United States Department of State

Washington, D.C. 20520

April 4, 2025

Case No. FL-2022-00062

Mr. Gary Ruskin
U.S. Right to Know
4096 Piedmont Avenue, #963
Oakland, CA 94611

Dear Mr. Ruskin:

As we noted in our letter dated February 21, 2025, we are processing your request for material under the Freedom of Information Act ("FOIA"), 5 U.S.C. § 552. The Department of State ("Department") has identified 27 additional responsive records subject to the FOIA. Upon review, we have determined that 22 records may be released in part and 5 records may be released in full.

An enclosure explains the FOIA exemptions and other grounds for withholding material. Where we have made redactions, the applicable FOIA exemptions are marked on each record. Where applicable, the Department has considered the foreseeable harm standard when reviewing these records and applying FOIA exemptions. All non-exempt material that is reasonably segregable from the exempt material has been released and is enclosed.

We will keep you informed as your case progresses. If you have any questions, your attorney may contact Assistant United States Attorney Stephanie Johnson at stephanie.johnson5@usdoj.gov or (202) 252-7874. Please refer to the case number, FL-2022-00062, and the civil action number, 22-cv-01130, in all correspondence about this case.

Sincerely,

Terry Gordon

Terry Gordon
Supervisory Government Information Specialist
Office of Information Programs and Services

Enclosures: As stated.

The Freedom of Information Act (5 USC 552)

FOIA Exemptions

(b)(1) Information specifically authorized by an executive order to be kept secret in the interest of national defense or foreign policy. Executive Order 13526 includes the following classification categories:

1.4(a) Military plans, systems, or operations
1.4(b) Foreign government information
1.4(c) Intelligence activities, sources or methods, or cryptology
1.4(d) Foreign relations or foreign activities of the US, including confidential sources
1.4(e) Scientific, technological, or economic matters relating to national security, including defense against transnational terrorism
1.4(f) U.S. Government programs for safeguarding nuclear materials or facilities
1.4(g) Vulnerabilities or capabilities of systems, installations, infrastructures, projects, plans, or protection services relating to US national security, including defense against transnational terrorism
1.4(h) Weapons of mass destruction

(b)(2) Related solely to the internal personnel rules and practices of an agency

(b)(3) Specifically exempted from disclosure by statute (other than 5 USC 552), for example:

ARMSEXP	Arms Export Control Act, 50a USC 2411(c)
CIA PERS/ORG	Central Intelligence Agency Act of 1949, 50 USC 403(g)
EXPORT CONTROL	Export Administration Act of 1979, 50 USC App. Sec. 2411(c)
FS ACT	Foreign Service Act of 1980, 22 USC 4004
INA	Immigration and Nationality Act, 8 USC 1202(f), Sec. 222(f)
IRAN	Iran Claims Settlement Act, Public Law 99-99, Sec. 505

(b)(4) Trade secrets and confidential commercial or financial information

(b)(5) Interagency or intra-agency communications forming part of the deliberative process, attorney-client privilege, or attorney work product

(b)(6) Personal privacy information

(b)(7) Law enforcement information whose disclosure would:
(A) interfere with enforcement proceedings
(B) deprive a person of a fair trial
(C) constitute an unwarranted invasion of personal privacy
(D) disclose confidential sources
(E) disclose investigation techniques
(F) endanger life or physical safety of an individual

(b)(8) Prepared by or for a government agency regulating or supervising financial institutions

(b)(9) Geological and geophysical information and data, including maps, concerning wells

Other Grounds for Withholding

NR Material not responsive to a FOIA request excised with the agreement of the requester

PERSPECTIVE

https://doi.org/10.1038/s41467-020-19149-2 OPEN

Check for updates

The biosecurity benefits of genetic engineering attribution

Gregory Lewis[1,2]✉, Jacob L. Jordan[3], David A. Relman[4,5], Gregory D. Koblentz[6], Jade Leung[1], Allan Dafoe[1], Cassidy Nelson[1], Gerald L. Epstein[7], Rebecca Katz[8], Michael Montague[9], Ethan C. Alley[2,10,11], Claire Marie Filone[12], Stephen Luby[4], George M. Church[2,11], Piers Millett[1,13], Kevin M. Esvelt[2,10], Elizabeth E. Cameron[3] & Thomas V. Inglesby[9]

Biology can be misused, and the risk of this causing widespread harm increases in step with the rapid march of technological progress. A key security challenge involves attribution: determining, in the wake of a human-caused biological event, who was responsible. Recent scientific developments have demonstrated a capability for detecting whether an organism involved in such an event has been genetically modified and, if modified, to infer from its genetic sequence its likely lab of origin. We believe this technique could be developed into powerful forensic tools to aid the attribution of outbreaks caused by genetically engineered pathogens, and thus protect against the potential misuse of synthetic biology.

Biotechnology is in an era of rapid and accelerating progress. Qualitative breakthroughs such as CRISPR and artificial gene drives unlock new capabilities, and quantitative trends show biotechnology as an area of increasing investment, decreasing costs, and expanding access.

However, alongside the benefits of this advancing technology for science, medicine, agriculture, and industry, there are concerns over its potential for accidental or deliberate misuse. Laboratory accidents have caused outbreaks before. The 2007 Foot and Mouth disease outbreak in the UK was attributed to a leaking pipe at Institute of Animal Health at Pirbright[1]. The last known cases of smallpox and SARS were both caused by laboratory exposures, and involved secondary transmission from infected researchers to individuals outside of the laboratory[2]. The 1977 influenza pandemic was caused by a strain closely related to those isolated in the 1950s, suggesting an anthropogenic origin[3].

Both state and non-state actors have attempted to develop biological weapons in the last century. Although 183 states are party to the Biological Weapons Convention, which categorically bans the development and production of biological weapons, multiple states have been

[1] Future of Humanity Institute, Oxford University, Oxford, UK. [2] Alt. Technology Labs, Inc., Berkeley, CA, USA. [3] Nuclear Threat Initiative, Washington, DC, USA. [4] Department of Medicine, Stanford University School of Medicine, Stanford, CA, USA. [5] Department of Microbiology & Immunology, Stanford University School of Medicine; and Center for International Security and Cooperation, Stanford University, Stanford, CA, USA. [6] Schar School of Policy and Government, George Mason University, Washington, DC, USA. [7] Center for the Study of Weapons of Mass Destruction, National Defense University, Washington, DC, USA. [8] Center for Global Health Science and Security, Georgetown University, Washington, DC, USA. [9] Center for Health Security, Johns Hopkins University, Baltimore, MD, USA. [10] Media Laboratory, Massachusetts Institute of Technology, Cambridge, MA, USA. [11] Department of Genetics, Harvard Medical School, Boston, MA, USA. [12] The Johns Hopkins University Applied Physics Laboratory, Laurel, MA, USA. [13] International Genetically Engineered Machine Competition, Boston, MA, USA. ✉email: gregory.lewis@zoo.ox.ac.uk

alleged to have initiated the attack. Non-state actors have also sought to use biological weapons[4,5]: notable among these are Al-Qaeda's unsuccessful attempts to develop biological weapons[6]; Aum Shinrikyo's ineffectual bioterrorist attacks[7]; and the Rajneeshee cult's use of *Salmonella* to cause 751 cases of food poisoning in Oregon in 1984.

Technological progress magnifies these dangers: falling barriers to entry increases the risk that reckless or malicious actors will access biotechnology. Emerging capabilities may worsen the potential impact if this risk is realised. The 2011 'gain of function' influenza experiments raised concern that adapting a highly virulent avian influenza strain to be transmissible between mammals posed an unacceptable risk since a laboratory escape could lead to a pandemic[8]. The increasing ease and accuracy of genetic engineering both widens the possibilities and lowers the barriers to entry to research that could be misused to produce pathogens more dangerous than naturally arising strains[9].

The attribution gap

Addressing these biological threats is an urgent and formidable challenge. One element of this challenge is attribution: being able to determine, in the wake of a human-caused biological event, who was responsible. Attribution has three main security benefits. First, knowledge of who was responsible can inform response efforts by shedding light on motives and capabilities, and so mitigate the event's consequences. Second, it can identify the responsible parties for appropriate civil, criminal, or diplomatic penalty. Third, successful attribution followed by meaningful actions to hold perpetrators accountable can deter those inclined to reckless or malicious practice in the first place.

Information for attribution can be roughly divided into three categories. The first category includes non-technical indicators that provide contextual clues to intent, such as the victims, the location of the event, and epidemiological features. For example, if an incident occurs in the midst of an ongoing conflict, suspicion falls on the belligerents, while if it occurs near laboratories working on the causative agent, there is a greater chance of it being attributed to an accidental release.

Another category informing attribution is intelligence. This ranges from human sources, such as informers or whistleblowers; to intercepted communications; to surveillance data. All can potentially identify those responsible for the release of a biological agent.

The final category is technical forensics: the properties and characteristics of the agent that caused a given outbreak may provide clues as to who made it and/or who was responsible for releasing it.

The nascent field of microbial forensics helped the FBI identify a suspected lab of origin for the anthrax used in the 2001 attack and a suspected perpetrator responsible for the attack[10]. Nonetheless, further improvement of these forensic capabilities are a recognised need[11]. Two capabilities would be important: first, to establish whether the causative organism was genetically engineered; and second, if it was engineered, to identify the actor who engineered it.

To detect engineering, tools are being developed which can interrogate the genome of the causative organism for indicators of genetic engineering. The IARPA Finding Engineering-Linked Indicators project, FELIX, seeks to develop new experimental and computational tools for this purpose[12]. Under the auspices of the UN Secretary-General's mechanism for investigating alleged biological attacks, there are separate efforts to develop an international trusted laboratory network that would provide forensic support to such investigations. As performance across laboratories in detecting genetic modifications is currently variable, the methods may be strengthened through additional tools and access to existing technologies[13].

Identification of the engineer poses a further challenge, since determining that an organism has been genetically engineered, and what that engineering involved, does not establish who the engineer was. A given set of edits could conceivably be performed by a multitude of different actors: from individuals working out of a community lab, to university research groups, to industrial laboratories, to a state-run bioweapons facility.

Towards genetic engineering attribution

Fortunately, the very diversity of design approaches and technical options that are now available to achieve a given result (e.g. which genes or genetic features to use, their origin, and how to incorporate these genes or features into the genome) offers a means to approach the attribution problem. Which option a genetic engineer chooses will be influenced by a variety of factors, including their training, prior experience, habits, and available resources. In aggregate, these choices compose a 'methodological signature', and thus a way of tracing these design choices back to the likely designer.

That machine learning could be used to detect and interpret these signatures was demonstrated in late 2018[14], although with a limited accuracy of 48%. Most recently, Alley and colleagues deployed deep learning techniques to predict lab-of-origin for plasmids submitted to the Addgene database - the largest repository of its kind, with 70,000 submissions from labs in 37 countries. Their approach offers an accuracy of 70% when distinguishing between over 1000 labs[15].

They also pioneered further capabilities: uncertainty estimation, tracking 'genealogies' of genetic engineering groups, and inferring the nation in which the originating laboratory is located. Each of these has security promise: uncertainty estimation enhances robustness and can aid the integration of technical indicators with other available information for making an overall attribution decision; tracking lineages may identify other groups who knowingly or otherwise assisted the actor responsible; and the nation of the originating laboratory may provide a useful investigative clue in the absence of finer-grained information.

The security potential of genetic engineering attribution

These rapid developments have potential as techniques, alongside publications and patents, to help understand patterns of influence and performance within the synthetic biology community, and also a means to identify and protect intellectual property. Our interest is in the biosecurity promise of using these advances to develop forensic tools which can aid attribution of genetically engineered agents and organisms.

The central benefit would be an increase in the actual and perceived accuracy of attribution decisions. This increases the likelihood of the right people being implicated in any misuse of genetic engineering in case of either an accident or an attack. The converse—avoiding mistaken attribution—is also key, given the potentially catastrophic consequences of one state mistakenly believing it is a victim of a biological attack.

An indirect effect of this improved accuracy is deterrence of misuse in the first place. Some actors may be incentivized to be reckless if they believe they are unlikely to be held accountable for any accidents arising from their actions. Malicious actors may be attracted to biological weapons as a means of clandestine violence. Better attribution tools deter both by increasing the risk of discovery.

Three additional features of genetic engineering forensics make it particularly attractive as a biodefense technology. First, unlike other instances where the interests of science and security

conflict, the development of genetic engineering forensic tools does not impede scientific enquiry. If anything, it offers co-benefits for the overwhelming majority of well-intentioned and responsible genetic engineers: further means of receiving due credit and recognition, and further safeguards of their intellectual property.

Second, biodefense activity can paradoxically worsen security, by what is known as a security dilemma[16]. A given state's biodefense activity, even if wholly defensive in intent, may nonetheless provoke concern in other states that this activity could both harbour and be co-opted for offensive purposes. Mutual suspicion can drive an arms race. Compared to other aspects of biodefense, genetic engineering forensics has more limited prospects for offensive use, and so state investment in this aspect of biodefense poses a lower risk of triggering suspicions and insecurity in its peers.

Third, the efficacy of genetic engineering attribution is coupled to biotechnological progress, so the trends that make misuse more concerning also enhance this approach to help address them. The rapidly growing corpus of genetically engineered sequence information provides more data that can be fed into these forensic tools; the increasing diversity of biotechnological methods also increases the diversity of 'methodological signatures' among practitioners.

Challenges and next steps

The security benefits of genetic engineering attribution, even in the ideal case, would have limits. Attribution techniques are not techniques to detect whether engineering occurred in the first place: determining attribution is a process that would follow detection of engineering, and is not a substitute for it. Great caution should apply to using genetic engineering attribution as an improvised means of genetic engineering detection. Inability to attribute does not rule out genetic engineering: a sequence may show clear signs of engineering even if the engineer cannot be identified. There are also risks of false positives: improper use of genetic engineering attribution could 'attribute' non-existent engineering, such as identifying the 'engineer' of a wild-type pathogen genome.

Genetic engineering attribution is also not applicable to releases of non-engineered agents or organisms, for which other forensics methods remain necessary. Technical forensics may help identify the designer of the genetically engineered organism, but this may not be the actor who misuses it (although identifying the source of genetic engineering which is subsequently misused could be important information, for example in a case of suspected state-sponsored bioterrorism).

The deterrence value of attribution, and thus of better forensic tools to inform it, is sensitive to political context. Forensic identification offers little deterrence to actors intending to claim rather than conceal responsibility, nor to those who plan to evade the consequences of being held responsible by disinformation campaigns or other political means (although genetic engineering forensics may prove a harder target for disinformation if its techniques become public and well-characterised).

Realistic circumstances, rather than ideal ones, imply further limitations. 70% accuracy is far from a smoking gun, and although this may improve further, the performance ceiling is not known. Genetic engineering forensics should be seen as an important forensic tool in the attribution toolkit, instead of a standalone silver bullet.

A key uncertainty is that genetic engineering forensics has so far been developed on—and tested against—data from genetic engineers operating 'in the clear': those who publish their sequences to public repositories and make no attempt to conceal authorship. In the case of an attack rather than accident, sophisticated adversaries may also attempt to find ways of obfuscating or misdirecting attribution indicators—genetic engineering forensics included. For example, an attacker could attempt to adopt the 'methodological signature' associated with other practitioners in an attempt to deflect attribution or at least confuse the analysis.

Such attempts could leave their own trace, and forecasting how any potential contest between forensics and counter-forensics would play out is difficult; one side or the other may have an intrinsic advantage. Yet even in the worst case where an adversary is justifiably confident that they can evade genetic engineering forensics, doing so imposes a further cost, a further design constraint, and a residual risk of discovery. Each is a disincentive.

Genetic engineering forensics is at an early stage; there is a long way to go from published proof of principle studies to a robust forensic capability. These next steps include: First, starting a dialogue with the forensics and biodefense communities for what capabilities would be useful, and how technical forensic innovations can be brought into practice. Second, corralling further sources of data to improve accuracy and assess how performance scales. Third, leveraging ongoing improvements in machine learning and the creativity of practitioners to further improve the state of the art.

As biotechnology continues to pose a security challenge, it promises new tools to address the same. We believe it is the responsibility of the scientific and policy communities to identify opportunities to create these tools, like genetic engineering attribution, which reduce the risk of misuse. By engaging in this enterprise pro-actively, we can continue to realize the benefits of rapidly improving biotechnology while safeguarding biological security.

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Published online: 08 December 2020

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Acknowledgements

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Author contributions

G.J.L. wrote and prepared the paper. J.L.J., E.E.C., D.A.R., G.D.K, J.J, A.D. C.N., G.L.E., R.K., M.M., E.C.A, C.M.F, S.L., and K.M.E. provided edits. All authors have contributed to conceptualisation and review.

