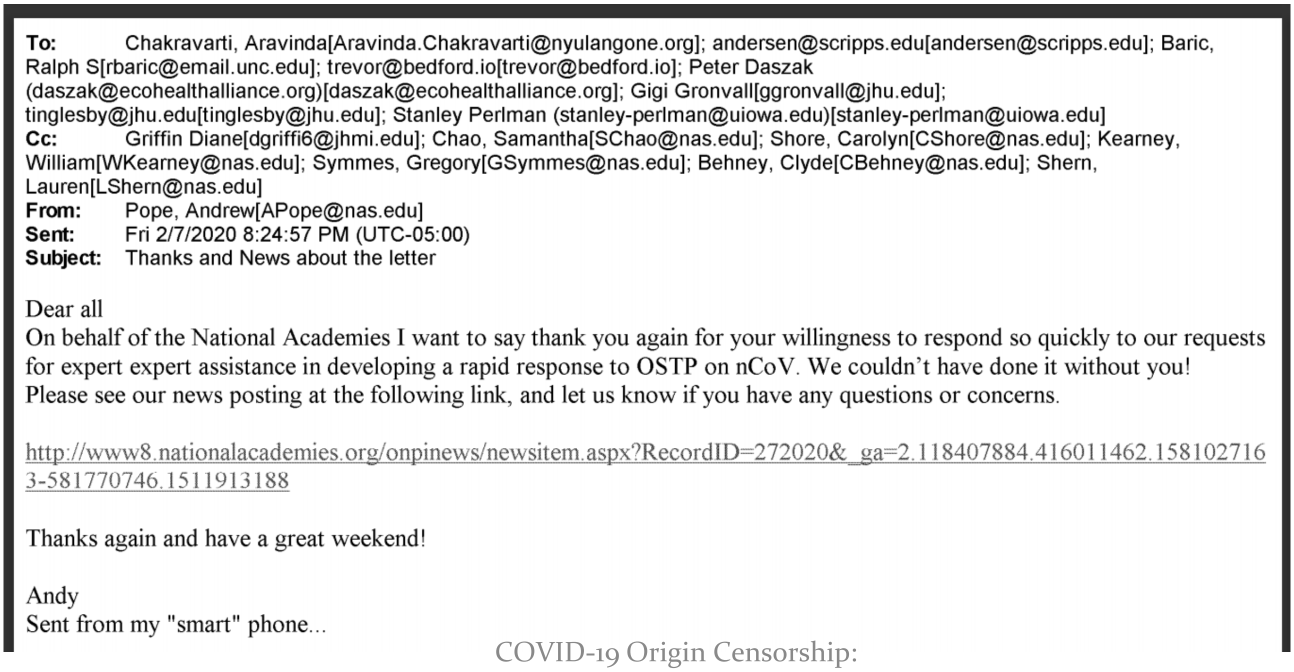


From: Hume Field <hume.field@ecohealthalliance.org>
Sent: Thursday, 6 February 2020 4:35 PM
To: 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Ralph Baric (rbaric@email.unc.edu)' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'jmhughe@emory.edu' <jmhughe@emory.edu>; 'Rita Colwell' <rita.colwell@cosmosid.com>; 'rcolwell@umiacs.umd.edu' <rcolwell@umiacs.umd.edu>; 'rcolwell@umd.edu' <rcolwell@umd.edu>; 'Wang Linfa' <linfa.wang@duke-nus.edu.sg>
Cc: Alison Andre <andre@ecohealthalliance.org>; Aleksei Chmura <chmura@ecohealthalliance.org>; Hongying Li <li@ecohealthalliance.org>; William B. Karesh <karesh@ecohealthalliance.org>; Robert Kessler <kessler@ecohealthalliance.org>
Subject: RE: A Statement in support of the scientists, public health and medical professionals of China

Count me in Peter. I had thought/hoped that this conspiracy stuff would fade, but clearly not. So yes, I agree it's time to actively counter it, and express peer support for the world class Chinese scientists doing such great work, yet being publicly and professionally impugned.

Well done mate.
Hume

Hume Field BVSc MSc PhD MACVS
Honorary Professor | **University of Queensland** | Australia
Science & Policy Advisor | **EcoHealth Alliance** | USA
Director | **Jeppesen Field Consulting** | Australia



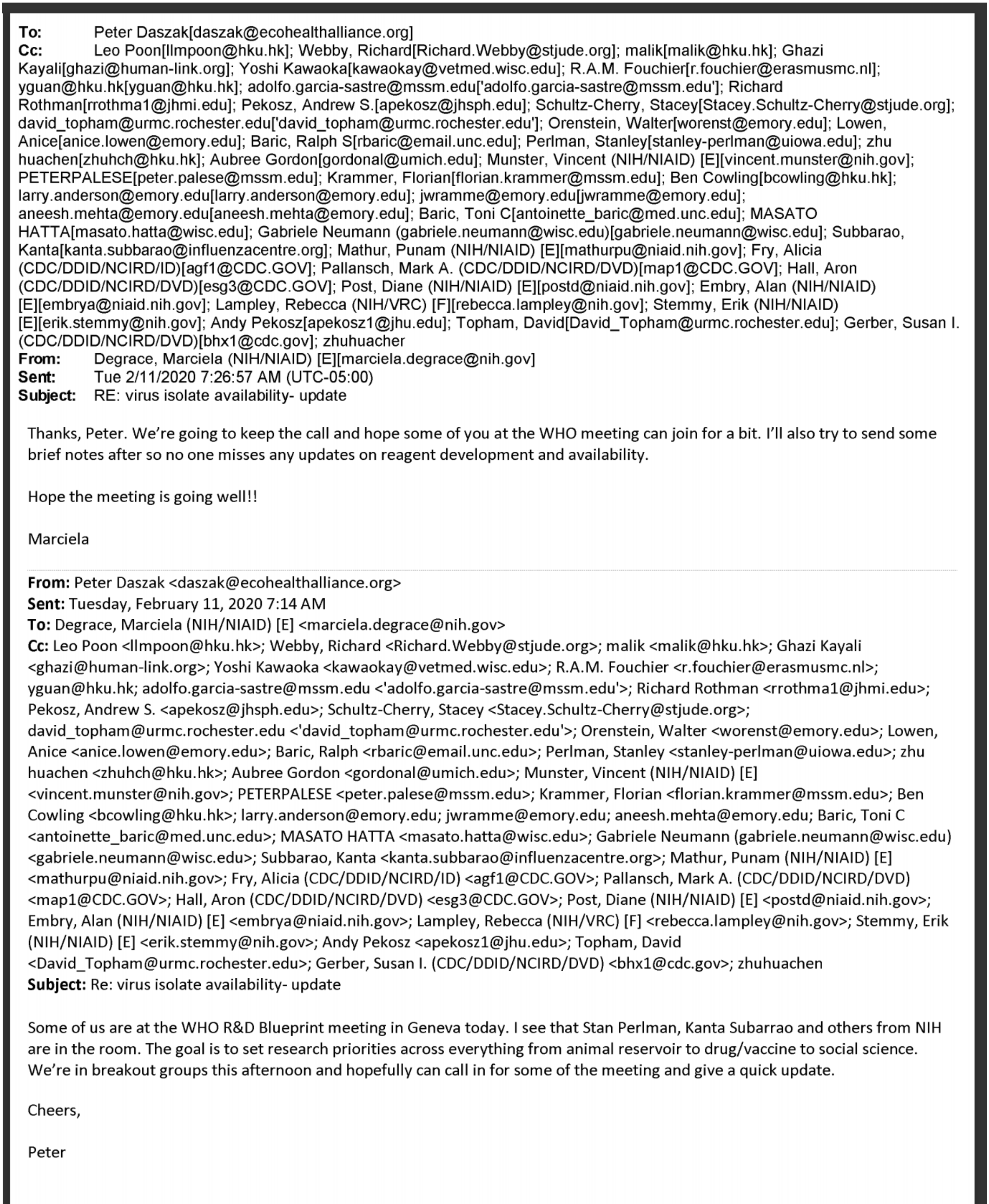
To: Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; andersen@scripps.edu[andersen@scripps.edu]; Baric, Ralph S[rbaric@email.unc.edu]; trevor@bedford.io[trevor@bedford.io]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Gigi Gronvall[ggronvall@jhu.edu]; tinglesby@jhu.edu[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]
Cc: Griffin Diane[dgriffi6@jhmi.edu]; Chao, Samantha[SChao@nas.edu]; Shore, Carolyn[CShore@nas.edu]; Kearney, William[WKearney@nas.edu]; Symmes, Gregory[GSymmes@nas.edu]; Behney, Clyde[CBehney@nas.edu]; Shern, Lauren[LShern@nas.edu]
From: Pope, Andrew[APope@nas.edu]
Sent: Fri 2/7/2020 8:24:57 PM (UTC-05:00)
Subject: Thanks and News about the letter

Dear all
On behalf of the National Academies I want to say thank you again for your willingness to respond so quickly to our requests for expert expert assistance in developing a rapid response to OSTP on nCoV. We couldn't have done it without you!
Please see our news posting at the following link, and let us know if you have any questions or concerns.

http://www8.nationalacademies.org/onpinews/newsitem.aspx?RecordID=272020&_ga=2.118407884.416011462.1581027163-581770746.1511913188

Thanks again and have a great weekend!

Andy
Sent from my "smart" phone...



To: Peter Daszak[daszak@ecohealthalliance.org]
Cc: Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; adolfo.garcia-sastre@mssm.edu['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@stjude.org]; david_topham@urmc.rochester.edu['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Krammer, Florian[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@urmc.rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuacher
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Tue 2/11/2020 7:26:57 AM (UTC-05:00)
Subject: RE: virus isolate availability- update

Thanks, Peter. We're going to keep the call and hope some of you at the WHO meeting can join for a bit. I'll also try to send some brief notes after so no one misses any updates on reagent development and availability.

Hope the meeting is going well!!

Marciela

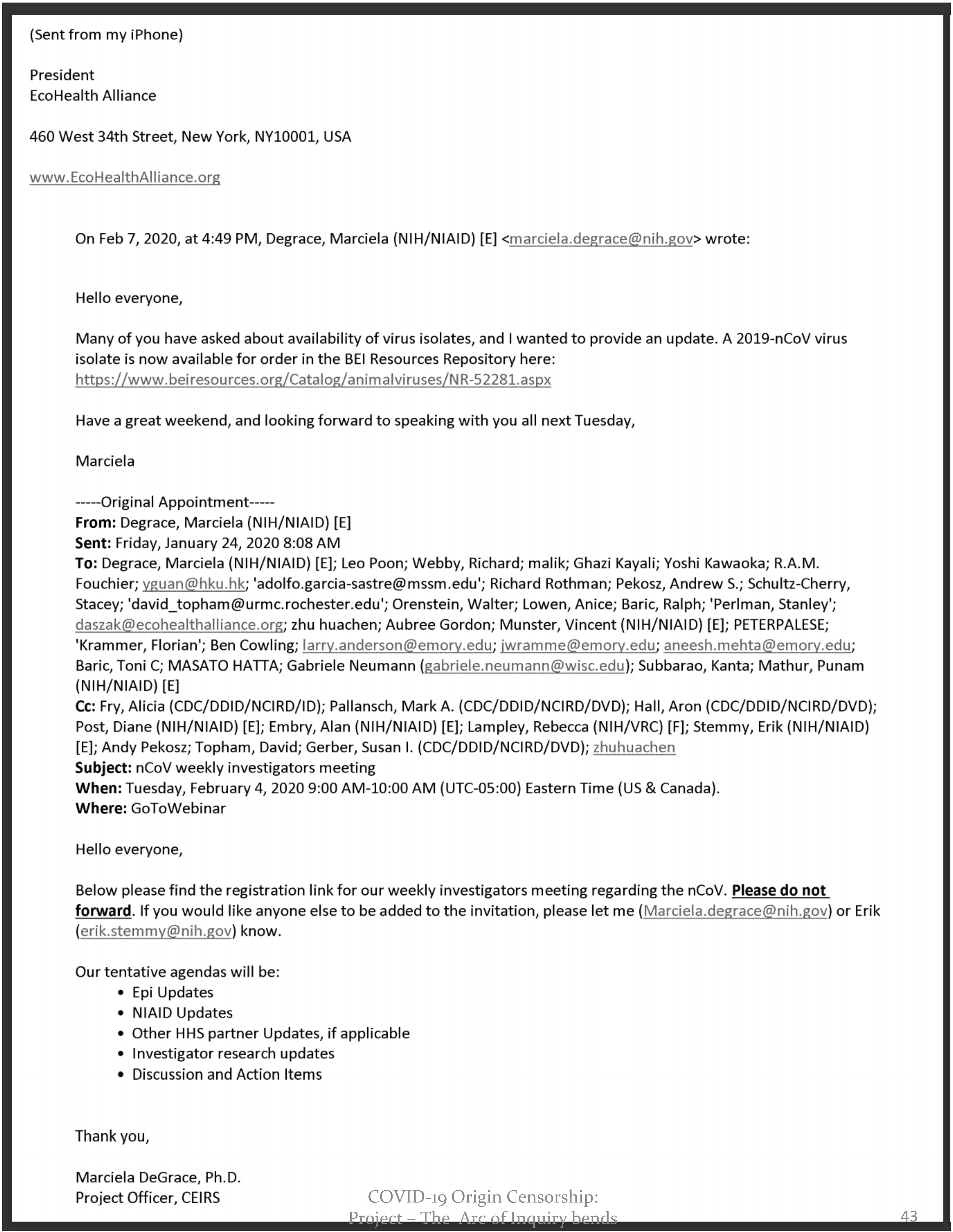
From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Tuesday, February 11, 2020 7:14 AM
To: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>
Cc: Leo Poon <llmpoon@hku.hk>; Webby, Richard <Richard.Webby@stjude.org>; malik <malik@hku.hk>; Ghazi Kayali <ghazi@human-link.org>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; yguan@hku.hk; adolfo.garcia-sastre@mssm.edu <'adolfo.garcia-sastre@mssm.edu'>; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@stjude.org>; david_topham@urmc.rochester.edu <'david_topham@urmc.rochester.edu'>; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>; Baric, Ralph <rbaric@email.unc.edu>; Perlman, Stanley <stanley-perlman@uiowa.edu>; zhu huachen <zhuhch@hku.hk>; Aubree Gordon <gordonal@umich.edu>; Munster, Vincent (NIH/NIAID) [E] <vincent.munster@nih.gov>; PETERPALESE <peter.palese@mssm.edu>; Krammer, Florian <florian.krammer@mssm.edu>; Ben Cowling <bcowling@hku.hk>; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C <antoinette_baric@med.unc.edu>; MASATO HATTA <masato.hatta@wisc.edu>; Gabriele Neumann (gabriele.neumann@wisc.edu) <gabriele.neumann@wisc.edu>; Subbarao, Kanta <kanta.subbarao@influenzacentre.org>; Mathur, Punam (NIH/NIAID) [E] <mathurpu@niaid.nih.gov>; Fry, Alicia (CDC/DDID/NCIRD/ID) <agf1@CDC.GOV>; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD) <map1@CDC.GOV>; Hall, Aron (CDC/DDID/NCIRD/DVD) <esg3@CDC.GOV>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Lampley, Rebecca (NIH/VRC) [F] <rebecca.lampley@nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Andy Pekosz <apekosz1@jhu.edu>; Topham, David <David_Topham@urmc.rochester.edu>; Gerber, Susan I. (CDC/DDID/NCIRD/DVD) <bhx1@cdc.gov>; zhuhuachen
Subject: Re: virus isolate availability- update

Some of us are at the WHO R&D Blueprint meeting in Geneva today. I see that Stan Perlman, Kanta Subarrao and others from NIH are in the room. The goal is to set research priorities across everything from animal reservoir to drug/vaccine to social science. We're in breakout groups this afternoon and hopefully can call in for some of the meeting and give a quick update.

Cheers,

Peter

Peter Daszak



(Sent from my iPhone)

President
EcoHealth Alliance

460 West 34th Street, New York, NY10001, USA

www.EcoHealthAlliance.org

On Feb 7, 2020, at 4:49 PM, Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov> wrote:

Hello everyone,

Many of you have asked about availability of virus isolates, and I wanted to provide an update. A 2019-nCoV virus isolate is now available for order in the BEI Resources Repository here: https://www.beiresources.org/Catalog/animalviruses/NR-52281.aspx

Have a great weekend, and looking forward to speaking with you all next Tuesday,

Marciela

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen
Subject: nCoV weekly investigators meeting
When: Tuesday, February 4, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hello everyone,

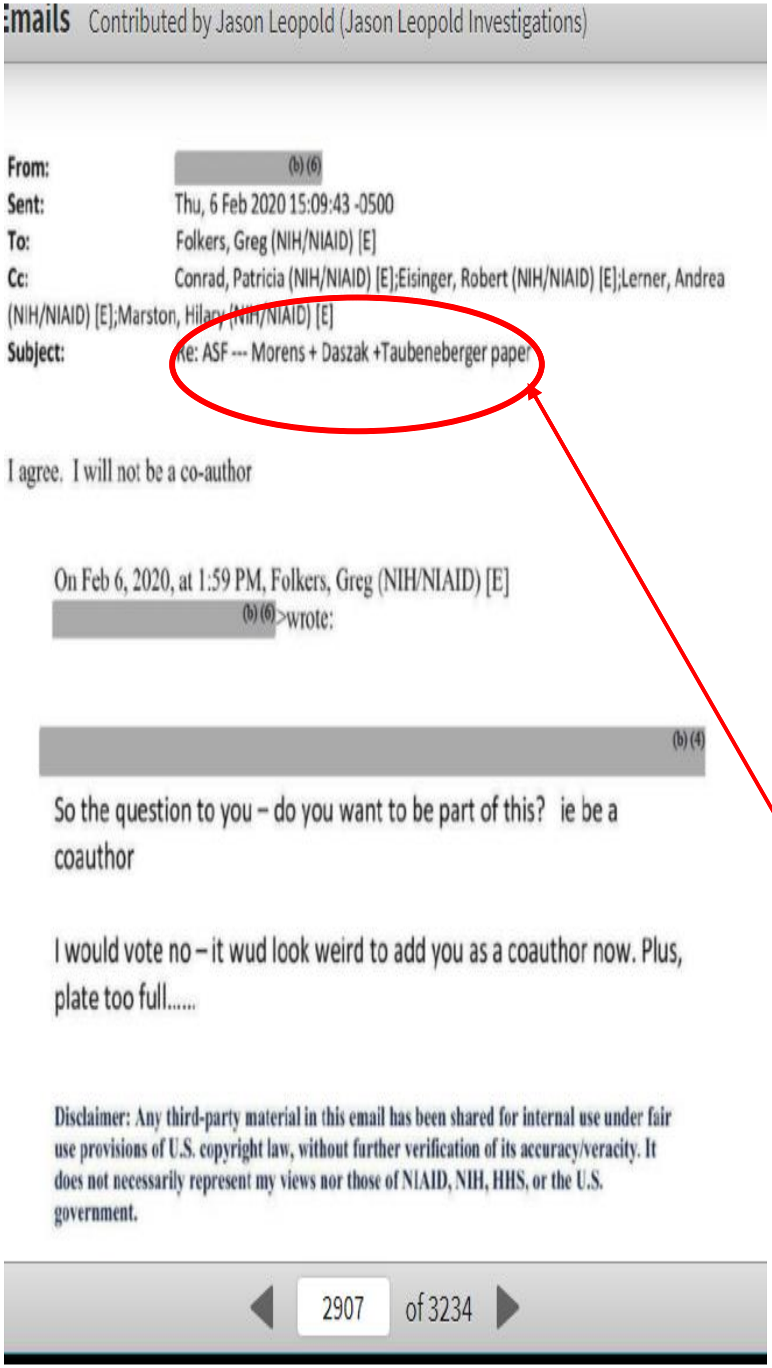
Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS



mails Contributed by Jason Leopold (Jason Leopold Investigations)

From: [redacted] (b)(6)
Sent: Thu, 6 Feb 2020 15:09:43 -0500
To: Folkers, Greg (NIH/NIAID) [E]
Cc: Conrad, Patricia (NIH/NIAID) [E];Eisinger, Robert (NIH/NIAID) [E];Lerner, Andrea (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Subject: Re: ASF --- Morens + Daszak +Taubeneberger paper

I agree. I will not be a co-author

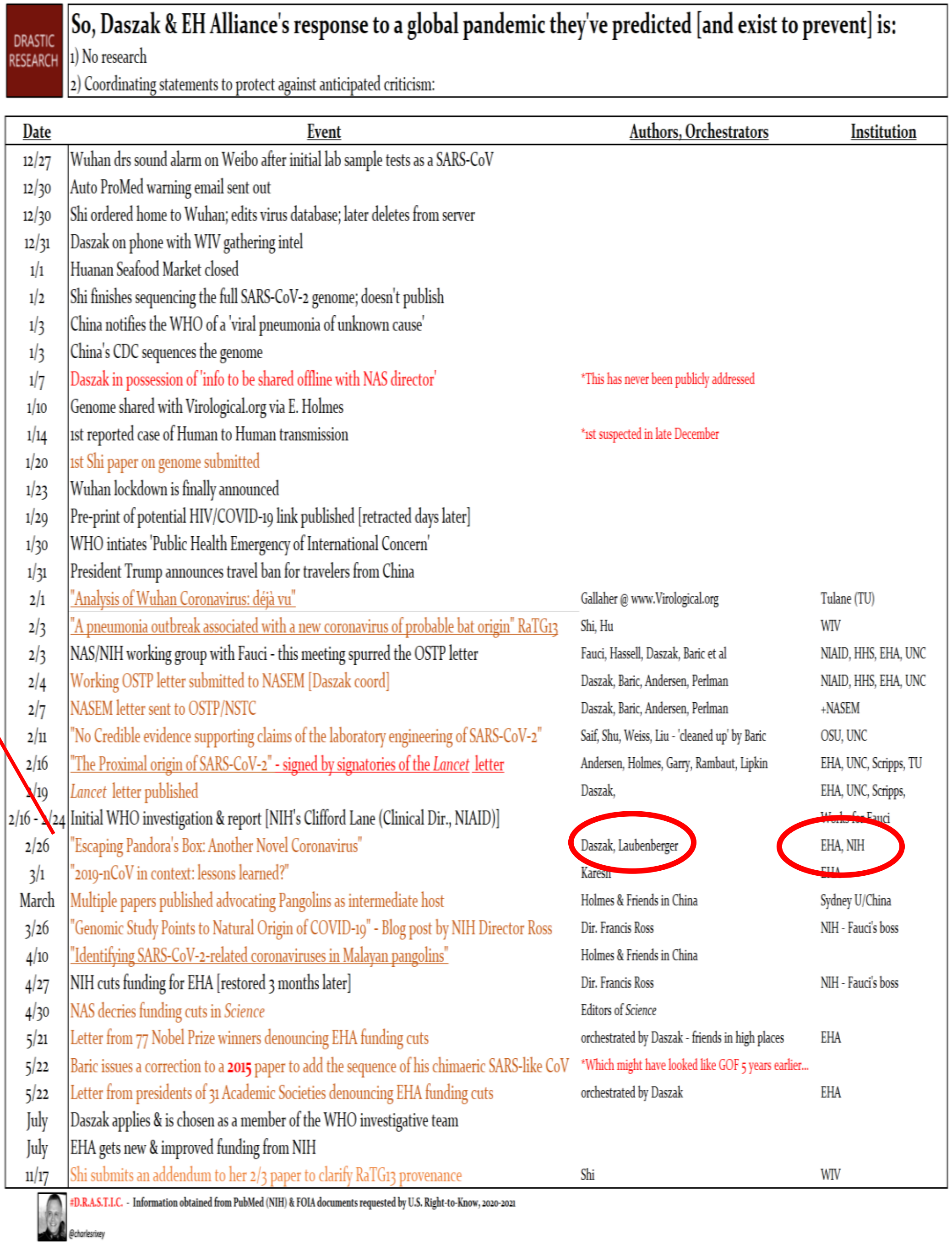
On Feb 6, 2020, at 1:59 PM, Folkers, Greg (NIH/NIAID) [E]
[redacted] (b)(6)>wrote:

[redacted] (b)(4)

So the question to you – do you want to be part of this? ie be a coauthor

I would vote no – it wud look weird to add you as a coauthor now. Plus, plate too full......

Disclaimer: Any third-party material in this email has been shared for internal use under fair use provisions of U.S. copyright law, without further verification of its accuracy/veracity. It does not necessarily represent my views nor those of NIAID, NIH, HHS, or the U.S. government.

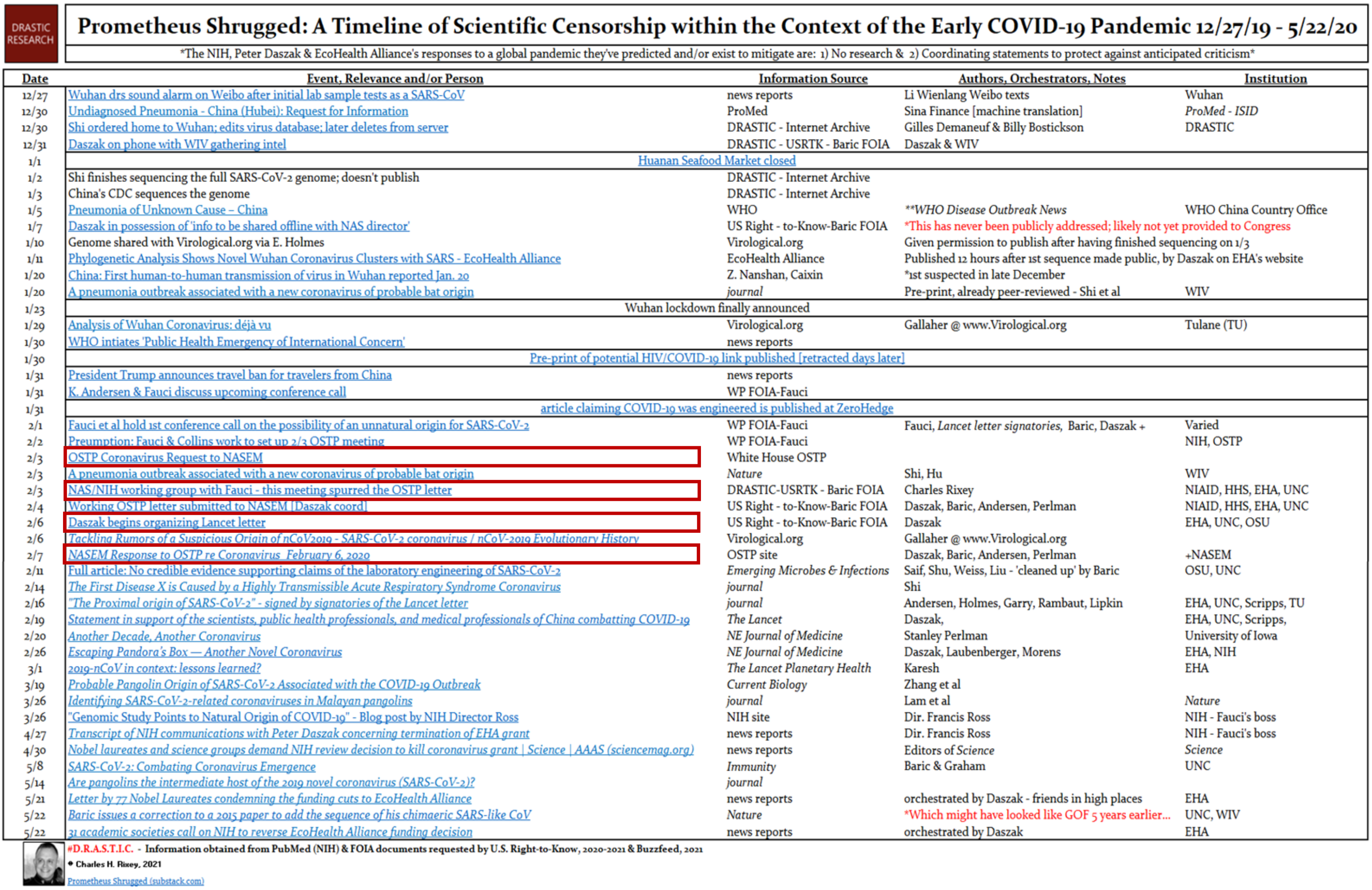


DRASTIC RESEARCH

So, Daszak & EH Alliance's response to a global pandemic they've predicted [and exist to prevent] is:
1) No research
2) Coordinating statements to protect against anticipated criticism:

Date	Event	Authors, Orchestrators	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV		
12/30	Auto ProMed warning email sent out		
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server		
12/31	Daszak on phone with WIV gathering intel		
1/1	Huanan Seafood Market closed		
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish		
1/3	China notifies the WHO of a 'viral pneumonia of unknown cause'		
1/3	China's CDC sequences the genome		
1/7	Daszak in possession of 'info to be shared offline with NAS director'	*This has never been publicly addressed	
1/10	Genome shared with Virological.org via E. Holmes		
1/14	1st reported case of Human to Human transmission	*1st suspected in late December	
1/20	1st Shi paper on genome submitted		
1/23	Wuhan lockdown is finally announced		
1/29	Pre-print of potential HIV/COVID-19 link published [retracted days later]		
1/30	WHO intiates 'Public Health Emergency of International Concern'		
1/31	President Trump announces travel ban for travelers from China		
2/1	"Analysis of Wuhan Coronavirus: déjà vu"	Gallaher @ www.Virological.org	Tulane (TU)
2/3	"A pneumonia outbreak associated with a new coronavirus of probable bat origin" RaTG13	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	Fauci, Hassell, Daszak, Baric et al	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/7	NASEM letter sent to OSTP/NSTC	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	"No Credible evidence supporting claims of the laboratory engineering of SARS-CoV-2"	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/16	"The Proximal origin of SARS-CoV-2" - signed by signatories of the *Lancet* letter	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Lancet* letter published	Daszak,	EHA, UNC, Scripps,
2/16 - 2/24	Initial WHO investigation & report [NIH's Clifford Lane (Clinical Dir., NIAID)]		Works for Fauci
2/26	"Escaping Pandora's Box: Another Novel Coronavirus"	Daszak, Laubenberger	EHA, NIH
3/1	"2019-nCoV in context: lessons learned?"	Karesh	EHA
March	Multiple papers published advocating Pangolins as intermediate host	Holmes & Friends in China	Sydney U/China
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	Dir. Francis Ross	NIH - Fauci's boss
4/10	"Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins"	Holmes & Friends in China	
4/27	NIH cuts funding for EHA [restored 3 months later]	Dir. Francis Ross	NIH - Fauci's boss
4/30	NAS decries funding cuts in *Science*	Editors of *Science*	
5/21	Letter from 77 Nobel Prize winners denouncing EHA funding cuts	orchestrated by Daszak - friends in high places	EHA
5/22	Baric issues a correction to a **2015** paper to add the sequence of his chimaeric SARS-like CoV	*Which might have looked like GOF 5 years earlier...	
5/22	Letter from presidents of 31 Academic Societies denouncing EHA funding cuts	orchestrated by Daszak	EHA
July	Daszak applies & is chosen as a member of the WHO investigative team		
July	EHA gets new & improved funding from NIH		
11/17	Shi submits an addendum to her 2/3 paper to clarify RaTG13 provenance	Shi	WIV

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021
@charlesrixey



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories*, Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier…	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

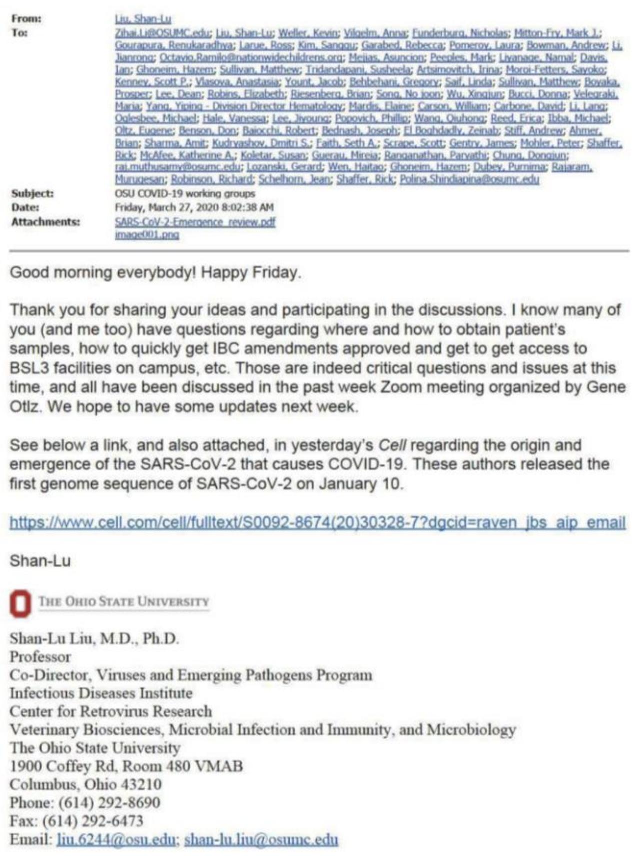
#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

• Charles H. Rixey, 2021

Prometheus Shrugged (substack.com)

Colwell, Linda Saif & Ralph Baric

These highlight further coordination , this time in support of the ***Lancet* letter.** Source: US Right-to-Know FOIA documents for Linda Saif & Rita Colwell



From: Liu, Shan-Lu
To: Zihai.Li@OSUMC.edu; Liu, Shan-Lu; Weller, Kevin; Vilgelm, Anna; Funderburg, Nicholas; Mitton-Fry, Mark J.; Gourapura, Renukaradhya; Larue, Ross; Kim, Sanggu; Garabed, Rebecca; Pomeroy, Laura; Bowman, Andrew; Li, Jianrong; Octavio.Ramilo@nationwidechildrens.org; Mejias, Asuncion; Peeples, Mark; Liyanage, Namal; Davis, Ian; Ghoneim, Hazem; Sullivan, Matthew; Tridandapani, Susheela; Artsimovitch, Irina; Moroi-Fetters, Sayoko; Kenney, Scott P.; Vlasova, Anastasia; Yount, Jacob; Behbehani, Gregory; Saif, Linda; Sullivan, Matthew; Boyaka, Prosper; Lee, Dean; Robins, Elizabeth; Riesenberg, Brian; Song, No joon; Wu, Xingjun; Bucci, Donna; Velegraki, Maria; Yang, Yiping - Division Director Hematology; Mardis, Elaine; Carson, William; Carbone, David; Li, Lang; Oglesbee, Michael; Hale, Vanessa; Lee, Jiyoung; Popovich, Phillip; Wang, Qiuhong; Reed, Erica; Ibba, Michael; Oltz, Eugene; Benson, Don; Baiocchi, Robert; Bednash, Joseph; El Boghdadly, Zeinab; Stiff, Andrew; Ahmer, Brian; Sharma, Amit; Kudryashov, Dmitri S.; Faith, Seth A.; Scrape, Scott; Gentry, James; Mohler, Peter; Shaffer, Rick; McAfee, Katherine A.; Koletar, Susan; Guerau, Mireia; Ranganathan, Parvathi; Chung, Dongjun; raj.muthusamy@osumc.edu; Lozanski, Gerard; Wen, Haitao; Ghoneim, Hazem; Dubey, Purnima; Rajaram, Murugesan; Robinson, Richard; Schelhorn, Jean; Shaffer, Rick; Polina.Shindiapina@osumc.edu
Subject: OSU COVID-19 working groups
Date: Friday, March 27, 2020 8:02:38 AM
Attachments: SARS-CoV-2-Emergence_review.pdf
image001.png

Good morning everybody! Happy Friday.