Competing interests

G.L, E.C.A., G.M.C., P.M., K.M.E., and T.V.L. are involved in a genetic engineering attribution challenge hosted by drivendata (https://www.drivendata.org/competitions/63/genetic-engineering attribution/). A full list of G.M.C.'s tech transfer, advisory roles, and funding sources can be found on the lab's website http://arep.med.harvard.edu/gmc/tech.html. All other authors declare no competing interests.

Additional information

Correspondence and requests for materials should be addressed to G.L.

Peer review information *Nature Communications* thanks Cedric Invernizzi, Kenneth Oye and the other, anonymous, reviewer(s) for their contribution to the peer review of this work.

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From: "Feith, David" (b)(6) @state.gov>
To: Ortagus, Morgan D (b)(6) @state.gov>; (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
CC: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: RE: Wuhan statement
Date: Fri, 15 Jan 2021 19:38:45 +0000

Thanks all. Attached is the properly formatted Memo.

(b)(6) as Press Office will send to S approvers.

Thanks --

~~SENSITIVE BUT UNCLASSIFIED~~

From: Ortagus, Morgan D (b)(6) @state.gov>
Sent: Friday, January 15, 2021 2:30 PM
To: Feith, David (b)(6) @state.gov>; (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Cc: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: RE: Wuhan statement

Thanks guys

Richard—please have your team put the statement and fact sheet into its proper format for S, list clearances, etc. and then get it up to the line.

Morgan D. Ortagus
Spokesperson
U.S. Dept of State

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Friday, January 15, 2021 2:25 PM
To: (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Cc: Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Roger, thanks. Attached is the fully updated clean text. It accounts for the one tweak (b)(6) approved an hour ago, and not the second; also removes the yellow/green coloring.

Morgan – do you want to read and then you will pass to S?

Thanks much.

~~SENSITIVE BUT UNCLASSIFIED~~

From (b)(6) @state.gov>
Sent: Friday, January 15, 2021 1:38 PM
To: Feith, David (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Cc: Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

They should be, yes

From: Feith, David (b)(6) @state.gov>
Sent: Friday, January 15, 2021 1:35 PM
To: (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Cc: Stilwell, David R <(b)(6) @state.gov>
Subject: RE: Wuhan statement

(Smaller distro to limit spam.)

Roger that.

Also — can we confirm that the statement and fact sheet won't be separated upon publication? That is, they'll be together on website, in email that goes out, etc?

Thanks again for pushing this through.

On January 15, 2021 at 1:15:39 PM EST (b)(6) @state.gov> wrote:
I clear the first edit but not the second

~~SENSITIVE BUT UNCLASSIFIED~~

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David <(b)(6) @state.gov>
Sent: Friday, January 15, 2021 12:34 PM
To: (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>
Cc: Eckels-Currie, Kelley <(b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Biegun, Stephen E <BiegunSE@state.gov>; (b)(6) @state.gov>; Keshap, Atul

(b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>
Subject: RE: Wuhan statement

(b)(6) Morgan -- sorry, just two fly-specking further edits in the attached.

(b)(5) Deliberative Process

Thanks.

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David
Sent: Friday, January 15, 2021 12:17 PM
To: (b)(6) @state.gov>
Cc: Eckels-Currie, Kelley (b)(6) @state.gov>; (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Biegun, Stephen E (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>
Subject: RE: Wuhan statement

Good for EAP, thanks.

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6) @state.gov>
Sent: Friday, January 15, 2021 12:13 PM
To: Feith, David (b)(6) @state.gov>
Cc: Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(5) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Biegun, Stephen E (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>
Subject: RE: Wuhan statement

Back to you. I concur with Miles (b)(5) Deliberative Process
(b)(5) That language is fine; see where I inserted.

Clear on my end with these edits.

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Friday, January 15, 2021 11:52 AM
To: (b)(6) @state.gov>
Cc: Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R

(b)(6) @state.gov>; Biegun, Stephen E (b)(6) @state.gov>; (b)(6)
(b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>
Subject: RE: Wuhan statement

(b)(6) - as discussed, I understand that D (who is CC'ed) gave A/S Stilwell the thumbs up on this statement.

So attached is the Public Statement Decision Memo with track-changes reflecting what's happened since you last saw. The tweaks in the yellow text are from DNI, and the tweaks on the military section come from T/Billingslea.

For reference, I'm also attaching a clean version separately.

Thanks for everyone's work here.

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6) @state.gov>
Sent: Thursday, January 14, 2021 6:06 AM
To: Feith, David (b)(6) @state.gov>
Cc: Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Biegun, Stephen E (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>
Subject: Re: Wuhan statement

Ok. Please let me know when there's a final draft to review. Thank you.
Sent from my iPhone

On Jan 14, 2021, at 12:20 AM, Feith, David (b)(6) @state.gov> wrote:

(b)(6) thanks. Attached is updated text reflecting the latest input from DNI (see yellow text especially) and T/Amb Billingslea (see section on WIV military ties).

D staff indicated that D will review in the morning.

All best,
David

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 9:52 PM
To: Feith, David (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell,

David R (b)(6) @state.gov>; Biegun, Stephen E (b)(6) @state.gov>
Subject: Re: Wuhan statement

Checking in. What is the status of this statement, and were there any suggested changes from interagency? Thank you.
Sent from my iPhone

On Jan 13, 2021, at 3:09 PM, (b)(6) @state.gov> wrote:

Sounds good, thank you David

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 3:09 PM
To: (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Many thanks (b)(6) received. We're coordinating with DNI (which has required a language tweaks that you'll see) and on clearances. Will come back to you with subsequent changes.

Thanks again --

~~SENSITIVE BUT UNCLASSIFIED~~

From: Kissel, Mary E (S) (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 1:47 PM
To: Feith, David (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Reattaching edit to ensure it goes through.

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6)
Sent: Wednesday, January 13, 2021 1:46 PM
To: Feith, David (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles <YuMM@state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Back to you. Please see redlined edits. The clearances aren't marked at the bottom of the page. Please send me the final drat when it has been cleared. The order is: bureau, me, SPOX, S.

A few notes:

(b)(5) Deliberative Process

One question for you in CAPS, in the text.

Again, if there are any subsequent changes, I need to read and clear before it goes to SPOX and S.

Thank you!

Best,
(b)(6)

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 12:38 PM
To: (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Yes, thanks, re-attached here with some small tweaks to memo background language. Thanks.

EAP meanwhile is finalizing coordination with DNI.

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 12:14 PM
To: Feith, David (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Great. Is this the final draft you want me to clear?

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 11:55 AM
To: Eckels-Currie, Kelley (b)(6) @state.gov>; (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>; Ortagus, Morgan D (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Subject: RE: Wuhan statement

Kelley, thanks for the great edits and the call.

Please see attached as discussed, which I've cleaned up but with highlights of the key areas we discussed. (It also keeps the yellow highlight in and adds green to a phrase that may need (b)(review but should work.)

+ A/S, Morgan.

Thanks all.

~~SENSITIVE BUT UNCLASSIFIED~~

From: Eckels-Currie, Kelley (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 10:56 AM
To: Feith, David (b)(6) @state.gov>; (b)(6) @state.gov>; Yu, Miles (b)(6) @state.gov>
Cc: Buangan, Richard L (b)(6) @state.gov>
Subject: Re: Wuhan statement

David

(b)(5) Deliberative Process

See attached raising these points and with a few line edits. Happy to discuss further when I'm in the office.

Thanks
K

Kelley E. Currie
Ambassador-at-Large
Secretary's Office of Global Women's Issues (S/GWI)
Department of State
Washington DC 20520
(b)(6)

From: Feith, David (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 7:39:03 AM
To: (b)(6) @state.gov>; Yu, Miles <(b)(6) @state.gov>
Cc: Eckels-Currie, Kelley (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Subject: Re: Wuhan statement

Many thanks all. The (b)(6) and Kelley versions are both strong, and I imagine a marriage of them can work well. Just two flags as we proceed, (b)(5) Deliberative

(b)(5) Deliberative Process

Thanks again all, really appreciate everyone's collaboration here in difficult circumstances.

+ Richard.

--
David Feith
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
(b)(6)
(b)(6) @state.gov
On January 13, 2021 at 7:21:02 AM EST (b)(6) @state.gov> wrote:

Good morning... Please marry this to the EAP statement I edited and provided extensive comments on last night, and send me whatever final draft you want me to clear. Please coordinate with Richard so we don't hVe multiple versions floating around. Thank you!
Sent from my iPhone

On Jan 13, 2021, at 6:41 AM, Yu, Miles (b)(6) @state.gov> wrote:
This is much better. I can live with this version.

Dr. M Miles Yu
Office of the Secretary
Department of State
Washington. DC
(b)(6)

Send from my iPhone

On Jan 13, 2021, at 1:34 AM, Eckels-Currie, Kelley(b)(6) @state.gov> wrote:

Take a look at the attached. There's still some duplicative language in here, but I want to get your feedback on the overall approach.
K

Kelley E. Currie
Ambassador-at-Large
Secretary's Office of Global Women's Issues (S/GWI)
Department of State
Washington DC 20520
(b)(6)

<COVID declass draft S statement MY DF CB.docx>
<EAP Declass Memo 01 13 master.docx>

Sender: "Feith, David" (b)(6))state.gov>

Recipient: Ortagus, Morgan D (b)(6))@state.gov>;
(b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
(b)(6) @state.gov>;
(b)(6) @state.gov>

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

EAP: David R. Stilwell [DRS]

Drafted: EAP Front Office

Clearances:
S: (b)(6) (ok)
EAP/FO: Atul Keshap (ok)
EAP/FO: David Feith (ok)
EAP/FO: Richard Buangan (ok)
EAP/FO: Jonathan Fritz (ok)
D: (b)(6) (ok)
P: (b)(6) (ok)
T: Marshall Billingslea (ok)
S/P: Miles Yu (ok)
SPOX: Morgan Ortagus (ok)
DNI (b)(6) (ok)
DOD (b)(6) (ok)

From: "Feith, David"
To: (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
CC: Stilwell, David R (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: RE: Urgent HHS statement for review
Date: Fri, 4 Dec 2020 22:02:55 +0000

(b)(6) here attached with an additional edit if possible.

Do we know who at HHS is running point on this?

Thanks.

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 2:08 PM
To: Buangan, Richard L (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>
Cc: Stilwell, David R (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: Re: Urgent HHS statement for review

Roger.

From: Buangan, Richard L (b)(6) @state.gov>
Sent: Friday, December 4, 2020 2:00 PM
To: Feith, (b)(6) @state.gov>
Cc: (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: Re: Urgent HHS statement for review

We're good with Feith's edits. Stilwell is talking for about one more hour. Move it forward.

Richard L. Buangan
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)

U.S. Department of State
Email (b)(6) @state.gov

On Dec 4, 2020, at 12:53, Feith, David (b)(6) @state.gov> wrote:

Many thanks. Please see edits in track-changes attached. Also clean copied here for the traveling party:

State/EAP edits to draft HHS statement
December 4, 2020

(b)(5) Deliberative Process

(b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:28 PM
To: Feith, David (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul <(b)(6) @state.gov>
Subject: Re: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Standing by and waiting for your edits/comments.

(b)(

From: Feith, David (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:26 PM
To: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: RE: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Hi all – please confirm we are not/not sending EAP clearance on this yet. Thanks.

From: Feith, David
Sent: Friday, December 4, 2020 1:11 PM
To: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: RE: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Seeing this now, will send suggestions in a minute --

From: Stilwell, David R (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:06 PM
To: (b)(6) @state.gov>
Cc: Fritz, Jonathan D <(b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: Re: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Good. There's some great reporting out of Taiwan on this topic. Can we point them to TACRO?

Get Outlook for iOS

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 11:30:57 AM
To: Stilwell, David R <(b)(6) @state.gov>
Cc: Fritz, Jonathan D <(b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

A/S Stilwell,
Please see the statement below in response to the WSJ article that PRC is using to claim COVID did not start in Wuhan. CM has made edits below in yellow.

Apologies for the short fuse. Would appreciate your earliest clearance so that we can get our edits in.

Thank you,

(b)(6)

(b)(5) Deliberative Process

(b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 12:13 PM
To: (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: EAP-Press <EAP-Press@state.gov>
Subject: RE: FOR (b)(6) CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Clear for CM. FO should see this one – recommend including Feith when you send it up to Buangan and Fritz.

(b)(6)
Director, Office of Chinese and Mongolian Affairs
Bureau of East Asian and Pacific Affairs
(b)(6) @@state.gov
(b)(6)

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 12:04 PM

To: (b)(6) @state.gov>; EAP-CM-Global-DL <EAP-CM-Global-DL@state.gov>; EAP-CM-Bilat Unit-DL <EAPCMBilatUnit@state.gov>; EAP-CM-ECON-DL <EAP-CM-ECON-DL@state.gov>
Cc: EAP-Press <EAP-Press@state.gov>
Subject: Re: CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

H (b)(6)

Some edits for CM/Econ below in yellow highlights. Since the CDC study was about cases before the President stopped travel from China, it does not show how that helped as implied in the third paragraph.

(b)(6)

Environment, Science, Technology, and Health Officer

Office of Chinese and Mongolian Affairs

U.S. Department of State

(b)(6)

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 10:16 AM
To: EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; IO-Press-DL <IO-Press-DL@state.gov>
Cc: OES-PA-DG <OES-PA-DG@state.gov>
Subject: 11:30 AM: Urgent HHS statement for review

Hello, please see HHS reactive statement below in response to the WSJ article that China is using to claim COVID did not start in Wuhan. I would appreciate your comments/clearance by 11:30.

Thank you.

(b)(6)

OES/PPO

****

The draft reactive statement below is in response to the WSJ article that China is using to claim COVID did not start in Wuhan. Once HHS comments have been received, it will go to State Dept for review.

https://www.wsj.com/articles/covid-19-likely-in-u-s-in-mid-december-2019-cdc-scientists-report-11606782449

(b)(5) Deliberative Process

(b)(5) Deliberative Process

Sender: "Feith, David"

Recipient: (b)(6) @state.gov>;
Buangan, Richard (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
EAP-Press <EAP-Press@state.gov>;
(b)(6) @state.gov>;
Keshap, Atul (b)(6) @state.gov>

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

From: "Asher, David" (b)(6) @state.gov>
To: Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) state.gov>; Gross, Laura J (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Paulopol, Andreea I (b)(6) @state.gov>
CC: (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Re: SBU COVID Timeline v06
Date: Tue, 29 Dec 2020 14:50:59 +0000

We don't lack unclassified evidence due to the timeline—it is more than sufficient to address Laura's concerns about evidence (b)(5) Deliberative Process

(b)(5) Deliberative Process

I'll been in the SCIF around 1130.

Hope everyone had a wonderful holiday.

David

From: Gibbs, Jeffrey J (b)(6) @state.gov>
Sent: Tuesday, December 29, 2020 9:36 AM
To: (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Paulopol, Andreea I (b)(6) @state.gov>
Cc: (b)(6) @state.gov>; (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>
Subject: Re: SBU COVID Timeline v06

Thanks, (b)(6 Great work - very helpful.

Jeff Gibbs
Senior Adviser AVC
SSD/AVC
(b)(6)

From: (b)(6) @state.gov>
Sent: Monday, December 28, 2020 7:01 PM
To: DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; (b)(6) <(b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; Paulopol, Andreea I (b)(6) @state.gov>
Cc: (b)(6) @state.gov>; (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>
Subject: SBU COVID Timeline v06

Attached FYI: I have updated the SBU version of the timeline to format it to print on legal size paper with page numbering (all tabs). As previously mentioned to some, it contains 606 unique excerpts from 1985 to 11/11/2020. Along with the complete timeline (first/red tab), I have extracted several thematic timelines which you can find in the tabs to the right. In order left to right they are labeled:

- "Censorship of health info"
- "Delayed admitting human xmsn"
- "Limited, false, delayed reporting"
- "Exporting the virus"
- "Catastrophic missteps"
- "Efforts to counter lab hypthsis"
- "WHO as PRC cheerleader"
- "GOF research"
- "Handling lethal pathogens"
- "Poor safety, lab leak history"
- "US offers of support"

(b)(6)

PS: As of tomorrow, I will only be reachable via this email and my cell (b)(6) until the 6th.

(b)(6)
Bureau of Arms Control, Verification and Compliance
US Department of State
(b)(6)
NSTS: (b)(6) *(NSTS)*
JWICS: (b)(6) *@state.ic.gov*
SIPR (b)(6) *@state.sgov.gov*

~~SENSITIVE BUT UNCLASSIFIED~~

Sender: "Asher, David" (b)(6) @state.gov>
Recipient: Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; (b)(6) <(b)(6) @state.gov>; Paulopol, Andreea I (b)(6) @state.gov>;

(b)(6) @state.gov>;
(b)(6) @state.gov>

From: "Keshap, Atul" (b)(6) @state.gov>

To: Feith, David (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>;
(b)(6) @state.gov>;
(b)(6) @state.gov>

Subject: RE: Peter Daszak, RaTG13, and "the freezer"

Date: Mon, 4 Jan 2021 19:53:38 +0000

And this guy is on the WHO investigative team? I look forward to their report, which will no doubt praise the WIV and the PRC for exemplary stewardship of the health of the human species.