Thank you for sharing your ideas and participating in the discussions. I know many of you (and me too) have questions regarding where and how to obtain patient's samples, how to quickly get IBC amendments approved and get to get access to BSL3 facilities on campus, etc. Those are indeed critical questions and issues at this time, and all have been discussed in the past week Zoom meeting organized by Gene Otlz. We hope to have some updates next week.

See below a link, and also attached, in yesterday's *Cell* regarding the origin and emergence of the SARS-CoV-2 that causes COVID-19. These authors released the first genome sequence of SARS-CoV-2 on January 10.

https://www.cell.com/cell/fulltext/S0092-8674(20)30328-7?dgcid=raven_jbs_aip_email

Shan-Lu

THE OHIO STATE UNIVERSITY

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Leading Edge
Commentary

Cell

A Genomic Perspective on the Origin and Emergence of SARS-CoV-2

Yong-Zhen Zhang[1] **and Edward C. Holmes**[1,2,*]
[1]Shanghai Public Health Clinical Center and School of Life Science, Fudan University, Shanghai, China
[2]Marie Bashir Institute for Infectious Diseases and Biosecurity, School of Life and Environmental Sciences and School of Medical Sciences, The University of Sydney, Sydney, Australia
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https://doi.org/10.1016/j.cell.2020.03.035

The ongoing pandemic of a new human coronavirus, SARS-CoV-2, has generated enormous global concern. We and others in China were involved in the initial genome sequencing of the virus. Herein, we describe what genomic data reveal about the emergence SARS-CoV-2 and discuss the gaps in our understanding of its origins.

A New Human Coronavirus

The first reports of a novel pneumonia (COVID-19) in Wuhan city, Hubei province, China, occurred in late December 2019, although retrospective analyses have identified a patient with symptom onset as early as December 1st. Because the number of SARS-CoV-2 cases is growing rapidly and spreading globally, we will refrain from citing the number of confirmed infections. However, it is likely that the true number of cases will be substantially greater than reported because very mild or asymptomatic infections will often be excluded from counts. Any under-reporting of case numbers obviously means that the case fatality rate (CFR) associated with COVID-19 in the worst-hit regions will be lower than that currently cited. CFRs will also vary geographically, between age groups and temporally. Although these uncertainties will likely not be resolved without large-scale serological surveys, from current data it is clear that the CFR for COVID-19 is substantially higher than that of seasonal influenza but lower than that of two closely related coronaviruses that have similarly recently emerged in humans: SARS-CoV, responsible for the SARS outbreak of 2002–2003, and MERS-CoV that since 2015 has been responsible for the ongoing outbreak of MERS largely centered on the Arabian peninsula. However, it is also evident that SARS-CoV-2 is more infectious than both SARS-CoV and MERS-CoV and that individuals can transmit the virus when asymptomatic or presymptomatic, although how frequently remains uncertain.

An important early association was observed between the first reported cases of COVID-19 and the Huanan seafood and wildlife market in Wuhan city (which we both visited several years ago) where a variety of mammalian species were available for purchase at the time of the outbreak (Figure 1). Given that SARS-CoV-2 undoubtedly has a zoonotic origin, the link to such a "wet" market should come as no surprise. However, as not all of the early cases were market associated, it is possible that the emergence story is more complicated than first suspected. Genome sequences of "environmental samples"—likely surfaces—from the market have now been obtained, and phylogenetic analysis reveals that they are very closely related to viruses sampled from the earliest Wuhan patients. While this again suggests that the market played an important role in virus emergence, it is not clear whether the samples were derived from people who inadvertently deposited infectious material or from animals or animal matter present at that location. Unfortunately, the apparent lack of direct animal sampling in the market may mean that it will be difficult, perhaps even impossible, to accurately identify any animal reservoir at this location.

After clinical cases began to appear, our research team, along with a number of others, attempted to determine the genome sequence of the causative pathogen (Lu et al., 2020; Wu et al., 2020; Zhou et al., 2020; Zhu et al., 2020). We focused on a patient admitted to the Central Hospital of Wuhan on December 26, 2019, six days after the onset of symptoms (Wu et al., 2020). This patient was experiencing fever, chest tightness, cough, pain, and weakness, along with lung abnormalities indicative of pneumonia that appear to be commonplace in COVID-19 (Huang et al., 2020). Fortunately, next-generation meta-transcriptomic sequencing enabled us to obtain a complete viral genome from this patient on January 5, 2020. Initial analysis revealed that the virus was closely related to those of SARS-like viruses (family *Coronaviridae*). This result was immediately reported to the relevant authorities, and an annotated version of the genome sequence (strain Wuhan-Hu-1) was submitted to NCBI/GenBank on the same day. Although the GenBank sequence (GenBank: MN908947) was the first of SARS-CoV-2 available, it was subsequently corrected to ensure its accuracy. With the help of Dr. Andrew Rambaut (University of Edinburgh), we released the genome sequence of the virus on the open access Virological website (http://virological.org/) early on January 11, 2020. Afterwards, the China CDC similarly released SARS-CoV-2 genome sequences (with associated epidemiological data) on the public access GISAID database (https://www.gisaid.org/). At the time of writing, almost 200 SARS-CoV-2 genomes are publicly available, representing the genomic diversity of the virus in China and beyond and providing a freely accessible global resource. Importantly, the release of the SARS-CoV-2 genome sequence data facilitated the rapid development of diagnostic tests (Corman et al., 2020) and now an infectious clone (Thao et al., 2020). The race to develop an effective vaccine and antivirals is ongoing, with trails of the latter underway (Wang et al., 2020).

Figure 1. The Huanan Seafood and Wildlife Market in Wuhan, China
The photographs (credit: E.C.H.) were taken when both authors visited the market together in October 2014 and highlight some of the wide variety of wildlife on sale, providing a potent mechanism for zoonotic transmission. Importantly, although many of the early COVID 19 cases were linked to this market, its role in the initial emergence of SARS CoV 2 remains uncertain.

Comparisons between SARS-CoV-2 and Other Coronaviruses

The earliest genomic genome sequence data made it clear that SARS-CoV-2 was a member of the genus *Betacoronavirus* and fell within a subgenus (*Sarbecovirus*) that includes SARS-CoV (MERS-CoV falls in a separate subgenus, *Merbecovirus*) (Lu et al., 2020; Wu et al., 2020; Zhou et al., 2020; Zhu et al., 2020). Indeed, initial comparisons revealed that SARS-CoV-2 was approximately 79% similar to SARS-CoV at the nucleotide level. Of course, patterns of similarity vary greatly between genes, and SARS-CoV and SARS-CoV-2 exhibit only ~72% nucleotide sequence similarity in the spike (S) protein, the key surface glycoprotein that interacts with host cell receptors.

Given these close evolutionary relationships, it is unsurprising that the genome structure of SARS-CoV-2 resembles those of other betacoronaviruses, with the gene order 5′-replicase ORF1ab-S-envelope(E)-membrane(M)-N-3′. The long replicase ORF1ab gene of SARS-CoV-2 is over 21 kb in length and contains 16 predicted non-structural proteins and a number of downstream open reading frames (ORFs) likely of similar function to those of SARS-CoV. Comparative genomic analysis has been greatly assisted by the availability of a related virus from a *Rhinolophus affinis* (i.e., horseshoe) bat sampled in Yunnan province, China, in 2013 (Zhou et al., 2020). This virus, denoted RaTG13, is ~96% similar to SARS-CoV-2 at the nucleotide sequence level. Despite this sequence similarity, SARS-CoV-2 and RaTG13 differ in a number of key genomic features, arguably the most important of which is that SARS-CoV-2 contains a polybasic (furin) cleavage site insertion (residues PRRA) at the junction of the S1 and S2 subunits of the S protein (Coutard et al., 2020). This insertion, which may increase the infectivity of the virus, is not present in related betacoronaviruses, although similar polybasic insertions are present in other human coronaviruses, including HCoV-HKU1, as well as in highly pathogenic strains of avian influenza virus. In addition, the receptor binding domain (RBD) of SARS-CoV-2 and RaTG13 are only ~85% similar and share just one of six critical amino acid residues. Both sequence and structural comparisons suggest that the SARS-CoV-2 RBD is well suited for binding to the human ACE2 receptor that was also utilized by SARS-CoV (Wrapp et al., 2020). Importantly, an independent insertion(s) of the amino acids PAA at the S1/S2 cleavage site was recently observed in a virus (RmYN02) sampled in mid-2019 from another *Rhinolophus* bat in Yunnan province, indicating that these insertion events reflect a natural part of ongoing coronavirus evolution (Zhou et al., 2020). While RmYN02 is relatively divergent from SARS-CoV-2 in the S protein (~72% sequence similarity), it is the closest relative (~97% nucleotide sequence similarity) of the human virus in the long replicase gene.

Although SARS-CoV and MERS-CoV are both closely related to SARS-CoV-2 and have bat reservoirs, the biological differences between these viruses are striking. As noted above, SARS-CoV-2 is markedly more infectious, resulting in very different epidemiological dynamics to those of SARS-CoV and MERS-CoV. In these latter two viruses, there was a relatively slow rise in case numbers, and MERS-CoV has never been able to fully adapt to human transmission: the majority of the cases are due to spillover from camels on the Arabian peninsula with only sporadic human-to-human transmission (Sabir et al., 2016). In contrast, the remarkable local and global spread of SARS-CoV-2 caught most by surprise. Determining the virological characteristics that underpin such transmissibility is clearly a priority.

The Zoonotic Origins of SARS-CoV-2

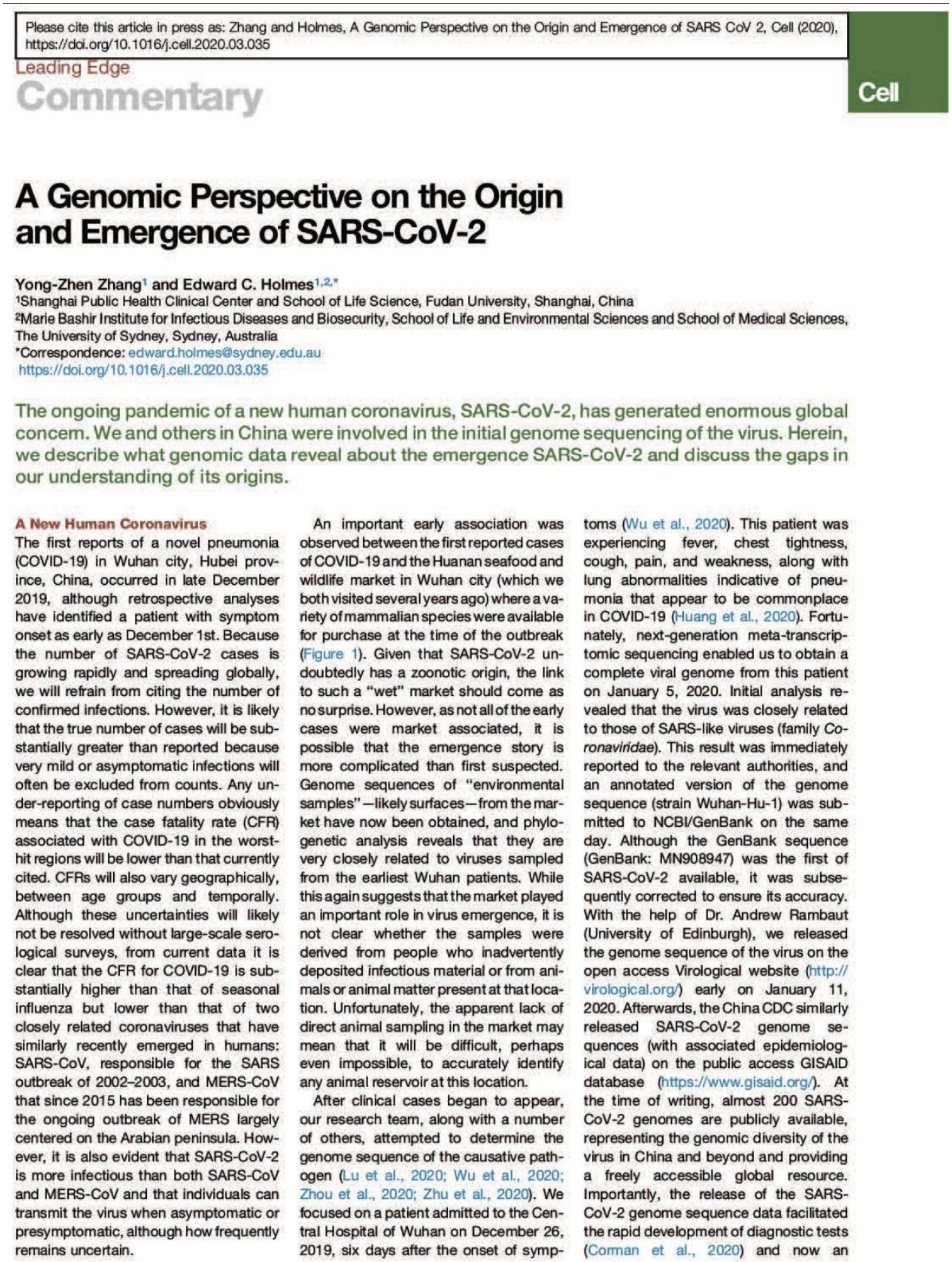
The emergence and rapid spread of COVID-19 signifies a perfect epidemiological storm. A respiratory pathogen of relatively high virulence from a virus family that has an unusual knack of jumping species boundaries, that emerged in a major population center and travel hub shortly before the biggest travel period of the year: the Chinese Spring Festival. Indeed, it is no surprise that epidemiological modeling suggests that SARS-CoV-2 had already spread widely in China before the city of Wuhan was placed under strict quarantine (Chinazzi et al., 2020).

It was also no surprise that early genomic comparisons revealed that the most closely related viruses to SARS-CoV-2 came from bats (Zhou et al., 2020). Sampling in recent years has identified an impressive array of bat coronaviruses, including RaTG13 and RmYN02 (Hu et al., 2017; Yang et al., 2015). Hence, bats are undoubtedly important reservoir species for a diverse range of coronaviruses (Cui et al., 2019). Despite this, the exact role played by bats in the zoonotic origin of SARS-CoV-2 is not established. In particular, the bat viruses most closely related to SARS-CoV-2 were sampled from animals in Yunnan province, over 1,500 km from Wuhan. There are relatively few bat coronaviruses from Hubei province, and those that have been sequenced are relatively distant to SARS-CoV-2 in phylogenetic trees (Lin et al., 2017). The simple inference from this is that our sampling of bat viruses is strongly biased toward some geographical locations. This will need to be rectified in future studies. In addition, although sequence similarity values of 96%–97% make it sound like the available bat viruses are very closely related to SARS-CoV-2, in reality this likely represents more than 20 years of sequence evolution (although the underlying molecular clock may tick at an uncertain rate if there was strong adaptive evolution of the virus in humans). It is therefore almost a certainty that more sampling will identify additional bat viruses that are even closer relatives of SARS-CoV-2. A key issue is whether these viruses, or those from any other animal species, contain the key RBD mutations and the same furin-like cleavage site insertion as found in SARS-CoV-2.

Although bats are likely the reservoir hosts for this virus, their general ecological separation from humans makes it probable that other mammalian species act as "intermediate" or "amplifying" hosts, within which SARS-CoV-2 was able to acquire some or all of the mutations needed for efficient human transmission. In the case of SARS and MERS, civets and camels, respectively, played the role of intermediate hosts, although as MERS-CoV was likely present in camels for some decades before it emerged in humans during multiple cross-species events, these animals may be better thought of as true reservoir hosts (Sabir et al., 2016). To determine what these intermediate host species might be, it is imperative to perform a far wider sampling of animals from wet markets or that live close to human populations. This is highlighted by the recent discovery of viruses closely related to SARS-CoV-2 in Malayan pangolins (*Manis javanica*) illegally imported into southern China (Guangdong and Guangxi provinces). The Guangdong pangolin viruses are particularly closely related to SARS-CoV-2 in the RBD, containing all six of the six key mutations thought to shape binding to the ACE2 receptor and exhibiting 97% amino acid sequence similarity (although they are more divergent from SARS-CoV-2 in the remainder of the genome). Although pangolins are of great interest because of how frequently they are involved in illegal trafficking and their endangered status, that they carry a virus related to SARS-CoV-2 strongly suggests that a far greater diversity of related betacoronaviruses exists in a variety of mammalian species but has yet to be sampled.

While our past experience with coronaviruses suggests that evolution in animal hosts, both reservoirs and intermediates, is needed to explain the emergence of SARS-CoV-2 in humans, it cannot be excluded that the virus acquired some of its key mutations during a period of "cryptic" spread in humans prior to its first detection in December 2019. Specifically, it is possible that the virus emerged earlier in human populations than envisaged (perhaps not even in Wuhan) but was not detected because asymptomatic infections, those with mild respiratory symptoms, and even sporadic cases of pneumonia were not visible to the standard systems used for surveillance and pathogen identification. During this period of cryptic transmission, the virus could have gradually acquired the key mutations, perhaps including the RBD and furin cleavage site insertions, that enabled it to adapt fully to humans. It wasn't until a cluster of pneumonia cases occurred that we were able to detect COVID-19 via the routine surveillance system. Obviously, retrospective serological or meta-genomic studies of respiratory infection will go a long way to determining whether this scenario is correct, although such early cases may never be detected.

Another issue that has received considerable attention is whether SARS-CoV-2 is a recombinant virus, and whether such recombination might have facilitated its emergence (Lu et al., 2020; Wu et al., 2020). The complicating factor here is that sarbeviruses, and coronaviruses more broadly, experience widespread recombination, so that distinguishing recombination that assisted virus emergence from "background" recombination events is not trivial. Recombination is visible at multiple locations across the sarbevirus genome, including in the S protein, and in bat viruses closely related to SARS-CoV-2. For example, there is some evidence for recombination among SARS-CoV-2, RaTG13, and the Guangdong pangolin CoVs (Lam et al., 2020), and the genome of RmYN02 has similarly been widely impacted by recombination (Zhou et al., 2020). However, trying to



Please cite this article in press as: Zhang and Holmes, A Genomic Perspective on the Origin and Emergence of SARS CoV 2, Cell (2020), https://doi.org/10.1016/j.cell.2020.03.035

Leading Edge

Commentary

Cell

A Genomic Perspective on the Origin and Emergence of SARS-CoV-2

Yong-Zhen Zhang[1] **and Edward C. Holmes**[1,2,*]
[1]Shanghai Public Health Clinical Center and School of Life Science, Fudan University, Shanghai, China
[2]Marie Bashir Institute for Infectious Diseases and Biosecurity, School of Life and Environmental Sciences and School of Medical Sciences, The University of Sydney, Sydney, Australia
*Correspondence: edward.holmes@sydney.edu.au
https://doi.org/10.1016/j.cell.2020.03.035

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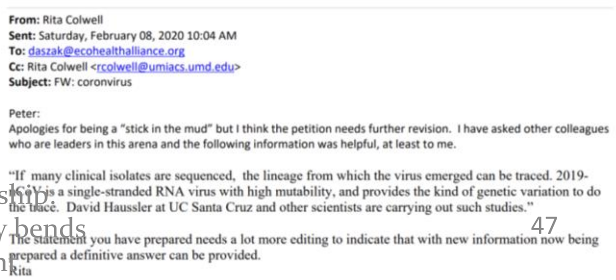

From: Rita Colwell
Sent: Saturday, February 08, 2020 10:04 AM
To: daszak@ecohealthalliance.org
Cc: Rita Colwell <rcolwell@umiacs.umd.edu>
Subject: FW: coronvirus

Peter:
Apologies for being a "stick in the mud" but I think the petition needs further revision. I have asked other colleagues who are leaders in this arena and the following information was helpful, at least to me.

"If many clinical isolates are sequenced, the lineage from which the virus emerged can be traced. 2019-nCoV is a single-stranded RNA virus with high mutability, and provides the kind of genetic variation to do the trace. David Haussler at UC Santa Cruz and other scientists are carrying out such studies."

The statement you have prepared needs a lot more editing to indicate that with new information now being prepared a definitive answer can be provided.
Rita

February 6, 2020

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy
1650 Pennsylvania Avenue, NW
Washington, D.C. 20504

Dear Dr. Droegemeier:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the declaration of a public health emergency and potential for misinformation to confound the response.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health. We wanted their views about the data needs that could help elucidate the origin and evolution of 2019-nCoV.

Research studies to better understand the origin of 2019-nCoV and how it relates to viruses found in bats and other species are already underway.[3] The closest known relative of 2019-nCoV appears to be a coronavirus identified from bat-derived samples collected in China.[4] The experts informed us that additional genomic sequence data from geographically- and temporally-diverse viral samples are needed to determine the origin and evolution of the virus. Samples collected as early as possible in the outbreak in Wuhan and samples from wildlife would be particularly valuable. Understanding the driving forces behind viral evolution would help facilitate the development of more effective strategies for managing the 2019-nCoV outbreak and for preventing future outbreaks. In this regard, we understand from Chunli Bai, President, Chinese Academy of Sciences, and the Alliance of International Science Organizations (ANSO), that the Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences is willing to share isolates of the 2019-nCoV with the international community and is working with the University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. International collaboration of this kind is more important than ever to overcome these types of global challenges.

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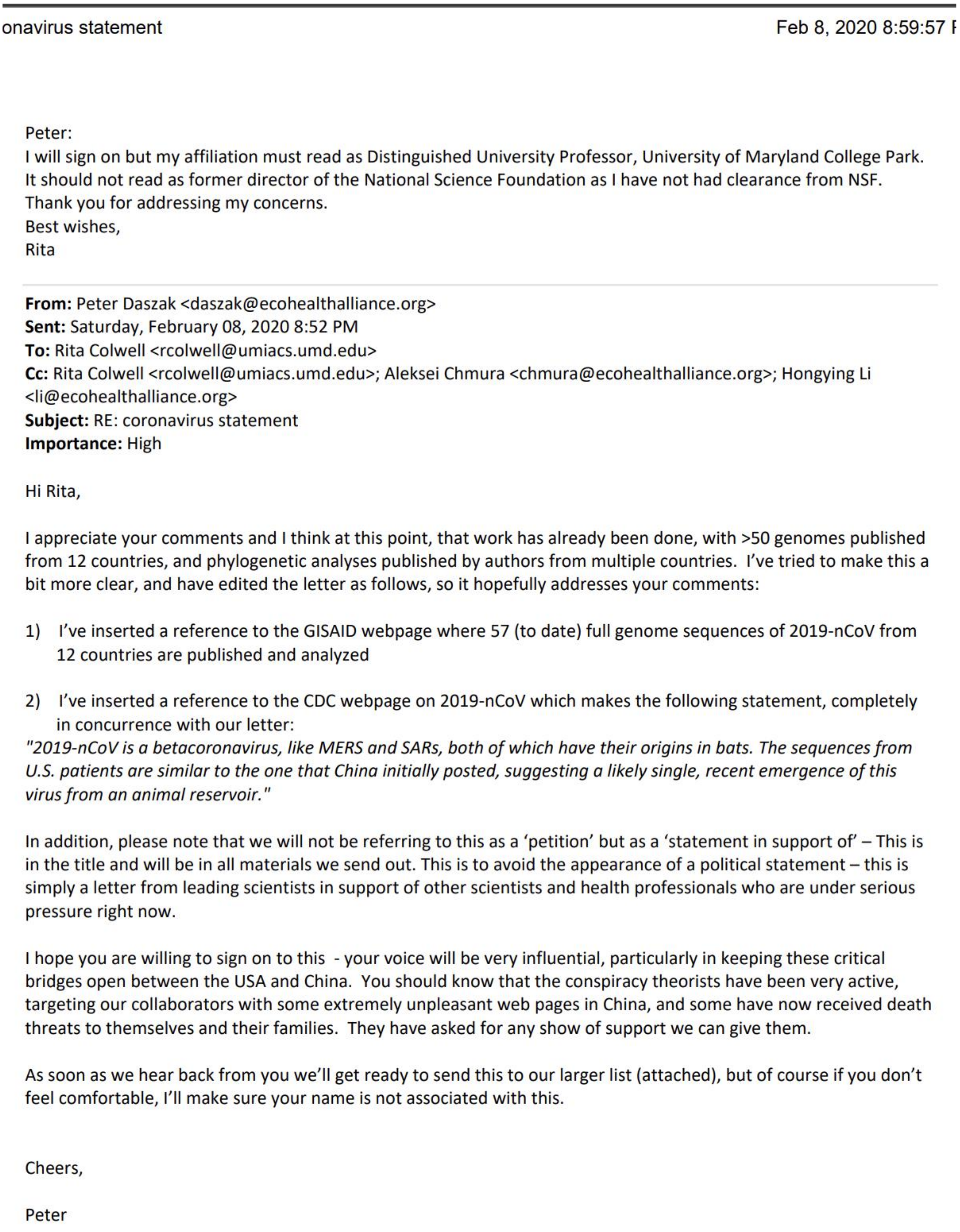
[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] Experts consulted: Kristian G. Andersen (Scripps Research Institute), Ralph Baric (UNC School of Public Health), Trevor Bedford (Fred Hutchinson Cancer Institute), Aravinda Chakravarti (New York University School of Medicine), Peter Daszak (EcoHealth Alliance), Gigi K. Gronvall (Johns Hopkins Bloomberg School of Public Health), Tom Inglesby (Johns Hopkins Center for Health Security), and Stanley Perlman (University of Iowa).

[3] Latinne *et al*. "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications*, in review.

[4] Zhou *et. al*. "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 2020. https://doi.org/10.1038/s41586-020-2012-7 (2020).



onavirus statement Feb 8, 2020 8:59:57

Peter:
I will sign on but my affiliation must read as Distinguished University Professor, University of Maryland College Park.
It should not read as former director of the National Science Foundation as I have not had clearance from NSF.
Thank you for addressing my concerns.
Best wishes,
Rita

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Saturday, February 08, 2020 8:52 PM
To: Rita Colwell <rcolwell@umiacs.umd.edu>
Cc: Rita Colwell <rcolwell@umiacs.umd.edu>; Aleksei Chmura <chmura@ecohealthalliance.org>; Hongying Li <li@ecohealthalliance.org>
Subject: RE: coronavirus statement
Importance: High

Hi Rita,

I appreciate your comments and I think at this point, that work has already been done, with >50 genomes published from 12 countries, and phylogenetic analyses published by authors from multiple countries. I've tried to make this a bit more clear, and have edited the letter as follows, so it hopefully addresses your comments:

1) I've inserted a reference to the GISAID webpage where 57 (to date) full genome sequences of 2019-nCoV from 12 countries are published and analyzed

2) I've inserted a reference to the CDC webpage on 2019-nCoV which makes the following statement, completely in concurrence with our letter:

"2019-nCoV is a betacoronavirus, like MERS and SARs, both of which have their origins in bats. The sequences from U.S. patients are similar to the one that China initially posted, suggesting a likely single, recent emergence of this virus from an animal reservoir."

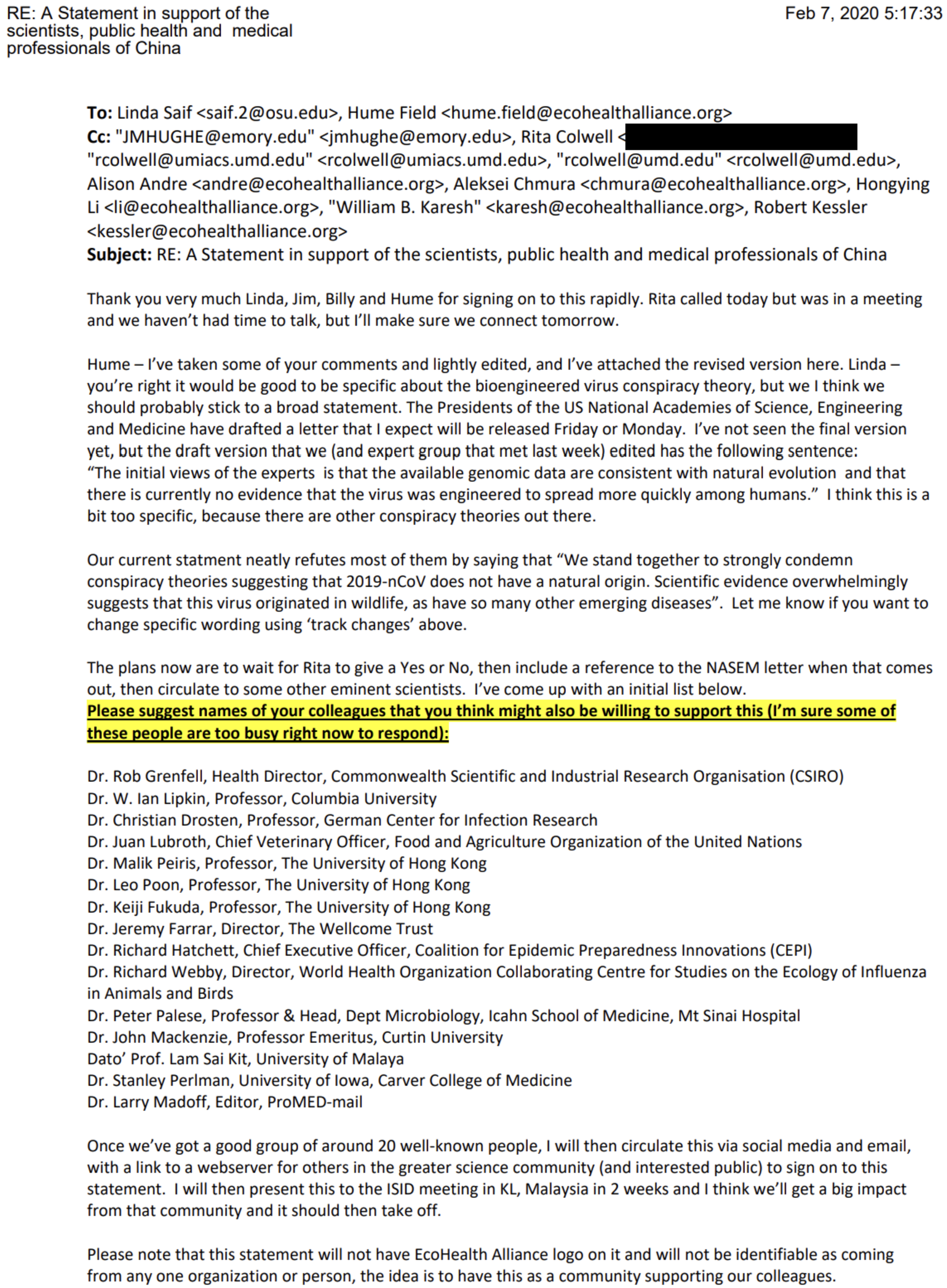
In addition, please note that we will not be referring to this as a 'petition' but as a 'statement in support of' – This is in the title and will be in all materials we send out. This is to avoid the appearance of a political statement – this is simply a letter from leading scientists in support of other scientists and health professionals who are under serious pressure right now.

I hope you are willing to sign on to this - your voice will be very influential, particularly in keeping these critical bridges open between the USA and China. You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. They have asked for any show of support we can give them.

As soon as we hear back from you we'll get ready to send this to our larger list (attached), but of course if you don't feel comfortable, I'll make sure your name is not associated with this.

Cheers,

Peter



RE: A Statement in support of the scientists, public health and medical professionals of China

Feb 7, 2020 5:17:33

To: Linda Saif <saif.2@osu.edu>, Hume Field <hume.field@ecohealthalliance.org>
Cc: "JMHUGHE@emory.edu" <jmhughe@emory.edu>, Rita Colwell <[redacted] "rcolwell@umiacs.umd.edu" <rcolwell@umiacs.umd.edu>, "rcolwell@umd.edu" <rcolwell@umd.edu>, Alison Andre <andre@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>, "William B. Karesh" <karesh@ecohealthalliance.org>, Robert Kessler <kessler@ecohealthalliance.org>
Subject: RE: A Statement in support of the scientists, public health and medical professionals of China

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Hume – I've taken some of your comments and lightly edited, and I've attached the revised version here. Linda – you're right it would be good to be specific about the bioengineered virus conspiracy theory, but we I think we should probably stick to a broad statement. The Presidents of the US National Academies of Science, Engineering and Medicine have drafted a letter that I expect will be released Friday or Monday. I've not seen the final version yet, but the draft version that we (and expert group that met last week) edited has the following sentence: "The initial views of the experts is that the available genomic data are consistent with natural evolution and that there is currently no evidence that the virus was engineered to spread more quickly among humans." I think this is a bit too specific, because there are other conspiracy theories out there.

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Dr. John Mackenzie, Professor Emeritus, Curtin University
Dato' Prof. Lam Sai Kit, University of Malaya
Dr. Stanley Perlman, University of Iowa, Carver College of Medicine
Dr. Larry Madoff, Editor, ProMED-mail

Once we've got a good group of around 20 well-known people, I will then circulate this via social media and email, with a link to a webserver for others in the greater science community (and interested public) to sign on to this statement. I will then present this to the ISID meeting in KL, Malaysia in 2 weeks and I think we'll get a big impact from that community and it should then take off.

Please note that this statement will not have EcoHealth Alliance logo on it and will not be identifiable as coming from any one organization or person, the idea is to have this as a community supporting our colleagues.

Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

We, the undersigned, are emerging infectious disease scientists who have closely followed the emergence of 2019-nCoV, and are deeply concerned about its current and potential global impact on human~~people's~~ health and well-being. We have watched as the scientists, public health and medical professionals of China have worked diligently and effectively ~~heroically~~ to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort, notwithstanding the benefit of hindsight, has been remarkable.

We sign this statement in solidarity with all scientists, public health, and medical professionals in China who continue to save lives and protect *global* human health during the challenge of this novel coronavirus outbreak. We ~~want you to know that we~~ are all in this together, with our Chinese counterparts~~you in~~ in the fore~~front of us on the battlefield~~ , against this new virus threat~~the novel coronavirus~~.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientific evidence overwhelmingly suggests that this virus originated in wildlife, as have so many other emerging diseases (*1-4*). This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent (INSERT REF). Conspiracy theories ~~will~~ do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We need to promote~~prioritize~~ scientific evidence and unity over misinformation and conjecture now. We want you, the science and health professionals of China, ~~all~~ to know that **we stand with you**~~, the science and health professionals of China,~~ in your fight against this virus.