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David (b)(6) @state.gov>
Sent: Monday, January 4, 2021 2:49 PM
To: Stilwell, David R (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Peter Daszak, RaTG13, and "the freezer"

Peter Daszak -- CEO of the USG-funded EcoHealth Alliance, longtime close collaborator with the WIV, and now member of the WHO investigative team – told Wired in February that the WIV had effectively done no work on RaTG13 over the years, after finding it in a cave in Yunnan in 2013 following the death of several miners with SARS-like symptoms. "We were looking for SARS-related virus, and this one was 20 percent different. We thought it was interesting, but not high risk. So we didn't do anything about it and put it in the freezer." (https://www.wired.co.uk/article/coronavirus-bats-snakes-pangolins)

Well, not exactly. We now know from various sources -- including some of the WIV's own online records that have since been scrubbed -- that the WIV did work with RaTG13 over the years.

From NY Mag today: "Of the fragmentary bits of virus Shi retrieved from the mine shaft, one was SARS-like, and Shi sequenced it and called it BtCoV/4991 and published a paper about it. Several times — in 2016 and 2018 and 2019 — this most interesting sample, a portion of what we now know as RaTG13, was taken out of the freezers in Shi's lab and worked on in undisclosed ways. (Peter Daszak claims that these samples have disintegrated and can't be validated or studied.) Samples of the nameless human disease also traveled back to the Wuhan Institute of Virology — few specifics about these valuable specimens have been released by Chinese sources, however."
(https://nymag.com/intelligencer/article/coronavirus-lab-escape-theory.html)

As discussed, Daszak has been supported by scores of millions of dollars of USG funding. The NY Mag article, by the way, takes a direct shot at Daszak's whole operation: "We need to stop hunting for new exotic diseases in the wild, shipping them back to laboratories, and hot-wiring their genomes to prove how dangerous to human life they might become."

Recall the Upton Sinclair line: "It is difficult to get a man to understand something, when his salary depends on his not understanding it."

--
David Feith
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
(b)(6) (o)
(c)
(b)(6) @state.gov

~~SENSITIVE BUT UNCLASSIFIED~~

Sender: "Keshap, Atul" (b)(6) @state.gov>

Recipient: Feith, David (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>;
(b)(6) @state.gov>;
(b)(6) @state.gov>

From: (b)(6) @state.gov>
To: Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: RE: Major Taiwan News of COV19 origins at WIV.....
Date: Tue, 12 Jan 2021 13:01:51 +0000

It certainly adds to the growing unclassified circumstantial case – almost to the point where "there are too many circumstances for it to be circumstantial".

From: Gibbs, Jeffrey J (b)(6) @state.gov>
Sent: Tuesday, January 12, 2021 7:54 AM
To: (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Re: Major Taiwan News of COV19 origins at WIV.....

(b)(5) Deliberative Process

Jeff Gibbs
Senior Adviser AVC
SSD/AVC
(b)(6)

From: Feith, David (b)(6) @state.gov>
Sent: Monday, January 11, 2021 9:40 PM
To: David Asher (b)(6) @hudson.org>
Cc: (b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Re: Major Taiwan News of COV19 origins at WIV.....

Thanks. Sure is interesting, Hu Ben and the rest.

--
David Feith
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
(b)(6)
(b)(6) @state.gov

On January 11, 2021 at 9:32:16 PM EST, David Asher (b)(6) @hudson.org> wrote:

David, See note below from perceptive Professor Muller. Enjoy Taipei and please get the whole story of this. As suspected Taipei knows a lot more. Now that we treat them normally a lot more will come out. David PS- Note "Hu Ben." Dr. Strangelove's Chinese bio cousin. Dasic, Baric, et al. Wow.

David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW
Fourth Floor
Washington, DC 20004
(b)(6)
https://www.hudson.org/experts/1299-david-asher

Begin forwarded message:

From: Richard Muller (b)(6) @gmail.com>
Date: January 11, 2021 at 21:11:17 EST
To: David Asher <(b)(6) @vitalfin.com>
Subject: Taiwan News

Dave

This article is must be devastating to the GOF community. The fact that the WIV was infected humanized mice with bat coronavirus — that's something that the public can easily understand, easier than "gain of function". This article names names, including Daszak and Baric.

I'm guessing that this is one of the things you knew about but couldn't tell me.

Rich

<Taiwan News Wuhan lab infected 'humanized mice' with bat coronaviruses in 2019 _ Taiwan News _ 2021_01_11.pdf>

Sender: (b)(6) (b)(6) @state.gov>

Recipient: Gibbs, Jeffrey J <(b)(6) @state.gov>; (b)(6) @state.gov>

From: "Fritz, Jonathan D" (b)(6) @state.gov>
To: Feith, David (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Re: Major Taiwan News of COV19 origins at WIV.....
Date: Tue, 12 Jan 2021 03:34:22 +0000

Wow. The wave is building.

Get Outlook for iOS
From: Feith, David (b)(6) @state.gov>
Sent: Monday, January 11, 2021 9:55:17 PM
To: Stilwell, David R (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>
Subject: Fwd: Major Taiwan News of COV19 origins at WIV.....

---------- Forwarded message ----------

From: David Asher (b)(6) @hudson.org>
Date: January 11, 2021 at 9:32:16 PM EST
Subject: Major Taiwan News of COV19 origins at WIV.....
To: Feith, David (b)(6) @state.gov>
Cc: (b)(6) (b)(6) @state.gov>,Gibbs, Jeffrey J (b)(6) @state.gov>,DiNanno, Thomas G (b)(6) @state.gov>,Yu, Miles (b)(6) @state.gov>(b)(6) (b)(6) @state.gov>(b)(6) @state.gov>(b)(6) (b)(6) @state.gov>

David, See note below from perceptive Professor Muller. Enjoy Taipei and please get the whole story of this. As suspected Taipei knows a lot more. Now that we treat them normally a lot more will come out. David PS- Note "Hu Ben." Dr. Strangelove's Chinese bio cousin. Dasic, Baric, et al. Wow.

David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW

Fourth Floor
Washington, DC 20004
(b)(6)
https://www.hudson.org/experts/1299-david-asher

Begin forwarded message:

From: Richard Muller (b)(6) @gmail.com>
Date: January 11, 2021 at 21:11:17 EST
To: David Asher (b)(6) @vitalfin.com>
Subject: Taiwan News

Dave

This article is must be devastating to the GOF community. The fact that the WIV was infected humanized mice with bat coronavirus — that's something that the public can easily understand, easier than "gain of function". This article names names, including Daszak and Baric.

I'm guessing that this is one of the things you knew about but couldn't tell me.

Rich

Sender: "Fritz, Jonathan D" (b)(6) @state.gov>
Recipient: Feith, David (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
Keshap, Atul (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>;
(b)(6) @state.gov>

From: "DiNanno, Thomas G" (b)(6) @state.gov>
To: (b)(6) (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>
CC: (b)(6) @state.gov>
Subject: Re: Fwd: Draft cable to China on consultations under Article V of the BWC
Date: Sat, 26 Dec 2020 23:11:29 +0000

(b)(6)

Can you come back to us as to when you can review or if you have further thoughts. I'd like to get cable out for review ASAP. Sorry understand it's a holiday weekend.
Thx
TD

On December 26, 2020 at 3:08:50 PM EST, DiNanno, Thomas G (b)(6) @state.gov> wrote:
I'd leave out the edit- it's implied with the consistent with peaceful purposes language.

On December 26, 2020 at 3:04:33 PM EST, (b)(6) (b)(6) @state.gov> wrote:
Tom and (b)(6)

I need your OK to move forward. Also please let me know if David's edit is OK.

Thanks,

(b)(6)
Director, AVC/VPO
(b)(6)
(b)(6) @state.gov

From: Asher, David (b)(6) @state.gov>
Sent: Saturday, December 26, 2020 2:09 PM
To: (b)(6) DiNanno, Thomas G; (b)(6) Gibbs, Jeffrey J; (b)(
(b)(6) (b)(6)
Subject: Re: Draft cable to China on consultations under Article V of the BWC

Looks good to go.(b)(5) Deliberative Process
(b)(5) Deliberative Process

From:(b)(6) (b)(6) @state.gov>
Sent: Saturday, December 26, 2020 12:18 PM
To: DiNanno, Thomas G (b)(6) @state.gov>;(b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) @state.gov>; Asher, David(b)(6) @state.gov>;(b)(6) @state.gov>
Subject: Draft cable to China on consultations under Article V of the BWC

Attached is a clean copy of the BWC cable to China that reflects edits and comments received as of now. Please review this and let me know ASAP if you have other edits. Per Tom's direction, I plan to circulate this today.

Thanks,

(b)(6)
Director, Verification, Planning, and Outreach
Currently Teleworking

Sender: "DiNanno, Thomas G"(b)(6) @state.gov>
Recipient: (b)(6) (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; (b)(6) @state.gov>

From: "Feith, David"
To: Stilwell, David R (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>
CC: (b)(6) @state.gov>
Subject: Re: FW: FW: WP: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses
Date: Tue, 14 Apr 2020 21:28:47 +0000

He's got personal background and network on ties between Galveston and Wuhan Institute. He could shed light on what happened Jan. 24 when Beijing prevented Wuhan Institute from sharing some info with Galveston. And possibly other such things.

(b)(5) Deliberative Process

--
David Feith
Senior Advisor
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
(b)(6)
(b)(6) @state.gov

On April 14, 2020 at 5:26:38 PM EDT, Stilwell, David R (b)(6) @state.gov> wrote:
Do we want to talk to LeDuc? (b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Tuesday, April 14, 2020 5:23 PM
To: Stilwell, David R (b)(6) @state.gov>
Subject: Re: FW: WP: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Dave,
Below were the speakers.

Kristian Andersen, Associate Professor, Department of Immunology and Microbiology, Scripps Research

James LeDuc, Director of the Galveston National Laboratory, The University of Texas Medical Branch

Jay Schnitzer, VP and CTO, MITRE Corporation.

Best,(b)(6)

Sent from Workspace ONE Boxer
On April 14, 2020 at 5:13:21 PM EDT, Stilwell, David R (b)(6) @state.gov> wrote:
(b)(6)
What was the name of the researcher from Texas who spoke about his personal involvement with the Wuhan Institute of Virology? We're taking questions on this article.
Thanks
Dave

The Chinese researchers at WIV were receiving assistance from the Galveston National Laboratory at the University of Texas Medical Branch and other U.S. organizations, but the Chinese requested additional help. The cables argued that the United States should give the Wuhan lab further support, mainly because its research on bat coronaviruses was important but also dangerous.

From: Buangan, Richard L (b)(6) @state.gov>
Sent: Tuesday, April 14, 2020 7:15 AM
To: Stilwell, David R (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; Fritz, Jonathan D (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) (Beijing) (b)(6) @state.gov>; (b)(6) (Shenyang) (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Fwd: WP: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Rogin's piece is out.

State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Josh Rogin

Two years before the novel coronavirus pandemic upended the world, U.S. Embassy officials visited a Chinese research facility in the city of Wuhan several times and sent two official warnings back to Washington about inadequate safety at the lab, which was conducting risky studies on coronaviruses from bats. The cables have fueled discussions inside the U.S. government about whether this or another Wuhan lab was the source of the virus — even though conclusive proof has yet to emerge.

In January 2018, the U.S. Embassy in Beijing took the unusual step of repeatedly sending U.S. science diplomats to the Wuhan Institute of Virology (WIV), which had in 2015 become China's first laboratory to achieve the highest level of international bioresearch safety (known as BSL-4). WIV issued a news release in English about the last of these visits, which occurred on March 27, 2018. The U.S. delegation was led by Jamison Fouss, the consule general in Wuhan, and Rick Switzer, the embassy's counselor of environment, science, technology and health. Last week, WIV erased that statement from its website, though it remains archived on the Internet.

What the U.S. officials learned during their visits concerned them so much that they dispatched two diplomatic cables categorized as Sensitive But Unclassified back to Washington. The cables warned about safety and management weaknesses at the WIV lab and proposed more attention and help. The first cable, which I obtained, also warns that the lab's work on bat coronaviruses and their potential human transmission represented a risk of a new SARS-like pandemic."During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory," states the Jan. 19, 2018, cable, which was drafted by two officials from the embassy's environment, science and health sections who met with the WIV scientists. (The State Department declined to comment on this and other details of the story.)

The Chinese researchers at WIV were receiving assistance from the Galveston National Laboratory at the University of Texas Medical Branch and other U.S. organizations, but the Chinese requested additional help. The cables argued that the United States should give the Wuhan lab further support, mainly because its research on bat coronaviruses was important but also dangerous.

As the cable noted, the U.S. visitors met with Shi Zhengli, the head of the research project, who had been publishing studies related to bat coronaviruses for many years. In November 2017, just before the U.S. officials' visit, Shi's team had published research showing that horseshoe bats they had collected from a cave in Yunnan province were very likely from the same bat population that spawned the SARS coronavirus in 2003.

"Most importantly," the cable states, "the researchers also showed that various SARS-like coronaviruses can interact with ACE2, the human receptor identified for SARS-coronavirus. This finding strongly suggests that SARS-like coronaviruses from bats can be transmitted to humans to cause SARS-like diseases. From a public health perspective, this makes the continued surveillance of SARS-like coronaviruses in bats and study of the animal-human interface critical to future emerging coronavirus outbreak prediction and prevention."

The research was designed to prevent the next SARS-like pandemic by anticipating how it might emerge. But even in 2015, other scientists questioned whether Shi's team was taking unnecessary risks. In October 2014, the U.S. government had imposed a moratorium on funding of any research that makes a virus more deadly or contagious, known as "gain-of-function" experiments.

As many have pointed out, there is no evidence that the virus now plaguing the world was engineered; scientists largely agree it came from animals. But that is not the same as saying it didn't come from the lab, which spent years testing bat coronaviruses in animals, said Xiao Qiang, a research scientist at the School of Information at the University of California at Berkeley.

"The cable tells us that there have long been concerns about the possibility of the threat to public health that came from this lab's research, if it was not being adequately conducted and protected," he said.

There are similar concerns about the nearby Wuhan Center for Disease Control and Prevention lab, which operates at biosecurity level 2, a level significantly less secure than the level-4 standard claimed by the Wuhan Insititute of Virology lab, Xiao said. That's important because the Chinese government still refuses to answer basic questions about the origin of the novel coronavirus while suppressing any attempts to examine whether either lab was involved.

Sources familiar with the cables said they were meant to sound an alarm about the grave safety concerns at the WIV lab, especially regarding its work with bat coronaviruses. The embassy officials were calling for more U.S. attention to this lab and more support for it, to help it fix its problems.

"The cable was a warning shot," one U.S. official said. "They were begging people to pay attention to what was going on."

No extra assistance to the labs was provided by the U.S. government in response to these cables. The cables began to circulate again inside the administration over the past two months as officials debated whether the lab could be the origin of the pandemic and what the implications would be for the U.S. pandemic response and relations with China.

Inside the Trump administration, many national security officials have long suspected either the WIV or the Wuhan Center for Disease Control and Prevention lab was the source of the novel coronavirus outbreak. According to the New York Times, the intelligence community has provided no evidence to confirm this. But one senior administration official told me that the cables provide one more piece of evidence to support the possibility that the pandemic is the result of a lab accident in Wuhan.

"The idea that is was just a totally natural occurrence is circumstantial. The evidence it leaked from the lab is circumstantial. Right now, the ledger on the side of it leaking from the lab is packed with bullet points and there's almost nothing on the other side," the official said.

As my colleague David Ignatius noted, the Chinese government's original story — that the virus emerged from a seafood market in Wuhan — is shaky. Research by Chinese experts published in the Lancet in January showed the first known patient, identified on Dec. 1, had no connection to the market, nor did more than one-third of the cases in the first large cluster. Also, the market didn't sell bats.

Shi and other WIV researchers have categorically denied this lab was the origin for the novel coronavirus. On Feb. 3, her team was the first to publicly report the virus known as 2019-nCoV was a bat-derived coronavirus.

The Chinese government, meanwhile, has put a total lockdown on information related to the virus origins. Beijing has yet to provide U.S. experts with samples of the novel coronavirus collected from the earliest cases. The Shanghai lab that published the novel coronavirus genome on Jan. 11 was quickly shut down by authorities for "rectification." Several of the doctors and journalistswho reported on the spread early on have disappeared.

On Feb. 14, Chinese President Xi Jinping called for a new biosecurity law to be accelerated. On Wednesday, CNN reported the Chinese government has placed severe restrictions requiring approval before any research institution publishes anything on the origin of the novel coronavirus.