- Dr. Jim Hughes, Professor, Emory University -- agreed
- Dr. Rita Colwell, former Director of National Science Foundation -- pending
- Dr. Linda Saif, Distinguished University Professor, The Ohio State University -- agreed
- Dr. Billy Karesh, Vice President, EcoHealth Alliance – agreed
- Dr. Peter Daszak, President, EcoHealth Alliance -- agreed
- Dr. Hume Field, Honorary Professor, The University of Queensland – agreed
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- From Kevin
- Dr. John Brownstein, Harvard University, HealthMap?
- Dr. Dennis Carroll, former USAID?
- Dr. Charles Calisher, Colorado State University
- Dr. Vincent Munster, NIH Rocky Mountain Laboratories
- Dr. Supaporn Wacharapluesadee, Chulalongkorn University
- From Linda Saif
- Dr. Marion Koopmans, Erasmus Medical Center, The Netherlands
- Dr. Bart Haagmans, Erasmus Medical Center, The Netherlands
- Dr. Luis Enjuanes, National Center of Biotechnology, Madrid, Spain
- Dr. Eric Snijder, Leiden University Medical Center, The Netherlands
- Dr. Alexander Gobalenya, Leiden University Medical Center, The Netherlands
- Dr. Mark Denison, Professor, Vanderbilt University, USA
- Dr. Yoshi Kawaoka, Professor, University of Wisconsin, USA
- From Jon
- Dr. Tony Schountz, Professor, Colorado State University
- Dr. Jonna Mazet. Professor, University of California, Davis
- Dr. Stephen Morse, Professor, Columbia University
- Dr. Christopher Broder, Professor, Uniformed Services University of the Health Sciences
- Dr. Marion Koopmans, Professor, Erasmus University Medical Center
- Dr. Ab Osterhaus, Emeritus Professor, Erasmus University Rotterdam
- Dr. Susan Lau, Hong Kong University?
- Dr. Charles Calisher, Emeritus Professor, Colorado State University
- Dr. Wanda Markotter, Professor, University of Pretoria

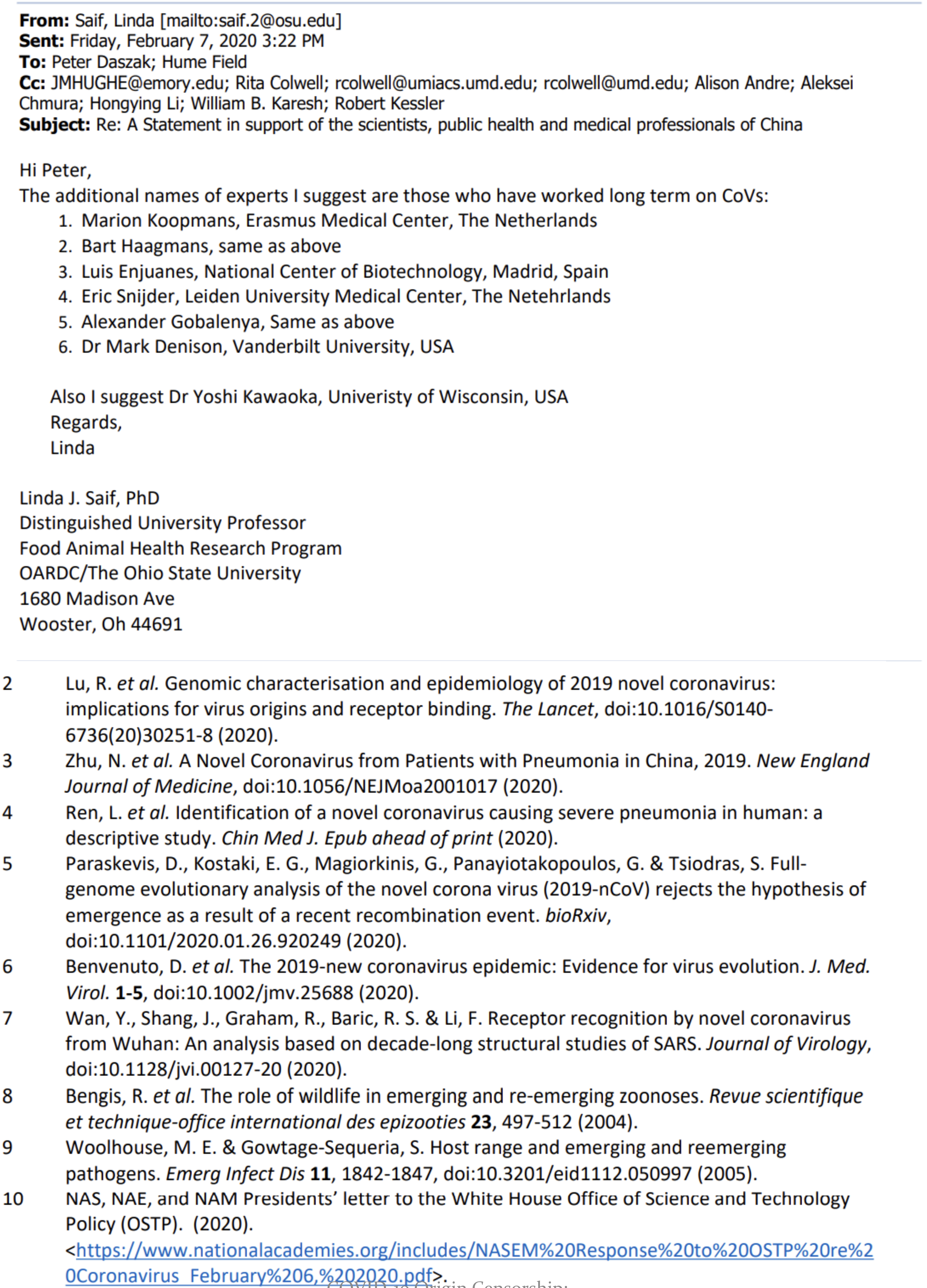
RE: A Statement in support of the scientists, public health and medical professionals of China

Feb 6, 2020 1:35:14

Count me in Peter. I had thought/hoped that this conspiracy stuff would fade, but clearly not. So yes, I agree it's time to actively counter it, and express peer support for the world class Chinese scientists doing such great work, yet being publicly and professionally impugned.

Well done mate.
Hume

Hume Field BVSc MSc PhD MACVS
Honorary Professor | **University of Queensland** | Australia
Science & Policy Advisor **| EcoHealth Alliance** | USA
Director | **Jeppesen Field Consulting** | Australia.



From: Saif, Linda [mailto:saif.2@osu.edu]
Sent: Friday, February 7, 2020 3:22 PM
To: Peter Daszak; Hume Field
Cc: JMHUGHE@emory.edu; Rita Colwell; rcolwell@umiacs.umd.edu; rcolwell@umd.edu; Alison Andre; Aleksei Chmura; Hongying Li; William B. Karesh; Robert Kessler
Subject: Re: A Statement in support of the scientists, public health and medical professionals of China

Hi Peter,
The additional names of experts I suggest are those who have worked long term on CoVs:

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4. Eric Snijder, Leiden University Medical Center, The Netehrlands
5. Alexander Gobalenya, Same as above
6. Dr Mark Denison, Vanderbilt University, USA

Also I suggest Dr Yoshi Kawaoka, Univeristy of Wisconsin, USA
Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

2 Lu, R. *et al.* Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, doi:10.1016/S0140-6736(20)30251-8 (2020).

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6 Benvenuto, D. *et al.* The 2019-new coronavirus epidemic: Evidence for virus evolution. *J. Med. Virol.* **1-5**, doi:10.1002/jmv.25688 (2020).

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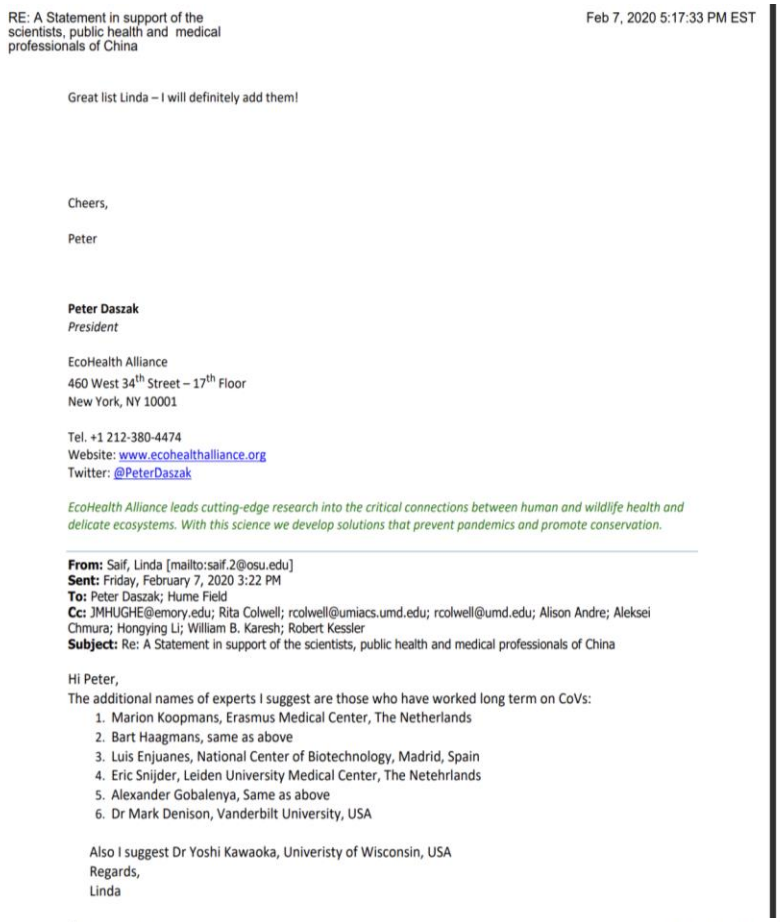
10 NAS, NAE, and NAM Presidents' letter to the White House Office of Science and Technology Policy (OSTP). (2020). <https://www.nationalacademies.org/includes/NASEM%20Response%20to%20OSTP%20re%20Coronavirus_February%206,%202020.pdf>.



RE: A Statement in support of the scientists, public health and medical professionals of China

Feb 7, 2020 5:17:33 PM EST

Great list Linda – I will definitely add them!

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

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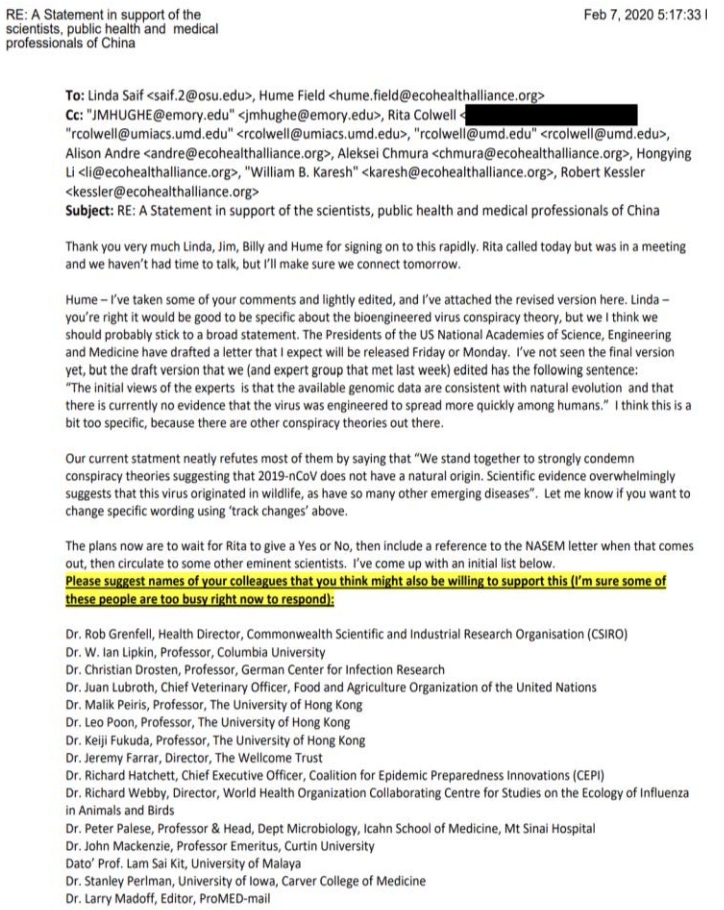

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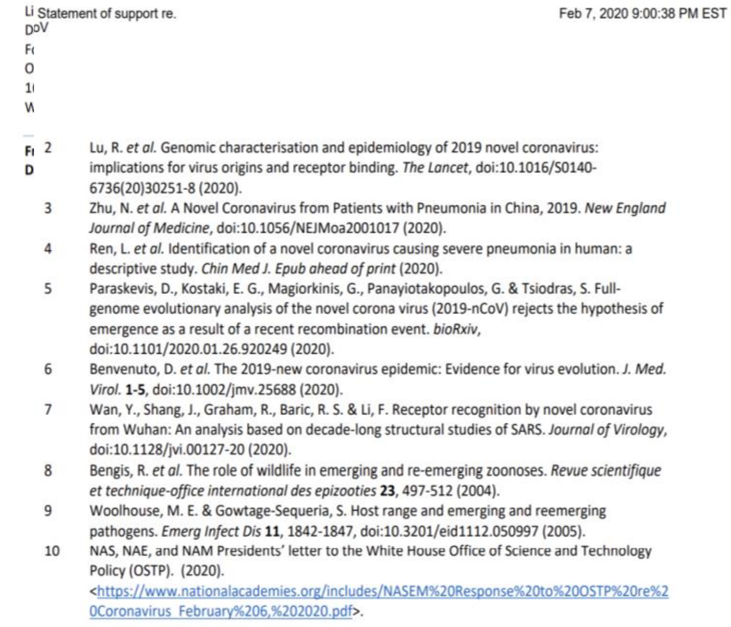

Li Statement of support re.
DoV

Feb 7, 2020 9:00:38 PM EST

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2 Lu, R. *et al.* Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, doi:10.1016/S0140-6736(20)30251-8 (2020).
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Revised Statement of support re. 2019nCoV

Feb 7, 2020 9:00:38 PM E

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Hume

Hume Field BVSc MSc PhD MACVS
Honorary Professor | **University of Queensland** | Australia
Science & Policy Advisor **| EcoHealth Alliance** | USA
Director | **Jeppesen Field Consulting** | Australia.

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From: Rita Colwell
Sent: Saturday, February 08, 2020 10:04 AM
To: daszak@ecohealthalliance.org
Cc: Rita Colwell <rcolwell@umiacs.umd.edu>
Subject: FW: coronvirus

Peter:
Apologies for being a "stick in the mud" but I think the petition needs further revision. I have asked other colleagues who are leaders in this arena and the following information was helpful, at least to me.

"If many clinical isolates are sequenced, the lineage from which the virus emerged can be traced. 2019-nCoV is a single-stranded RNA virus with high mutability, and provides the kind of genetic variation to do the trace. David Haussler at UC Santa Cruz and other scientists are carrying out such studies."

The statement you have prepared needs a lot more editing to indicate that with new information now being prepared a definitive answer can be provided.
Rita

From: Rita Colwell [mailto:rcolwell@umiacs.umd.edu]
Sent: Saturday, February 8, 2020 10:15 AM
To: Peter Daszak
Cc: rcolwell@umiacs.umd.edu
Subject: FW: coronvirus

Peter: resending. The email sent bounced.
Rita

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Saturday, February 08, 2020 8:52 PM
To: Rita Colwell <rcolwell@umiacs.umd.edu>
Cc: Rita Colwell <rcolwell@umiacs.umd.edu>; Aleksei Chmura <chmura@ecohealthalliance.org>; Hongying Li <li@ecohealthalliance.org>
Subject: RE: coronavirus statement
Importance: High

Hi Rita,

I appreciate your comments and I think at this point, that work has already been done, with >50 genomes published from 12 countries, and phylogenetic analyses published by authors from multiple countries. I've tried to make this a bit more clear, and have edited the letter as follows, so it hopefully addresses your comments:

1) I've inserted a reference to the GISAID webpage where 57 (to date) full genome sequences of 2019-nCoV from 12 countries are published and analyzed

2) I've inserted a reference to the CDC webpage on 2019-nCoV which makes the following statement, completely in concurrence with our letter:

"2019-nCoV is a betacoronavirus, like MERS and SARs, both of which have their origins in bats. The sequences from U.S. patients are similar to the one that China initially posted, suggesting a likely single, recent emergence of this virus from an animal reservoir."

In addition, please note that we will not be referring to this as a 'petition' but as a 'statement in support of' – This is in the title and will be in all materials we send out. This is to avoid the appearance of a political statement – this is simply a letter from leading scientists in support of other scientists and health professionals who are under serious pressure right now.

I hope you are willing to sign on to this - your voice will be very influential, particularly in keeping these critical bridges open between the USA and China. You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. They have asked for any show of support we can give them.

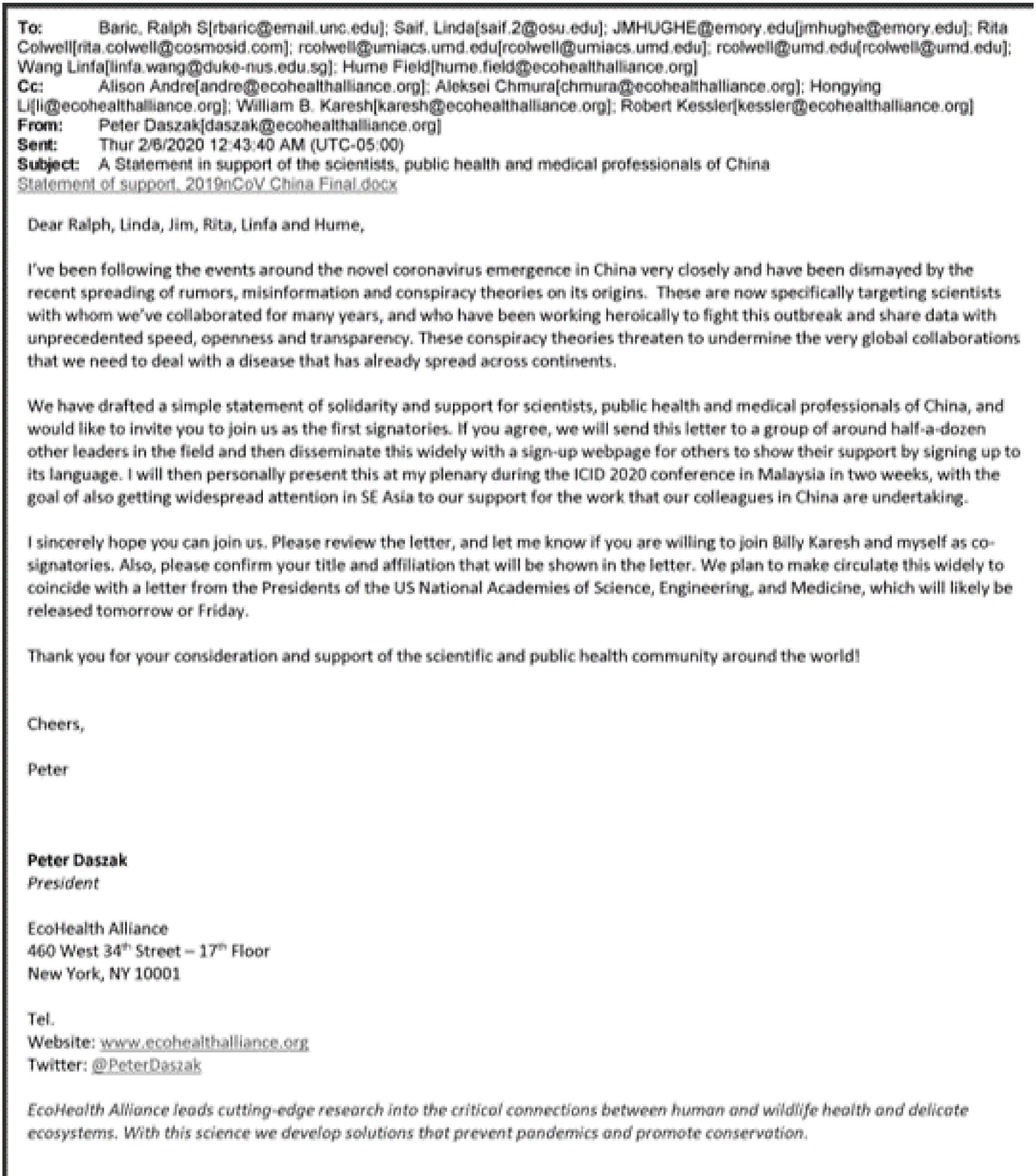
As soon as we hear back from you we'll get ready to send this to our larger list (attached), but of course if you don't feel comfortable, I'll make sure your name is not associated with this.

Cheers,

Peter

Peter Daszak
President

Peter:
I will sign on but my affiliation must read as Distinguished University Professor, University of Maryland College Park. It should not read as former director of the National Science Foundation as I have not had clearance from NSF.
Thank you for addressing my concerns.
Best wishes,
Rita



To: Baric, Ralph S[rbaric@email.unc.edu]; Saif, Linda[saif.2@osu.edu]; JMHUGHE@emory.edu[jmhughe@emory.edu]; Rita Colwell[rita.colwell@cosmosid.com]; rcolwell@umiacs.umd.edu[rcolwell@umiacs.umd.edu]; rcolwell@umd.edu[rcolwell@umd.edu]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Hume Field[hume.field@ecohealthalliance.org]
Cc: Alison Andre[andre@ecohealthalliance.org]; Aleksei Chmura[chmura@ecohealthalliance.org]; Hongying Li[li@ecohealthalliance.org]; William B. Karesh[karesh@ecohealthalliance.org]; Robert Kessler[kessler@ecohealthalliance.org]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Thur 2/6/2020 12:43:40 AM (UTC-05:00)
Subject: A Statement in support of the scientists, public health and medical professionals of China
Statement of support, 2019nCoV China Final.docx

Dear Ralph, Linda, Jim, Rita, Linfa and Hume,

I've been following the events around the novel coronavirus emergence in China very closely and have been dismayed by the recent spreading of rumors, misinformation and conspiracy theories on its origins. These are now specifically targeting scientists with whom we've collaborated for many years, and who have been working heroically to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents.

We have drafted a simple statement of solidarity and support for scientists, public health and medical professionals of China, and would like to invite you to join us as the first signatories. If you agree, we will send this letter to a group of around half-a-dozen other leaders in the field and then disseminate this widely with a sign-up webpage for others to show their support by signing up to its language. I will then personally present this at my plenary during the ICID 2020 conference in Malaysia in two weeks, with the goal of also getting widespread attention in SE Asia to our support for the work that our colleagues in China are undertaking.

I sincerely hope you can join us. Please review the letter, and let me know if you are willing to join Billy Karesh and myself as co-signatories. Also, please confirm your title and affiliation that will be shown in the letter. We plan to make circulate this widely to coincide with a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, which will likely be released tomorrow or Friday.

Thank you for your consideration and support of the scientific and public health community around the world!

Cheers,

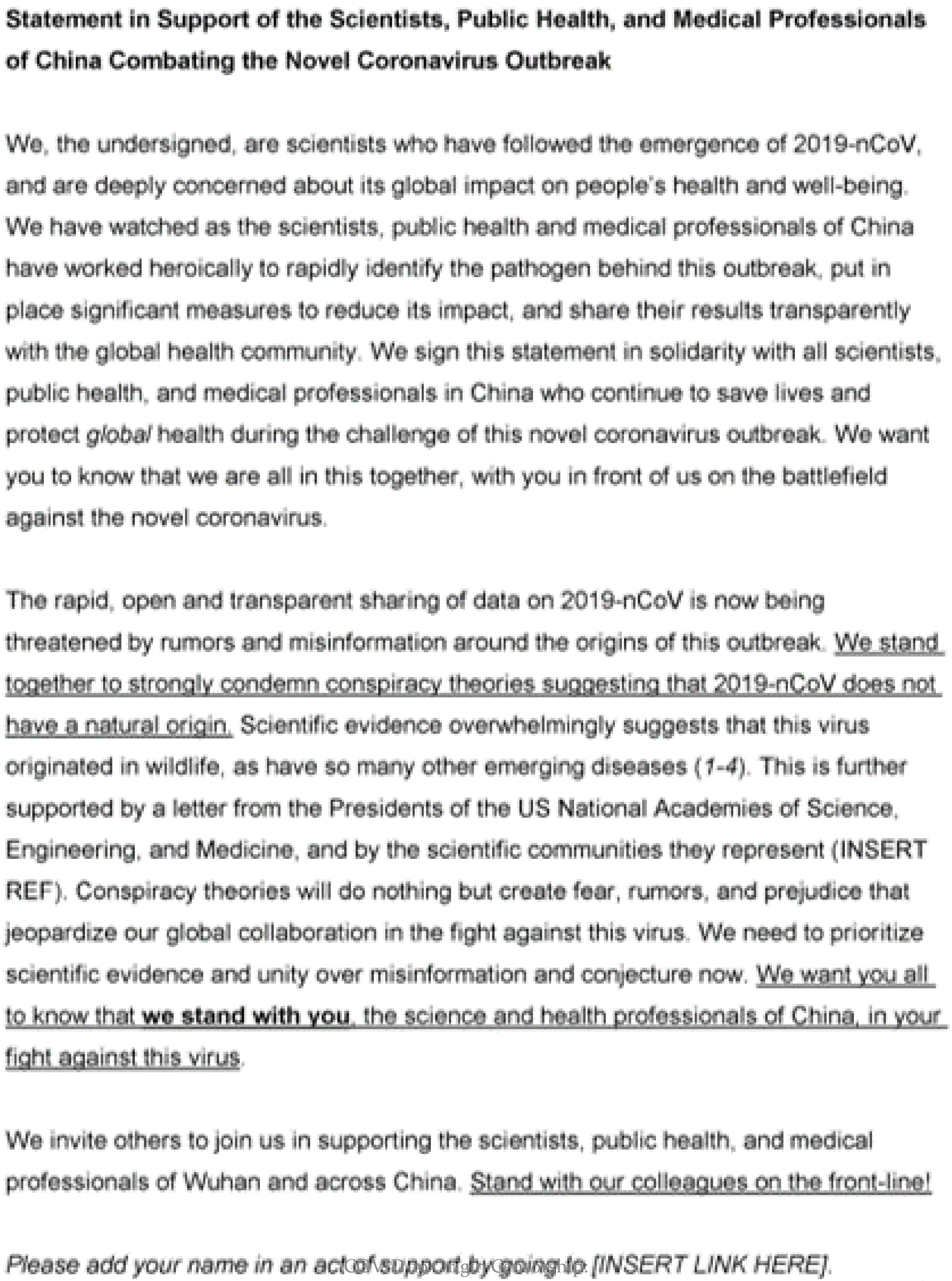
Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel.
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.



Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

We, the undersigned, are scientists who have followed the emergence of 2019-nCoV, and are deeply concerned about its global impact on people's health and well-being. We have watched as the scientists, public health and medical professionals of China have worked heroically to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. We sign this statement in solidarity with all scientists, public health, and medical professionals in China who continue to save lives and protect *global* health during the challenge of this novel coronavirus outbreak. We want you to know that we are all in this together, with you in front of us on the battlefield against the novel coronavirus.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientific evidence overwhelmingly suggests that this virus originated in wildlife, as have so many other emerging diseases (*1-4*). This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent (INSERT REF). Conspiracy theories will do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We need to prioritize scientific evidence and unity over misinformation and conjecture now. We want you all to know that **we stand with you**, the science and health professionals of China, in your fight against this virus.

We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

Please add your name in an act of support by going to [INSERT LINK HERE].

A Statement in support of the
scientists, public health and medical
professionals of China

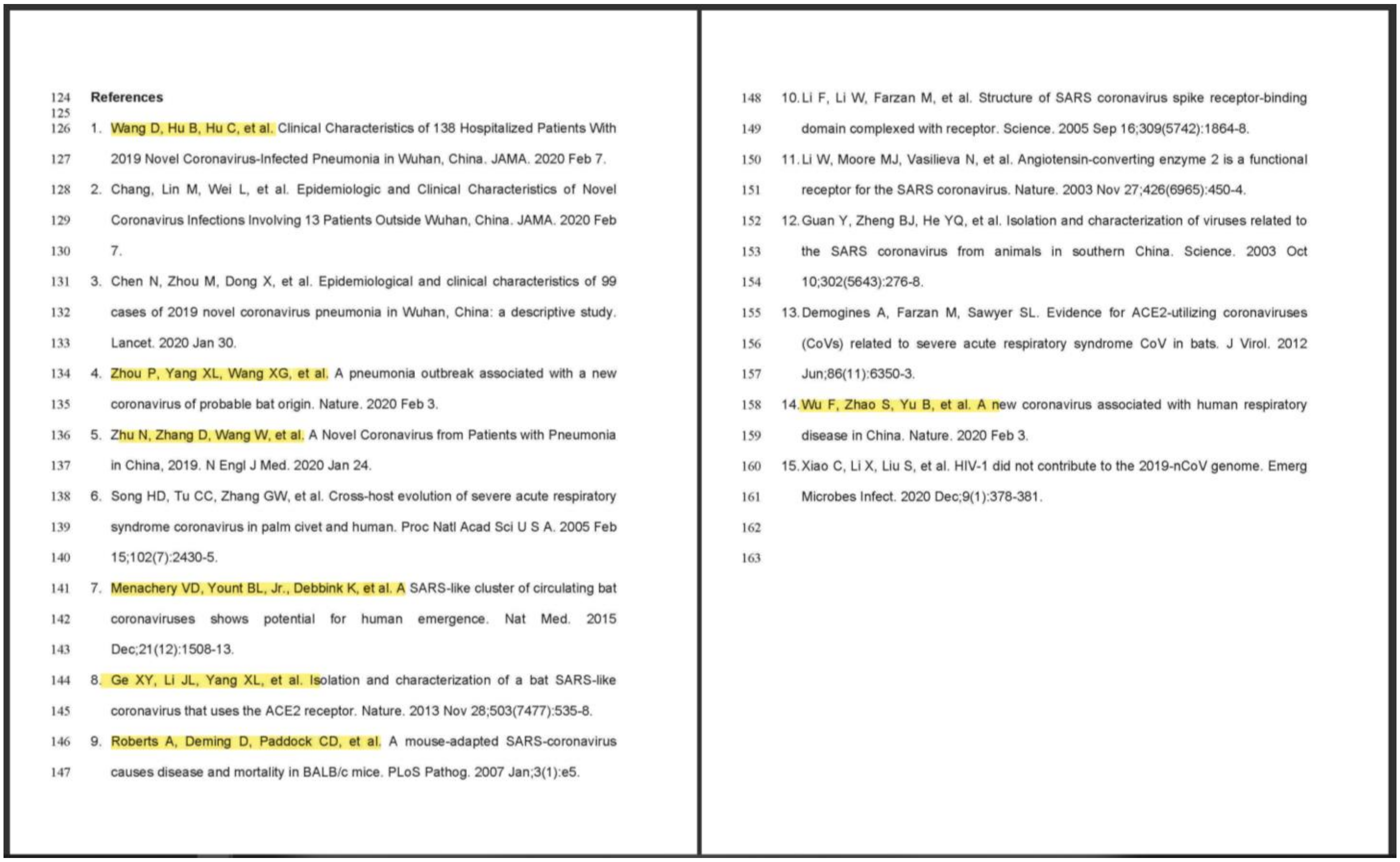
Feb 6, 2020 12:43:40 AM EST

Signatories

Dr. Peter Daszak, President, EcoHealth Alliance
Dr. Jim Hughes, Professor Emeritus, Emory University
Dr. Rita Colwell, former Director of National Science Foundation
Dr. Ralph Baric, Professor, The University of North Carolina, Chapel Hill
Dr. Linda Saif, Distinguished University Professor, The Ohio State University
Dr. Billy Karesh, Executive Vice President, EcoHealth Alliance
Dr. Linfa Wang, Professor, Duke-NUS Medical School
Dr. Hume Field, Honorary Professor, The University of Queensland

References

1. P. Zhou *et al.*, A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, (2020).
2. R. Lu *et al.*, Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, (2020).
3. N. Zhu *et al.*, A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*, (2020).
4. L. Ren *et al.*, Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. *Chin Med J. Epub ahead of print*, (2020).



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3. Chen N, Zhou M, Dong X, et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet. 2020 Jan 30.
4. Zhou P, Yang XL, Wang XG, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature. 2020 Feb 3.
5. Zhu N, Zhang D, Wang W, et al. A Novel Coronavirus from Patients with Pneumonia in China, 2019. N Engl J Med. 2020 Jan 24.
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11. Li W, Moore MJ, Vasilieva N, et al. Angiotensin-converting enzyme 2 is a functional receptor for the SARS coronavirus. Nature. 2003 Nov 27;426(6965):450-4.
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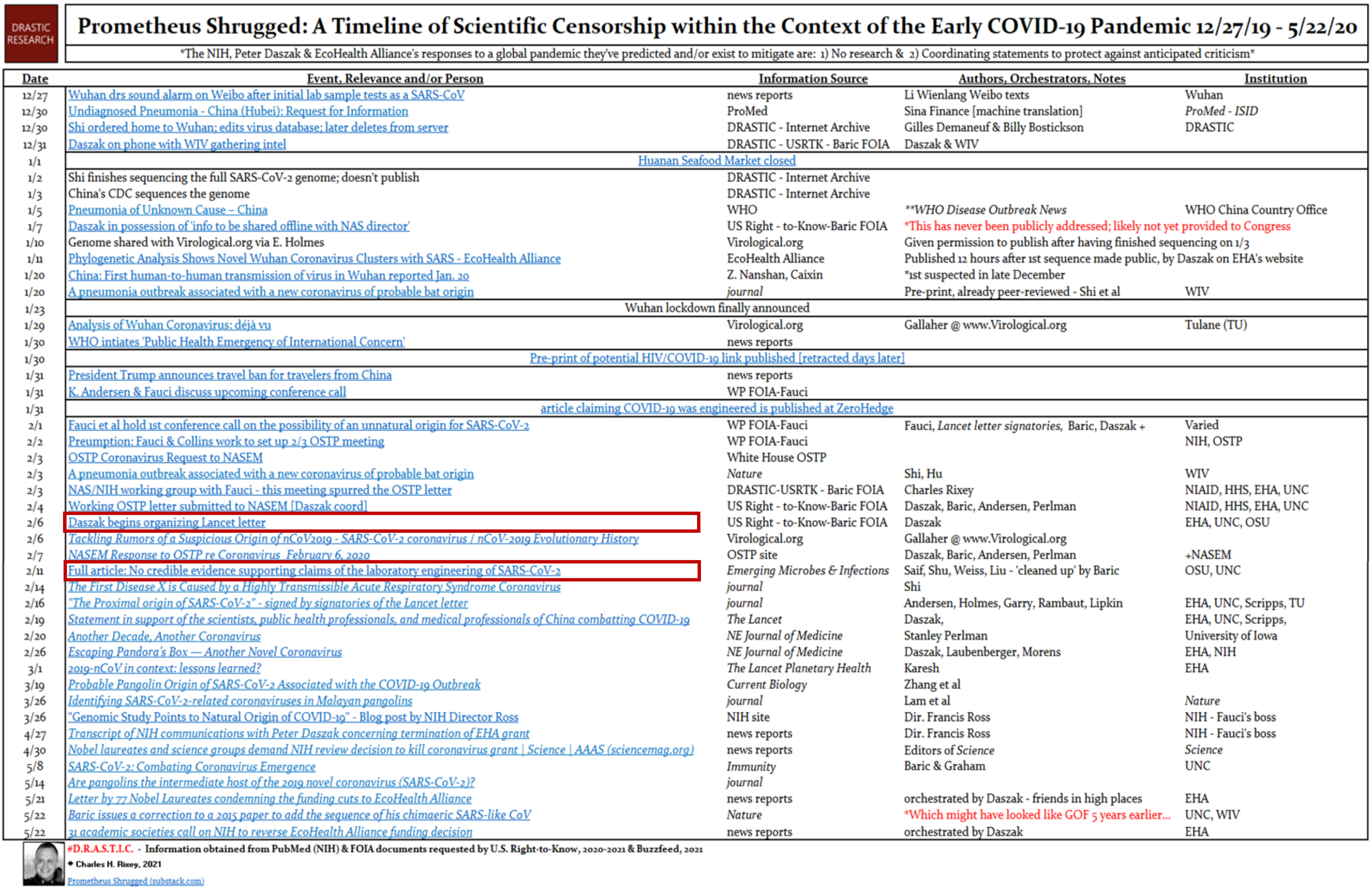
14. Wu F, Zhao S, Yu B, et al. A new coronavirus associated with human respiratory disease in China. Nature. 2020 Feb 3.
15. Xiao C, Li X, Liu S, et al. HIV-1 did not contribute to the 2019-nCoV genome. Emerg Microbes Infect. 2020 Dec;9(1):378-381.