The origin story is not just about blame. It's crucial to understanding how the novel coronavirus pandemic started because that informs how to prevent the next one. The Chinese government must be transparent and answer the questions about the Wuhan labs because they are vital to our scientific understanding of the virus, said Xiao.

We don't know whether the novel coronavirus originated in the Wuhan lab, but the cable pointed to the danger there and increases the impetus to find out, he said.
"I don't think it's a conspiracy theory. I think it's a legitimate question that needs to be investigated and answered," he said. "To understand exactly how this originated is critical knowledge for preventing this from happening in the future."

Sender: "Feith, David"

Recipient: Stilwell, David R (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
(b)(6) @state.gov>

From: "Asher, David" (b)(6) @state.gov>
To: Stilwell, David R <(b)(6) @state.gov>
CC: Feith, David <(b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>
Subject: Re: Federal Grants and Contracts Awarded to EcoHealth Alliance
Date: Sun, 3 Jan 2021 20:56:59 +0000

You need to see this tweet translating a CCP expert on TV discussing genetic warfare from 2016.
https://twitter.com/G_Translators6/status/1345515712593457153?s=09

From: Stilwell, David R (b)(6) @state.gov>
Sent: Saturday, December 19, 2020 6:45 PM
To: Asher, David <(b)(6) @state.gov>
Cc: Feith, David (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>; (b)(6) <(b)(6) @state.gov>
Subject: RE: Federal Grants and Contracts Awarded to EcoHealth Alliance

David
This is excellent.

(b)(5) Deliberative Process

Best
Dave

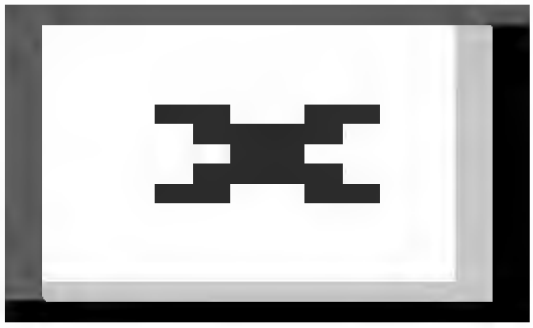
From: Asher, David (b)(6) @state.gov>
Sent: Thursday, December 17, 2020 6:58 PM
To: Stilwell, David R <(b)(6) @state.gov>
Cc: Feith, David (b)(6) @state.gov>; Keshap, Atul <(b)(6) @state.gov>; (b)(6) <(b)(6) @state.gov>
Subject: Fw: Federal Grants and Contracts Awarded to EcoHealth Alliance

If you want a glance at how much U5G money was going to support PRC gain of function research on COVID/SARS via the "Eco Health alliance," see attached. This smells of a UFD link to me as well....

EcoHealth Alliance Orchestrated Key Scientists' Statement on "natural origin" of SARS-CoV-2

by Sainath Suryanarayanan of U.S. Right to Know

Emails obtained by U.S. Right to Know show that a statement in *The Lancet* authored by 27 prominent public health scientists condemning "conspiracy theories suggesting that COVID-19 does not have a natural origin" was organized by employees of EcoHealth Alliance, a non-profit group that has received millions of dollars of U.S. taxpayer funding to genetically manipulate coronaviruses with scientists at the Wuhan Institute of Virology.



Peter Daszak of the Ecohealth Alliance

The emails obtained via public records requests show that EcoHealth Alliance President Peter Daszak drafted the *Lancet* statement, and that he intended it to "not be identifiable as coming

from any one organization or person" but rather to be seen as "simply a letter from leading scientists". Daszak wrote that he wanted "to avoid the appearance of a political statement". The scientists' letter appeared in *The Lancet* on February 18, just one week after the World Health Organization announced that the disease caused by the novel coronavirus would be named COVID-19.

The 27 authors "strongly condemn[ed] conspiracy theories suggesting that COVID-19 does not have a natural origin," and reported that scientists from multiple countries "overwhelmingly conclude that this coronavirus originated in wildlife." The letter included no scientific references to refute a lab-origin theory of the virus. One scientist, Linda Saif, asked via email 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 occuring? Seems critical to scientifically refute such claims!" Daszak responded, "I think we should probably stick to a broad statement."

Growing calls to investigate the Wuhan Institute of Virology as a potential source of SARS-CoV-2 have led to increased scrutiny of EcoHealth Alliance. The emails show how members of EcoHealth Alliance played an early role in framing questions about possible lab origin of SARS-CoV-2 as "crackpot theories that need to be addressed," as Daszak told *The Guardian*.

Although the phrase "EcoHealth Alliance" appeared only once in *The Lancet* statement, in association with co-author Daszak, several other co-authors also have direct ties to the group that were not disclosed as conflicts of interest. Rita Colwell and James Hughes are members of the Board of Directors of EcoHealth Alliance, William Karesh is the group's Executive Vice President for Health and Policy, and Hume Field is Science and Policy Advisor.

The statement's authors also claimed that the "rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins." Today, however, little is known about the origins of SARS-CoV-2, and investigations into its origins by the World Health Organization and *The Lancet* COVID-19 commission have been shrouded in secrecy and mired by conflicts of interests.

Peter Daszak, Rita Colwell, and *The Lancet* Editor Richard Horton did not provide comments in response to our requests for this story.

This article is reprinted from the website of US Right to Know.

For more information:

A link to the entire batch of EcoHealth Alliance emails can be found here: **EcoHealth Alliance emails: University of Maryland** (466 pages)

From: (b)(6) <(b)(6) @state.gov>
Sent: Thursday, December 17, 2020 7:40 AM
To: DiNanno, Thomas G <(b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) N <(b)(6) @state.gov>
Cc: (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>
Subject: Federal Grants and Contracts Awarded to EcoHealth Alliance

Attached is a formatted listing of federal grant and contract data for EcoHealth Alliance, sorted by agency and period of performance start. DoD awards records are highlighted.

Note:

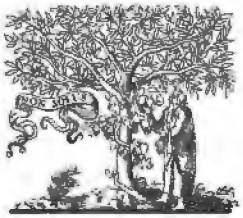
- All but one of the DoD grants to EcoHealth Alliance grants were for "SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION". Most grants were awarded by DTRA.
- All of the DoD contracts for EcoHealth Alliance were awarded by DTRA.
- The latest $4.9M DoD contract for EcoHealth Alliance was terminated for cause in June.

Complete raw data CSV files also available. Source:
https://www.usaspending.gov/keyword_search/%22ecohealth%20alliance%22

(b)(6)
Bureau of Arms Control, Verification and Compliance
US Department of State
(b)(6)
JWICS (b)(6) *@state.ic.gov*
SIPR (b)(6) *@state.sgov.gov*

Sender: "Asher, David" (b)(6) @state.gov>

Recipient: Stilwell, David R (b)(6) @state.gov>;
Feith, David (b)(6) @state.gov>;
Keshap, Atul (b)(6) @state.gov>;
(b)(6) @state.gov>;
DiNanno, Thomas G (b)(6) @state.gov>;
Gibbs, Jeffrey J (b)(6) @state.gov>

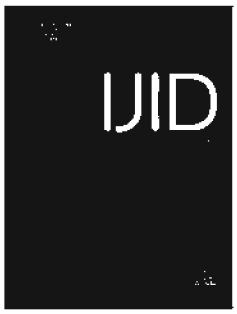


ELSEVIER

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Journal Pre-proof



High prevalence of pre-existing serological cross-reactivity against SARS-CoV-2 in sub-Sahara Africa

For Yue Tso, Salum J. Lidenge, Phoebe B. Peña, Ashley A. Clegg, John R. Ngowi, Julius Mwaiselage, Owen Ngalamika, Peter Julius, John T. West, Charles Wood

PII: S1201-9712(20)32310-9

DOI: https://doi.org/10.1016/j.ijid.2020.10.104

Reference: IJID 4826

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Accepted Date: 31 October 2020

Please cite this article as: { doi: https://doi.org/

High prevalence of pre-existing serological cross-reactivity against SARS-CoV-2 in sub-Sahara Africa

For Yue Tso[a,b], Salum J. Lidenge[a,b,d,e], Phoebe B. Peña[a,b], Ashley A. Clegg[a,b], John R. Ngowi[d], Julius Mwaiselage[d,e], Owen Ngalamika[f], Peter Julius[g], John T. West[a,c] and Charles Wood[a,b,c,*].

[a]Nebraska Center for Virology, Lincoln, NE, USA

[b]School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA

[c]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE, USA

[d]Ocean Road Cancer Institute, Dar es Salaam, Tanzania

[e]Muhimbili University of Health and Allied Sciences, Dar es Salaam, Tanzania

[f]Dermatology and Venereology Section, University Teaching Hospitals, University of Zambia School of Medicine, Lusaka, Zambia

[g]Department of Pathology and Microbiology, University of Zambia School of Medicine, Lusaka, Zambia

[*]Corresponding author: Charles Wood, cwood1@unl.edu. Nebraska Center for Virology, 4240 Fair Street, East Campus, Lincoln, Nebraska 68583-0900.

Highlights

- High prevalence of serological cross-reactivity against SARS-CoV-2 in pre-COVID-19 pandemic plasma samples from sub-Sahara Africa.
- Pre-COVID-19 pandemic plasma displayed strong reactivity against other human coronaviruses.
- Exposure to other coronaviruses may induce cross-reactive antibodies against SARS-CoV-2 in sub-Sahara Africa.

Abstract

Objective: Significant morbidity and mortality from SARS-CoV-2 has been experienced in America, Europe and Asia; whereas, the number of infections and deaths in sub-Sahara Africa (SSA) has remained comparatively low. One hypothesis is that population in SSA has been exposed to other coronaviruses prior to the COVID-19 pandemic and resulted in some degree of cross-protection against SARS-CoV-2 infection and pathogenesis. Our goal was to evaluate this hypothesis by comparing SARS-CoV-2 cross-reactive antibodies in pre-pandemic plasma samples collected from SSA and USA.

Method: Pre-COVID-19 pandemic plasma samples from SSA and USA were collected and tested by immunofluorescence assay against the spike and nucleocapid proteins of all known human coronaviruses (HCoV).

Results: Significantly higher prevalence of SARS-CoV-2 serological cross-reactivity was detected in samples from SSA compared to USA. Majority of these cross-reactive samples cross-recognized SARS-CoV-2 nucleocapsid protein together with recognition of spike proteins from other HCoVs. Since nucleocapsid proteins from HCoV-NL63 and HCoV-229E were detected by majority of samples, it implicates prior exposure to these two HCoVs as the likely source for cross-reactive antibodies against SARS-CoV-2.

Conclusion: Low SARS-CoV-2 infection and disease in SSA appears to correlate with pre-pandemic serological cross-recognition of HCoVs, which are substantially more prevalent in SSA than USA.

Keywords: SARS-CoV-2; COVID-19; cross-reactivity; sub-Sahara Africa; serology; human coronavirus; HCoV-NL63; HCoV-229E.

Introduction

Since the first case of the COVID-19 pandemic was reported in Wuhan, China in late 2019, its causative agent severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) has spread rapidly worldwide (Lu et al., 2020). SARS-CoV-2 is a betacoronavirus and a close relative to the original SARS and Middle East respiratory syndrome coronavirus (MERS) which both cause lethal diseases in human (Chen et al., 2020, Gussow et al., 2020). There are four other less pathogenic human coronaviruses (HCoV), HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E that cause mild upper respiratory tract disease referred to as the "common cold" (Chen et al., 2020, Gussow et al., 2020).

At the time of writing, the COVID-19 pandemic has resulted in over 31 million confirmed SARS-CoV-2 infections and nearly a million deaths, with the USA alone contributing nearly 22% of the confirmed cases and 21% of the confirmed deaths (Nuzzo et al., 2020). A number of factors would lend support to the expectation that populations in sub-Sahara Africa (SSA) might be more susceptible to coronaviral infection and disease. These include the high infectious disease burden (Ebola, yellow fever and cholera outbreaks as well as endemic high prevalence HIV-1, tuberculosis, malaria and parasitic diseases), a multiplicity of socioeconomic factors, poor hygiene and nutritional sufficiency, and lack of health care access in rural areas (Oleribe et al., 2015, Semeere et al., 2016). While infrastructure for diagnostics and epidemiological surveillance is suboptimal in Africa, where large scale testing has been possible the COVID-19 case mortality rates are lower than elsewhere in the world. There are no reports of any abnormal increase in the number of respiratory diseases or deaths – the hallmark of the COVID-19 pandemic - in SSA. Despite the high number of COVID-19 cases and case-mortality in America, Europe and Asia, the COVID-19 disease burden in SSA has remained surprisingly low (Nuzzo et al., 2020). A potential factor could be the relatively younger African populations as compared to that in America or Europe. This may result in more asymptomatic cases (Gaye et al., 2020). Additionally, if the onerous high infectious disease burden in SSA includes exposure to human coronaviruses, this could elicit humoral responses against conserved epitopes among coronaviruses that might engender cross-protection. This prior exposure to other coronaviruses may offer some level of cross-protective immune responses against SARS-CoV-2 infection, thereby, reducing either the number and/or severity of COVID-19 cases.

To investigate this hypothesis, we examined pre-COVID-19 pandemic Tanzanian, Zambian and USA plasma samples for serological cross-reactivity against the spike and

nucleocapsid proteins of SARS-CoV-2 and other human coronaviruses (SARS, MERS, HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E), as well as whether HIV-1 infection, which is endemic in SSA, could affect the prevalence of serological cross-reactive against SARS-CoV-2. We found that pre-COVID-19 pandemic sub-Saharan African samples have a significantly higher prevalence of serological cross-reactivity against SARS-CoV-2 than samples from the USA. Additionally, SARS-CoV-2 cross-reactive plasma samples strongly recognized the spike and nucleocapsid proteins from specific human seasonal coronaviruses, suggesting prior exposure to these other coronaviruses may induce partially protective responses against SAR-CoV-2.

Material and methods

Study cohort and samples

The study cohort was comprised of 289 consenting subjects, ≥18 years of age and of both genders from Dar es Salaam, Tanzania; Lusaka, Zambia; and Lincoln, Nebraska, USA. The Tanzanian samples included 105 plasma samples collected from voluntary blood donors collected between March and May of 2019. Zambian samples included 99 plasma samples collected between 2017 and early 2019. USA plasma samples were from 85 blood donors collected in 2005, 2007 and 2009 in Lincoln, Nebraska and were also evaluated for comparison. All study procedures were approved by the institutional review boards from the Tanzania National Institute for Medical Research, Ocean Road Cancer Institute, University of Zambia Biomedical Research Ethics Committee, and the University of Nebraska-Lincoln.

HIV serological testing

HIV-1 serology was determined by HIV Rapid Test Algorithm (United Republic of Tanzania, 2007) in Tanzania and Alere Determine HIV-1/2 Ag/Ab Combo test in Zambia. The serological results were verified in our lab at Lincoln, Nebraska using HIV-1-2.0 First Response kit (Premier Medical Corporation Limited, Daman, India).

Immunofluorescence assay against SARS-CoV-2 and other human coronaviruses

To detect the presence of serological cross-reactivity against SARS-CoV-2 and other human coronaviruses, we used an immunofluorescence assay (IFA) against the spike and nucleocapsid proteins of SARS, SARS-CoV-2, MERS, HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E. Briefly, HEK-293T cells (ATCC, USA) were transfected with mammalian expression plasmids encoding either the spike or nucleocapsid proteins of the respective coronaviruses (Addgene and Sino Biological, USA). After 48-hours, the transfected cells were fixed and seeded onto 12-well polytetrafluoroethylene (PTFE) printed slides (Electron Microscopy Sciences, USA) where each well contained either spike, nucleocapsid or mock transfected cells and followed by permeabilization with 0.3% H_2O_2 methanol solution. The prepared IFA slides were stored at -80°C.

Plasma samples were diluted 1:20 with PBS, 0.1% Tween-20 and incubated at room temperature for 30 minutes. The prepared IFA slides were thawed and incubated with PBS, 0.1% Tween-20 for 30 minutes at 37°C. Each diluted plasma sample was then added onto cells expressing each HCoV antigen or control wells and incubated for 1 hour at 37°C. Following primary antibody binding and washing, secondary mouse monoclonal anti-human IgG antibody (ATCC, USA) was bound for 1 hour at 37°C followed by washes to remove excess unbound antibodies. Tertiary CY2-conjugated donkey anti-mouse IgG (Jackson Immuno Research Laboratories, USA) was then added and incubated for 1 hour at 37°C. Finally, the slides were

counterstained with 0.004% Evans blue solution for 30 seconds. All IFA slides were washed three times with PBS after each incubation step. The stained IFA slides were read by three independent readers on a Nikon Eclipse 50i fluorescence microscope. Positive cells were enumerated by green fluorescence against a red cellular counterstain. A well was only considered positive or negative if at least two independent readers were concordant in reporting the outcome. Summarized results and statistical analysis (two-tailed Fishers' exact test) were conducted and plotted using GraphPad (GraphPad Software, USA).