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

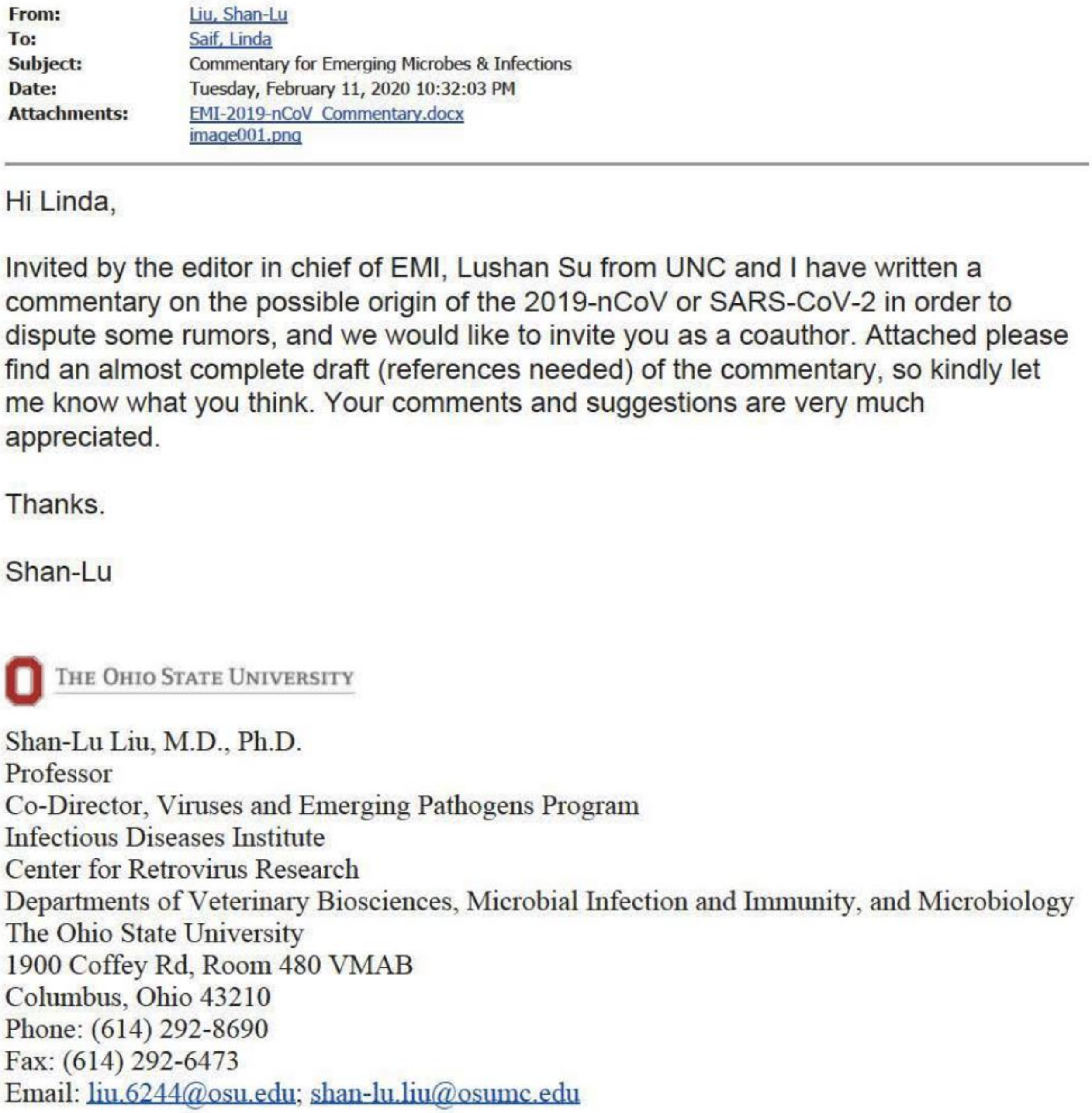
• Charles H. Rixey, 2021

Prometheus Shrugged (substack.com)

FOIA Emails: Linda Saif & Ralph Baric

These highlight further coordination , this time in support of **another pro-zoonosis article** .

Source: US Right-to-Know FOIA documents for Linda Saif



From: Liu, Shan-Lu
To: Saif, Linda
Subject: Commentary for Emerging Microbes & Infections
Date: Tuesday, February 11, 2020 10:32:03 PM
Attachments: EMI-2019-nCoV_Commentary.docx
image001.png

Hi Linda,

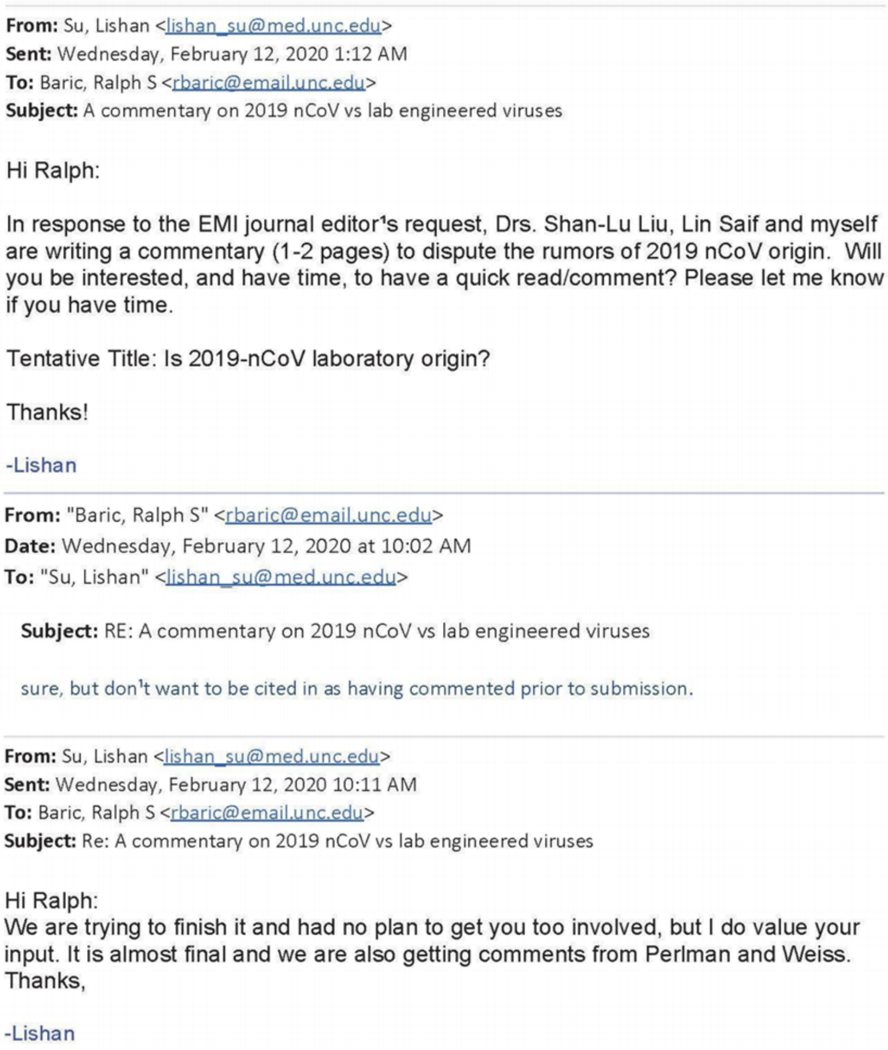
Invited by the editor in chief of EMI, Lushan Su from UNC and I have written a commentary on the possible origin of the 2019-nCoV or SARS-CoV-2 in order to dispute some rumors, and we would like to invite you as a coauthor. Attached please find an almost complete draft (references needed) of the commentary, so kindly let me know what you think. Your comments and suggestions are very much appreciated.

Thanks.

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu



From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 1:12 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: A commentary on 2019 nCoV vs lab engineered viruses

Hi Ralph:

In response to the EMI journal editor's request, Drs. Shan-Lu Liu, Lin Saif and myself are writing a commentary (1-2 pages) to dispute the rumors of 2019 nCoV origin. Will you be interested, and have time, to have a quick read/comment? Please let me know if you have time.

Tentative Title: Is 2019-nCoV laboratory origin?

Thanks!

-Lishan

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Wednesday, February 12, 2020 at 10:02 AM
To: "Su, Lishan" <lishan_su@med.unc.edu>

Subject: RE: A commentary on 2019 nCoV vs lab engineered viruses

sure, but don't want to be cited in as having commented prior to submission.

From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 10:11 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: A commentary on 2019 nCoV vs lab engineered viruses

Hi Ralph:
We are trying to finish it and had no plan to get you too involved, but I do value your input. It is almost final and we are also getting comments from Perlman and Weiss.
Thanks,

-Lishan

From: "rbaric@email.unc.edu" <rbaric@email.unc.edu>
Date: Wednesday, February 12, 2020 12:32 PM
To: "Su, Lishan" <lishan_su@med.unc.edu>
Cc: Linda Saif <saif.2@osu.edu>
Subject: RE: A commentary on 2019 nCoV vs lab engineered viruses

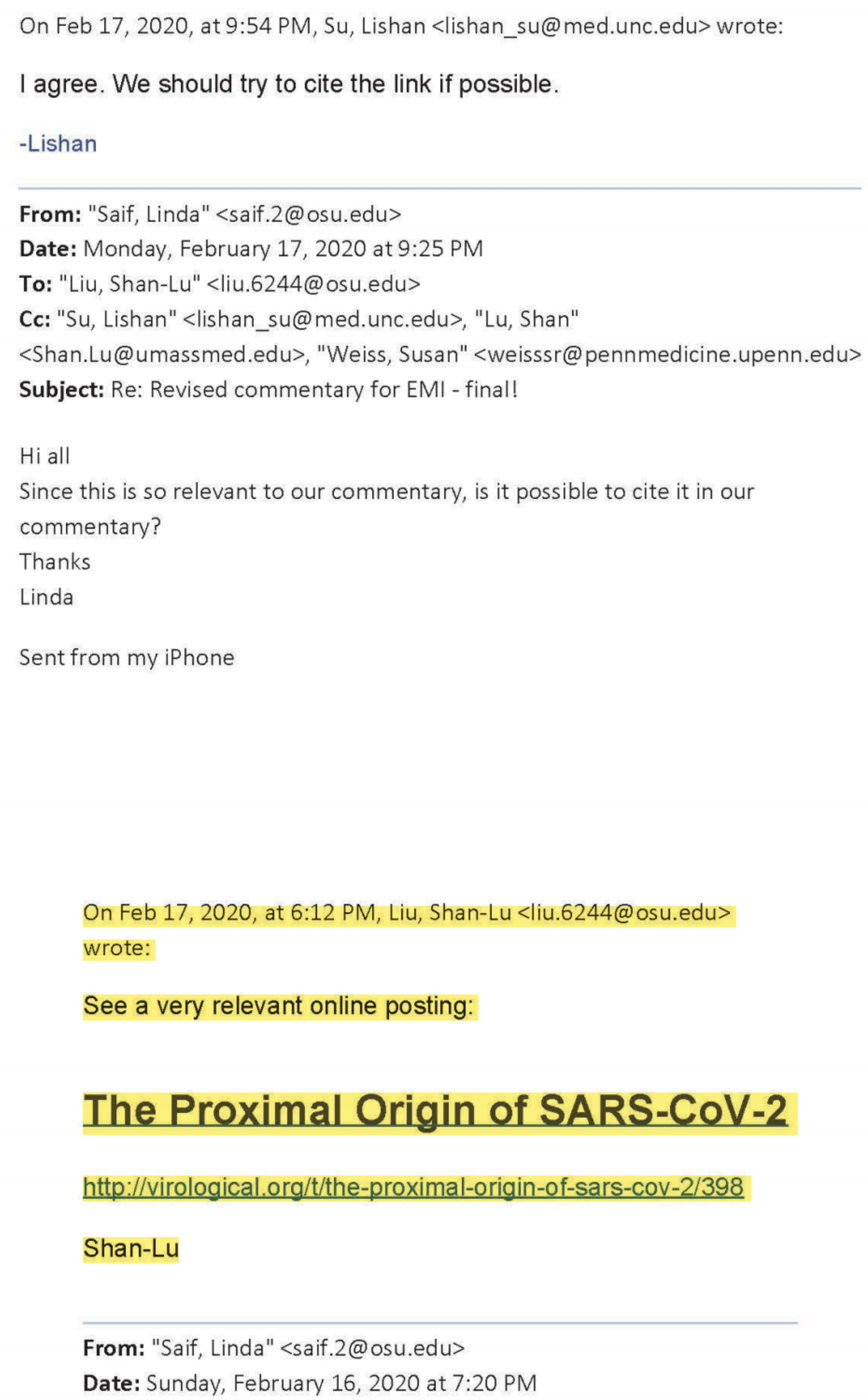
My comments. I've included an excel file comparing the differences in the genome length sequences of the parental and chimeric viruses. Also made some text changes. I think the community needs to write these editorials and I thank you for your efforts. ralph

---

From:	Saif, Linda
To:	Liu, Shan-Lu; lishan_su@med.unc.edu
Subject:	FW: A commentary on 2019 nCoV vs lab engineered viruses
Date:	Wednesday, February 12, 2020 1:28:39 PM
Attachments:	EMI-2019-nCoV_Commentary LJS_SLL_Refs-rsb.docx

Hi
Please note that Ralph made these changes on an earlier copy sent to him so hopefully the 2 of you can incorporate them into the updated draft I sent this AM!
Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University



On Feb 17, 2020, at 9:54 PM, Su, Lishan <lishan_su@med.unc.edu> wrote:

I agree. We should try to cite the link if possible.

-Lishan

From: "Saif, Linda" <saif.2@osu.edu>
Date: Monday, February 17, 2020 at 9:25 PM
To: "Liu, Shan-Lu" <liu.6244@osu.edu>
Cc: "Su, Lishan" <lishan_su@med.unc.edu>, "Lu, Shan" <Shan.Lu@umassmed.edu>, "Weiss, Susan" <weisssr@pennmedicine.upenn.edu>
Subject: Re: Revised commentary for EMI - final!

Hi all
Since this is so relevant to our commentary, is it possible to cite it in our commentary?
Thanks
Linda

Sent from my iPhone

On Feb 17, 2020, at 6:12 PM, Liu, Shan-Lu <liu.6244@osu.edu> wrote:

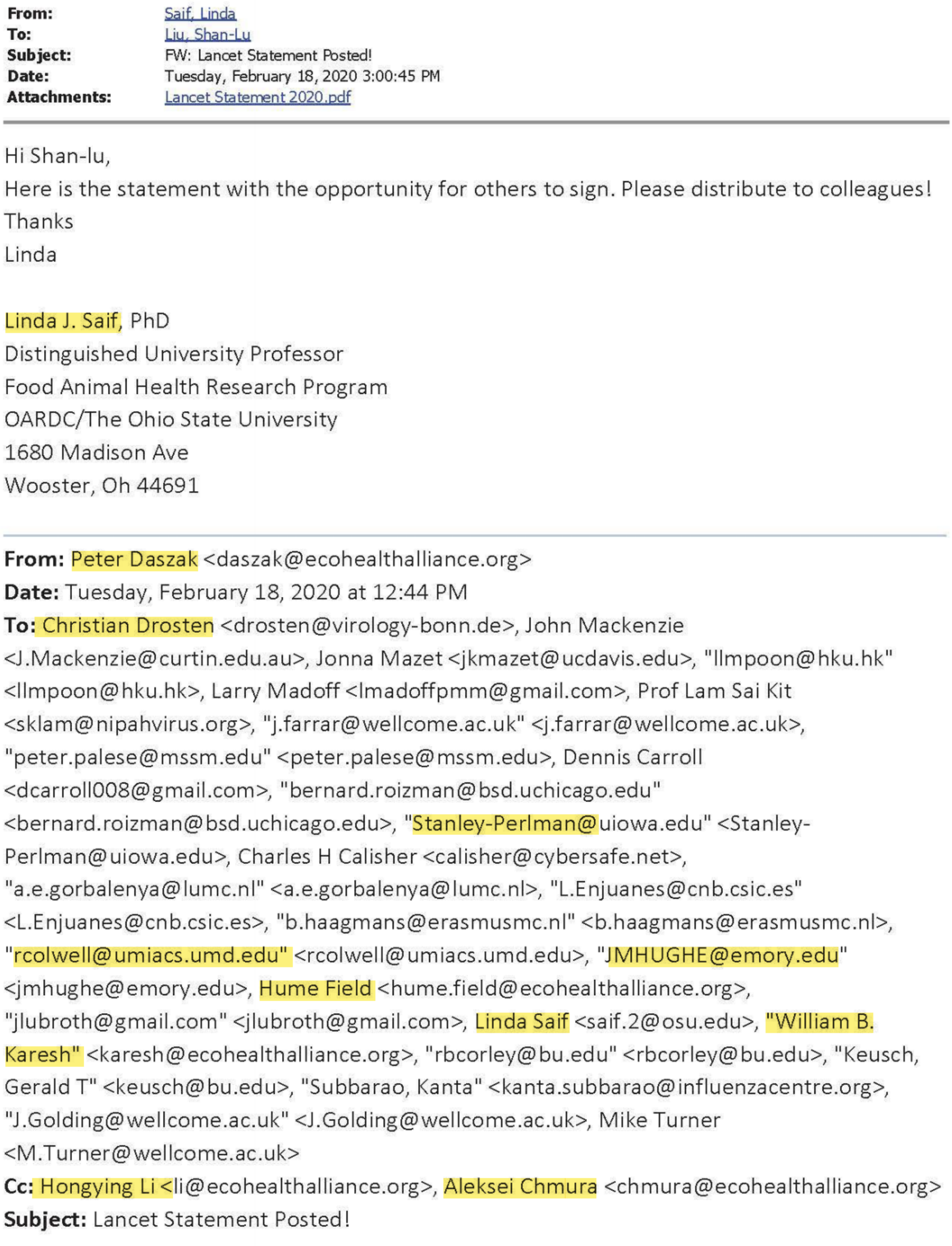
See a very relevant online posting:

The Proximal Origin of SARS-CoV-2

http://virological.org/t/the-proximal-origin-of-sars-cov-2/398

Shan-Lu

From: "Saif, Linda" <saif.2@osu.edu>
Date: Sunday, February 16, 2020 at 7:20 PM



From: Saif, Linda
To: Liu, Shan-Lu
Subject: FW: Lancet Statement Posted!
Date: Tuesday, February 18, 2020 3:00:45 PM
Attachments: Lancet Statement 2020.pdf

Hi Shan-lu,

Here is the statement with the opportunity for others to sign. Please distribute to colleagues!

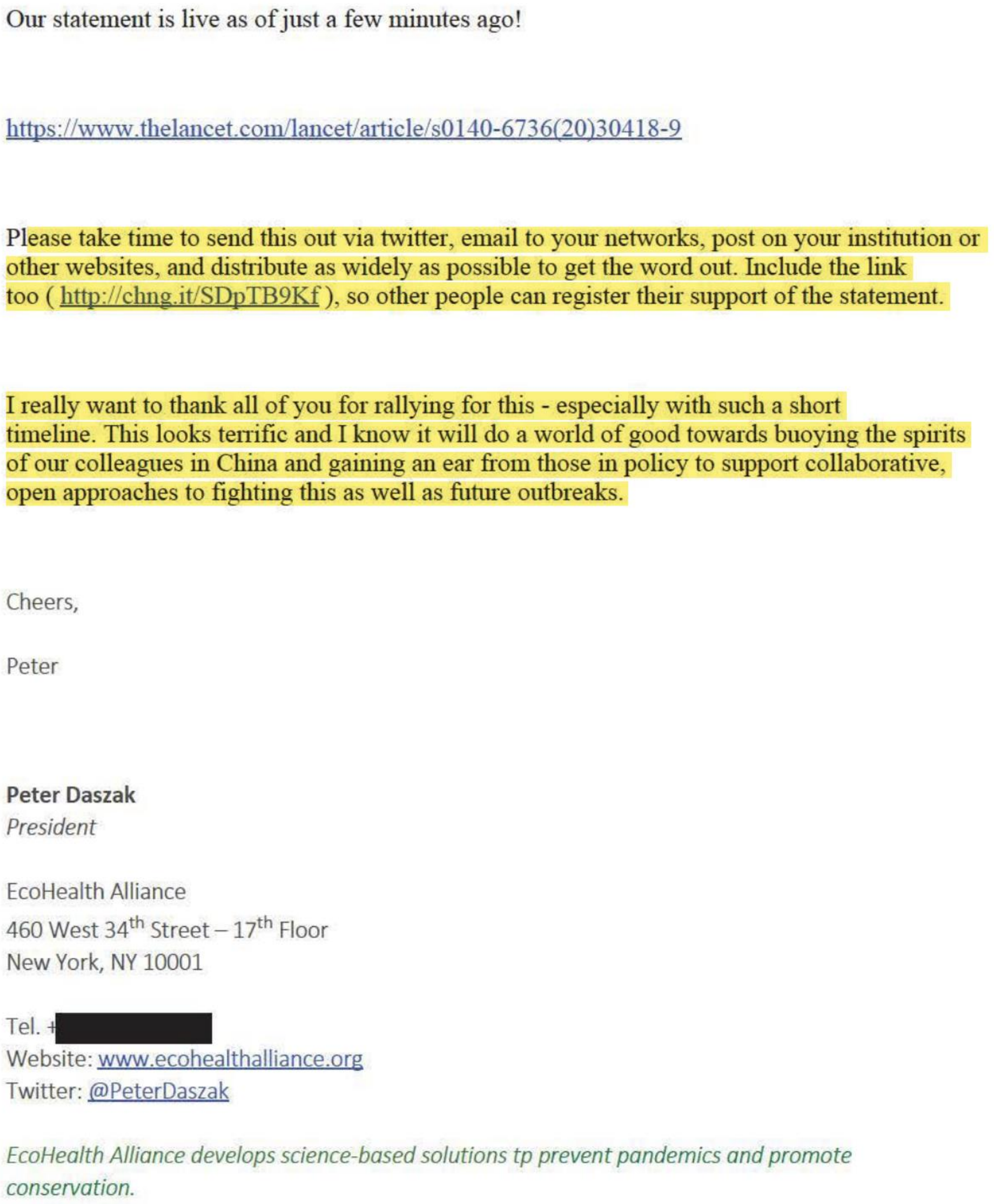
Thanks

Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

From: Peter Daszak <daszak@ecohealthalliance.org>
Date: Tuesday, February 18, 2020 at 12:44 PM
To: Christian Drosten <drosten@virology-bonn.de>, John Mackenzie <J.Mackenzie@curtin.edu.au>, Jonna Mazet <jkmazet@ucdavis.edu>, "llmpoon@hku.hk" <llmpoon@hku.hk>, Larry Madoff <lmadoffpmm@gmail.com>, Prof Lam Sai Kit <sklam@nipahvirus.org>, "j.farrar@wellcome.ac.uk" <j.farrar@wellcome.ac.uk>, "peter.palese@mssm.edu" <peter.palese@mssm.edu>, Dennis Carroll <dcarroll008@gmail.com>, "bernard.roizman@bsd.uchicago.edu" <bernard.roizman@bsd.uchicago.edu>, "Stanley-Perlman@uiowa.edu" <Stanley-Perlman@uiowa.edu>, Charles H Calisher <calisher@cybersafe.net>, "a.e.gorbalenya@lumc.nl" <a.e.gorbalenya@lumc.nl>, "L.Enjuanes@cnb.csic.es" <L.Enjuanes@cnb.csic.es>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "rcolwell@umiacs.umd.edu" <rcolwell@umiacs.umd.edu>, "JMHUGHE@emory.edu" <jmhughe@emory.edu>, Hume Field <hume.field@ecohealthalliance.org>, "jlubroth@gmail.com" <jlubroth@gmail.com>, Linda Saif <saif.2@osu.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>, "rbcorley@bu.edu" <rbcorley@bu.edu>, "Keusch, Gerald T" <keusch@bu.edu>, "Subbarao, Kanta" <kanta.subbarao@influenzacentre.org>, "J.Golding@wellcome.ac.uk" <J.Golding@wellcome.ac.uk>, Mike Turner <M.Turner@wellcome.ac.uk>
Cc: Hongying Li <li@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: Lancet Statement Posted!

Dear All,



Our statement is live as of just a few minutes ago!

https://www.thelancet.com/lancet/article/s0140-6736(20)30418-9

Please take time to send this out via twitter, email to your networks, post on your institution or other websites, and distribute as widely as possible to get the word out. Include the link too (http://chng.it/SDpTB9Kf), so other people can register their support of the statement.

I really want to thank all of you for rallying for this - especially with such a short timeline. This looks terrific and I know it will do a world of good towards buoying the spirits of our colleagues in China and gaining an ear from those in policy to support collaborative, open approaches to fighting this as well as future outbreaks.

Cheers,

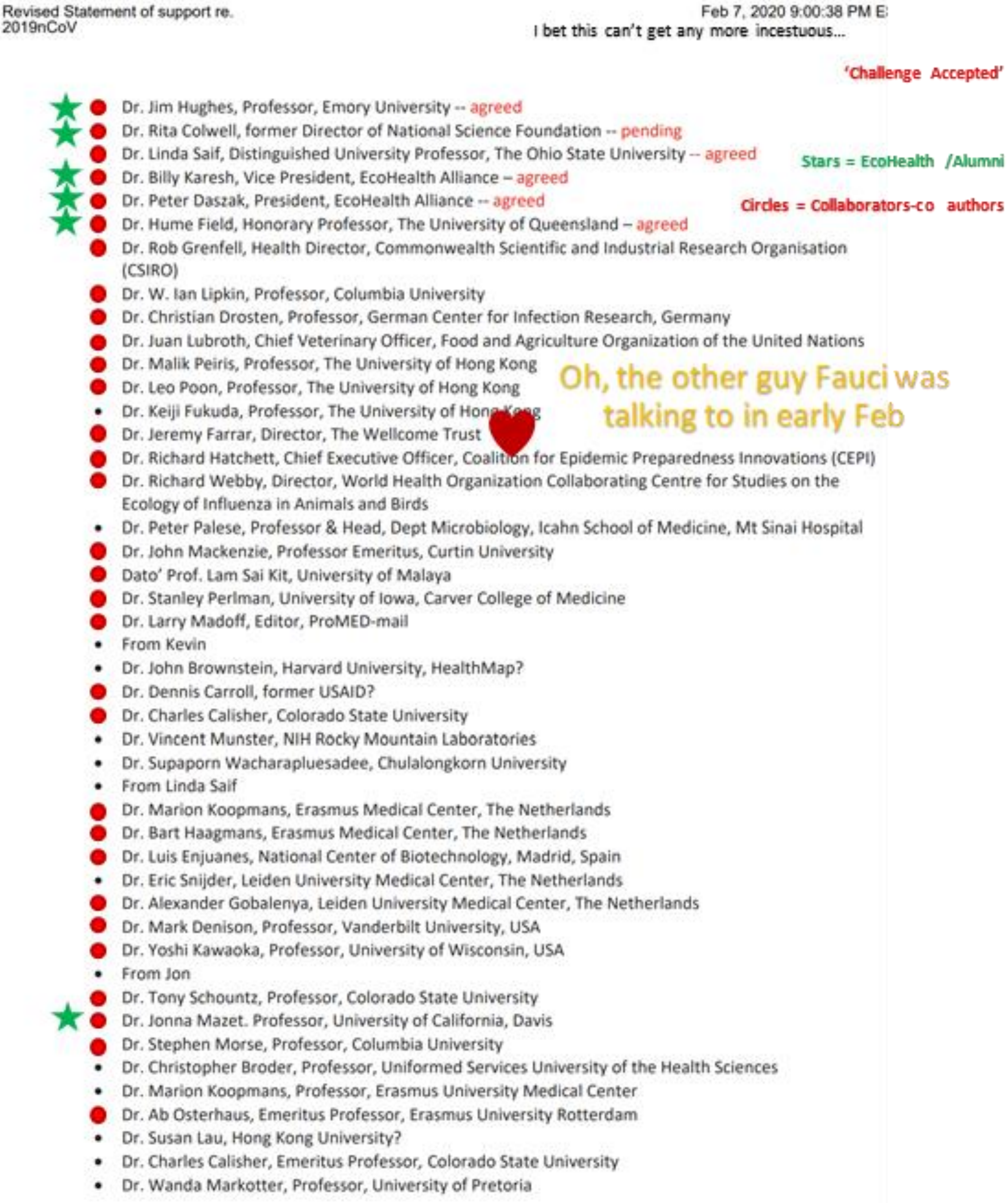
Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +[redacted]
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions tp prevent pandemics and promote conservation.



Revised Statement of support re. 2019nCoV

Feb 7, 2020 9:00:38 PM E

I bet this can't get any more incestuous...

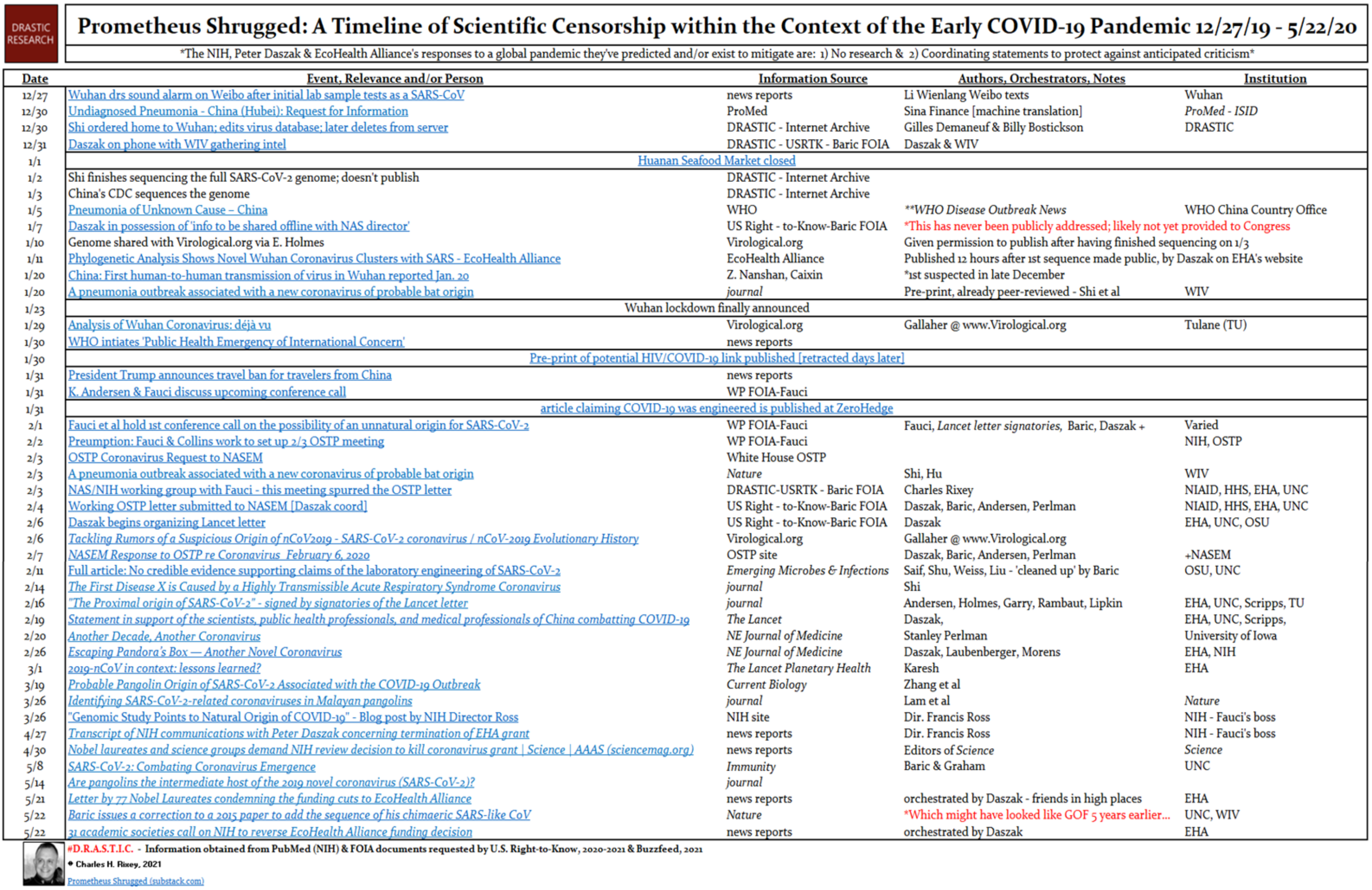
'Challenge Accepted'

Stars = EcoHealth /Alumni

Circles = Collaborators-co authors

- ★ ● Dr. Jim Hughes, Professor, Emory University -- agreed
- ★ ● Dr. Rita Colwell, former Director of National Science Foundation -- pending
- ● Dr. Linda Saif, Distinguished University Professor, The Ohio State University -- agreed
- ★ ● Dr. Billy Karesh, Vice President, EcoHealth Alliance – agreed
- ★ ● Dr. Peter Daszak, President, EcoHealth Alliance -- agreed
- ★ ● Dr. Hume Field, Honorary Professor, The University of Queensland – agreed
- ● Dr. Rob Grenfell, Health Director, Commonwealth Scientific and Industrial Research Organisation (CSIRO)
- ● Dr. W. Ian Lipkin, Professor, Columbia University
- ● Dr. Christian Drosten, Professor, German Center for Infection Research, Germany
- ● Dr. Juan Lubroth, Chief Veterinary Officer, Food and Agriculture Organization of the United Nations
- ● Dr. Malik Peiris, Professor, The University of Hong Kong
- ● Dr. Leo Poon, Professor, The University of Hong Kong
- Dr. Keiji Fukuda, Professor, The University of Hong Kong
- ● Dr. Jeremy Farrar, Director, The Wellcome Trust
- ● Dr. Richard Hatchett, Chief Executive Officer, Coalition for Epidemic Preparedness Innovations (CEPI)
- ● Dr. Richard Webby, Director, World Health Organization Collaborating Centre for Studies on the Ecology of Influenza in Animals and Birds
- Dr. Peter Palese, Professor & Head, Dept Microbiology, Icahn School of Medicine, Mt Sinai Hospital
- ● Dr. John Mackenzie, Professor Emeritus, Curtin University
- ● Dato' Prof. Lam Sai Kit, University of Malaya
- ● Dr. Stanley Perlman, University of Iowa, Carver College of Medicine
- ● Dr. Larry Madoff, Editor, ProMED-mail
- From Kevin
- Dr. John Brownstein, Harvard University, HealthMap?
- ● Dr. Dennis Carroll, former USAID?
- ● Dr. Charles Calisher, Colorado State University
- Dr. Vincent Munster, NIH Rocky Mountain Laboratories
- Dr. Supaporn Wacharapluesadee, Chulalongkorn University
- From Linda Saif
- ● Dr. Marion Koopmans, Erasmus Medical Center, The Netherlands
- ● Dr. Bart Haagmans, Erasmus Medical Center, The Netherlands
- ● Dr. Luis Enjuanes, National Center of Biotechnology, Madrid, Spain
- Dr. Eric Snijder, Leiden University Medical Center, The Netherlands
- ● Dr. Alexander Gobalenya, Leiden University Medical Center, The Netherlands
- ● Dr. Mark Denison, Professor, Vanderbilt University, USA
- ● Dr. Yoshi Kawaoka, Professor, University of Wisconsin, USA
- From Jon
- ● Dr. Tony Schountz, Professor, Colorado State University
- ★ ● Dr. Jonna Mazet. Professor, University of California, Davis
- ● Dr. Stephen Morse, Professor, Columbia University
- Dr. Christopher Broder, Professor, Uniformed Services University of the Health Sciences
- Dr. Marion Koopmans, Professor, Erasmus University Medical Center
- ● Dr. Ab Osterhaus, Emeritus Professor, Erasmus University Rotterdam
- Dr. Susan Lau, Hong Kong University?
- Dr. Charles Calisher, Emeritus Professor, Colorado State University
- Dr. Wanda Markotter, Professor, University of Pretoria

Oh, the other guy Fauci was talking to in early Feb



DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

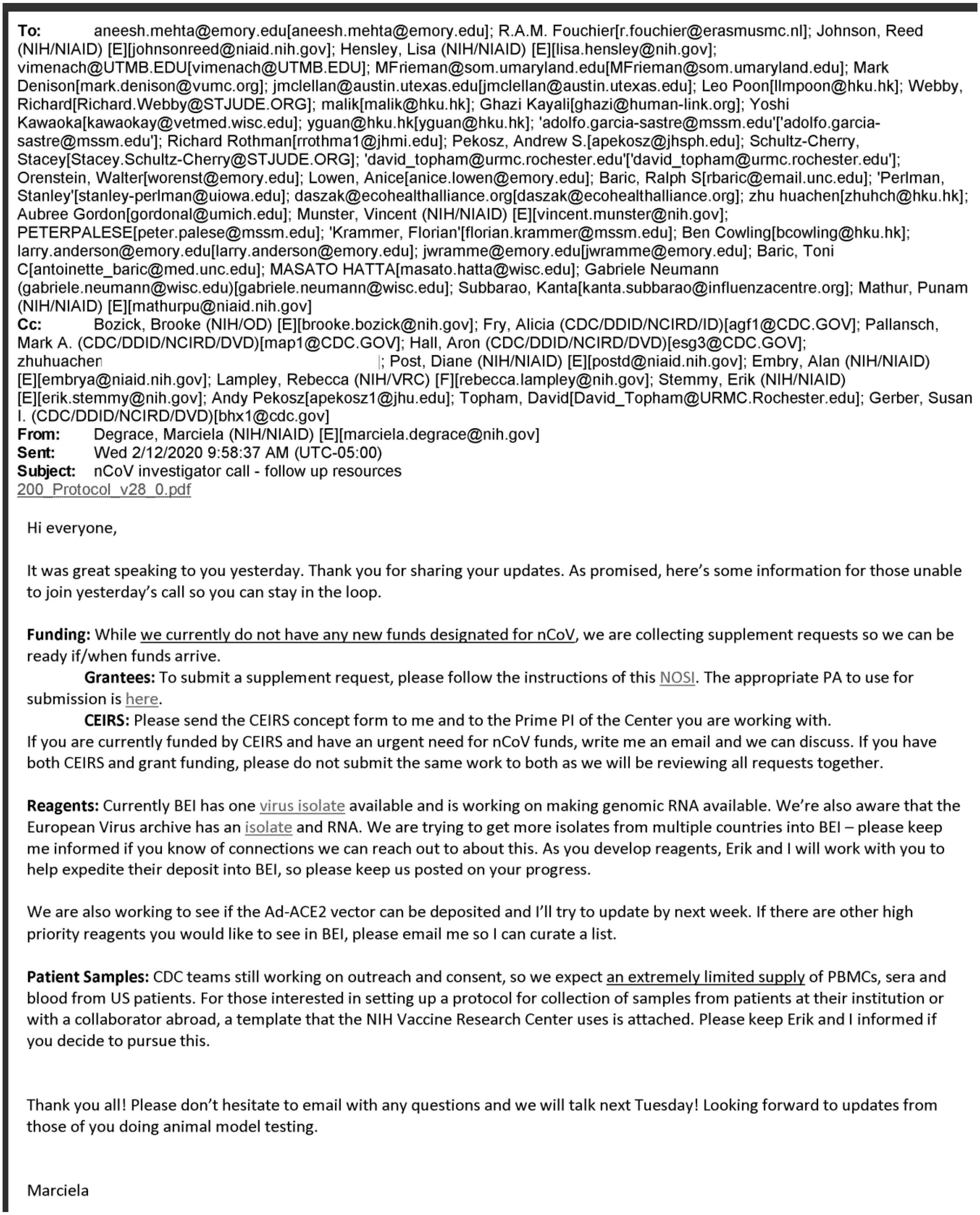
• Charles H. Rixey, 2021

Prometheus Shrugged (substack.com)

FOIA Emails: China fights for a new name

These highlight the efforts by Chinese scientists to get the international organization that assigns names to new microorganism species to not name it SARS-CoV-2, which would remind people of their failures in 2003

Source: US Right-to-Know FOIA documents for Ralph Baric



To: aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; vimenach@UTMB.EDU[vimenach@UTMB.EDU]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Mark Denison[mark.denison@vumc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]
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Subject: nCoV investigator call - follow up resources
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Hi everyone,

It was great speaking to you yesterday. Thank you for sharing your updates. As promised, here's some information for those unable to join yesterday's call so you can stay in the loop.

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Grantees: To submit a supplement request, please follow the instructions of this NOSI. The appropriate PA to use for submission is here.

CEIRS: Please send the CEIRS concept form to me and to the Prime PI of the Center you are working with.
If you are currently funded by CEIRS and have an urgent need for nCoV funds, write me an email and we can discuss. If you have both CEIRS and grant funding, please do not submit the same work to both as we will be reviewing all requests together.

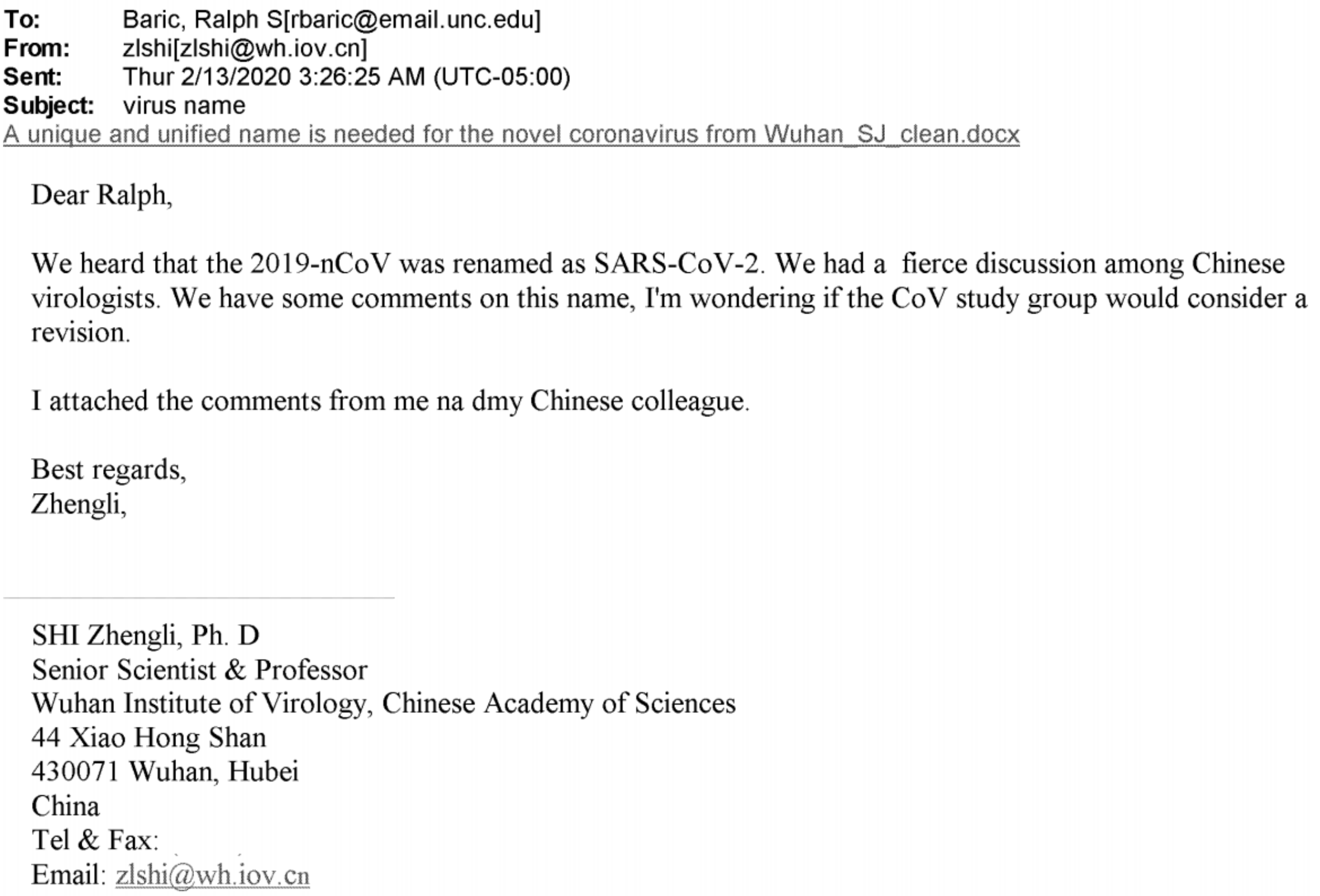
Reagents: Currently BEI has one virus isolate available and is working on making genomic RNA available. We're also aware that the European Virus archive has an isolate and RNA. We are trying to get more isolates from multiple countries into BEI – please keep me informed if you know of connections we can reach out to about this. As you develop reagents, Erik and I will work with you to help expedite their deposit into BEI, so please keep us posted on your progress.

We are also working to see if the Ad-ACE2 vector can be deposited and I'll try to update by next week. If there are other high priority reagents you would like to see in BEI, please email me so I can curate a list.

Patient Samples: CDC teams still working on outreach and consent, so we expect an extremely limited supply of PBMCs, sera and blood from US patients. For those interested in setting up a protocol for collection of samples from patients at their institution or with a collaborator abroad, a template that the NIH Vaccine Research Center uses is attached. Please keep Erik and I informed if you decide to pursue this.

Thank you all! Please don't hesitate to email with any questions and we will talk next Tuesday! Looking forward to updates from those of you doing animal model testing.

Marciela



To: Baric, Ralph S[rbaric@email.unc.edu]
From: zlshi[zlshi@wh.iov.cn]
Sent: Thur 2/13/2020 3:26:25 AM (UTC-05:00)
Subject: virus name
A unique and unified name is needed for the novel coronavirus from Wuhan_SJ_clean.docx

Dear Ralph,

We heard that the 2019-nCoV was renamed as SARS-CoV-2. We had a fierce discussion among Chinese virologists. We have some comments on this name, I'm wondering if the CoV study group would consider a revision.

I attached the comments from me na dmy Chinese colleague.

Best regards,
Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
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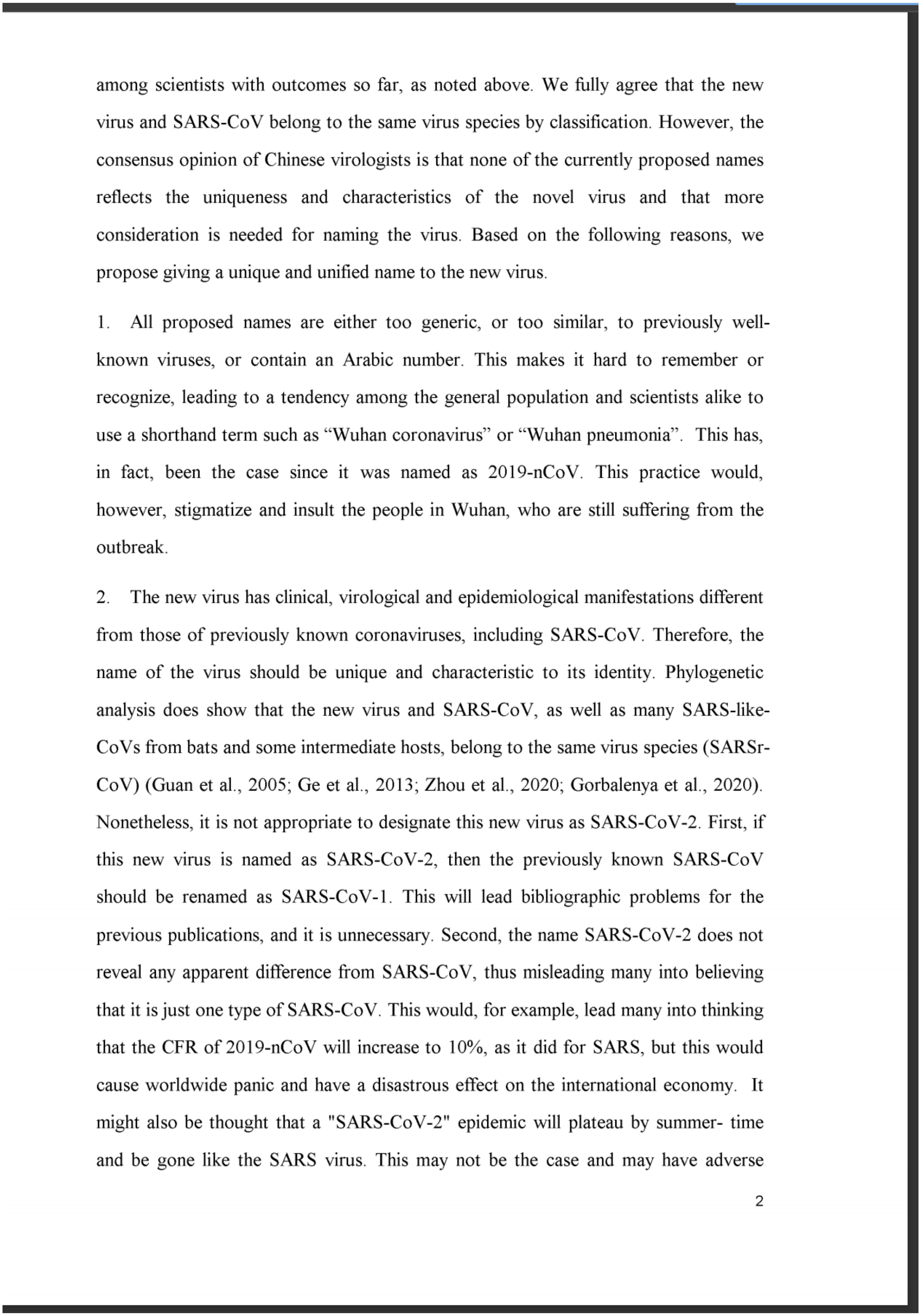
China
Tel & Fax:
Email: zlshi@wh.iov.cn

Suggestion to the Coronavirus Study Group (CSG) of ICTV

A unique and unified name is needed for the novel coronavirus identified from Wuhan

An outbreak of unusual pneumonia of unknown cause in Wuhan, China was first reported in December, 2019. By 5 January, 2020, Chinese scientists had quickly identified the causative agent as a new type of coronavirus (CoV) belonging to the *Betacoronavirus* genus of the *Coronaviridae* family that also includes severe acute respiratory syndrome (SARS)-CoV and Middle East respiratory syndrome (MERS)-CoV (Zhu et al., 2020; Zhou et al., 2020; Wu et al., 2020; Chen et al., 2020). On 12 January 2020, the World Health Organization (WHO) temporarily named the virus as **2019 novel coronavirus (2019-nCoV)** (WHO webpage). On 30 January, WHO recommended naming the disease as "2019-nCoV acute respiratory disease" (WHO webpage). On 8 February 2020, the China National Health Commission (CNHC) announced naming the disease as **"Novel Coronavirus Pneumonia" (NCP)** (CNHC webpage). On 11 February 2020, WHO renamed the disease as "**coronavirus disease 2019" (COVID-19)** (WHO webpage). On 7 February 2020, the Coronavirus Study Group (CSG) of the International Committee on Virus Taxonomy (ICTV) posted a manuscript at bioRxiv and suggested designating the novel coronavirus as "**severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)**" based on the phylogenetic analysis of related coronaviruses (Gorbalenya et al., 2020).

By 11 February 2020, the new coronavirus had caused more than 40,000 confirmed infections and more than 1000 deaths, mostly in mainland China, in spite of efforts by the Chinese government and its people to contain spread of the virus in past weeks. It goes without saying that the effects of the epidemic on all the aspects of Chinese life are devastating and, possibly, irreversible. Consequently, appropriately naming the virus and disease becomes a matter of importance to the Chinese people, in general, and virologists, in specific, and the issue has been fervently discussed and debated



among scientists with outcomes so far, as noted above. We fully agree that the new virus and SARS-CoV belong to the same virus species by classification. However, the consensus opinion of Chinese virologists is that none of the currently proposed names reflects the uniqueness and characteristics of the novel virus and that more consideration is needed for naming the virus. Based on the following reasons, we propose giving a unique and unified name to the new virus.

1. All proposed names are either too generic, or too similar, to previously well-known viruses, or contain an Arabic number. This makes it hard to remember or recognize, leading to a tendency among the general population and scientists alike to use a shorthand term such as “Wuhan coronavirus” or “Wuhan pneumonia”. This has, in fact, been the case since it was named as 2019-nCoV. This practice would, however, stigmatize and insult the people in Wuhan, who are still suffering from the outbreak.

2. The new virus has clinical, virological and epidemiological manifestations different from those of previously known coronaviruses, including SARS-CoV. Therefore, the name of the virus should be unique and characteristic to its identity. Phylogenetic analysis does show that the new virus and SARS-CoV, as well as many SARS-like-CoVs from bats and some intermediate hosts, belong to the same virus species (SARSr-CoV) (Guan et al., 2005; Ge et al., 2013; Zhou et al., 2020; Gorbalenya et al., 2020). Nonetheless, it is not appropriate to designate this new virus as SARS-CoV-2. First, if this new virus is named as SARS-CoV-2, then the previously known SARS-CoV should be renamed as SARS-CoV-1. This will lead bibliographic problems for the previous publications, and it is unnecessary. Second, the name SARS-CoV-2 does not reveal any apparent difference from SARS-CoV, thus misleading many into believing that it is just one type of SARS-CoV. This would, for example, lead many into thinking that the CFR of 2019-nCoV will increase to 10%, as it did for SARS, but this would cause worldwide panic and have a disastrous effect on the international economy. It might also be thought that a "SARS-CoV-2" epidemic will plateau by summer- time and be gone like the SARS virus. This may not be the case and may have adverse

effects on the implementation of the outbreak control activities.

3. The new virus is still evolving, and it is still too early to predict the outcome of the current outbreak. However, it is already clear that the infection of the new virus has diverse symptoms, from asymptomatic infection to severe pneumonia and even death. It has less case-fatality rate and higher transmissibility than SARS-CoV, indicating its clear difference from SARS-CoV. Again, therefore, it is not appropriate to designate the new virus as SARS-CoV-2 before we know more properties of the virus.

4. In consideration of the above reasoning and in view of the contagiousness and transmissibility of the new virus, we suggest proposing a unique and easy-to-use name for it, such as "**Transmissible acute respiratory coronavirus (TARS-CoV)**" (Jiang and Shi, 2020). Another choice is "**Human acute respiratory coronavirus (HARS-CoV)**. In this way, the new coronavirus and SARS-CoV, as well as related bat SARS-like coronaviruses, would, together, comprise the biological species of SARSr-CoV, which complies with the conventions of the classification and nomenclature of ICTV.

Proposers:

Zhengli Shi, Wuhan Institute of Virology, Chinese Academy of Sciences
Shibo Jiang, Fudan University School of Medicine
Wenjie Tan, China Center for Disease Control and Prevention
Yuelong Shu, Sun Yat-sen University, School of Public Health (Shenzhen)
Deyin Guo, Sun Yat-sen University School of Medicine

References

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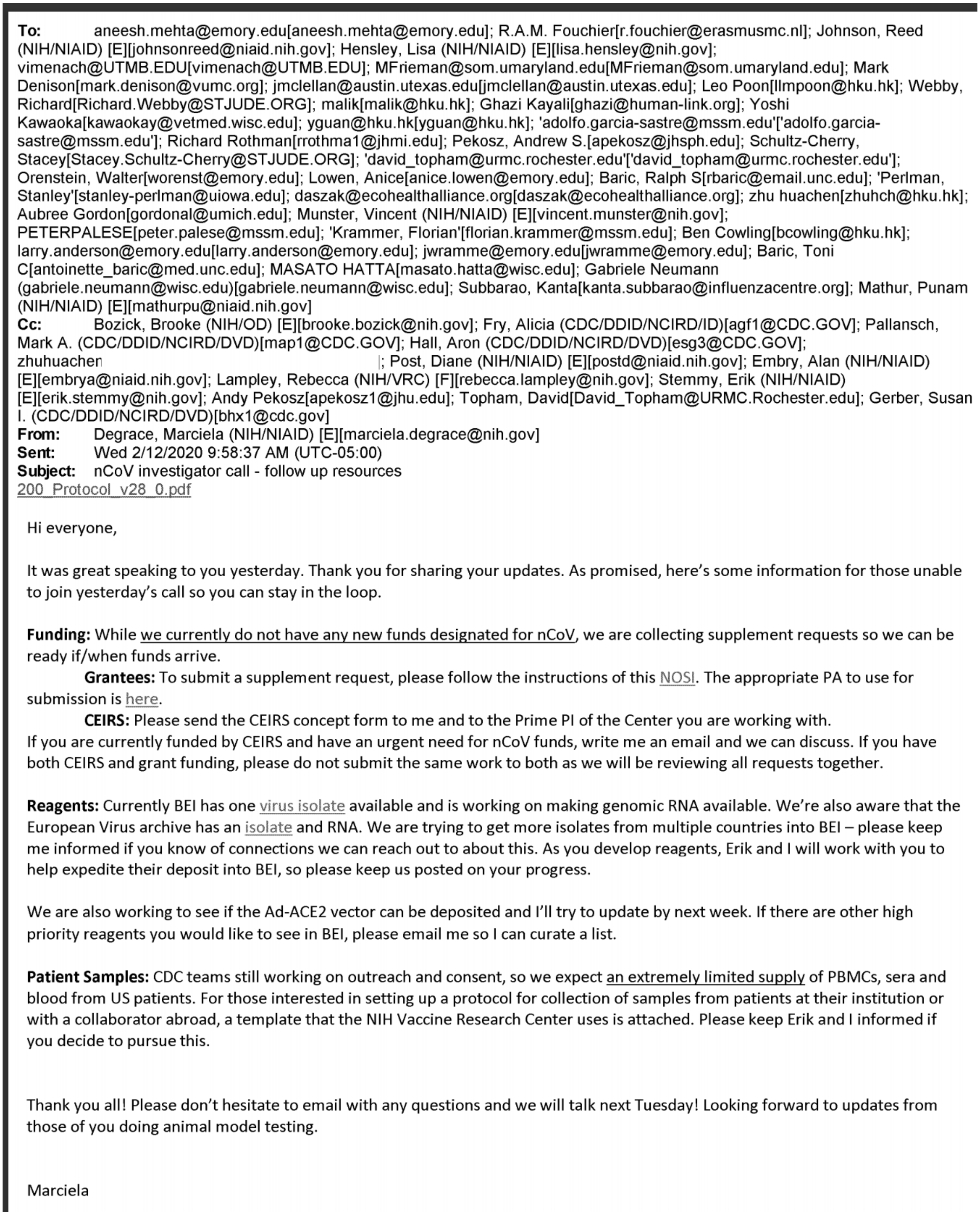
11. Zhou P, et al., A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature. 2020 Feb 3. doi: 10.1038/s41586-020-2012-7. [Epub ahead of print]

12. Zhu et al., (2020) A Novel Coronavirus from Patients with Pneumonia in China, 2019. N Engl J Med. 2020 Jan 24. doi: 10.1056/NEJMoa2001017. [Epub ahead of print]



To: aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; vimenach@UTMB.EDU[vimenach@UTMB.EDU]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Mark Denison[mark.denison@vumc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph S[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]
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Grantees: To submit a supplement request, please follow the instructions of this NOSI. The appropriate PA to use for submission is here.

CEIRS: Please send the CEIRS concept form to me and to the Prime PI of the Center you are working with.
If you are currently funded by CEIRS and have an urgent need for nCoV funds, write me an email and we can discuss. If you have both CEIRS and grant funding, please do not submit the same work to both as we will be reviewing all requests together.

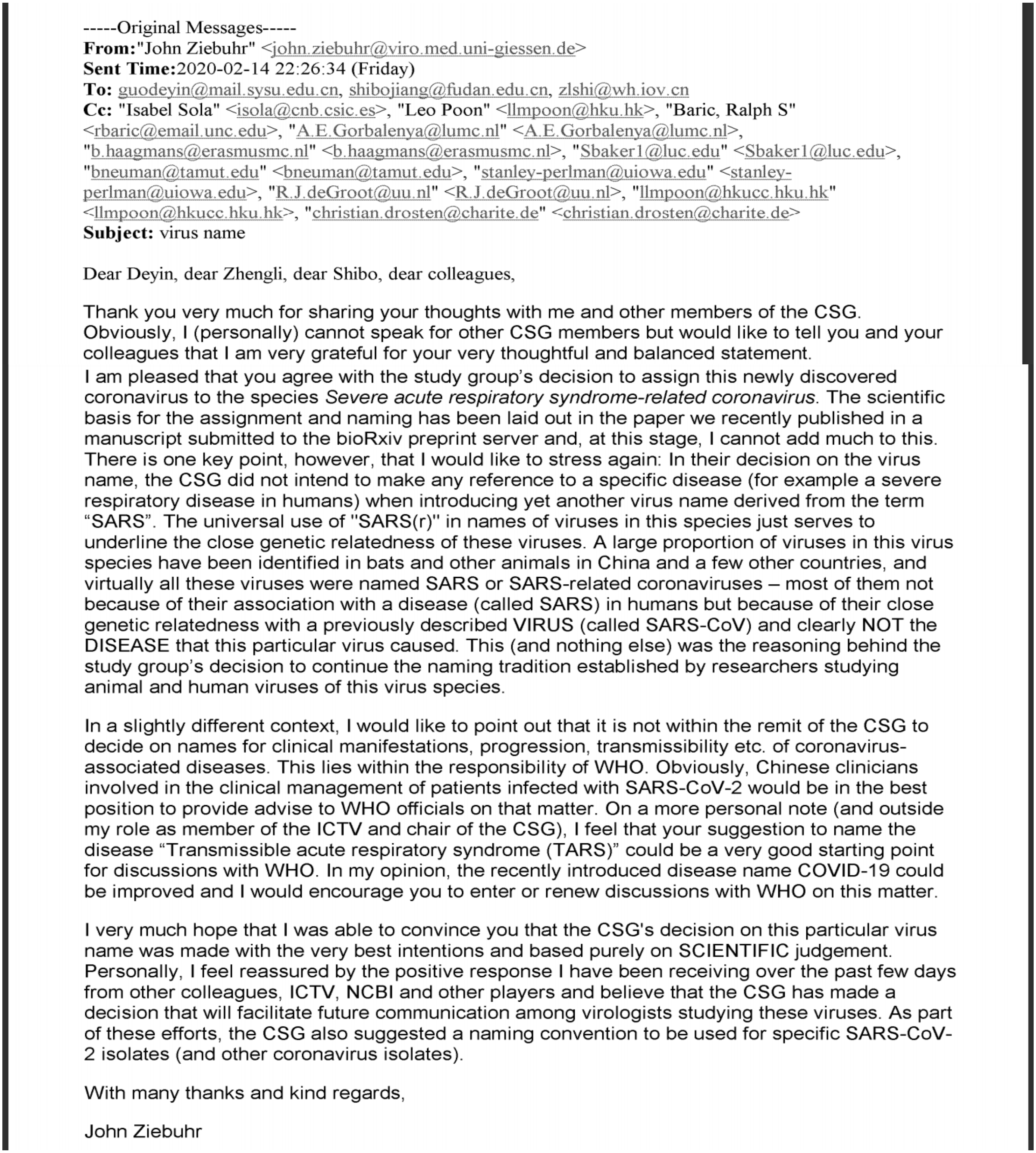
Reagents: Currently BEI has one virus isolate available and is working on making genomic RNA available. We're also aware that the European Virus archive has an isolate and RNA. We are trying to get more isolates from multiple countries into BEI – please keep me informed if you know of connections we can reach out to about this. As you develop reagents, Erik and I will work with you to help expedite their deposit into BEI, so please keep us posted on your progress.

We are also working to see if the Ad-ACE2 vector can be deposited and I'll try to update by next week. If there are other high priority reagents you would like to see in BEI, please email me so I can curate a list.

Patient Samples: CDC teams still working on outreach and consent, so we expect an extremely limited supply of PBMCs, sera and blood from US patients. For those interested in setting up a protocol for collection of samples from patients at their institution or with a collaborator abroad, a template that the NIH Vaccine Research Center uses is attached. Please keep Erik and I informed if you decide to pursue this.

Thank you all! Please don't hesitate to email with any questions and we will talk next Tuesday! Looking forward to updates from those of you doing animal model testing.

Marciela



-----Original Messages-----
From:"John Ziebuhr" <john.ziebuhr@viro.med.uni-giessen.de>
Sent Time:2020-02-14 22:26:34 (Friday)
To: guodeyin@mail.sysu.edu.cn, shibojiang@fudan.edu.cn, zlshi@wh.iov.cn
Cc: "Isabel Sola" <isola@cnb.csic.es>, "Leo Poon" <llmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "llmpoon@hkucc.hku.hk" <llmpoon@hkucc.hku.hk>, "christian.drosten@charite.de" <christian.drosten@charite.de>
Subject: virus name

Dear Deyin, dear Zhengli, dear Shibo, dear colleagues,

Thank you very much for sharing your thoughts with me and other members of the CSG. Obviously, I (personally) cannot speak for other CSG members but would like to tell you and your colleagues that I am very grateful for your very thoughtful and balanced statement.

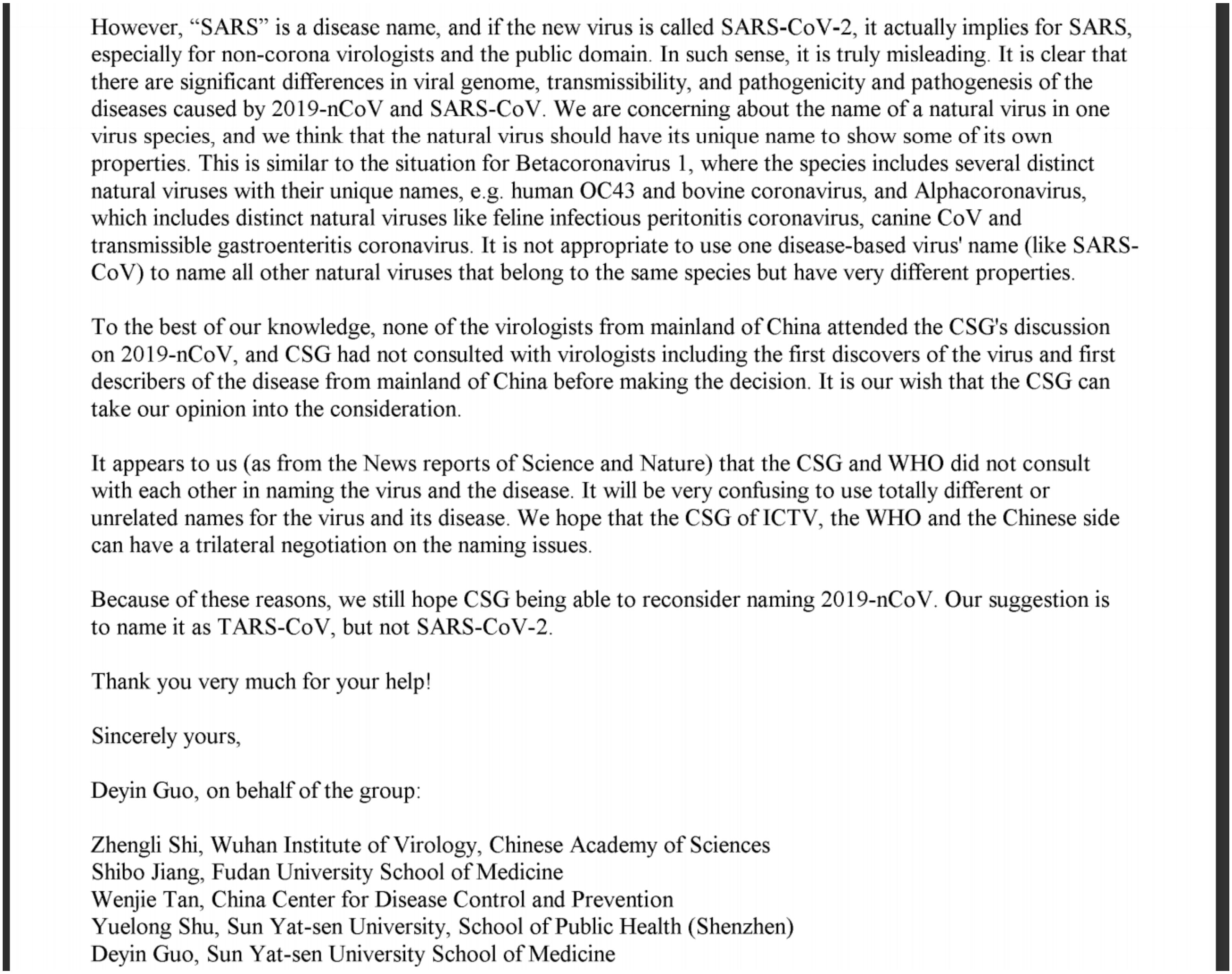
I am pleased that you agree with the study group's decision to assign this newly discovered coronavirus to the species *Severe acute respiratory syndrome-related coronavirus*. The scientific basis for the assignment and naming has been laid out in the paper we recently published in a manuscript submitted to the bioRxiv preprint server and, at this stage, I cannot add much to this. There is one key point, however, that I would like to stress again: In their decision on the virus name, the CSG did not intend to make any reference to a specific disease (for example a severe respiratory disease in humans) when introducing yet another virus name derived from the term "SARS". The universal use of "SARS(r)" in names of viruses in this species just serves to underline the close genetic relatedness of these viruses. A large proportion of viruses in this virus species have been identified in bats and other animals in China and a few other countries, and virtually all these viruses were named SARS or SARS-related coronaviruses – most of them not because of their association with a disease (called SARS) in humans but because of their close genetic relatedness with a previously described VIRUS (called SARS-CoV) and clearly NOT the DISEASE that this particular virus caused. This (and nothing else) was the reasoning behind the study group's decision to continue the naming tradition established by researchers studying animal and human viruses of this virus species.