Results

To evaluate the serological cross-reactivity against SARS-CoV-2 and other human coronaviruses, we obtained blood donor plasma samples from Tanzania (n = 105), Zambia (n = 99) and the USA (n = 85) (Table 1). These samples were collected between 2005 to May 2019 and therefore are from prior to the current COVID-19 pandemic; however, due to the retrospective nature of the study, synchronously sampled plasma were not available. Among our cohort, 6.7% and 43.4% of the Tanzania and Zambia samples, respectively, were HIV-1 positive. Whereas all plasma samples collected in the USA were HIV-1 negative. The high prevalence of HIV-1 infection in the Zambian samples does not reflect the national HIV-1 infection rates, but rather was intended to support comparison of cross-reactivity against SARS-CoV-2 and recognition of other coronaviruses between HIV-1 positive and negative subjects.

The plasma samples were screened for cross-reactivity against SARS-CoV-2 using IFA. As shown in figure 1, COVID-19 convalescent positive control plasma resulted in strong green fluorescence staining in cells expressing either SARS-CoV-2 spike or nucleocapsid proteins, but

not in mock transfected cells. There was no green fluorescence evident on antigen-expressing cells stained with negative control plasma, demonstrating the specificity of IFA to detect SARS-CoV-2 specific IgG antibodies. Interestingly, green fluorescence was evident on cells expressing either SARS-CoV-2 spike or nucleocapsid proteins when stained with some pre-COVID-19 pandemic plasma samples. This result indicates the presence of antibodies cross-reactive against SARS-CoV-2 prior to the current COVID-19 pandemic (Figure 1). Compared to samples from the USA (2.4%), the prevalence of serological cross-reactivity against SARS-CoV-2 was significantly higher in Tanzania (19%) ($P = 0.0002$) and Zambia (14.1%) ($P = 0.0069$) (Figure 2A). A breakdown of the anti-SARS-CoV-2 cross-reactivity indicates that most of the Tanzanian and Zambian cross-reactive responses targeted the SARS-CoV-2 nucleocapsid protein, 17.1% ($P = 0.0001$) and 13.1% ($P = 0.0018$), respectively, levels significantly higher than in samples from the USA 1.2% (Figure 2B). There was no statistical difference between the anti-SARS-CoV-2 spike cross-reactivity prevalence rates, with 2.9% in Tanzania, 4% in Zambia and 1.2% in USA (Figure 2C). Additionally, none of the cross-reactive samples from Tanzania are HIV-1 positive and only 5 out of 43 (11.6%) HIV-1 positive samples from Zambia were cross-reactive towards SARS-CoV-2. Whereas, 9 out of 56 (16%) HIV-1 negative samples from Zambia were cross-reactive towards SARS-CoV-2. Therefore, HIV-1 infected individuals seem to have lower cross-reactive response towards SARS-CoV-2. However, a larger sample size of an HIV-1 positive cohort will be needed to verify this observation.

To investigate whether anti-SARS-CoV-2 cross-reactivity correlated with past exposures to other human coronaviruses, pre-COVID-19 pandemic plasma samples that cross-reacted against SARS-CoV-2 were tested for their anti-HCoV responses. As demonstrated with a representative cross-reactive plasma sample 21854, IFA against the spike and nucleocapsid

proteins of different HCoV revealed IgG antibodies against HCoV-OC43, HKU-1, NL63 and 229E spike proteins (Figure 3). However, the same plasma sample only recognized the nucleocapsid of HCoV-NL63, suggesting that HCoV-NL63 could be the main source of antigenic exposure for this individual. When we analyzed all SARS-CoV-2 serologically cross-reactive samples, we found 100% recognized the spike proteins from all four HCoV that cause the common cold, but not that from SARS and MERS (Figure 4A). This recognition of common HCoV spike versus SARS and MERS spike proteins was statistically significant ($P < 0.0001$). Additionally, comparison of HCoV nucleocapsid recognition among all samples showed that the most commonly recognized nucleocapsid was that of HCoV-NL63, followed by HCoV-229E, at 92% and 50%, respectively (Figure 4B). This difference was statistically significant compared to recognition of the other HCoV, with P-values ranging from < 0.0001 to 0.0002 for HCoV-NL63 and P-values ranging from 0.0002 to 0.0054 for HCoV-229E (Figure 4B). Lastly, we compared how individuals from different countries responded against various HCoV nucleocapsid. Qualitatively, we found that the Zambian SARS-CoV-2 cross-reactive samples tended to recognize a wider range of HCoV compared to samples from Tanzania (Table 2). Some Zambian individuals recognized 4 up to 6 different HCoV, whereas Tanzanian individuals maximally recognized 3 different HCoV. However, the small sample size limited the statistical analysis of this difference.

Discussion

Despite the rapid spread of SARS-CoV-2 and causing nearly a million deaths worldwide to date, the SARS-CoV-2 burden in sub-Sahara Africa remains surprisingly low. This is despite a high prevalence of other diseases such as HIV-1, malaria, cancer and tuberculosis, and in

addition to insufficient health care and the impact of poverty. Coincidently, the current SARS-CoV-2 disease burden is much higher in the USA than sub-Saharan African countries. Whether this low prevalence of serological cross-reactivity to HCoV in the USA, as we report here, is directly associated with the outcomes of the USA COVID-19 pandemic remains unknown. Our data suggests that populations in sub-Sahara Africa had been pre-exposed to a spectrum of HCoVs that have provided some cross-reactivity against SARS-CoV-2 and may have limited infections or pathogenesis on the continent. In support of this hypothesis, our study detected serological cross-reactivity against SARS-CoV-2 antigens in pre-COVID-19 plasma samples from Tanzania and Zambia at levels nearly 8- and 6-fold, respectively, higher than the prevalence in samples from the USA. Additionally, by comparing the prevalence of serological cross-reactivity against SARS-CoV-2 between HIV-1 positive and negative Zambian individuals, we found that HIV-1 infection seem to lower the cross-reactive response towards SARS-CoV-2, which could be caused by a weakened immune response in HIV-1 infected individuals. However, a larger sample size of HIV-1 positive cohort will be needed to confirm this observation.

Among our study cohort, individuals reactive to SARS-CoV-2 antigens predominantly cross-reacted with SARS-CoV-2 nucleocapsid protein. Consistent with spike protein variation across coronaviruses, few individuals reacted with the SARS-CoV-2 spike protein. This reaffirmed that SARS-CoV-2 spike is a more specific target for serological testing for SARS-CoV-2 infection and humoral response to infection. Conversely, a recent study suggests that SARS-CoV-2 nucleocapsid is more sensitive than spike for early detection of SARS-CoV-2 infection (Burbelo et al., 2020) highlighting the distinction between sensitivity and specificity. Based on our analysis of pre-COVID-19 pandemic samples, we would support the notion that

detection of SARS-CoV-2 infection with nucleocapsid may generate a significant number of false positive results which could be country specify, with countries like Tanzania and Zambia potentially having a higher false positive rate than USA due to prior exposure to other coronaviruses.

To address the question of which human coronavirus was responsible for the observed cross-reactivity with SARS-CoV-2, we found that all SARS-CoV-2 cross-reactive samples strongly cross-reacted with the spike proteins from HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E, but not from SARS or MERS. This suggests that some immunogenic epitopes within the spike protein may be shared among all the known human coronaviruses. Additionally, the majority of our SARS-CoV-2 cross-reactive samples reacted strongly against the nucleocapsid of HCoV-NL63 and HCoV-229E, suggesting that these two HCoVs may have served as the source of antigenic exposure in sub-Saharan Africa prior to the COVID-19 pandemic. Although cross-reactivity against SARS-CoV-1 nucleocapsid as a result of exposure to human coronaviruses, such as HCoV-OC43, has been reported (Patrick et al., 2006), ours is the first study linking HCoV-NL63 and HCoV-229E to cross-reactivity against SARS-CoV-2 in the sub-Sahara Africa setting.

HCoV-NL63 and HCoV-229E are members of alphacoronavirus, whereas HCoV-OC43, HCoV-HKU-1 belongs to the same betacoronavirus as SARS-CoV-2 (Abdul-Rasool and Fielding, 2010). Additionally, HCoV-NL63 is the only other human coronavirus that uses angiotensin-converting enzyme (ACE) 2, the same receptor used by SARS and SARS-CoV-2 (Abdul-Rasool and Fielding, 2010, Hofmann et al., 2005). The epidemiology of HCoV-NL63 and HCoV-229E in adults is poorly defined. Some studies reported an 8.8% prevalence rate of HCoV-NL63 in the USA with less than 1% in UK (Esper et al., 2005, Gaunt et al., 2010). The

prevalence of HCoV-229E is unclear. Importantly, no epidemiological data exists for these two HCoVs in sub-Saharan Africa. Additionally, a recent bioinformatics study suggests that SARS-CoV-2 evolved from bat coronavirus and may have bats as a primary reservoir (Boni et al., 2020). Given the abundance wildlife, including multiple species of bats, in Africa and its often close proximity to humans, we cannot exclude the possibility of exposure to zoonotic coronaviruses that could elicit the observed cross-reactivity against SARS-CoV-2 and other human coronaviruses. Our results would suggest that infections with HCoV-NL63 or similar transmissible zoonotic agents were common in sub-Saharan Africa prior to the COVID-19 pandemic.

Lastly, the function of these SARS-CoV-2 cross-reactive antibodies and whether they provide any protection against SARS-CoV-2 infection or disease progression is still unclear and cannot be resolved with retrospective cross-sectional sampling. Since SARS-CoV-2 nucleocapsid is the major antigen that is recognized by these cross-reactive antibodies, we speculate that antibody-dependent effector mechanisms such as antibody-dependent cellular cytotoxicity could play some protective role. Our finding of SARS-CoV-2 cross-reactive antibodies in pre-COVID-19 pandemic samples mirrors and supports a recent study that showed exposure to HCoV/common cold induced SARS-CoV-2 cross-reactive T-cell responses in pre-pandemic samples (Mateus et al., 2020). Perhaps both adaptive responses may have offered some protection against COVID-19 pathogenesis, if not SARS-CoV-2 infection. A limitation of our study is that there were no peripheral blood mononuclear cells collected prior to the COVID-19 pandemic for analysis of potential cross-reactive T-cell response. Thus, a larger sample size and more in-depth longitudinal analysis of the function of these cross-reactive antibodies, as well as cross-reactive T-cell response will be needed in future studies.

Author contributions

FYT, SJL, PBP and AAC performed IFA. PBP and AAC performed HIV serological testing. ON, PJ, JRN, JM and JTW collected all plasma samples. FYT wrote the manuscript. CW supervised all aspect of the study. All authors reviewed and approved the manuscript.

Conflict of interest

All authors declare no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgement

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Table 1: Study cohort and sampling time period

Country	Sample size	HIV-1 positive (%)	Sampling time period
Tanzania	105	7 (6.7%)	March to May 2019
Zambia	99	43 (43.4%)	2017 to early 2019
USA	85	0 (0%)	2005, 2007 and 2009

Table 2: Individual cross-reactive responses against the nucleocapsid protein of SARS, MERS, HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E.

Country	Sample ID	SARS	MERS	OC43	HKU-1	NL63	229E
Tanzania	21850	-	-	-	-	+	-
Tanzania	21854	-	-	-	-	+	-
Tanzania	21868	-	-	-	-	+	+
Tanzania	21872	-	-	-	-	+	+
Tanzania	21873	-	-	-	-	+	-
Tanzania	21928	-	-	-	-	+	-
Tanzania	21933	-	-	-	-	+	-
Tanzania	211141	+	-	-	-	+	+
Tanzania	211145	-	-	-	-	+	+
Tanzania	211157	-	-	-	+	+	+
Tanzania	211176	+	-	-	-	+	-
Tanzania	211177	-	-	-	-	+	-
Tanzania	211181	-	-	-	-	+	+
Tanzania	211182	-	-	-	-	+	-
Tanzania	211185	-	-	-	+	+	+
Tanzania	211188	-	-	-	-	+	+
Tanzania	211192	-	+	-	-	+	+
Tanzania	211203	-	-	-	-	+	+
Tanzania	211205	-	-	-	-	+	+
Tanzania	211210	-	-	-	-	+	+
Zambia	C3076	+	-	-	-	+	-
Zambia	C3082	-	-	-	-	+	-
Zambia	C3154	-	-	-	-	+	-
Zambia	C3155	+	-	+	+	+	+
Zambia	C3156	-	-	-	-	+	+
Zambia	C3163	+	-	+	-	+	+
Zambia	C3166	-	+	-	-	+	-

Zambia	C3182	+	-	+	+	+	+
Zambia	C3187	-	-	-	-	-	-
Zambia	C3197	-	-	-	-	+	-
Zambia	C3202	+	+	+	+	+	+
Zambia	C3204	+	+	-	-	-	-
Zambia	N044	+	-	-	-	+	-
Zambia	N216	+	-	-	-	+	-
USA	KC-34	-	-	-	-	+	+
USA	KC-65	-	-	-	-	+	+

Figure 1. Immunofluorescence assay (IFA) against either mock, SARS-CoV-2 spike or nucleocapsid expressing cells. Representative pictures of IFA with negative control plasma, COVID-19 convalescence plasma (positive control) and pre-COVID-19 pandemic cross-reactive plasma samples 21928 and 21933. Sample 21928 displayed cross-reactivity against SARS-CoV-2 spike, but not its respective mock and SARS-CoV-2 nucleocapsid. Sample 21933 displayed cross-reactivity against SARS-CoV-2 nucleocapsid, but not its respective mock and SARS-CoV-2 spike. White arrows indicate positive cells. Scale bar represent 50 µm.

Figure 2. Percent prevalence of serological cross-reactivity against SARS-CoV-2 among Tanzania, Zambia and USA. (A) Combined serological cross-reactivity against SARS-CoV-2 spike and nucleocapsid. (B) Serological cross-reactivity against SARS-CoV-2 nucleocapsid. (C) Serological cross-reactivity against SARS-CoV-2 spike.

Figure 3. Immunofluorescence assay (IFA) against SARS, MERS, HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E spike or nucleocapsid expressing cells. Representative pictures of IFA with pre-COVID-19 pandemic cross-reactive plasma samples 21854. Sample 21854 strongly recognized the spike protein of HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E, but not SARS and MERS. Sample 21854 only recognized the nucleocapsid of HCoV-

NL63 and not the other human coronaviruses. White arrows indicate positive cells. Scale bar represent 50 µm.

Figure 4. Percent prevalence of serological cross-reactivity against SARS, MERS, HCoV-OC43, HCoV-HKU-1, HCoV-NL63 and HCoV-229E. (A) Spike. (B) Nucleocapsid.