In a slightly different context, I would like to point out that it is not within the remit of the CSG to decide on names for clinical manifestations, progression, transmissibility etc. of coronavirus-associated diseases. This lies within the responsibility of WHO. Obviously, Chinese clinicians involved in the clinical management of patients infected with SARS-CoV-2 would be in the best position to provide advise to WHO officials on that matter. On a more personal note (and outside my role as member of the ICTV and chair of the CSG), I feel that your suggestion to name the disease "Transmissible acute respiratory syndrome (TARS)" could be a very good starting point for discussions with WHO. In my opinion, the recently introduced disease name COVID-19 could be improved and I would encourage you to enter or renew discussions with WHO on this matter.

I very much hope that I was able to convince you that the CSG's decision on this particular virus name was made with the very best intentions and based purely on SCIENTIFIC judgement. Personally, I feel reassured by the positive response I have been receiving over the past few days from other colleagues, ICTV, NCBI and other players and believe that the CSG has made a decision that will facilitate future communication among virologists studying these viruses. As part of these efforts, the CSG also suggested a naming convention to be used for specific SARS-CoV-2 isolates (and other coronavirus isolates).

With many thanks and kind regards,

John Ziebuhr



However, “SARS” is a disease name, and if the new virus is called SARS-CoV-2, it actually implies for SARS, especially for non-corona virologists and the public domain. In such sense, it is truly misleading. It is clear that there are significant differences in viral genome, transmissibility, and pathogenicity and pathogenesis of the diseases caused by 2019-nCoV and SARS-CoV. We are concerning about the name of a natural virus in one virus species, and we think that the natural virus should have its unique name to show some of its own properties. This is similar to the situation for Betacoronavirus 1, where the species includes several distinct natural viruses with their unique names, e.g. human OC43 and bovine coronavirus, and Alphacoronavirus, which includes distinct natural viruses like feline infectious peritonitis coronavirus, canine CoV and transmissible gastroenteritis coronavirus. It is not appropriate to use one disease-based virus' name (like SARS-CoV) to name all other natural viruses that belong to the same species but have very different properties.

To the best of our knowledge, none of the virologists from mainland of China attended the CSG's discussion on 2019-nCoV, and CSG had not consulted with virologists including the first discovers of the virus and first describers of the disease from mainland of China before making the decision. It is our wish that the CSG can take our opinion into the consideration.

It appears to us (as from the News reports of Science and Nature) that the CSG and WHO did not consult with each other in naming the virus and the disease. It will be very confusing to use totally different or unrelated names for the virus and its disease. We hope that the CSG of ICTV, the WHO and the Chinese side can have a trilateral negotiation on the naming issues.

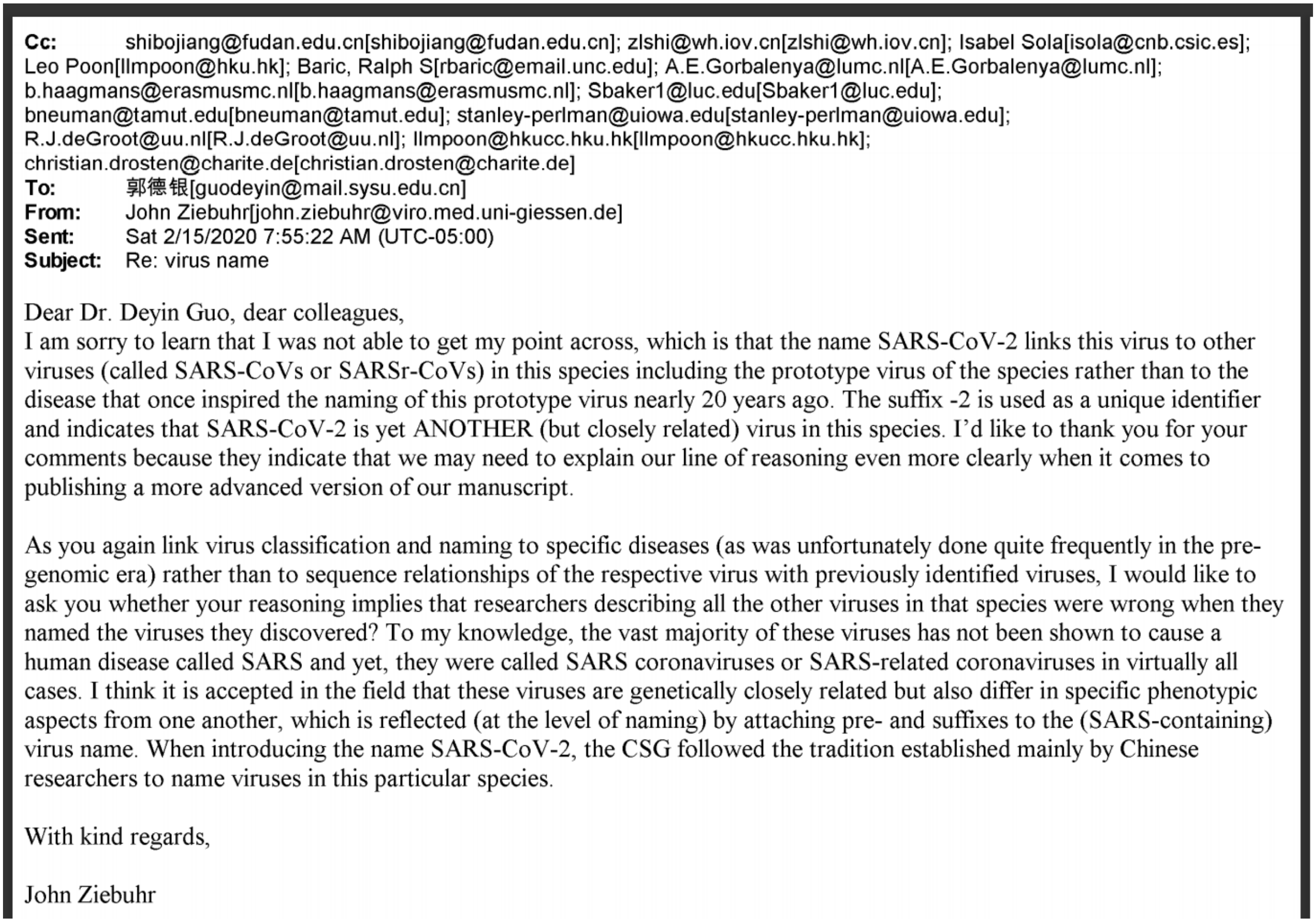
Because of these reasons, we still hope CSG being able to reconsider naming 2019-nCoV. Our suggestion is to name it as TARS-CoV, but not SARS-CoV-2.

Thank you very much for your help!

Sincerely yours,

Deyin Guo, on behalf of the group:

Zhengli Shi, Wuhan Institute of Virology, Chinese Academy of Sciences
Shibo Jiang, Fudan University School of Medicine
Wenjie Tan, China Center for Disease Control and Prevention
Yuelong Shu, Sun Yat-sen University, School of Public Health (Shenzhen)
Deyin Guo, Sun Yat-sen University School of Medicine



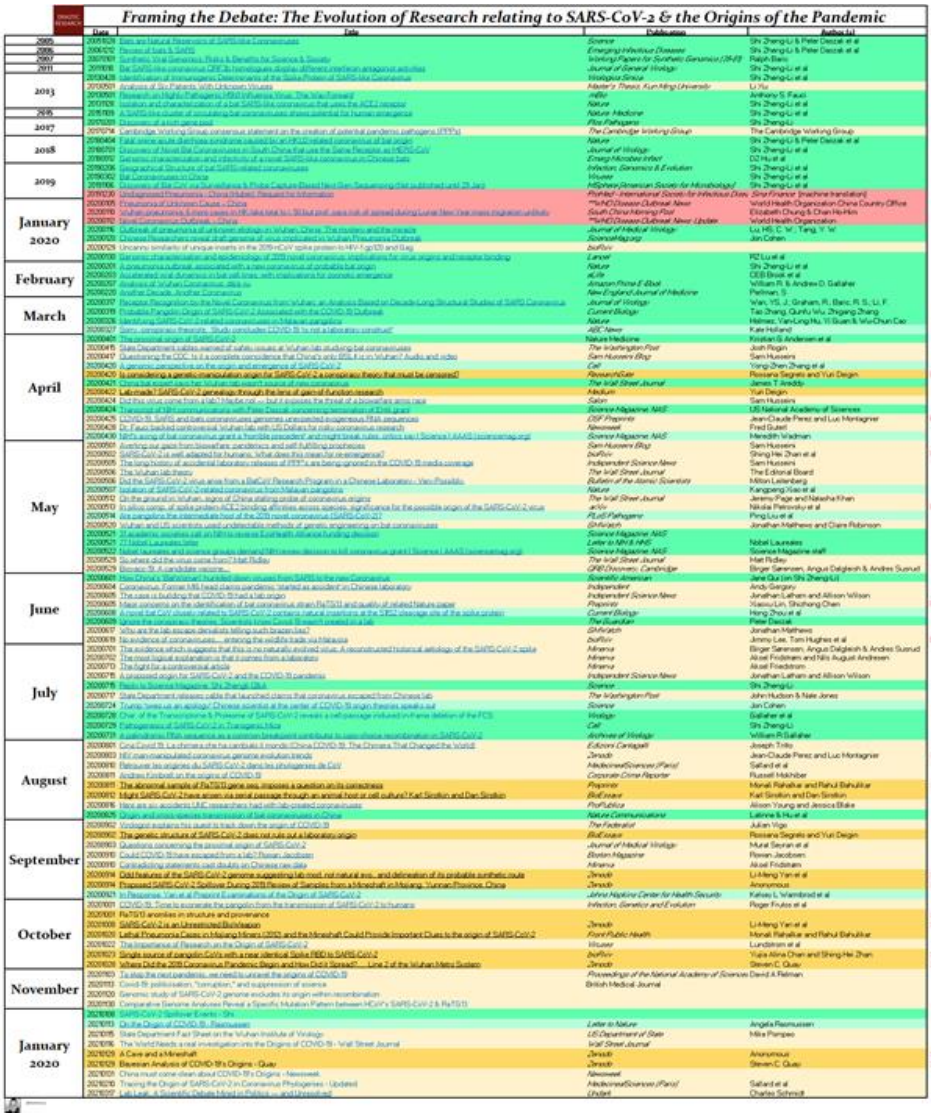
Cc: shibojiang@fudan.edu.cn[shibojiang@fudan.edu.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[llmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; christian.drosten@charite.de[christian.drosten@charite.de]
To: 郭德银[guodeyin@mail.sysu.edu.cn]
From: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]
Sent: Sat 2/15/2020 7:55:22 AM (UTC-05:00)
Subject: Re: virus name

Dear Dr. Deyin Guo, dear colleagues,
I am sorry to learn that I was not able to get my point across, which is that the name SARS-CoV-2 links this virus to other viruses (called SARS-CoVs or SARSr-CoVs) in this species including the prototype virus of the species rather than to the disease that once inspired the naming of this prototype virus nearly 20 years ago. The suffix -2 is used as a unique identifier and indicates that SARS-CoV-2 is yet ANOTHER (but closely related) virus in this species. I'd like to thank you for your comments because they indicate that we may need to explain our line of reasoning even more clearly when it comes to publishing a more advanced version of our manuscript.

As you again link virus classification and naming to specific diseases (as was unfortunately done quite frequently in the pre-genomic era) rather than to sequence relationships of the respective virus with previously identified viruses, I would like to ask you whether your reasoning implies that researchers describing all the other viruses in that species were wrong when they named the viruses they discovered? To my knowledge, the vast majority of these viruses has not been shown to cause a human disease called SARS and yet, they were called SARS coronaviruses or SARS-related coronaviruses in virtually all cases. I think it is accepted in the field that these viruses are genetically closely related but also differ in specific phenotypic aspects from one another, which is reflected (at the level of naming) by attaching pre- and suffixes to the (SARS-containing) virus name. When introducing the name SARS-CoV-2, the CSG followed the tradition established mainly by Chinese researchers to name viruses in this particular species.

With kind regards,

John Ziebuhr


Framing the Debate: The Evolution of Research relating to SARS-CoV-2 & the Origins of the Pandemic

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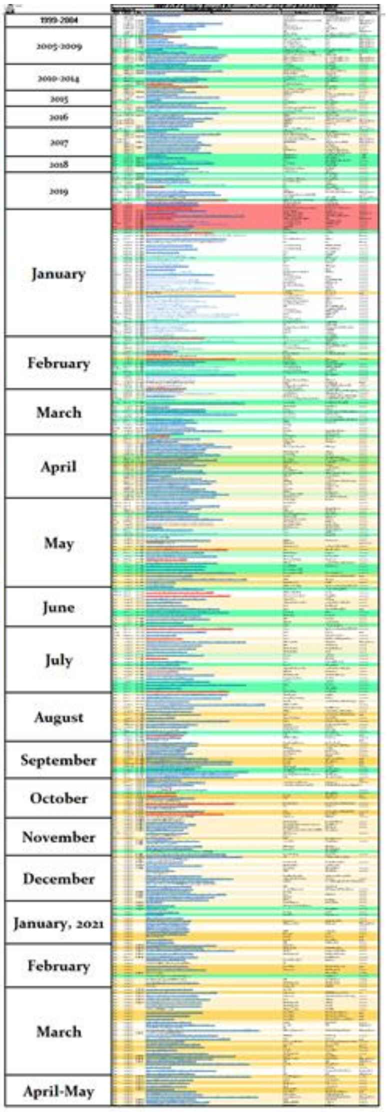
January 2020


1999-2004
2005-2009
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January, 2021
February
March
April-May

Shi, Baric, Dazsak, Andersen, Holmes & Collaborators

Scientist/Media directly or indirectly supporting GOF/Zoonosis

Outbreak in Wuhan: 12/19 - 1/20

Scientists/Media directly or indirectly questioning Zoonosis

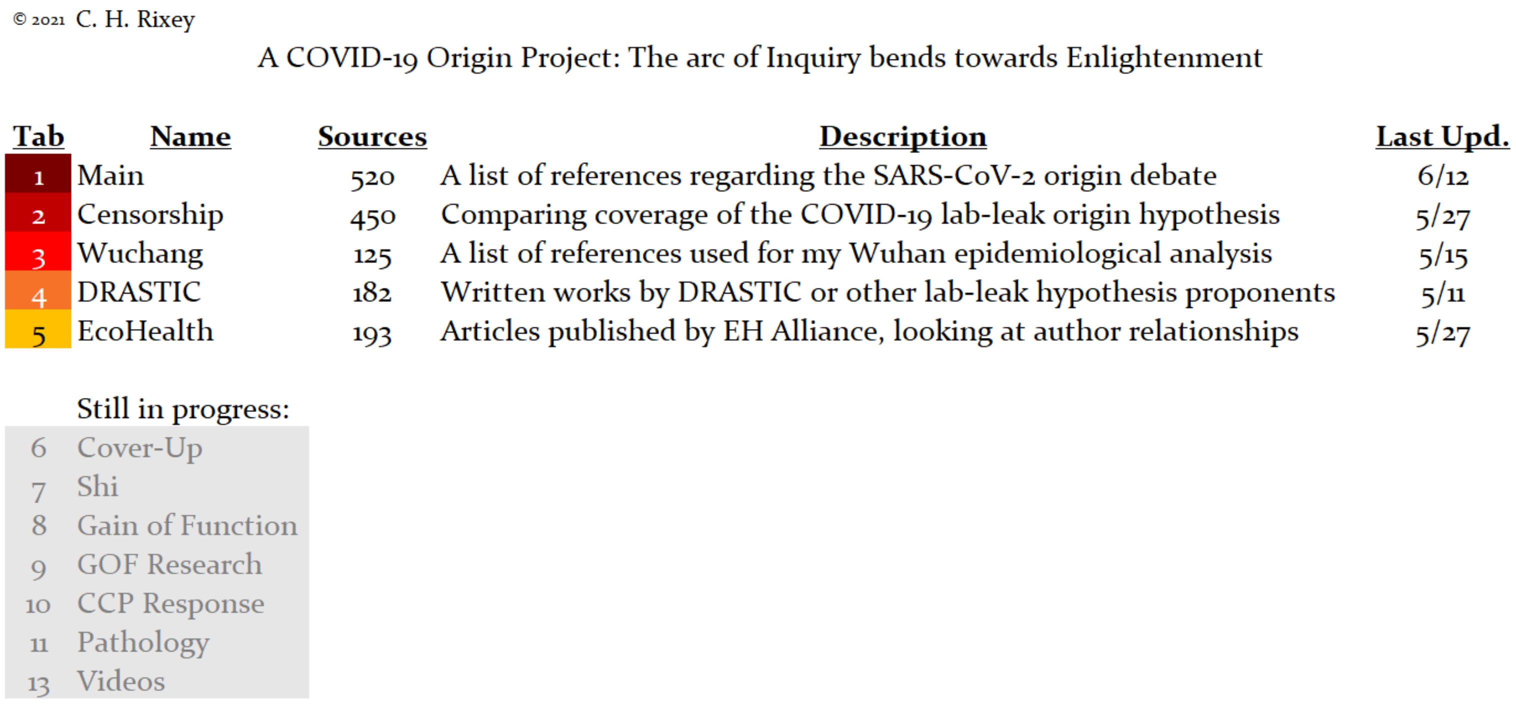
D.R.A.S.T.I.C., Collaborators & Li-Meng Yan

'The 'P' denotes an article published to a pre-print server

Tony Fauci's Legacy

The **effect of censorship** by the pro natural-origin supporters is far more obvious from a bird's-eye view

From my ongoing project on ResearchGate:
The Index of my Excel file analyzing research censorship



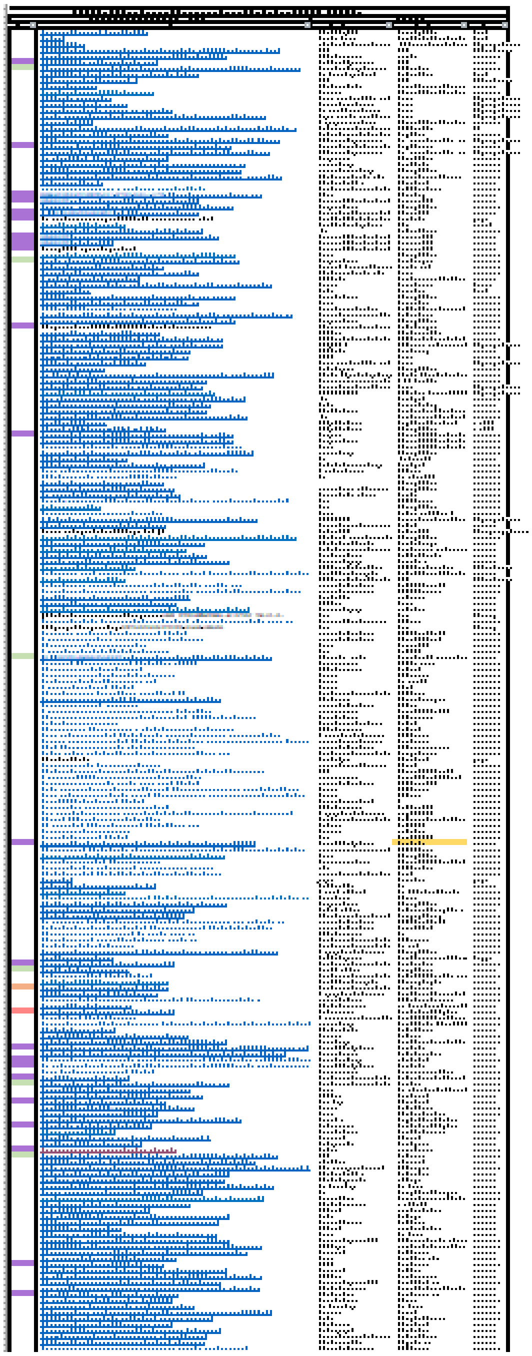
A COVID-19 Origin Project: The arc of Inquiry bends towards Enlightenment

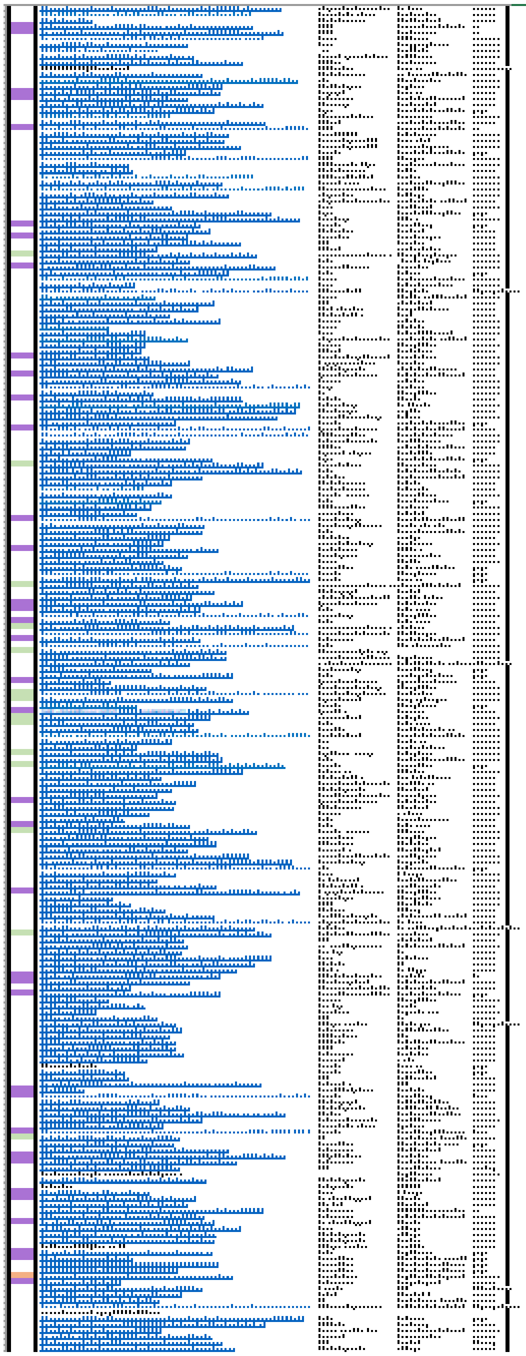
Tab	Name	Sources	Description	Last Upd.
1	Main	520	A list of references regarding the SARS-CoV-2 origin debate	6/12
2	Censorship	450	Comparing coverage of the COVID-19 lab-leak origin hypothesis	5/27
3	Wuchang	125	A list of references used for my Wuhan epidemiological analysis	5/15
4	DRASTIC	182	Written works by DRASTIC or other lab-leak hypothesis proponents	5/11
5	EcoHealth	193	Articles published by EH Alliance, looking at author relationships	5/27

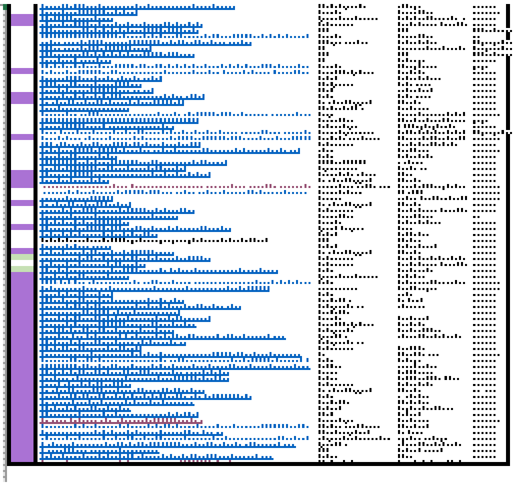
Still in progress:

6	Cover-Up
7	Shi
8	Gain of Function
9	GOF Research
10	CCP Response
11	Pathology
13	Videos

From my ongoing project on ResearchGate:
All 520 articles



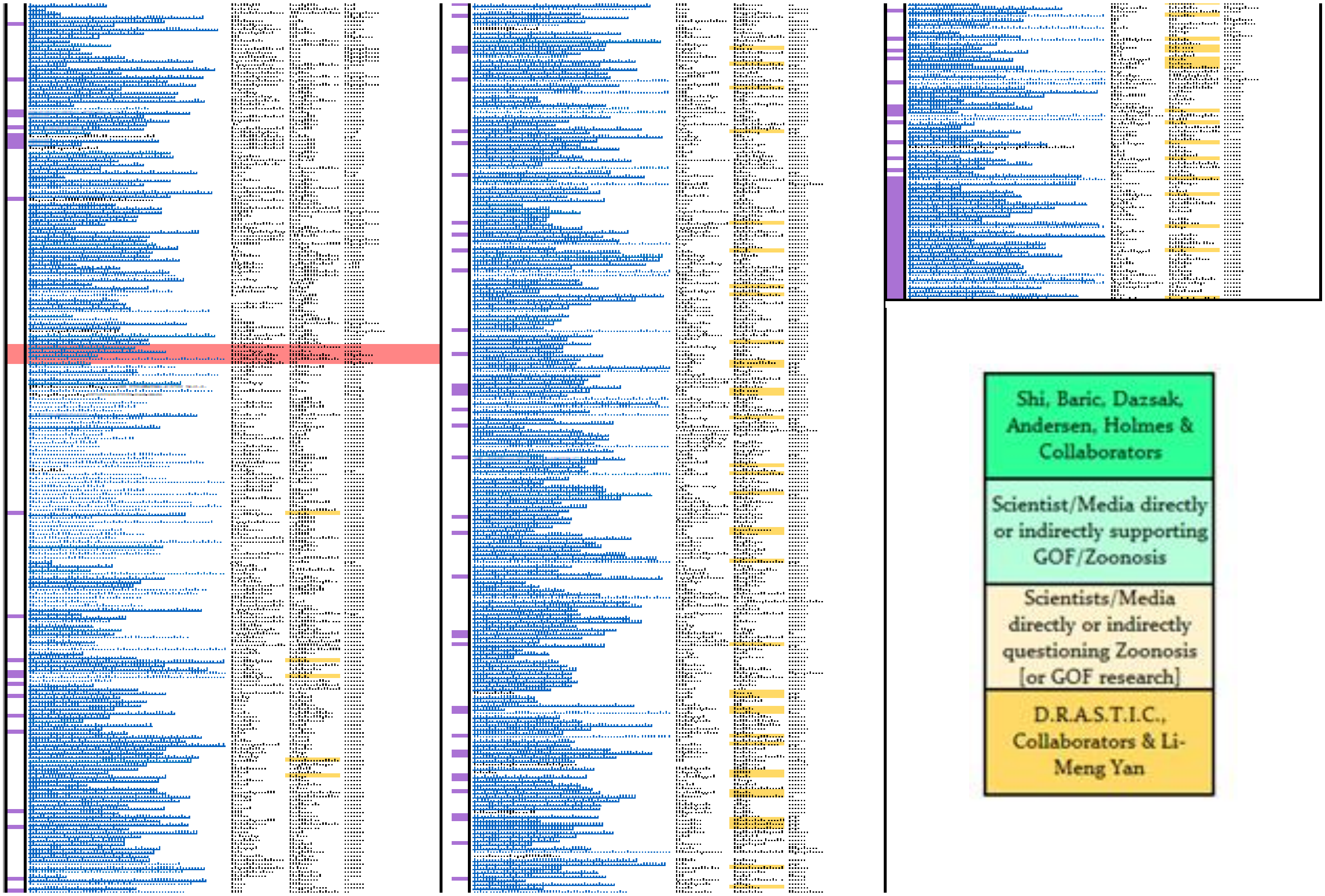


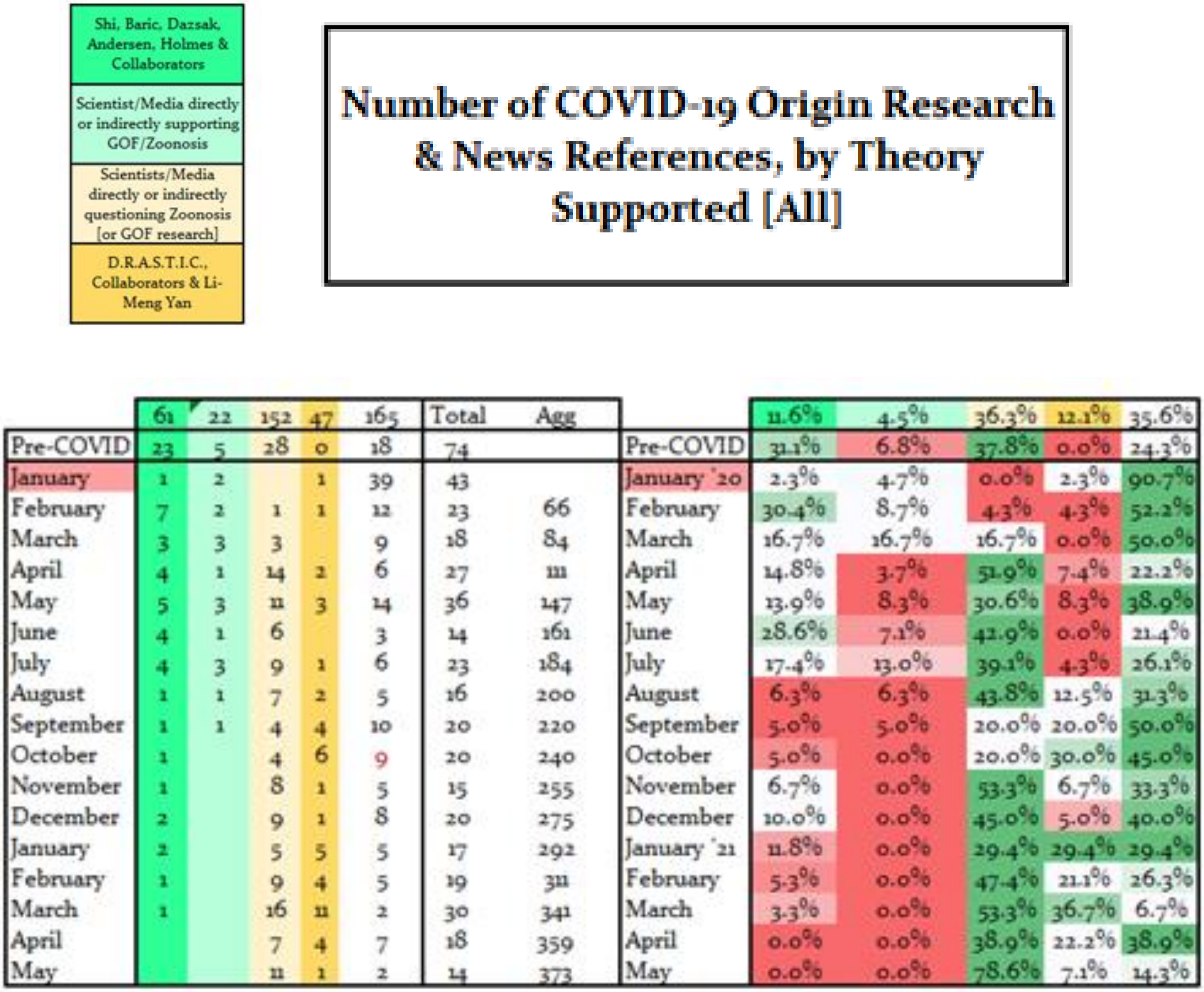


Sources	Date
14	7/30/2020
117	11/30/2020
142	1/7/2021
224	1/30/2021
387	5/5/2021
458	5/27/2021
520	6/13/2021

New Additions
are highlighted
in Purple

From my ongoing project on ResearchGate:
All Research & Commentary authored by members of D.R.A.S.T.I.C. [in yellow]





Shi, Baric, Dazsak, Andersen, Holmes & Collaborators

Scientist/Media directly or indirectly supporting GOF/Zoonosis

Scientists/Media directly or indirectly questioning Zoonosis [or GOF research]

D.R.A.S.T.I.C., Collaborators & Li-Meng Yan

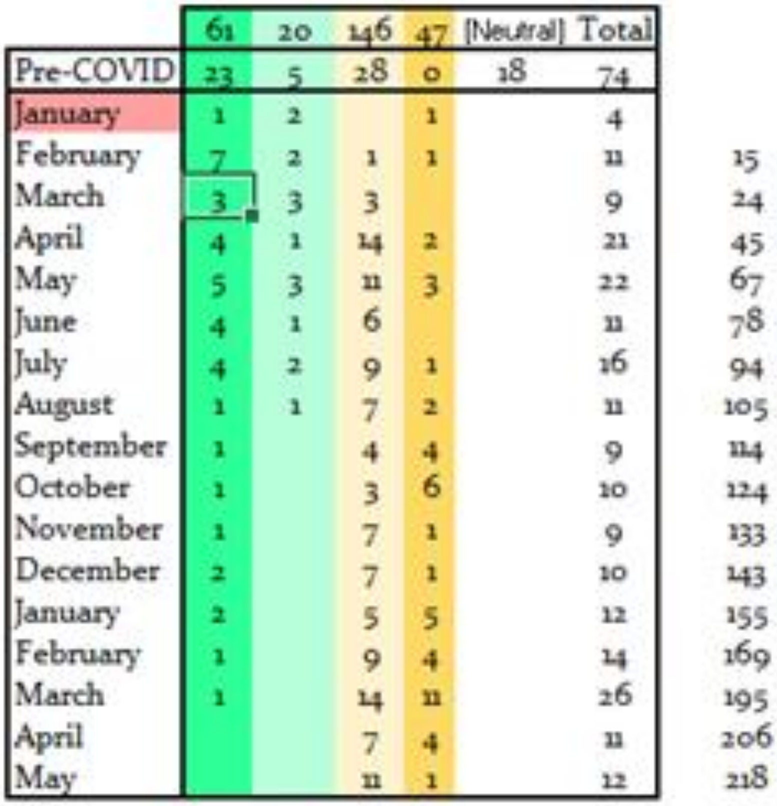
Number of COVID-19 Origin Research & News References, by Theory Supported [All]

	61	22	152	47	165	Total	Agg
Pre-COVID	23	5	28	0	18	74	
January	1	2		1	39	43	
February	7	2	1	1	12	23	66
March	3	3	3		9	18	84
April	4	1	14	2	6	27	111
May	5	3	11	3	14	36	147
June	4	1	6		3	14	161
July	4	3	9	1	6	23	184
August	1	1	7	2	5	16	200
September	1	1	4	4	10	20	220
October	1		4	6	9	20	240
November	1		8	1	5	15	255
December	2		9	1	8	20	275
January	2		5	5	5	17	292
February	1		9	4	5	19	311
March	1		16	11	2	30	341
April			7	4	7	18	359
May			11	1	2	14	373

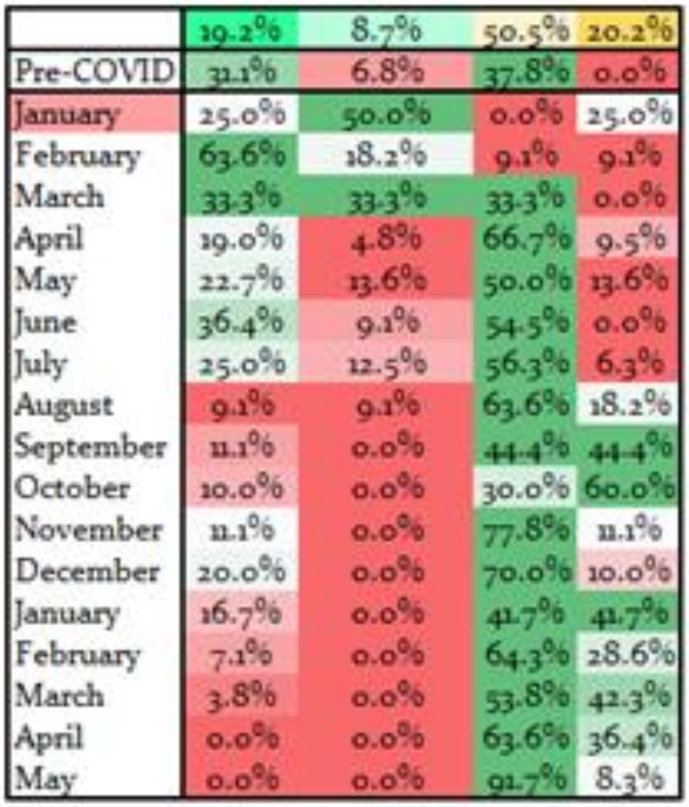
	11.6%	4.5%	36.3%	12.1%	35.6%
Pre-COVID	31.1%	6.8%	37.8%	0.0%	24.3%
January '20	2.3%	4.7%	0.0%	2.3%	90.7%
February	30.4%	8.7%	4.3%	4.3%	52.2%
March	16.7%	16.7%	16.7%	0.0%	50.0%
April	14.8%	3.7%	51.9%	7.4%	22.2%
May	13.9%	8.3%	30.6%	8.3%	38.9%
June	28.6%	7.1%	42.9%	0.0%	21.4%
July	17.4%	13.0%	39.1%	4.3%	26.1%
August	6.3%	6.3%	43.8%	12.5%	31.3%
September	5.0%	5.0%	20.0%	20.0%	50.0%
October	5.0%	0.0%	20.0%	30.0%	45.0%
November	6.7%	0.0%	53.3%	6.7%	33.3%
December	10.0%	0.0%	45.0%	5.0%	40.0%
January '21	11.8%	0.0%	29.4%	29.4%	29.4%
February	5.3%	0.0%	47.4%	21.1%	26.3%
March	3.3%	0.0%	53.3%	36.7%	6.7%
April	0.0%	0.0%	38.9%	22.2%	38.9%
May	0.0%	0.0%	78.6%	7.1%	14.3%

- 🟩 Shi, Baric, Dazsak, Andersen, Holmes & Collaborators
- 🟩 Scientist/Media directly or indirectly supporting GOF/Zoonosis
- 🟨 Scientists/Media directly or indirectly questioning Zoonosis [or GOF research]
- 🟨 D.R.A.S.T.I.C., Collaborators & Li-Meng Yan

Number of COVID-19 Origin Research & News References, by Theory Supported [No-Neutral Inc]



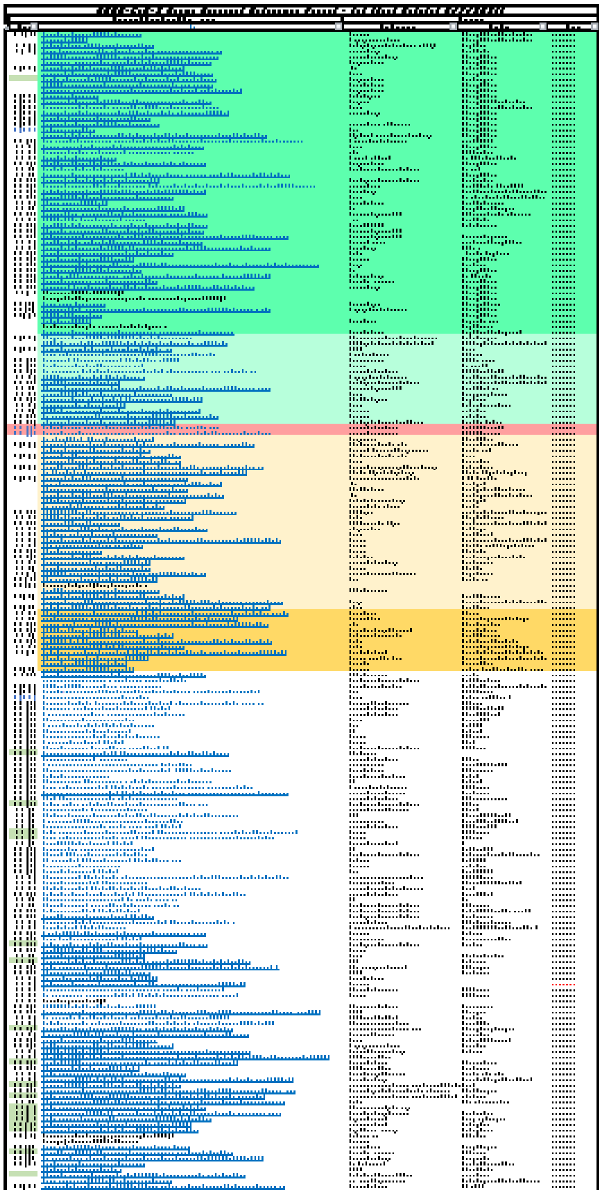
	61	20	146	47	[Neutral]	Total	
Pre-COVID	23	5	28	0	18	74	
January	1	2		1		4	
February	7	2	1	1		11	15
March	3	3	3			9	24
April	4	1	14	2		21	45
May	5	3	11	3		22	67
June	4	1	6			11	78
July	4	2	9	1		16	94
August	1	1	7	2		11	105
September	1		4	4		9	114
October	1		3	6		10	124
November	1		7	1		9	133
December	2		7	1		10	143
January	2		5	5		12	155
February	1		9	4		14	169
March	1		14	11		26	195
April			7	4		11	206
May			11	1		12	218



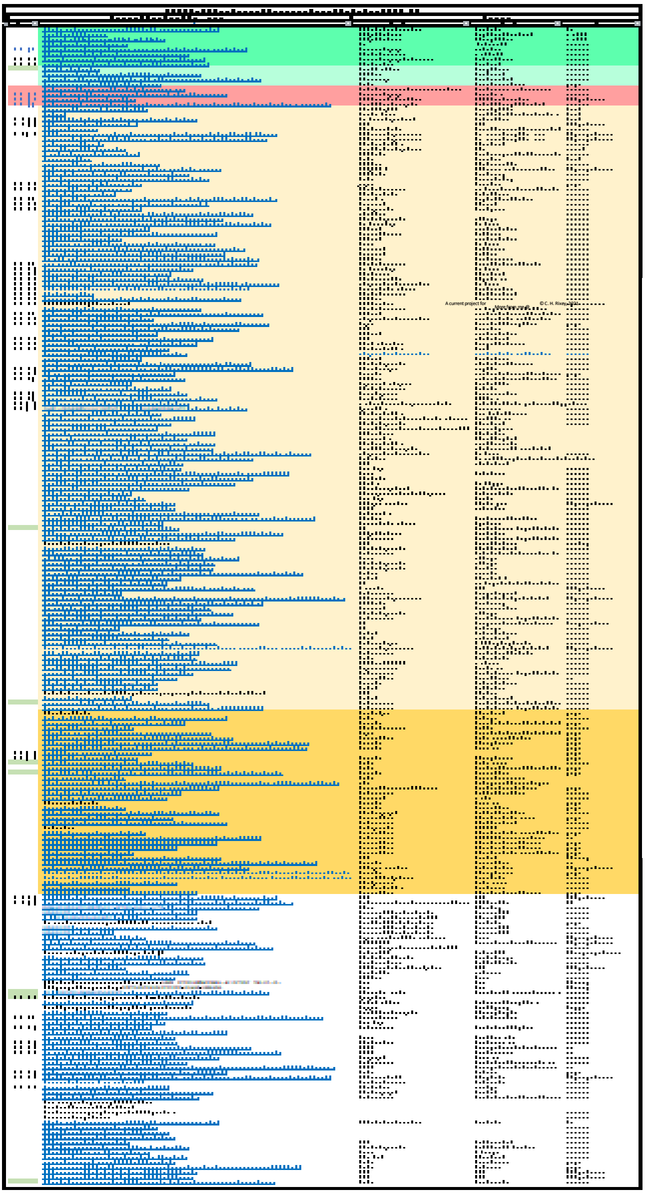
	19.2%	8.7%	50.5%	20.2%
Pre-COVID	31.1%	6.8%	37.8%	0.0%
January	25.0%	50.0%	0.0%	25.0%
February	63.6%	18.2%	9.1%	9.1%
March	33.3%	33.3%	33.3%	0.0%
April	19.0%	4.8%	66.7%	9.5%
May	22.7%	13.6%	50.0%	13.6%
June	36.4%	9.1%	54.5%	0.0%
July	25.0%	12.5%	56.3%	6.3%
August	9.1%	9.1%	63.6%	18.2%
September	11.1%	0.0%	44.4%	44.4%
October	10.0%	0.0%	30.0%	60.0%
November	11.1%	0.0%	77.8%	11.1%
December	20.0%	0.0%	70.0%	10.0%
January	16.7%	0.0%	41.7%	41.7%
February	7.1%	0.0%	64.3%	28.6%
March	3.8%	0.0%	53.8%	42.3%
April	0.0%	0.0%	63.6%	36.4%
May	0.0%	0.0%	91.7%	8.3%

From my ongoing project on ResearchGate:
“The Arc of Inquiry Bends towards Enlightenment”

205 Peer Reviewed Articles…….



233 of all other types of publications



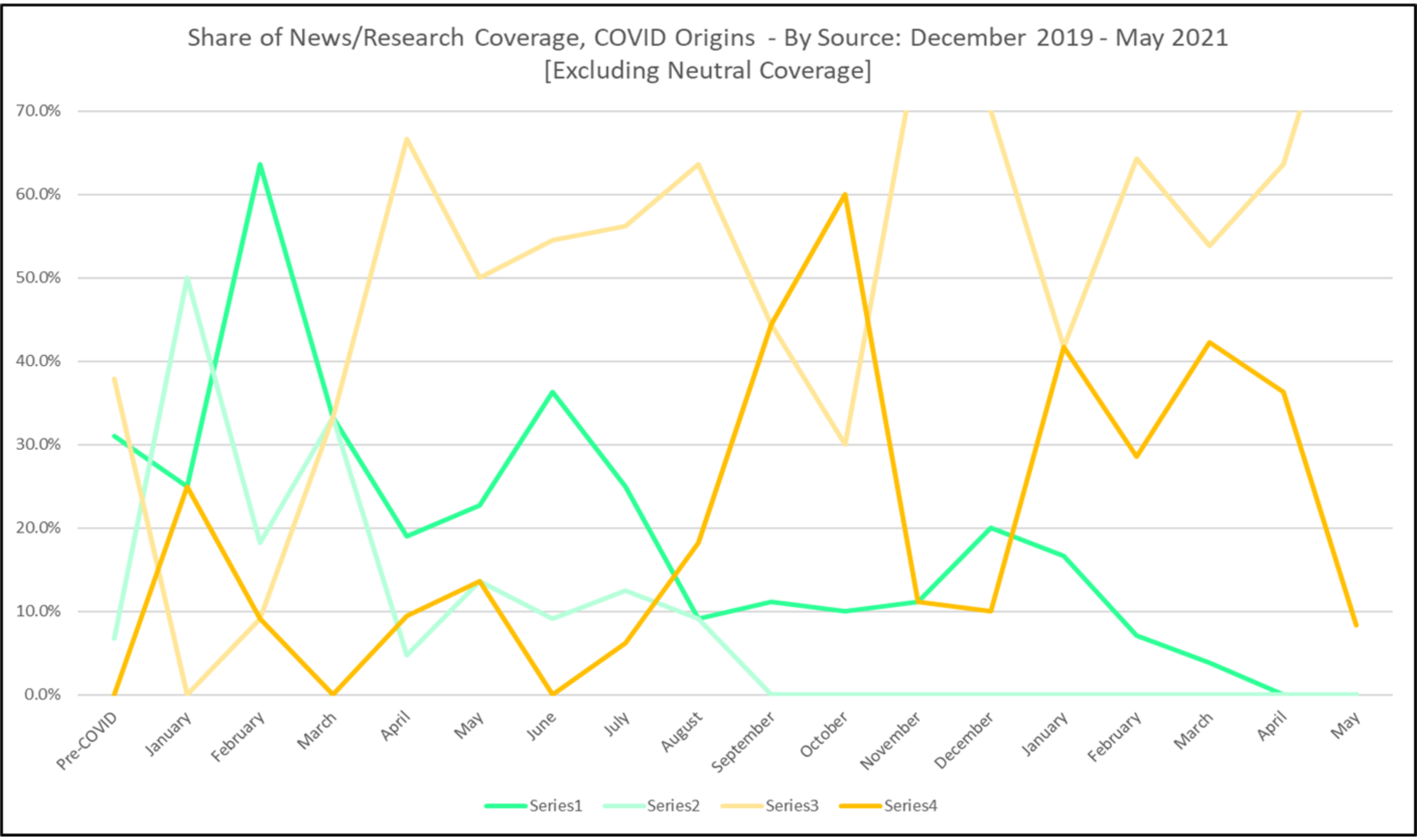
Shi, Baric, Dazsak, Andersen, Holmes & Collaborators

Scientist/Media directly or indirectly supporting GOF/Zoonosis

Outbreak in Wuhan: 12/30 - 1/10

Scientists/Media directly or indirectly questioning Zoonosis [or GOF research]

D.R.A.S.T.I.C., Collaborators & Li-Meng Yan


Share of News/Research Coverage, COVID Origins - By Source: December 2019 - May 2021
[Excluding Neutral Coverage]
70.0%
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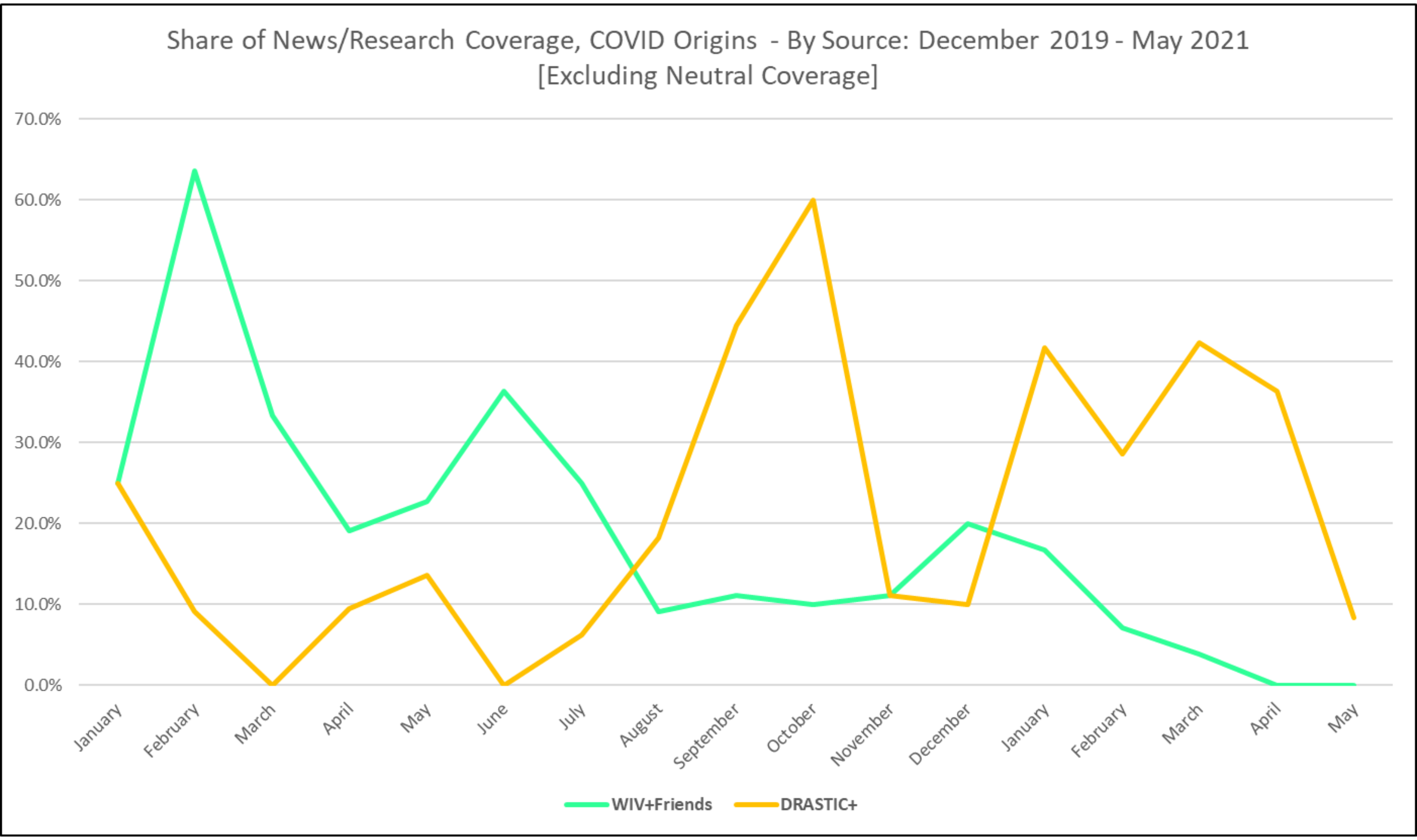
Series1
Series2
Series3
Series4


Share of News/Research Coverage, COVID Origins - By Source: December 2019 - May 2021
[Excluding Neutral Coverage]
70.0%
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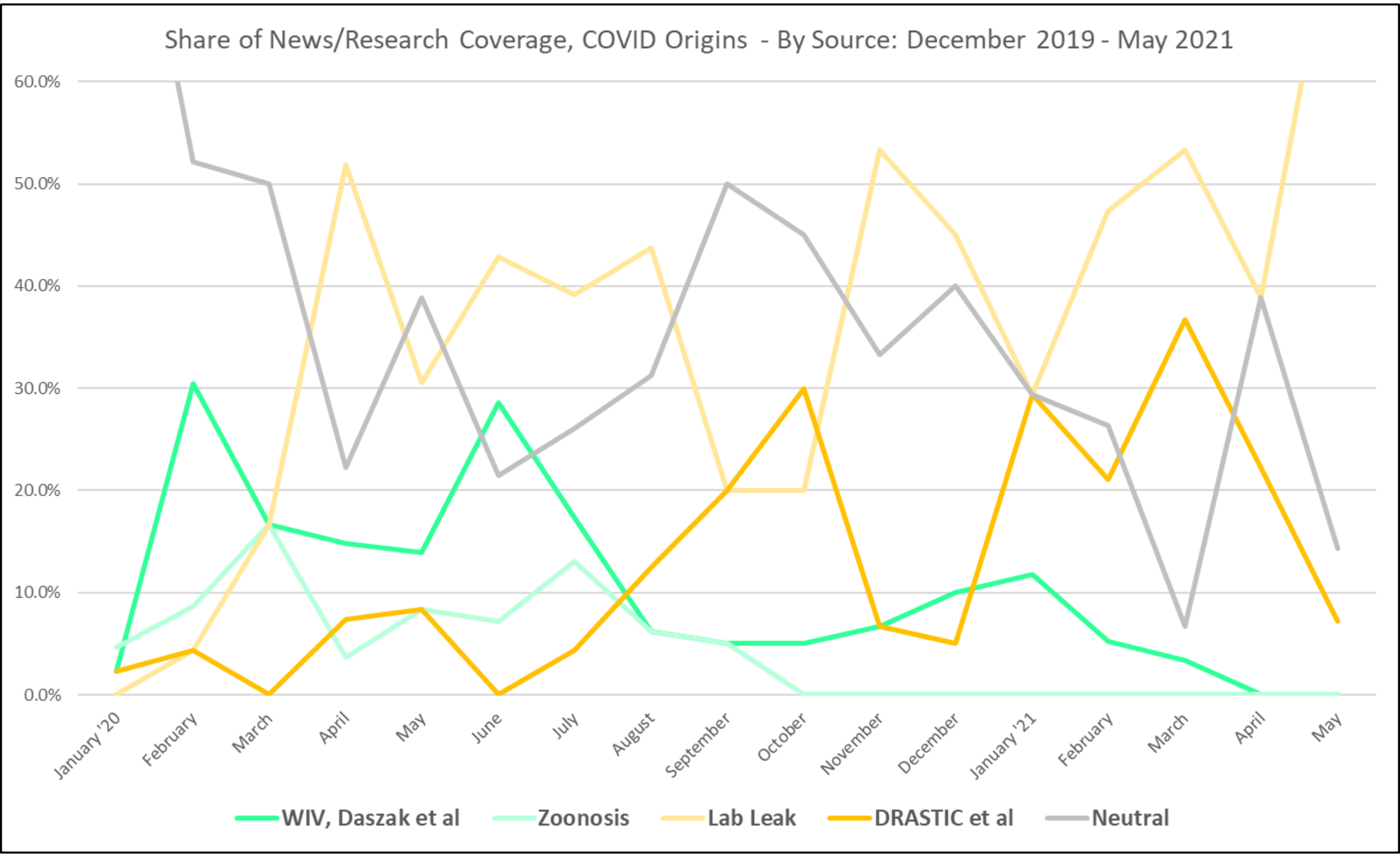
WIV+Friends
DRASTIC+


Share of News/Research Coverage, COVID Origins - By Source: December 2019 - May 2021
60.0%
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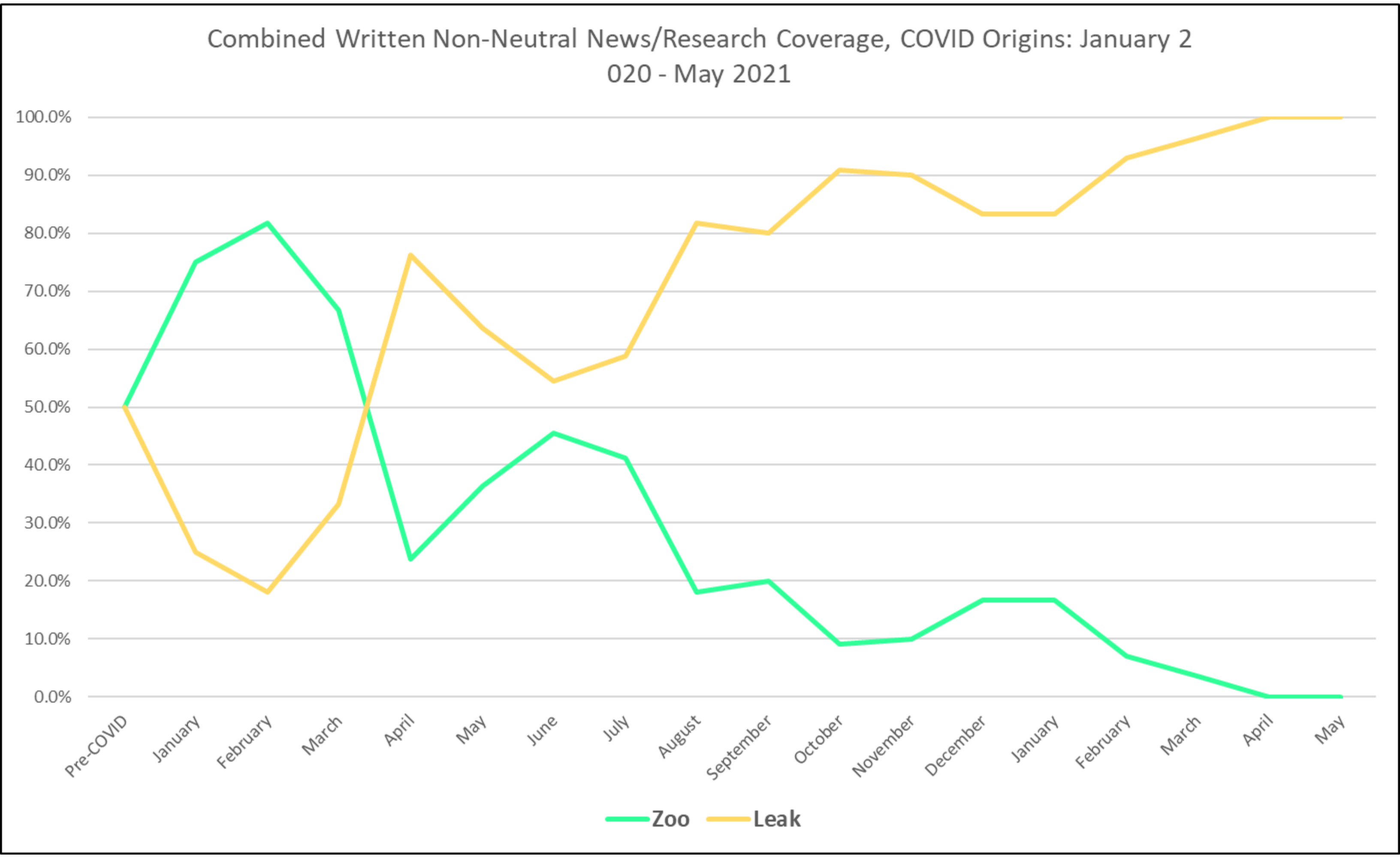
WIV, Daszak et al
Zoonosis
Lab Leak
DRASTIC et al
Neutral


Combined Written Non-Neutral News/Research Coverage, COVID Origins: January 2
020 - May 2021
100.0%
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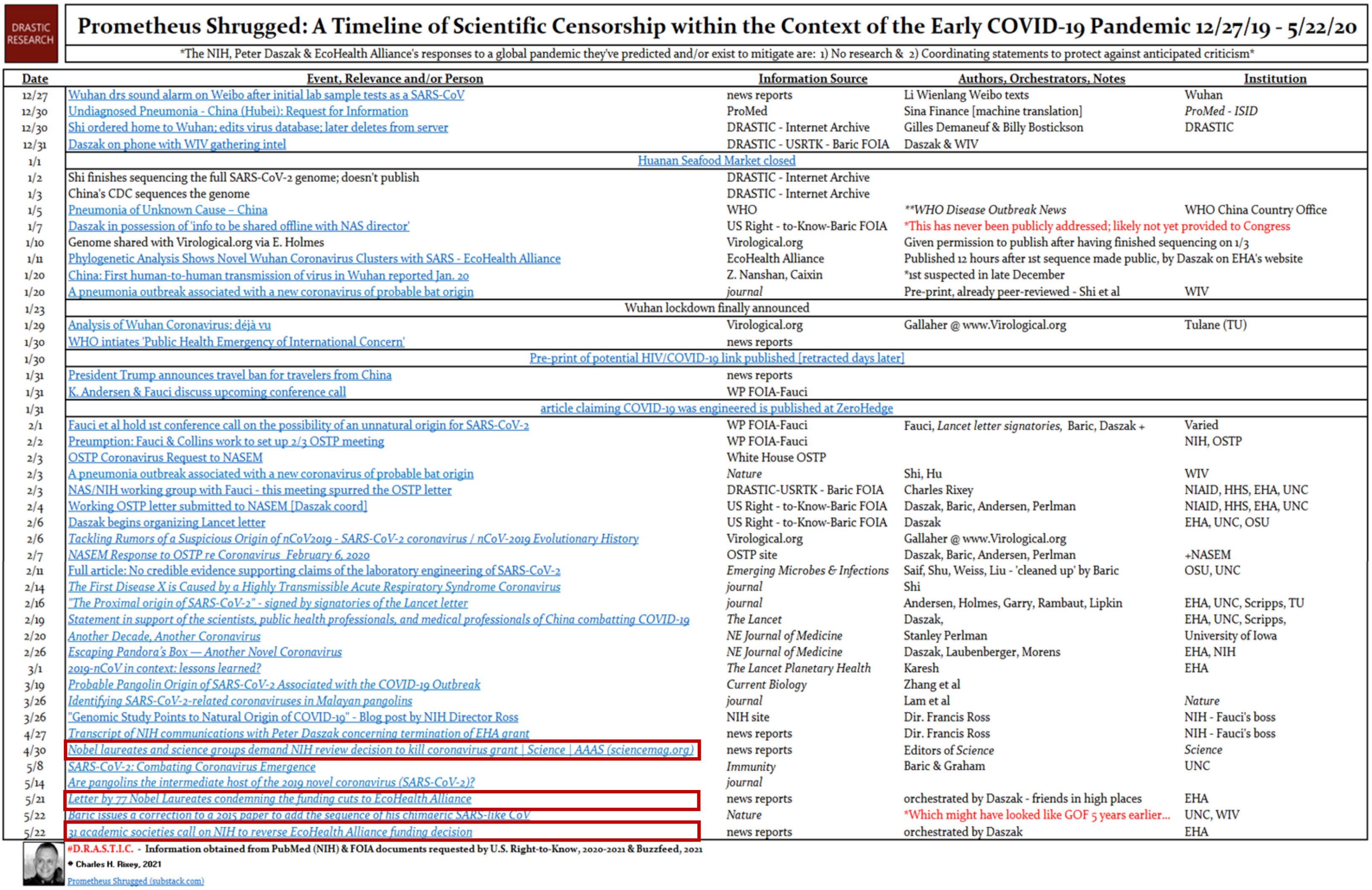

DRASTIC RESEARCH

Prometheus Shrugged: A Timeline of Scientific Censorship within the Context of the Early COVID-19 Pandemic 12/27/19 - 5/22/20

The NIH, Peter Daszak & EcoHealth Alliance's responses to a global pandemic they've predicted and/or exist to mitigate are: 1) No research & 2) Coordinating statements to protect against anticipated criticism

Date	Event, Relevance and/or Person	Information Source	Authors, Orchestrators, Notes	Institution
12/27	Wuhan drs sound alarm on Weibo after initial lab sample tests as a SARS-CoV	news reports	Li Wienlang Weibo texts	Wuhan
12/30	Undiagnosed Pneumonia - China (Hubei): Request for Information	ProMed	Sina Finance [machine translation]	*ProMed - ISID*
12/30	Shi ordered home to Wuhan; edits virus database; later deletes from server	DRASTIC - Internet Archive	Gilles Demaneuf & Billy Bostickson	DRASTIC
12/31	Daszak on phone with WIV gathering intel	DRASTIC - USRTK - Baric FOIA	Daszak & WIV	
1/1	Huanan Seafood Market closed			
1/2	Shi finishes sequencing the full SARS-CoV-2 genome; doesn't publish	DRASTIC - Internet Archive		
1/3	China's CDC sequences the genome	DRASTIC - Internet Archive		
1/5	Pneumonia of Unknown Cause – China	WHO	***WHO Disease Outbreak News*	WHO China Country Office
1/7	Daszak in possession of 'info to be shared offline with NAS director'	US Right - to-Know-Baric FOIA	*This has never been publicly addressed; likely not yet provided to Congress	
1/10	Genome shared with Virological.org via E. Holmes	Virological.org	Given permission to publish after having finished sequencing on 1/3	
1/11	Phylogenetic Analysis Shows Novel Wuhan Coronavirus Clusters with SARS - EcoHealth Alliance	EcoHealth Alliance	Published 12 hours after 1st sequence made public, by Daszak on EHA's website	
1/20	China: First human-to-human transmission of virus in Wuhan reported Jan. 20	Z. Nanshan, Caixin	*1st suspected in late December	
1/20	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*journal*	Pre-print, already peer-reviewed - Shi et al	WIV
1/23	Wuhan lockdown finally announced			
1/29	Analysis of Wuhan Coronavirus: déjà vu	Virological.org	Gallaher @ www.Virological.org	Tulane (TU)
1/30	WHO intiates 'Public Health Emergency of International Concern'	news reports		
1/30	Pre-print of potential HIV/COVID-19 link published [retracted days later]			
1/31	President Trump announces travel ban for travelers from China	news reports		
1/31	K. Andersen & Fauci discuss upcoming conference call	WP FOIA-Fauci		
1/31	article claiming COVID-19 was engineered is published at ZeroHedge			
2/1	Fauci et al hold 1st conference call on the possibility of an unnatural origin for SARS-CoV-2	WP FOIA-Fauci	Fauci, *Lancet letter signatories,* Baric, Daszak +	Varied
2/2	Preumption: Fauci & Collins work to set up 2/3 OSTP meeting	WP FOIA-Fauci		NIH, OSTP
2/3	OSTP Coronavirus Request to NASEM	White House OSTP		
2/3	A pneumonia outbreak associated with a new coronavirus of probable bat origin	*Nature*	Shi, Hu	WIV
2/3	NAS/NIH working group with Fauci - this meeting spurred the OSTP letter	DRASTIC-USRTK - Baric FOIA	Charles Rixey	NIAID, HHS, EHA, UNC
2/4	Working OSTP letter submitted to NASEM [Daszak coord]	US Right - to-Know-Baric FOIA	Daszak, Baric, Andersen, Perlman	NIAID, HHS, EHA, UNC
2/6	Daszak begins organizing Lancet letter	US Right - to-Know-Baric FOIA	Daszak	EHA, UNC, OSU
2/6	*Tackling Rumors of a Suspicious Origin of nCoV2019 - SARS-CoV-2 coronavirus / nCoV-2019 Evolutionary History*	Virological.org	Gallaher @ www.Virological.org	
2/7	*NASEM Response to OSTP re Coronavirus February 6, 2020*	OSTP site	Daszak, Baric, Andersen, Perlman	+NASEM
2/11	Full article: No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2	*Emerging Microbes & Infections*	Saif, Shu, Weiss, Liu - 'cleaned up' by Baric	OSU, UNC
2/14	*The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus*	*journal*	Shi	
2/16	*"The Proximal origin of SARS-CoV-2" - signed by signatories of the Lancet letter*	*journal*	Andersen, Holmes, Garry, Rambaut, Lipkin	EHA, UNC, Scripps, TU
2/19	*Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*	*The Lancet*	Daszak,	EHA, UNC, Scripps,
2/20	*Another Decade, Another Coronavirus*	*NE Journal of Medicine*	Stanley Perlman	University of Iowa
2/26	*Escaping Pandora's Box — Another Novel Coronavirus*	*NE Journal of Medicine*	Daszak, Laubenberger, Morens	EHA, NIH
3/1	*2019-nCoV in context: lessons learned?*	*The Lancet Planetary Health*	Karesh	EHA
3/19	*Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak*	*Current Biology*	Zhang et al	
3/26	*Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins*	*journal*	Lam et al	*Nature*
3/26	"Genomic Study Points to Natural Origin of COVID-19" - Blog post by NIH Director Ross	NIH site	Dir. Francis Ross	NIH - Fauci's boss
4/27	*Transcript of NIH communications with Peter Daszak concerning termination of EHA grant*	news reports	Dir. Francis Ross	NIH - Fauci's boss
4/30	*Nobel laureates and science groups demand NIH review decision to kill coronavirus grant | Science | AAAS (sciencemag.org)*	news reports	Editors of *Science*	*Science*
5/8	*SARS-CoV-2: Combating Coronavirus Emergence*	*Immunity*	Baric & Graham	UNC
5/14	*Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?*	*journal*		
5/21	*Letter by 77 Nobel Laureates condemning the funding cuts to EcoHealth Alliance*	news reports	orchestrated by Daszak - friends in high places	EHA
5/22	*Baric issues a correction to a 2015 paper to add the sequence of his chimaeric SARS-like CoV*	*Nature*	*Which might have looked like GOF 5 years earlier...	UNC, WIV
5/22	*31 academic societies call on NIH to reverse EcoHealth Alliance funding decision*	news reports	orchestrated by Daszak	EHA

#D.R.A.S.T.I.C. - Information obtained from PubMed (NIH) & FOIA documents requested by U.S. Right-to-Know, 2020-2021 & Buzzfeed, 2021

• Charles H. Rixey, 2021

Prometheus Shrugged (substack.com)

FOIA Emails: No Rest for the Wicked

These are further examples of Peter Daszak's shaping of the public narrative. He coordinated both a letter signed by 77 Nobel Prize winners & a letter signed by the presidents of 31 leading academic societies – all to protest the withdrawal of his funding by the NIH.