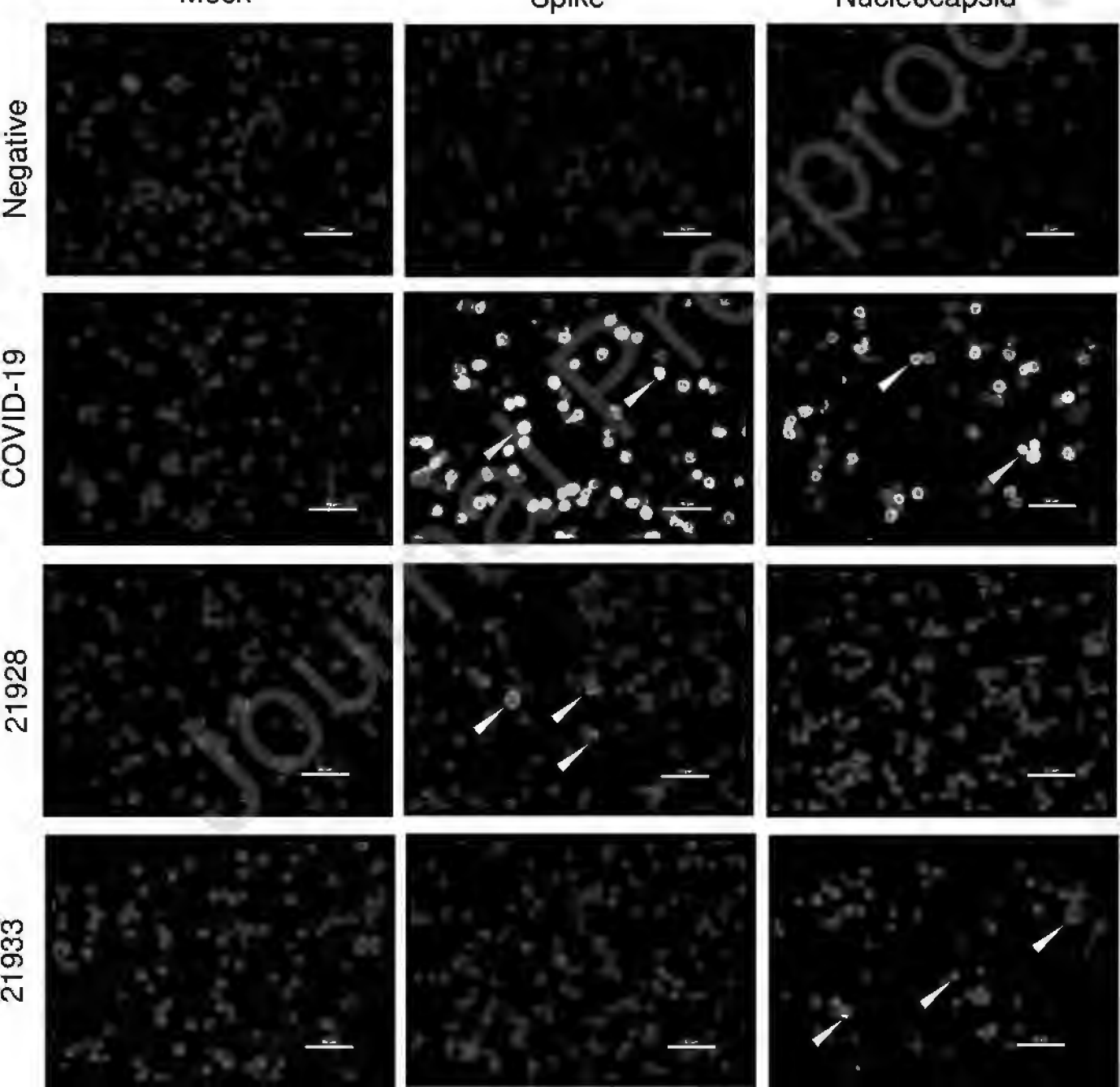
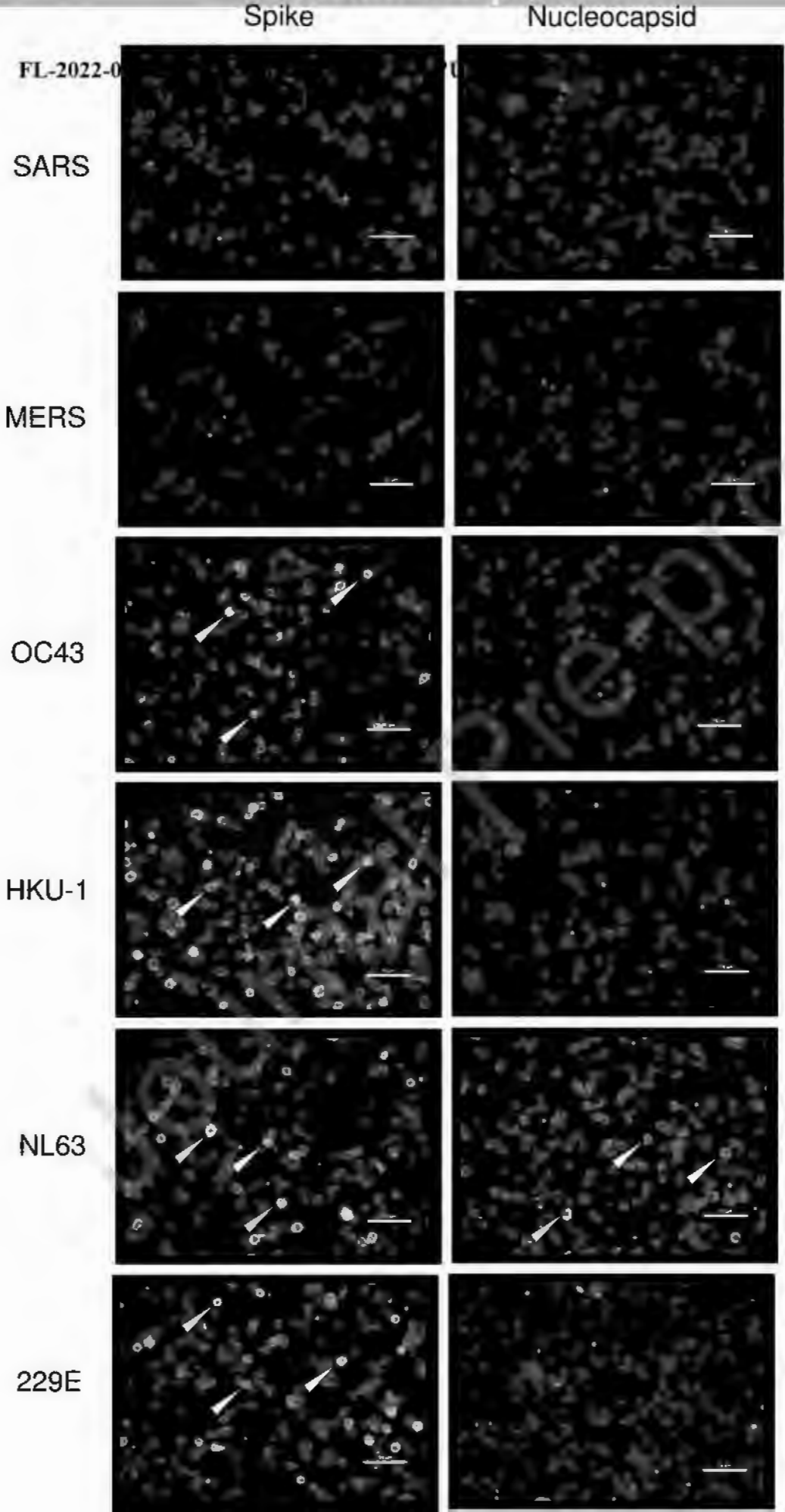
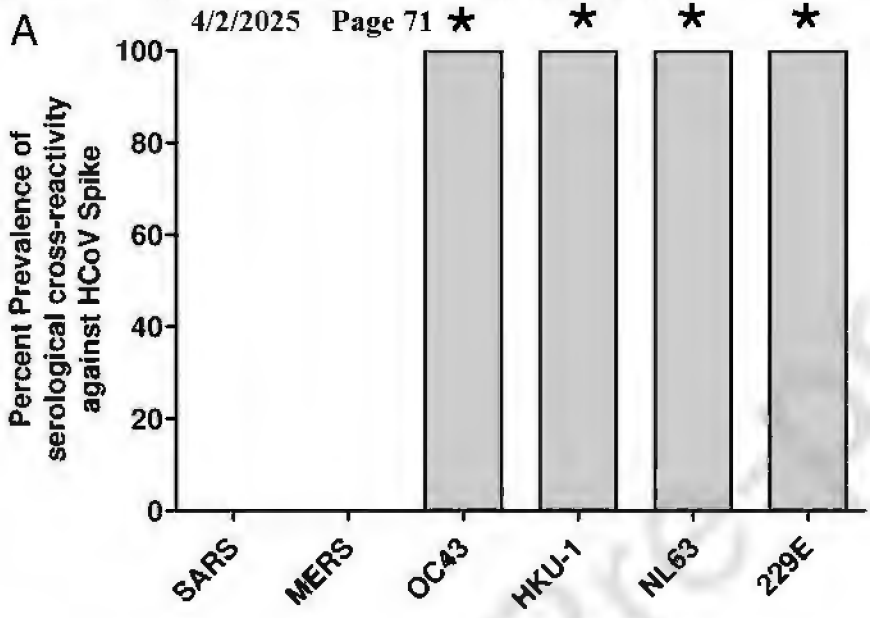
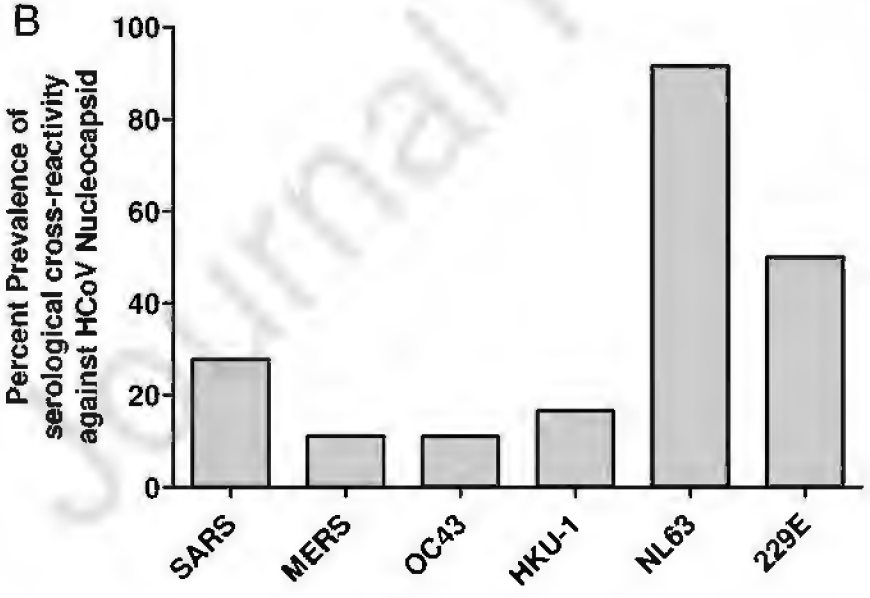


Figure 2

A
Percent Prevalence of serological cross-reactivity against SARS-CoV-2
0
5
10
15
20
Tanzania
Zambia
USA
P = 0.0002
P = 0.0069
B
Percent Prevalence of serological cross-reactivity against SARS-CoV-2 Nucleocapsid
0
5
10
15
20
Tanzania
Zambia
USA
P = 0.0001
P = 0.0018
Percent Prevalence of serological cross-reactivity against SARS-CoV-2 Spike
0
1
2
3
4
5
Tanzania
Zambia
USA







P-values table

	SARS	MERS	OC43	HKU-1	NL63	229E
SARS	-	ns	ns	ns	<0.0001	ns
MERS	ns	-	ns	ns	<0.0001	0.0007
OC43	ns	ns	-	ns	<0.0001	0.0007
HKU-1	ns	ns	ns	-	<0.0001	0.0054
NL63	<0.0001	<0.0001	<0.0001	<0.0001	-	0.0002
229E	ns	0.0007	0.0007	0.0054	0.0002	-

"ns" denotes non-significant

From: "Feith, David" (b)(6) @state.gov>
To: Ortagus, Morgan D (b)(6) @state.gov>; (b)(6) @state.gov>
CC: Stilwell, David R (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Subject: Fwd: Major Taiwan News of COV19 origins at WIV.....
Date: Tue, 12 Jan 2021 02:55:39 +0000

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David Feith
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
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(b)(6) @state.gov

---------- Forwarded message ----------

From: David Asher (b)(6) @hudson.org>
Date: January 11, 2021 at 9:32:16 PM EST
Subject: Major Taiwan News of COV19 origins at WIV.....
To: Feith, David (b)(6) @state.gov>
Cc: (b)(6) (b)(6) @state.gov>,Gibbs, Jeffrey J (b)(6) @state.gov>,DiNanno, Thomas G (b)(6) @state.gov>(b)(6) @state.gov>,(b)(6) (b)(6) @state.gov>(b)(6) @state.gov>(b)(6) (b)(6) @state.gov>

David, See note below from perceptive Professor Muller. Enjoy Taipei and please get the whole story of this. As suspected Taipei knows a lot more. Now that we treat them normally a lot more will come out. David PS- Note "Hu Ben." Dr. Strangelove's Chinese bio cousin. Dasic, Baric, et al. Wow.

David L. Asher, Ph.D
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https://www.hudson.org/experts/1299-david-asher

Begin forwarded message:

From: Richard Muller (b)(6) @gmail.com>
Date: January 11, 2021 at 21:11:17 EST
To: David Asher (b)(6) @vitalfin.com>
Subject: Taiwan News

Dave

This article is must be devastating to the GOF community. The fact that the WIV was infected humanized mice with bat coronavirus — that's something that the public can easily understand, easier than "gain of function". This article names names, including Daszak and Baric.

I'm guessing that this is one of the things you knew about but couldn't tell me.

Rich

Sender: "Feith, David" (b)(6) @state.gov>

Recipient: Ortagus, Morgan D (b)(6) @state.gov>;
(b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>

From: "Feith, David"

To: Stilwell, David R (b)(6) @state.gov>;
Atul Keshap (Colombo) (b)(6) @state.gov) (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>

Subject: FW: Wuhan statement

Date: Wed, 13 Jan 2021 14:47:21 +0000

Latest.

~~SENSITIVE BUT UNCLASSIFIED~~

From: Feith, David
Sent: Wednesday, January 13, 2021 9:46 AM
To: Yu, Miles (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Buangan, Richard L (b)(6) .@state.gov>
Cc: (b)(6) @state.gov>
Subject: RE: Wuhan statement

Team (with (b)(6) cc'ed) –

Sharing this DRAFT memo, including statement and fact sheet text, which makes a marriage of (b)(6) and Kelley's versions. This isn't yet final because I want this group's review, and I'm also sending it to Amb. Bremberg given his familiarity with WHO/HHS world. Also pasted below.

Appreciate your read. Thanks much.

--

(b)(5) Deliberative Process

(b)(5) Deliberative Process

###

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

(b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Wednesday, January 13, 2021 7:48 AM
To: Feith, David (b)(6) @state.gov>
Cc: Yu, Miles (b)(6) @state.gov>; Eckels-Currie, Kelley (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>
Subject: Re: Wuhan statement

Great. Please send me the final draft when it's ready to read.

Sent from my iPhone

On Jan 13, 2021, at 7:39 AM, Feith, David (b)(6) @state.gov> wrote:

Many thanks all. The (b)(6 and Kelley versions are both strong, and I imagine a marriage of them can work well. Just two flags as we proceed, both relating to IC issues:

(b)(5) Deliberative Process

Thanks again all, really appreciate everyone's collaboration here in difficult circumstances.

+ Richard.

--
David Feith
Deputy Assistant Secretary
Bureau of East Asian and Pacific Affairs (EAP)
U.S. Department of State
(b)(6) (o)
(c)
(b)(6) @state.gov

On January 13, 2021 at 7:21:02 AM EST, (b)(6) @state.gov> wrote:
Good morning... Please marry this to the EAP statement I edited and provided extensive comments on last night, and send me whatever final draft you want me to clear. Please coordinate with Richard so we don't hVe multiple versions floating around. Thank you!

Sent from my iPhone

On Jan 13, 2021, at 6:41 AM, Yu, Miles (b)(6) @state.gov> wrote:

This is much better.
I can live with this
version.

Dr. M Miles Yu
Office of the Secretary
Department of State
Washington. DC
(b)(6)

Send from my iPhone

On Jan 13, 2021, at 1:34 AM, Eckels-Currie, Kelley (b)(6) @state.gov> wrote:

Take a look at the attached. There's still some duplicative language in here, but I want to get your feedback on the overall approach.
K

Kelley E. Currie
Ambassador-at-Large
Secretary's Office of Global Women's Issues (S/GWI)
Department of State
Washington DC 20520
(b)(6)

<COVID declass draft S statement MY DF CB.docx>

Sender: "Feith, David"

Recipient: Stilwell, David R (b)(6) @state.gov>;
Atul Keshap (Colombo) (b)(6) @state.gov) (b)(6) @state.gov>;
Fritz, Jonathan D (b)(6) @state.gov>;
Buangan, Richard L (b)(6) @state.gov>

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

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Withheld pursuant to exemption

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Withheld pursuant to exemption

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Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

EAP: David R. Stilwell []

Drafted: EAP Front Office

Clearances:
EAP/FO: Atul Keshap ()
EAP/FO: Richard Buangan ()
EAP/FO: Jonathan Fritz ()
D: (b)(6)
P: (b)(6)
T: Chris Ford (ok)
S/P: Miles Yu ()
SPOX: Morgan Ortagus/Cale Brown

From: "Asher, David" (b)(6) @state.gov>
To: (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>
CC: Feith, David (b)(6) @state.gov>
Subject: Fw: SBU Timeline v7/ origins investigation
Date: Sun, 3 Jan 2021 23:34:00 +0000

Asher, David has shared a OneDrive for Business file with you. To view it, click the link below.

☒ SBU COVID Timeline v07c.xlsx

From: Asher, David (b)(6) @state.gov>
Sent: Sunday, January 3, 2021 6:31 PM
To: Ford, Christopher A (b)(6) @state.gov>
Cc: DiNanno, Thomas G <(b)(6) @state.gov>
Subject: Fw: SBU Timeline v7/ origins investigation

Chris,

For your edification see attached (b)(5) Deliberative Process

(b)(5) Deliberative Process

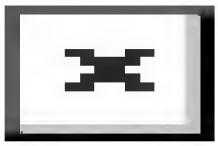
FYI- we will have a discussion with some top scientists later in the week to review a number of key papers on origins. You might wish to listen in. You bear full responsibility so we certainly are committed to supporting you at this critical time. You can count on us.

Happy New Year!

David

(b)(5) Deliberative Process

https://twitter.com/g_translators6/status/1345515712593457153?s=24

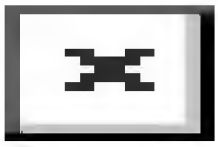


秘密翻译组 on Twitter

"CCP's military expert CHEN Hu, publicly discussed the CCP's bioweapon plan in 2016 in a Southeast China Military Watch show on Southeast Cable TV, but the Western world has been ignoring the fact either because they're naïve or ignorant or profit-driven, this is a ... (1/2) https://t.co/ogXjPuvXlR"

twitter.com

https://www.zerohedge.com/covid-19/top-us-official-says-growing-body-evidence-shows-covid-19-leaked-chinese-lab



Top US Official Says 'Growing Body Of Evidence' Shows COVID-19 Leaked From Chinese Lab | ZeroHedge

The most 'credible' theory about the origin of COVID-19 is that it escaped from a Chinese laboratory, according to US National Security Adviser Matthew Pottinger, who made the comment during a Zoom meeting with UK officials. "There is a growing body of evidence that the lab is likely the most credible source of the virus," said Pottinger, referring to the Wuhan Institute of Virology, according ...

www.zerohedge.com

Attached is a link to the latest version of the SBU timeline. So far I have been unable to attach the file. The best I can do from on the road is to provide a link to it. Recommend you save a copy to your computer/cloud storage in order to work with the file.

Changes since last version:

- Added the 239 new entries to bring the total to 845
- Added "Lab origin cover-up" and "Failed to follow IHR 6" breakout worksheet timelines

From: (b)(6)
Sent: Saturday, January 2, 2021 4:43 PM
To: Gibbs, Jeffrey J (b)(6) @state.gov>
Cc: (b)(6) @state.gov>; (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>
Subject: Additional unclassified timeline entries

Jeff -

For your reading pleasure, I have created 239 additional unclassified, tagged, and sourced timeline entries based on CRS, AP, NYT, and other reporting (see attached). Like before, I have broken out some of the entries by category and placed them in additional worksheets to the right of the first/master worksheet. I also created two new categories, "Failed to follow IHR 6" and "Cover-up". When combined with the master timeline some entries will be redundant, but they serve to provide additional sources and sometimes additional context.

I will add these new entries to the master U-SBU timeline and send it to you as a new version 7.

Best,

(b)(6)

Sender: "Asher, David" (b)(6) @state.gov>
(b)(6) @state.gov>;
(b)(6) @state.gov>;
Recipient: (b)(6) @state.gov>;
Gibbs, Jeffrey J (b)(6) @state.gov>;
Feith, David (b)(6) @state.gov>

From: "Asher, David" (b)(6) @state.gov>

To: Feith, David (b)(6) @state.gov>;
Yu, Miles (b)(6) @state.gov>

CC: DiNanno, Thomas G (b)(6) @state.gov>;
Gibbs, Jeffrey J (b)(6) @state.gov>;
(b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
(b)(6) (b)(6) @state.gov>;
(b)(6) @state.gov>;
Keshap, Atul (b)(6) @state.gov>

Subject: Fw: Re: Dr. Quay's comments and responses

Date: Thu, 7 Jan 2021 02:23:52 +0000

Miles, David, and David

I regret that you weren't included on the scientific debate related to Dr. Quay's original draft, which all agree is much enhanced due to the feedback of many leading experts. See attached.

Anyway, this analysis attached is in the weeds—no urgent need to peruse— but I want to assure you we are promoting an honest debate among scientists, not some framed up conspiracy as Ford, in effect accuses me, in particular, without knowledge and with no apparent attention to our research or methods. Moreover, I note next to no response to our specific questions from our valued IC. We asked Dr. Quay to provide a Bayesian response utilizing the available sequence data and disparities. We asked Dr. Lai at Harvard to present her work, with collaborators, using actual gain of function and other cutting edge techniques to evaluate the origins issue.

(b)(5) Deliberative Process

Tomorrow we will encourage allow scientists to discuss the COV 19 origins issue before us as observers. I encourage you to listen in. (b)(6) will make sure you are invited. In addition to numerous and highly distinguished American scientists at the forefront of the origins debate and others with great experience into the specific potential uses of viruses as bio WMD vectors, now we will have two special guests, Dr. Ralph Baric. Dr. Baric's research with Dr. Shi at the WIV has been controversial but whose motivations as a scientist and researcher we will respect and whose views on the origins we will hear from objectively and hope he give us some insight into what apparently happened at WIV in the late fall. In addition, we will welcome Dr. Ping-Ing Lee, who is spearheading Taipei's response to COV-19 and is a noted pediatric virologist. Dr. Lee will

be welcome to speak from the frontlines on their analysis of COV 19 that led to their extraordinarily successful pandemic response.

In any event, thanks for your support, advice, and leadership. (b)(5) Deliberative Process

(b)(5) Deliberative Process

Asher

From (b)(6) @state.gov>
Sent: Wednesday, January 6, 2021 1:22 PM
To: (b)(6) @stanford.edu <(b)(6) @stanford.edu>; Alina Chan <(b)(6) @broadinstitute.org>; Santarpia, Joshua L (b)(6) @unmc.edu>; Joshua Santarpia <(b)(6) @nsri.nebraskaresearch.gov>; (b)(6) @nsri.nebraskaresearch.gov <(b)(6) @nsri.nebraskaresearch.gov>; (b)(6) @lbl.gov <(b)(6) @lbl.gov>
Cc: Steven Quay, MD, PhD <(b)(6) drquay.com>; Lawrence Remmel <(b)(6) @gmail.com>; Gibbs, Jeffrey J <(b)(6) @state.gov>; (b)(6) <(b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; Christopher Yeaw <(b)(6) @nsri.nebraskaresearch.gov>; Turner, Bruce I (b)(6) @state.gov>
Subject: Re: Dr. Quay's comments and responses

Please find attached the following:

- Dr. Quay's Qs and As/Comments and Responses to "A Bayesian Analysis of the Origin of SARS-CoV-2;"
- Dr. Quay's paper;
- Dr. Chan's two papers (this version displays the charts in color); and
- Bios of the panel members.

Thank you!

(b)(6)

(b)(6)

Chief of Staff
Bureau of Arms Control, Verification and Compliance
U.S. Department of State
HST Room 5950

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Feith, David (b)(6) @state.gov>;
(b)(6) @state.gov>;
DiNanno, Thomas G (b)(6) @state.gov>;
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Recipient: (b)(6) @state.gov>;
Stilwell, David R (b)(6) @state.gov>;
(b)(6) @state.gov>;
(b)(6) @state.gov>;
Keshap, Atul (b)(6) @state.gov>

Questions and Answers

Comments and Responses

to

A Bayesian Analysis of the Origin of SARS-CoV-2

By

Steven C. Quay, MD, PhD

Steven@DrQuay.com

Website: www.DrQuay.com

Purpose. Following circulation of the first draft of the titled document comments and questions were received from a number of reviewers. The author acknowledges the very helpful work done by the reviewers with a short timeframe and over vacation time. Many of the comments were laudable and are appreciated but will not be covered here. This is reserved for the challenges.

This document will be the author's response to these comments and questions, which are in bold text for clarity.

The stated intent of this report is to "provide likelihoods of the alternative hypotheses zoonotic or laboratory, as to the origin of SARS-CoV-2." As pointed out, some elements of this report appear to stray from the stated intent, most notably the discussion of RaTG13.

The author agrees and the RaTG13 material has been moved to the Appendix. Its current probative value is to impeach the credibility of Dr. Zhengli Shi, coronavirus research expert at the Wuhan Institute of Virology (WIV), the likely architect of the synthetic biology project that created SARS-CoV-2 (CoV-2). Its future value, subject to more research and analysis, is as the source for the CoV-2 genomic backbone.

The adenoviral expression vector data assessment was also interesting, hut seems to stray from the stated intent. These data could be included as "additional supportive information", but the focus of the assessment should he on what are considered to be the key factors assessing the primary and alternative hypotheses.

Agree. This work is incomplete and so has been moved to the Appendix pending further work. I disagree with its import to the question of origin.

The finding of an adenovirus vector vaccine being given to patients the end of December 2019 would be strong evidence of possession of CoV-2 in laboratories months earlier, a finding that supports a laboratory origin.

I recommend this as a two-step process: 1) determine if evidence supports a natural or intentional mutation of the virus, 2) if evidence supports intentional mutation, determine if evidence supports accidental or intentional release.

An excellent conceptual approach. I have not given attention to how one would differentiate accidental versus intentional.

There are multiple probabilities stated in this report without a clear description of how they were each derived. A table of raw data or detailed description of how each probability was derived would enhance credibility.

Each evidence discussion now ends with a calculation box which shows the computations.

Arbitrary rules were set in the beginning as follows:

1. Evidence that favors one hypothesis over the other but cannot be easily quantified will be assigned a 51% likelihood for the 'winning' hypothesis and a 49% likelihood for the 'loosing' hypothesis. This is consistent with the civil law concept of a preponderance of the evidence.

2. Evidence that can be quantified but where the p-values are highly significant, where the likelihood is one in a hundred, thousand, million, etc. were not used directly as a single piece of such highly significant data would end the analysis simply because of the math. So no matter the magnitude of the effect size for a piece of data, the evidence will be given the accepted value for significance in science, a p-value of 0.05. This is equivalent to a probability of one out of 20.
3. Quantitative effect sizes that are between a 51% likelihood and a 95% likelihood (the latter being the statistical significance level of p=0.05) will be used directly.

The zoogeographic assessment is interesting and supports the theory that SARS-CoV-2 was not a natural emergent zoonotic infection but I would like to know more about the radius for animals brought into the market in Wuhan. From my experiences in Africa, animals sold at wet markets are typically local to the area, but it would be helpful to know if this is also typical for the Huanan Wholesale Market or if it is feasible for animals from the Yunnan province to be trafficked to this market.

Page 66 deals with this.

"The Huanan wholesale market is a large market (653 stalls and more than 1180 employees) mainly supplying seafood products but also fresh fruits and vegetables, meat, and live animals. In late December 2019, 10 stalls operators were trading live wild animals including **chipmunks, foxes, racoons, wild boar, giant salamanders, hedgehogs, sika deer**, among others. Farmed, wild and domestic animals were also traded at the market including **snakes, frogs, quails, bamboo rats, rabbits, crocodiles, and badgers.** The market was closed on 1 January 2020, and several investigations followed, including environmental sampling in the market, as well as sampling of frozen animal carcasses at the market. Of the 336 samples collected from animals, none were PCR positive for SARS-CoV-2, whereas 69 out of 842 environmental samples were positive by PCR for SARS-CoV-2. Sixty- one of those (88%) were from the western wing of the market. Of these, 22 samples were from 8 different drains and sewage, and 3 viruses were isolated, sequenced and shared on GISAID. These were virtually identical to the patient samples collected at the same time (>99.9 % homology)."

I have no data of the sources of the market animals to assess if Yunnan province animals would be a likely source. Yunnan is 1700 km south of Wuhan, the equivalent to the distance from the Everglades in Florida and New York City. So, it seems unlikely. In addition, if I could credibly report that animals in the Wuhan market were from Yunnan, the known origin of the ancestor to CoV-2 I would be broadcasting that information.

An assessment of the Chinese biosafety/biosecurity culture along with national policies and standards would be helpful to the discussion of safety and LAI reporting. While this information is important to the big picture and it can potentially help explain how a community infection can result accidentally from a laboratory incident it does not directly address the question of the origin of the virus. I would also recommend this be considered "additional supportive information."

On page 71 is the topic, "Evidence of Lax and disregard of laboratory safety protocols and regulations in China," which contains a hyperlink to a Mandarin site with abundant evidence of a low standard of safety compliance.

An example from this section states:

"The following document shows that in June 2019, the Chinese CDC was soliciting for the removal of 25-years of solid and liquid medical waste. The total is close to two tons including three kg of highly toxic waste.

Finally, a new evidence section has been identified related to a new biosafety law, first proposed in October 2019 but only recently finalized.[1] The English translation of the cover of the new law follows:

Wednesday, January 6, 2021 | National People's Daily

全国人民代表大会
The National People's Congress of the People's Republic of China

中国人大网

Home | Constitution | National People's Congress Organization | Chairman Li Zhanshu | Congress Meeting | Standing Committee Meeting | Chairman Meeting | Authoritative Release | Legislation | Supervision | news

Current Location: Home

Biosafety Law of the People's Republic of China

(Adopted at the 22nd Meeting of the Standing Committee of the 13th National People's Congress on October 17, 2020)

Source: Chinese National People's Congress web browser font size: Tai Zhong Small October 17, 2020 19:50:00

table of Contents

Chapter One General Provisions

Chapter II Biosafety Risk Prevention and Control System

Chapter III Prevention and Control of Major New Emergent Infectious Diseases, Animal and Plant Epidemics

Chapter 4 Biotechnology Research, Development and Application Security

Chapter 5 Biosafety of Pathogenic Microorganism Laboratory

Chapter VI Human Genetic Resources and Biological Resources Security

Chapter 7 Preventing Bioterrorism and Biological Weapons Threats

Chapter 8 Biosafety Capacity Building

Chapter 9 Legal Liability

Chapter 10 Supplementary Provisions

Chapter One General Provisions

Picture report More

legislation

- Use good laws and good governance
- Speeding up the stamp duty law
- Where can I download the national
- Top ten legislative contexts in
- "Code" brightens our lives | "self-

Supervise

- Improve the legal system to ensure
- Members of the Standing Committee
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- Feature In the face of audit
- Members of the Standing Committee

representative

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- [Video] The 13th NPC Standing
- [Video] The 13th NPC Standing

The most interesting sections of the new law are:

[1] http://www.npc.gov.cn/npc/c30834/202010/bb3bee5122854893a69acf4005a66059.shtml

Article 47 The pathogenic microbiology laboratory shall take measures to strengthen the management of experimental animals, prevent the escape of experimental animals, and treat the used experimental animals in a harmless manner in accordance with national regulations to realize the traceability of experimental animals. It is forbidden to introduce used experimental animals into the market.

Article 77 Anyone who, in violation of the provisions of this law, sends used experimental animals into the market shall be ordered by the science and technology department of the people's government at or above the county level to make corrections, confiscated the illegal gains, and impose a penalty of more than 200,000 yuan but less than 1 million yuan If the illegal income is more than 200,000 yuan, a fine of five to ten times the illegal income shall be imposed; if the circumstances are serious, the relevant permit shall be revoked by the issuing department.

I also agree that the math is lacking in many of the claims of probabilities. That should be rectified (though I'm sure that will only make the paper longer!).

Math calculations included in each section now.

I am not sure what the author is doing with the putative precursor virus, RATG13. I can't tell if he thinks the virus is the immediate ancestor of CoV-2, with some modifications, or if he thinks it's a complete fabrication. I think he needs to pick a line of reasoning and stick with it.

The observation of my ambivalence is astute and accurate. I have not decided if I believe RaTG13 is the precursor or not.

This criticism has led me to produce the following organization of my thoughts. The support for these ideas are now in the Appendix.

- Evidence for and against RaTG13 as the direct precursor of CoV-2. I have not made up my mind on this important hypothesis
    - To establish a precursor-product relationship for RaTG13 and CoV-2 a relative simple process must be proposed to make approximately 1140 nt changes in the 30,000 nt genome
    - Evidence in favor of the hypothesis:
        - While the nucleotide sequence data show these coronaviruses are only 96.2% homologous a comparison of their amino acid homology indicates they are 98.8% identical and as similar as the Civet SARS-CoV-1 and human SARS-CoV-1
        - About 26% of the entire genomes contain only synonymous mutations without any non-synonymous mutations, a highly improbably outcome in nature but an easy exercise in the laboratory to introduce. The motivation would be to obscure the closeness of the two genomes without worrying about introducing detrimental mutations. This represents about 200 of the nt differences

- There are two restriction enzyme sites in RaTG13 that begin at the receptor binding domain and end 3' to the furin cleavage site that use the 'No See 'Em' technology developed and patented by Ralph Baric, a Dr. Shi and WIV collaborator. Shi has used these enzymes herself. As expected for the technology, the sites are lost in CoV-2. However, they are not the "pure-form" of the Baric technology, are less hidden, and so I would be surprised if Shi did this less robust approach. Nonetheless, the likelihood these sites are there by chance is infinitesimal.
- CoV-2 and RaTG13 share a >100 nt insertion in the ORF1ab gene found no where else in sarbecoviruses. A very strange fact and significantly greater than the 12-nt furin site that has caught so much attention. I spent a day or so probing the function of the site, I believe it is nsp3 (from memory), but didn't find a smoking gun to warrant deeper work. Should be returned to.
- It is part of the nine viruses found in the Yunnan cave where miners died of a coronavirus-like illness.

o Evidence against RaTG13

- My proof that it did not come from the bat feces specimen as reported by Shi is troublesome for an hypothesis it is the critical precursor virus
- To my knowledge no has grown it and examination of its Spike Protein by numerous groups comes to the unlikely conclusion it will bind to ACE2 of most species or grow in a lab culture.
- Peter Daszak, who has said many things proven to be false, nonetheless has described RaTG13 as a "composite sequence" a term used for a really mixed specimen where metagenomics are used to obtain a "genome sequence" which in reality was pieced together artificially by the computers running the analysis
- I can reduce the 1140 nt difference to about 600 with two steps, the No See 'Em insertion of the CoV-2 RBD in the Spike Protein and using a synonymous mutation algorithm to create artificial phylogenetic distance. But a simple method of closing that 600 nt, mostly non-synonymous mutations, has not been identified.
- Shi collected nine beta coronaviruses in the mine but has published the sequence of only RaTG13. She voluntarily published RaTG13. It seems more likely that she would publish a virus close to CoV-2 to establish the bat origin in the medical field (the RaTG13 paper title was "A pneumonia outbreak associated with a new coronavirus of probable bat origin) but not publish the actual virus she used for the construction of CoV-2, in the unlikely event a 'bullet proof' connection that she hadn't thought of could be found.