Source: NASEM, *Science Magazine*

ASBMB
American Society for Biochemistry and Molecular Biology

American Society for
Biochemistry and Molecular Biology
11200 Rockville Pike, Suite 302
Rockville, Maryland
20852-3110

CONTACT: Benjamin Corb
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FOR IMMEDIATE RELEASE

ROCKVILLE, MD – Nearly one month ago, the National Institutes of Health took the unusual step of revoking a peer-reviewed research grant awarded in June 2019. The grant, which focused on how coronaviruses can be transferred from their natural hosts to humans, became the target of criticism from President Donald Trump because of the investigator's collaboration with experts in China.

Today, 31 scientific societies representing hundreds of thousands of scientists – led by the American Society for Biochemistry and Molecular Biology – sent a letter to NIH Director Francis S. Collins calling for transparency about the decision-making process and for the NIH to reconsider its decision. In the letter, the groups argue that revocation of the grant is "counterintuitive, given the urgent need to better understand the virus that causes COVID-19 and identify drugs that will save lives." It also says "it politicizes science at a time when, if we are to stamp out this scourge, we need the public to trust experts and to take collective action."

This effort is being led by Benjamin Corb, public affairs director for the ASBMB, who says, "Our aim with this effort is to stand up for a scientific enterprise that should be free of political influence on sound scientific research. This grant was peer reviewed, led to research that has numerous publications in scholarly journals, and was competitively renewed just last year."

Corb continues, "The continued politicization of science during this pandemic crisis is an alarming trend that is risking not only the integrity of science, but also the lives of citizens. Scientific research must remain clear of the partisanship that divides the nation and must be the foundation for sound policymaking during and beyond the COVID-19 pandemic."

A copy of the letter can be found here: https://www.asbmb.org/getmedia/dbb22a26-ee0f-45e5-a1ed-13af91275f07/Support-Science-Sign-on-Letter_1.pdf

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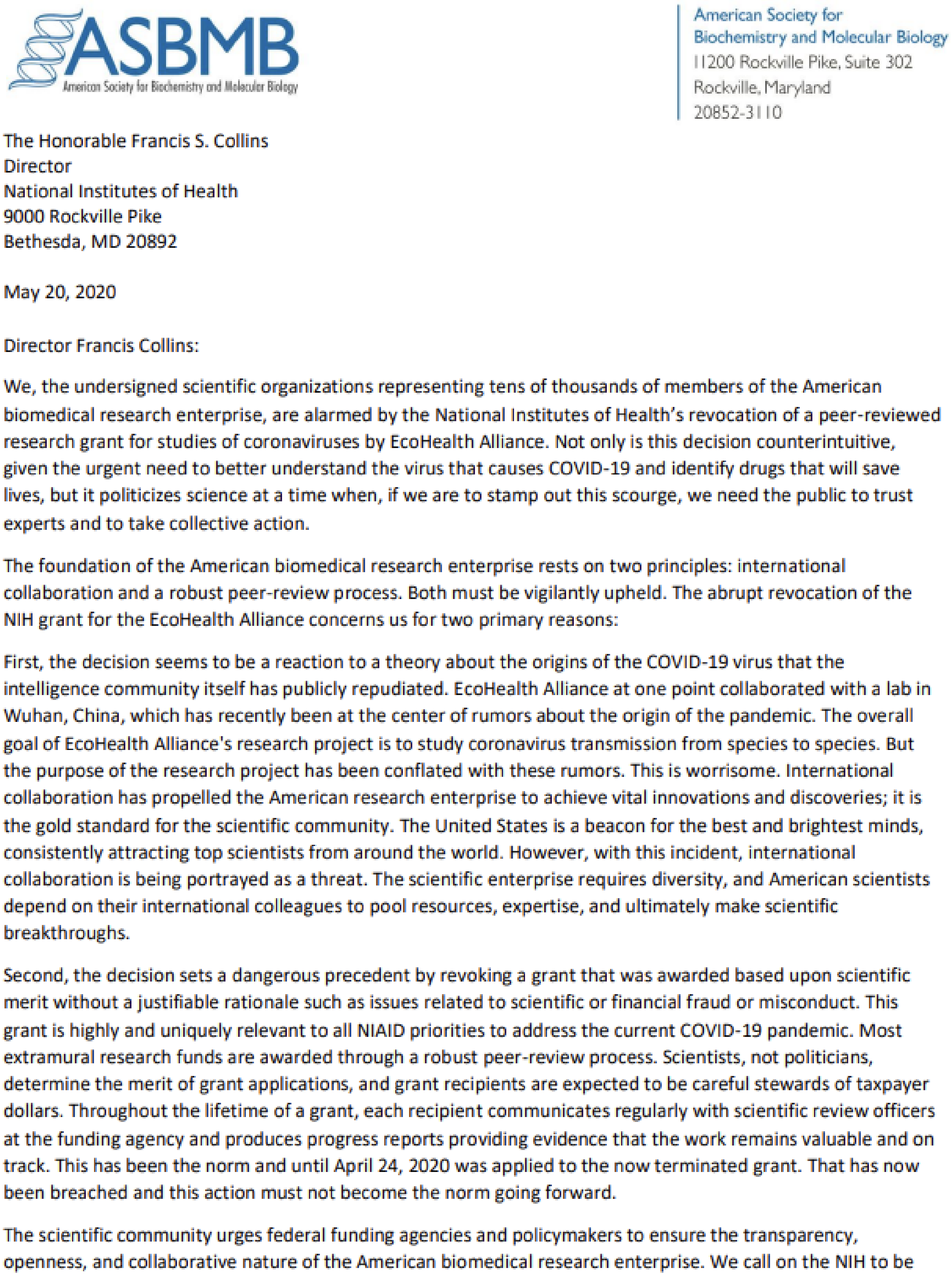


American Society for
Biochemistry and Molecular Biology
11200 Rockville Pike, Suite 302
Rockville, Maryland
20852-3110

The Honorable Francis S. Collins
Director
National Institutes of Health
9000 Rockville Pike
Bethesda, MD 20892

May 20, 2020

Director Francis Collins:

We, the undersigned scientific organizations representing tens of thousands of members of the American biomedical research enterprise, are alarmed by the National Institutes of Health's revocation of a peer-reviewed research grant for studies of coronaviruses by EcoHealth Alliance. Not only is this decision counterintuitive, given the urgent need to better understand the virus that causes COVID-19 and identify drugs that will save lives, but it politicizes science at a time when, if we are to stamp out this scourge, we need the public to trust experts and to take collective action.

The foundation of the American biomedical research enterprise rests on two principles: international collaboration and a robust peer-review process. Both must be vigilantly upheld. The abrupt revocation of the NIH grant for the EcoHealth Alliance concerns us for two primary reasons:

First, the decision seems to be a reaction to a theory about the origins of the COVID-19 virus that the intelligence community itself has publicly repudiated. EcoHealth Alliance at one point collaborated with a lab in Wuhan, China, which has recently been at the center of rumors about the origin of the pandemic. The overall goal of EcoHealth Alliance's research project is to study coronavirus transmission from species to species. But the purpose of the research project has been conflated with these rumors. This is worrisome. International collaboration has propelled the American research enterprise to achieve vital innovations and discoveries; it is the gold standard for the scientific community. The United States is a beacon for the best and brightest minds, consistently attracting top scientists from around the world. However, with this incident, international collaboration is being portrayed as a threat. The scientific enterprise requires diversity, and American scientists depend on their international colleagues to pool resources, expertise, and ultimately make scientific breakthroughs.

Second, the decision sets a dangerous precedent by revoking a grant that was awarded based upon scientific merit without a justifiable rationale such as issues related to scientific or financial fraud or misconduct. This grant is highly and uniquely relevant to all NIAID priorities to address the current COVID-19 pandemic. Most extramural research funds are awarded through a robust peer-review process. Scientists, not politicians, determine the merit of grant applications, and grant recipients are expected to be careful stewards of taxpayer dollars. Throughout the lifetime of a grant, each recipient communicates regularly with scientific review officers at the funding agency and produces progress reports providing evidence that the work remains valuable and on track. This has been the norm and until April 24, 2020 was applied to the now terminated grant. That has now been breached and this action must not become the norm going forward.

The scientific community urges federal funding agencies and policymakers to ensure the transparency, openness, and collaborative nature of the American biomedical research enterprise. We call on the NIH to be

transparent about their decision-making process on this matter. We urge federal funding agencies to safeguard the American biomedical research enterprise. The action taken by the NIH must be immediately reconsidered.

Respectfully,

The American Society for Biochemistry and Molecular Biology
The Academy for Radiology and Biomedical Imaging Research
The American Association for Anatomy
The American Institute of Biological Sciences
The American Physiological Society
The American Psychological Association
The American Society for Investigative Pathology
The American Society for Virology
The American Society of Ichthyologists and Herpetologists
The Association of Anatomy, Cell Biology and Neurobiology Chairs
The Association of Biomolecular Resource Facilities
The Association of Medical and Graduate Departments of Biochemistry
The Association of Schools and Programs of Public Health
The Biophysical Society
The Botanical Society of America
The Conference Board of Mathematical Sciences
The Endocrine Society
The Entomological Society of America
The Federation of American Societies for Experimental Biology
The Genetics Society of America
The HIV Medicine Association
The Infectious Diseases Society of America
The Natural Science Collections Alliance
The North American Vascular Biology Organization
The Shock Society
The Society for Freshwater Science
The Society for the Study of Amphibians and Reptiles
The Society for the Study of Reproduction
The Society of Toxicology

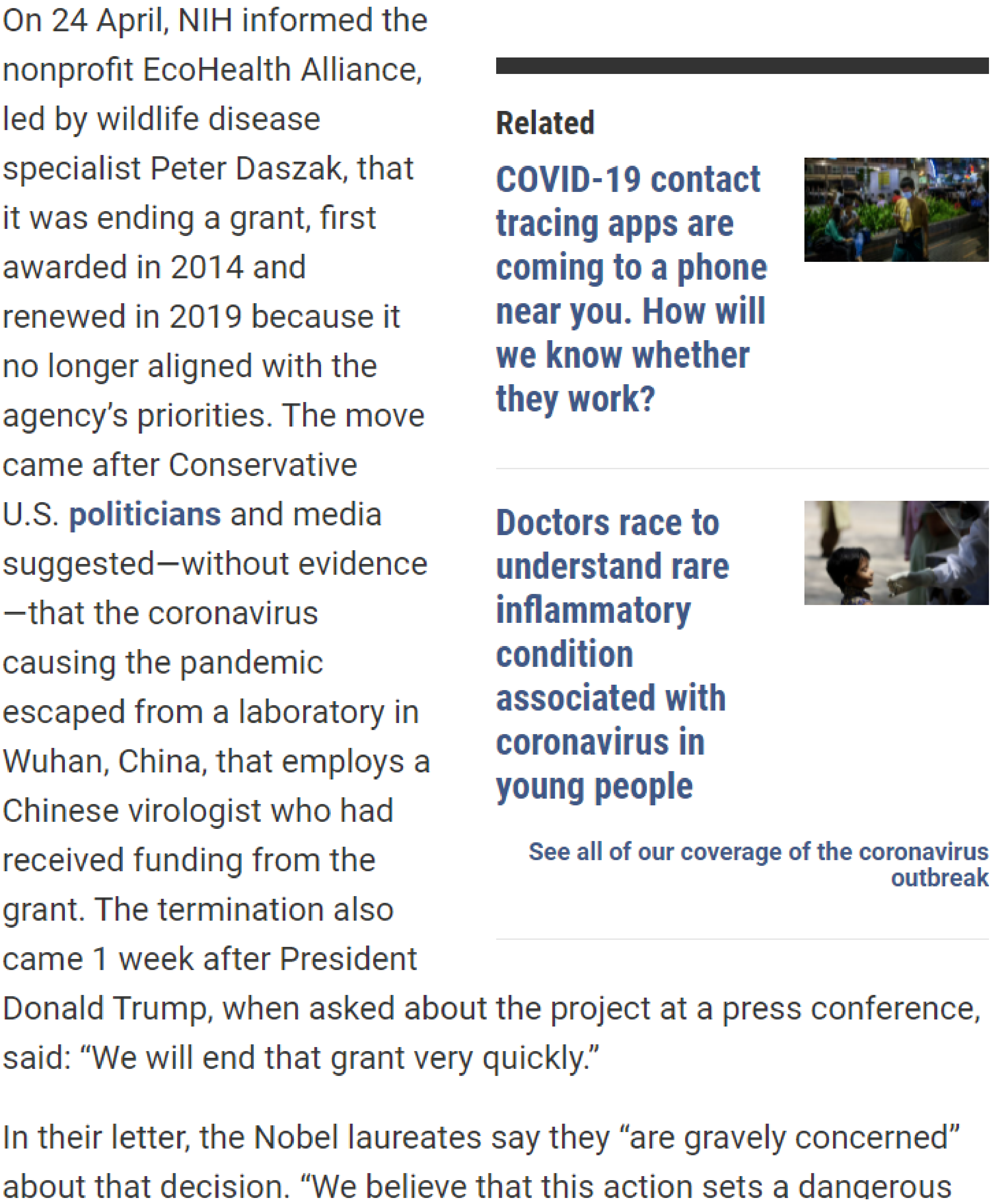
Nobel laureates and science groups demand NIH review decision to kill coronavirus grant

By **Science News Staff** | May. 21, 2020 , 6:40 PM

Seventy-seven U.S. scientists who have won a Nobel Prize today asked Francis Collins, director of the National Institutes of Health, and Alex Azar, secretary of Health and Human Services, to “act urgently” to review **a controversial NIH decision to terminate a grant** that supported research into bat coronaviruses in China. NIH’s explanation for killing the grant was “preposterous,” **the laureates write**.

Thirty-one scientific societies have also written to Collins, calling on NIH “to be transparent about their decision-making process on this matter. … The action taken by the NIH must be immediately reconsidered.”

reconsidered.”



On 24 April, NIH informed the nonprofit EcoHealth Alliance, led by wildlife disease specialist Peter Daszak, that it was ending a grant, first awarded in 2014 and renewed in 2019 because it no longer aligned with the agency's priorities. The move came after Conservative U.S. **politicians** and media suggested—without evidence—that the coronavirus causing the pandemic escaped from a laboratory in Wuhan, China, that employs a Chinese virologist who had received funding from the grant. The termination also came 1 week after President Donald Trump, when asked about the project at a press conference, said: "We will end that grant very quickly."

Related

COVID-19 contact tracing apps are coming to a phone near you. How will we know whether they work?

Doctors race to understand rare inflammatory condition associated with coronavirus in young people

See all of our coverage of the coronavirus outbreak

In their letter, the Nobel laureates say they "are gravely concerned" about that decision. "We believe that this action sets a dangerous public trust in the process of awarding federal funds for research. … Now is precisely the time when we need to support this kind of research if we aim to control the pandemic and prevent subsequent ones."

They write that "despite the high relevance of the studies to the current pandemic, and despite the very high priority score that his application for renewal had received during peer review, the NIH informed Dr. Daszak and his colleagues that the grant was being terminated because 'NIH does not believe that the current project outcomes align with the program goals and agency priorities.' Such explanations are preposterous under the circumstances."

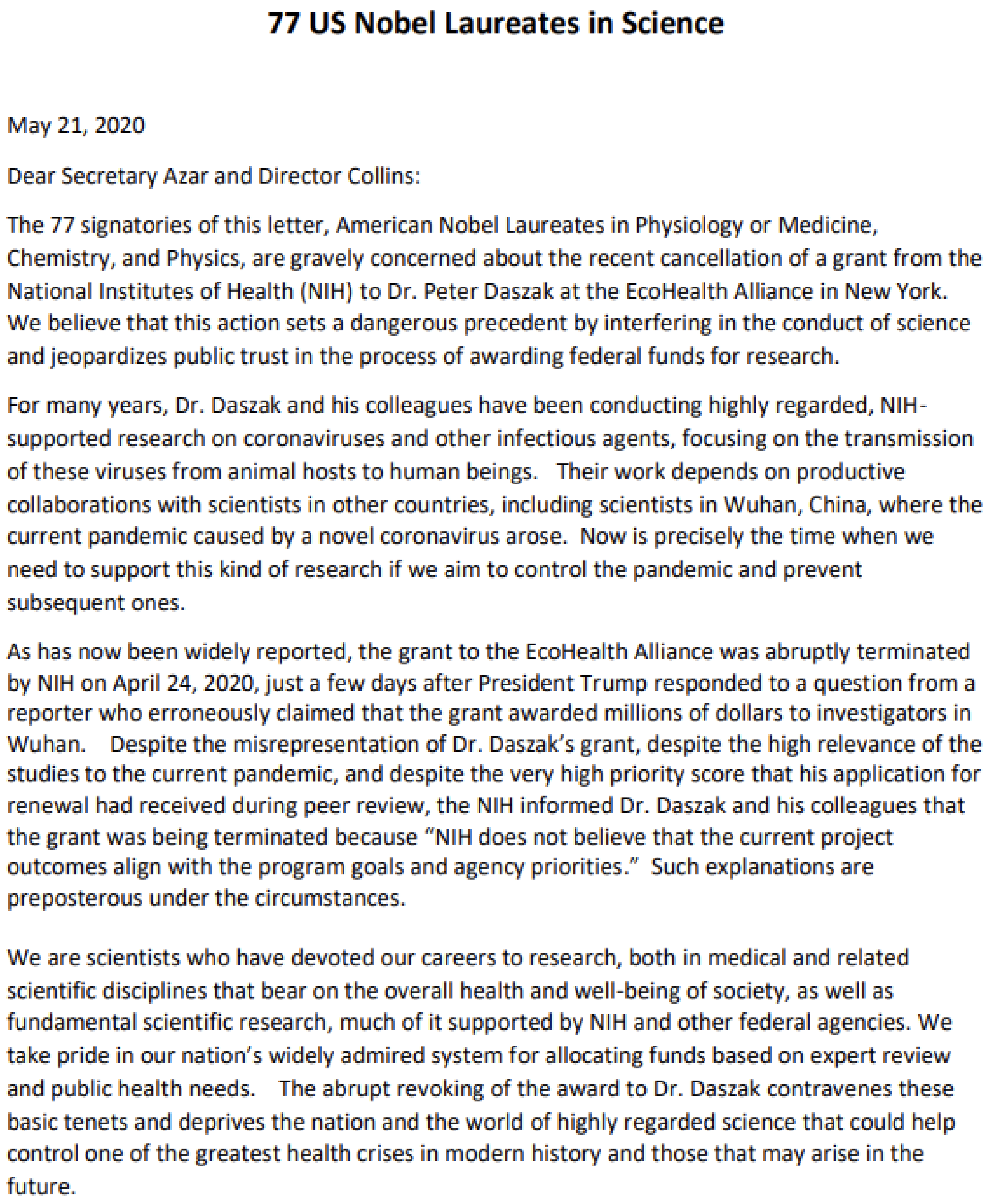
Azar and Collins should, they write, "act urgently to conduct and release a thorough review of the actions that led to the decision to terminate the grant, and that, following this review … take appropriate steps to rectify the injustices that may have been committed in revoking it."

The signers of the letter include researchers who won a Nobel Prize as recently as 2019, and as long ago as 1975.

The letter from the scientific societies was organized by the American Society for Biochemistry and Molecular Biology (ASBMB). "Our aim with this effort is to stand up for a scientific enterprise that should be free of political influence on sound scientific research," said Benjamin Corb, public affairs director for ASBMB, in a statement. "The continued politicization of science during this pandemic crisis is an alarming trend that is risking not only the integrity of science, but also the lives of citizens."

Posted in: **Science and Policy**, **Coronavirus**

doi:10.1126/science.abc9393



77 US Nobel Laureates in Science

May 21, 2020

Dear Secretary Azar and Director Collins:

The 77 signatories of this letter, American Nobel Laureates in Physiology or Medicine, Chemistry, and Physics, are gravely concerned about the recent cancellation of a grant from the National Institutes of Health (NIH) to Dr. Peter Daszak at the EcoHealth Alliance in New York. We believe that this action sets a dangerous precedent by interfering in the conduct of science and jeopardizes public trust in the process of awarding federal funds for research.

For many years, Dr. Daszak and his colleagues have been conducting highly regarded, NIH-supported research on coronaviruses and other infectious agents, focusing on the transmission of these viruses from animal hosts to human beings. Their work depends on productive collaborations with scientists in other countries, including scientists in Wuhan, China, where the current pandemic caused by a novel coronavirus arose. Now is precisely the time when we need to support this kind of research if we aim to control the pandemic and prevent subsequent ones.

As has now been widely reported, the grant to the EcoHealth Alliance was abruptly terminated by NIH on April 24, 2020, just a few days after President Trump responded to a question from a reporter who erroneously claimed that the grant awarded millions of dollars to investigators in Wuhan. Despite the misrepresentation of Dr. Daszak's grant, despite the high relevance of the studies to the current pandemic, and despite the very high priority score that his application for renewal had received during peer review, the NIH informed Dr. Daszak and his colleagues that the grant was being terminated because "NIH does not believe that the current project outcomes align with the program goals and agency priorities." Such explanations are preposterous under the circumstances.

We are scientists who have devoted our careers to research, both in medical and related scientific disciplines that bear on the overall health and well-being of society, as well as fundamental scientific research, much of it supported by NIH and other federal agencies. We take pride in our nation's widely admired system for allocating funds based on expert review and public health needs. The abrupt revoking of the award to Dr. Daszak contravenes these basic tenets and deprives the nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future.

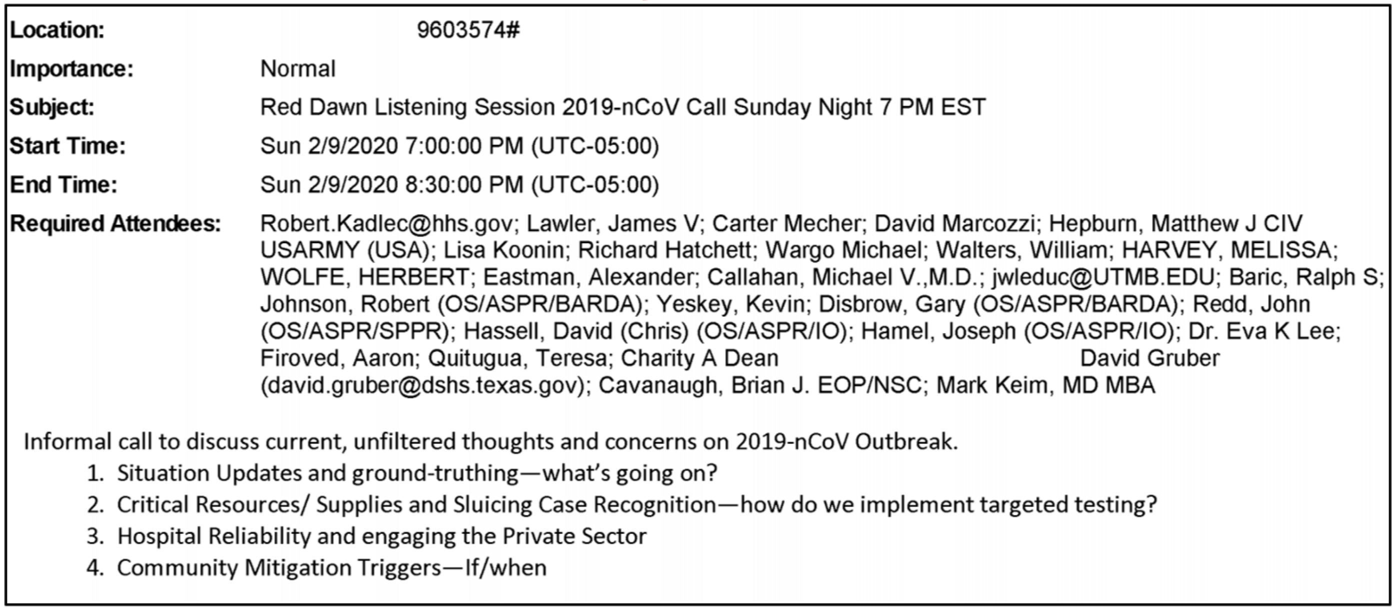
We ask that you act urgently to conduct and release a thorough review of the actions that led to the decision to terminate the grant, and that, following this review, you take appropriate steps to rectify the injustices that may have been committed in revoking it.

Peter Agre	Chemistry	2003	James P. Allison	Medicine	2018
Sidney Altman	Chemistry	1989	Frances H. Arnold	Chemistry	2018
David Baltimore	Medicine	1975	Barry Clark Barish	Physics	2017
Paul Berg	Chemistry	1980	J. Michael Bishop	Medicine	1989
Elizabeth H. Blackburn	Medicine	2009	Michael S. Brown	Medicine	1985
William C. Campbell	Medicine	2015	Mario R. Capecchi	Medicine	2007
Thomas R. Cech	Chemistry	1989	Martin Chalfie	Chemistry	2008
Steven Chu	Physics	1997	Elias James Corey	Chemistry	1990
Robert F. Curl Jr.	Chemistry	1996	Johann Deisenhofer	Chemistry	1988
Andrew Z. Fire	Medicine	2006	Edmond H. Fischer	Medicine	1992
Joachim Frank	Chemistry	2017	Jerome I. Friedman	Physics	1990
Walter Gilbert	Chemistry	1980	Sheldon Glashow	Physics	1979
Joseph L. Goldstein	Medicine	1985	Carol W. Greider	Medicine	2009
David J. Gross	Physics	2004	Roger Guillemin	Medicine	1977
Leland H. Hartwell	Medicine	2001	Dudley R. Herschbach	Chemistry	1986
Roald Hoffmann	Chemistry	1981	H. Robert Horvitz	Medicine	2002
Louis J. Ignarro	Medicine	1998	William G. Kaelin Jr.	Medicine	2019
Eric R. Kandel	Medicine	2000	Wolfgang Ketterle	Physics	2001
Brian K. Kobilka	Chemistry	2012	Roger D. Kornberg	Chemistry	2006
Robert J. Lefkowitz	Chemistry	2012	Anthony J. Leggett	Physics	2003
Michael Levitt	Chemistry	2013	Roderick MacKinnon	Chemistry	2003
John C. Mather	Physics	2006	Craig C. Mello	Medicine	2006
William E. Moerner	Chemistry	2014	Mario J. Molina	Chemistry	1995
Ferid Murad	Medicine	1998	Douglas D. Osheroff	Physics	1996
James Peebles	Physics	2019	Saul Perlmutter	Physics	2011
William D. Phillips	Physics	1997	H. David Politzer	Physics	2004
Sir Richard J. Roberts	Medicine	1993	Michael Rosbash	Medicine	2017
James E. Rothman	Medicine	2013	Randy W. Schekman	Medicine	2013
Richard R. Schrock	Chemistry	2005	Gregg L. Semenza	Medicine	2019
Phillip A. Sharp	Medicine	1993	Hamilton O. Smith	Medicine	1978
George P. Smith	Chemistry	2018	Horst L. Stormer	Physics	1998
Thomas C. Sudhof	Medicine	2013	Jack W. Szostak	Medicine	2009
Joseph H. Taylor Jr.	Physics	1993	Kip Stephen Thorne	Physics	2017
Susumu Tonegawa	Medicine	1987	Daniel C. Tsui	Physics	1998
Harold E. Varmus	Medicine	1989	Steve Weinberg	Physics	1979
Rainer Weiss	Physics	2017	Carl E. Wieman	Physics	2001
Eric F. Wieschaus	Medicine	1995	Torsten N. Wiesel	Medicine	1981
Frank Wilczek	Physics	2004	Robert Woodrow Wilson	Physics	1978
Michael W. Young	Medicine	2017			

US Right-To-Know's FOIA Emails - 1st Baric dump		
Pages	**File/String**	**Start**
5,508	**Vol. 1**	
	Red Dawn Wolverines	1/24
	Red Dawn Breaking	2/16
6,093	**Vol. 2**	
	Red Dawn Breaking (cont)	2/16
	Red Dawn Breaking Bad	2/24
	Red Dawn Rising	2/29
6,626	**Vol. 3**	
	Red Dawn Rising (cont)	2/29
14,359	**Vol. 4**	
	Red Dawn Raging	3/4
8,510	**Vol. 5**	(cont)
4,711	**Vol. 6**	(cont)
12,178	**Vol. 7**	(cont)
1,670	**Vol. 8**	
	Red Dawn Responding	3/16
16,505	**Vol. 9**	
	Red Dawn Reflux	3/19
	Red Dawn Suppression	3/23
	Red Dawn Pondering	3/27
	Red Dawn Rooster	4/2
	Red Dawn Rolling	4/6
	Red Dawn Setting	4/13
7,245	**Vol. 10**	
	Red Dawn Setting (cont)	4/13
	Red Dawn Posturing	5/5
	Red Dawn Rhapsodizing	7/2
83,405	**Total**	

	Title [in Feb. 2020]	Position [in Feb. 2020]
Carter Mecher	Sr. Medical Advisor	Department of Veterans Affairs, Public Health
Duane Caneva	Chief Medical Officer	Department of Homeland Security
Richard Hatchett	Director	Coalition for Epidemic Preparedness Innovations
Matthew Hepburn	Col. USA; Program Manager	DARPA
Robert Kadlec	A. Sec. for Prep & Response	Department of Health & Human Services
James Lawler	Director, Int. Programs & Innovation	U of NE
Ralph Baric	W.R. Kenan Dist. Prof. of Microbiology & Imm.	UNC
Eva Lee	Director, Center for Ops Research	Georgia Tech
David Marcozzi	A. CMO for Acute Care	University of Maryland MC
Michael Callahan	Vaccine & Immunotherapy Center	Massachusetts General Hospital
D. (Chris) Hassell*	Sr. Sci. Adv. to the A. Sec. for Prep & Response	Department of Health & Human Services

*Hassell is also the head of the PCO3 Adv. Board



Location: 9603574#

Importance: Normal

Subject: Red Dawn Listening Session 2019-nCoV Call Sunday Night 7 PM EST

Start Time: Sun 2/9/2020 7:00:00 PM (UTC-05:00)

End Time: Sun 2/9/2020 8:30:00 PM (UTC-05:00)

Required Attendees: Robert.Kadlec@hhs.gov; Lawler, James V; Carter Mecher; David Marcozzi; Hepburn, Matthew J CIV USARMY (USA); Lisa Koonin; Richard Hatchett; Wargo Michael; Walters, William; HARVEY, MELISSA; WOLFE, HERBERT; Eastman, Alexander; Callahan, Michael V.,M.D.; jwleduc@UTMB.EDU; Baric, Ralph S; Johnson, Robert (OS/ASPR/BARDA); Yeskey, Kevin; Disbrow, Gary (OS/ASPR/BARDA); Redd, John (OS/ASPR/SPPR); Hassell, David (Chris) (OS/ASPR/IO); Hamel, Joseph (OS/ASPR/IO); Dr. Eva K Lee; Firoved, Aaron; Quitugua, Teresa; Charity A Dean David Gruber (david.gruber@dshs.texas.gov); Cavanaugh, Brian J. EOP/NSC; Mark Keim, MD MBA

Informal call to discuss current, unfiltered thoughts and concerns on 2019-nCoV Outbreak.

1. Situation Updates and ground-truthing—what's going on?
2. Critical Resources/ Supplies and Sluicing Case Recognition—how do we implement targeted testing?
3. Hospital Reliability and engaging the Private Sector
4. Community Mitigation Triggers—If/when