I'll be honest, this needs a theory for how SARS-CoV-2 got to be what it is. If that theory involves the near de novo creation of it from parts and prices of other CoVs, I will call BS.

I agree that *de novo* synthesis is both unlikely and unnecessary.

A reasonably plausible theory, that might fit the arguments presented is that the actual immediate ancestor of CoV-2 has an undisclosed sequence, closer to that of the original CoV-2. RATG13 is a red herring sequence created from the ancestor to look like it is more distant and found in nature, giving a plausible natural evolution pathway. CoV-2 is the result of GOF experiments on the ancestor, probably to add the furin cleavage site. This slightly modified virus got out of the bag, either through a lab acquired infection, or the waste, or something. This is technologically reasonable and is supported by at least some of the data presented.

I agree with the suppositions above.

There is a fair bit of evidence in there that suggests that bat to human zoonosis isn't the start of the pandemic. Lack of serology in animals, codon usage in cleavage site, initial spread from human to human. Still, saying that it didn't exactly follow the jump pattern from animals to humans, that MERS did, really only says it's different from MERS, not that it's a lab escape.

In most cases I combine SARS-CoV-1 and MERS data but you are right it is a very small data set of only two for comparisons. Nonetheless, it is the way science is done. If my data shows CoV-2 is nothing like the previous epidemics the next question is what properties does the virus have to account for the difference and where did those come from. If a 99% human adapted receptor binding motif and a furin site is the secret to its success, where did it adapt without causing any seroconversion in Wuhan and where did the furin site come from with no recombination candidates from other sarbecoviruses.

And it should be admitted that a graduate level class, given the task on a Frida of increasing a coronavirus' infectivity as a weekend project, would arrive Monday morning with a plan to use humanized mice and serial passage and insertion of a canonical furin cleavage site. The fact this is so obviously easy and the alternative zoonotic hypothesis requires twisting in knots should be worth something in the analysis

There are numerous statistics thought the document (such as references to one in 13 million or one in a billion) that don't have calculations to support them.

These have been corrected for the most part.

The steady increase in likelihood (shown at the end of each section) seems qualitative to me. There was a formula given at the beginning, but the change reported at the end of each section seems subjective.

The author has attempted to address this criticism in the report.

The comparison between SARS-CoV-2 and MERS-CoV posterior diversity isn't really convincing to me. Honestly, I would expect those to be really different, since MERS never really got a strong foothold in the human population and seems to come in and out of animal reservoir, with camel to human and human to human transmission both continuing to occur, so I don't think that's the right model. If this is going to be more convincing, it

needs to be something else, maybe including comparison to SARS or pandemic influenza or something. I'm not really sure, but the comparison to MERS doesn't convince me.

An excellent observation which has been rectified with a comparison to SARS-CoV-1 as well. I have included it here for convenience, but it is found on page 25-6.

SARS-CoV-1. A similar pattern of clinical cases that do not show a common ancestor in the human population but instead is evidence of posterior diversity is shown in the Text-Table on the left for SARS-CoV-1[2] compared to CoV-2 on the right[3]. SARS-CoV-1 shows clusters of cases in humans that are connected only by phylogenetic branches that reach back in time (all of the branches inside the purple box. This is because of the extensive mutational background created while being in the intermediate host, the civet. With CoV-2 on the right, every clinical case descends from the first clinical case, in the 19A clade. There are no background mutations to account for. I will show elsewhere that the first Clade A patient was at the PLA Hospital about 3 km from the WIV.

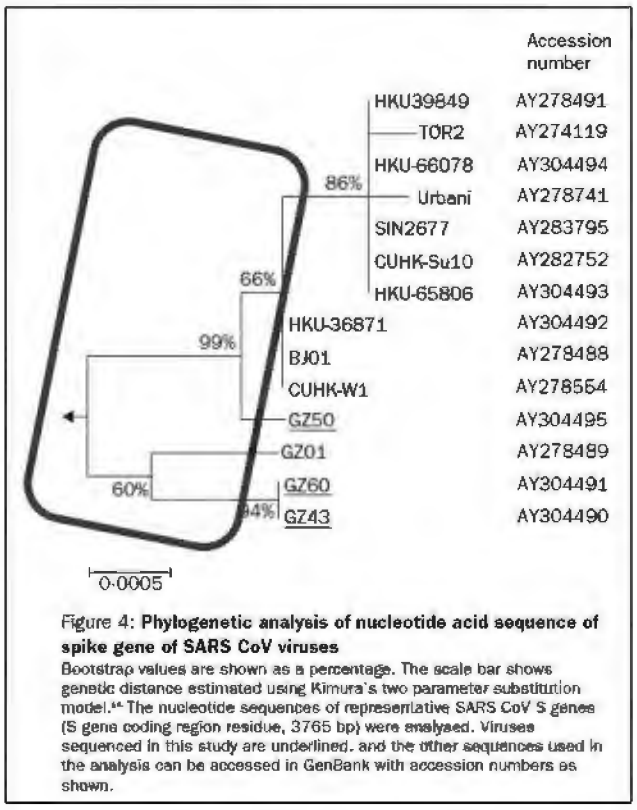
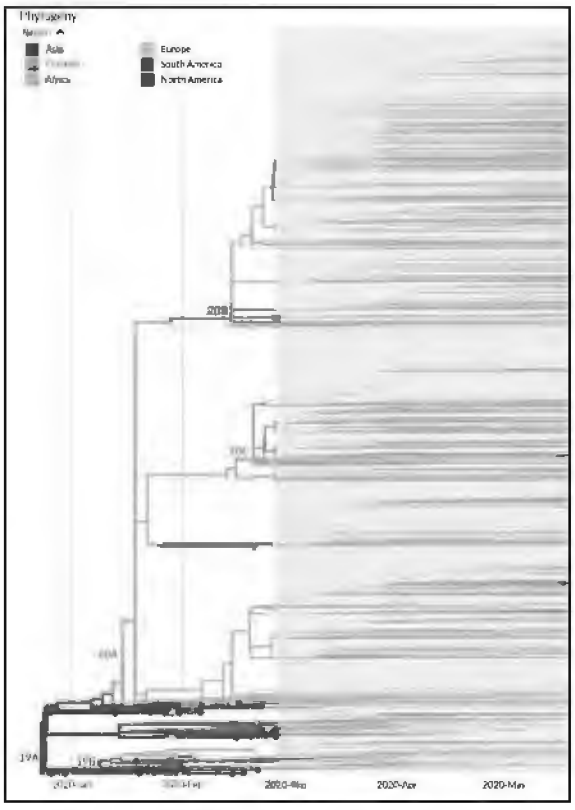
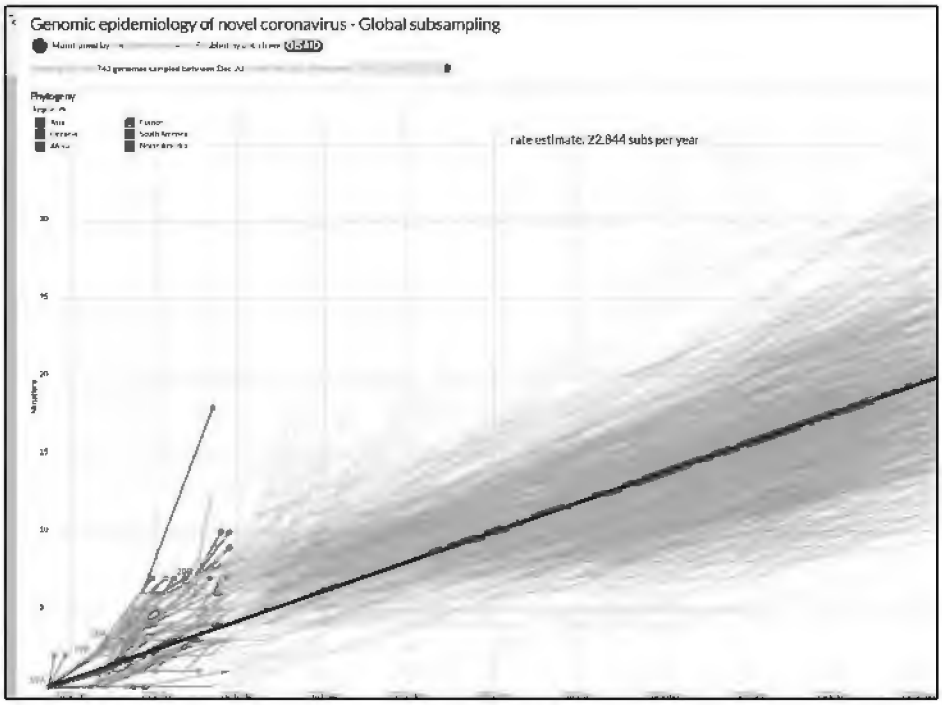


Figure 4: **Phylogenetic analysis of nucleotide acid sequence of spike gene of SARS CoV viruses**
Bootstrap values are shown as a percentage. The scale bar shows genetic distance estimated using Kimura's two parameter substitution model.[44] The nucleotide sequences of representative SARS CoV S genes (S gene coding region residue, 3765 bp) were analysed. Viruses sequenced in this study are underlined, and the other sequences used in the analysis can be accessed in GenBank with accession numbers as shown.



Given the rate of mutations of 22.8 per year for CoV-2 as shown in the Nextstrain graph below and a sequencing accuracy of about two calls per genome, CoV-2 could not have spent more than a few weeks in an intermediate host before a pattern of background mutations would be identified as posterior diversity. In the laboratory a pure culture on a single genome is used and the CoV-2 pattern is most consistent with a single pure culture infection a first human.

[2] https://pubmed.ncbi.nlm.nih.gov/14585636/
[3] https://nextstrain.org/



I will say that the author appears to occasionally typo CGG as CCG, and it makes my eyes cross.

A great comment and all six of my mistakes have been corrected!

The only CCG remaining is the search for the complimentary strand -CGG-CGG- pair in other sarbecoviruses as a possible substrate for a recombination event between a positive strand and a negative strand. No candidates were found.

That notwithstanding, I agree that the particular codon is underutilized in coronaviruses, but the table on page 93 indicates that an RR dimer that includes a single CGG is found in HKU1, an endemic human coronavirus. I'm not saying that the CGGCGG isn't unlikely, just that it wouldn't be impossible.

There are two sequences that have a single CGG codon in the furin site, HKU1 as noted above and BatCoV.

The following Table contains both the furin cleavage site amino acids of known coronaviruses with such sites, even from subgenera where recombination is unlikely. The furin site nt sequence is also shown. As noted, there are two with a single CGG but none with two together. The blue codons are arginine codons other that CGG. Given the frequency of 2/56 CGG codons in the collected furin sites being CGG and 0/56 being -CGG-CGG- I am saying that it is unlikely, with a probability of about (2/56)(2/56) or one in 784.

Description	Accession Number	Furin Cleavage Sequence -R-X-X-R-	Furin Score	Identity to CoV-2	RR Dimer	R at PCS	CGG for PCS	Nt Sequence	Total Arg in SP	Total CGG codon in SP	URL
SARS-CoV 2	MN996527.1	NSPRRAR/SV	0.62	100.0%	1	3	2	aat tct cct cgg cgg gca cgt agt gta	42	2	https://www.ncbi.nlm.nih.gov/nuccore/MN996527.1
Rat-CoV	JF792617.1	TAHRARR/SV	0.88	36.3%	1	3	0	acc gct cac cgt gct cgt agg tct gtc	46	2	https://www.ncbi.nlm.nih.gov/nuccore/JF792617.1
MHV	EF682498.1	TSHRARR/SI	0.86	36.9%	1	3	0	acg tca cat cgt gct cgt agg tcc atc	43	2	https://www.ncbi.nlm.nih.gov/nuccore/EF682498.1
Canine-CoV	DQ682406.1	TQRRSRR/SI	0.83	37.1%	2	4	0	aca cag aga cgg agt cgt aga tcg att	36	2	https://www.ncbi.nlm.nih.gov/nuccore/DQ682406.1
Equine-CoV	LC061274.1	TARRQRR/SP	0.82	37.1%	2	4	0	act gca cgt cgt cag cgt agg tca cct	44	5	https://www.ncbi.nlm.nih.gov/nuccore/LC061274.1
Rodent-CoV	KY370043.1	TARRKRR/AL	0.80	37.3%	2	4	0	aca gct cgt cgt aag cgc aga gct ctc	40	3	https://www.ncbi.nlm.nih.gov/nuccore/KY370043.1
Bovine-CoV	MK989624.1	TKRRSRR/AI	0.78	37.5%	2	4	0	aca aaa aga cga agt cgt aga gcg att	31	1	https://www.ncbi.nlm.nih.gov/nuccore/MK989624.1
BCoV-ENT	NC_003045.1	TKRRSRR/SI	0.78	NA	2	4	0	aca aaa aga cga agt cgt aga tcg att	34	1	https://www.ncbi.nlm.nih.gov/nuccore/NC_003045.1
Porcine-CoV	KY419106.1	TSLRSRR/SL	0.76	36.1%	1	3	0	acn tca cti aga tca cgt aga tct cti	41	0	https://www.ncbi.nlm.nih.gov/nuccore/KY419106.1
Beta-CoVsp	MH687976.1	ATRRAKR/DL	0.75	35.9%	1	3	1	gct act cgg cgt gcc aag agn gat tta	37	2	https://www.ncbi.nlm.nih.gov/nuccore/MH687976.1
HCoV-HKU1	KF430197.1	SSRRKRR/GI	0.74	36.8%	2	4	1	tct tct cgg cgt aag cgt aga ggt att	37	2	https://www.ncbi.nlm.nih.gov/nuccore/KF430197.1
Human-CoV OC43	KU131570.1	KTRRSRR/AI	0.73	36.8%	2	4	0	aaa acc aga cga agt cgt aga gcg att	37	2	https://www.ncbi.nlm.nih.gov/nuccore/KU131570.1
Camel-CoV HKU23	KT368891.1	IDRRARR/AI	0.72	36.5%	2	4	0	ata gat aga cga agc cgt aga gcg att	35	1	https://www.ncbi.nlm.nih.gov/nuccore/KT368891.1
Bat-CoV HKU5	KC522102.1	PSARLAR/SD	0.70	37.1%	0	2	0	cct tct gca cgt cti gca agt tca gat	40	3	https://www.ncbi.nlm.nih.gov/nuccore/KC522102.1
Rabbit-CoV HKU14	JN874560.1	TQLPSRR/AI	0.63	37.7%	1	2	0	aca cau tta cgg agt cgt aga gcg att	33	3	https://www.ncbi.nlm.nih.gov/nuccore/JN874560.1
AcCoV-JC34	NC_034972.1	TFSRRAR/AR	0.65	NA	1	3	0	aca ttt tca cgt cgt gcc aga gcc cgt	33	2	https://virology.biomedcentral.com/articles/10.1186/s12985-017-0746-9
MERS-CoV	MK564474.1	LTPRSVR/SV	0.56	35.0%	0	2	0	ctc aca cct cga agt gtg cgc tct gtt	43	2	https://www.ncbi.nlm.nih.gov/nuccore/MK564474.1
Bat-SL-CoV	MG772934.1	HTASILR/ST	0.17	80.3%	0	1	0	cat acg gct tct ata tta cgt agt aca	41	0	https://www.ncbi.nlm.nih.gov/nuccore/MG772934.1
Bat-CoV-RaTG13	MN996532.1	QTQTNSR/SV	0.15	97.4%	0	1	0	cag act caa act aat tca cgt agt gtg	39	0	https://www.ncbi.nlm.nih.gov/nuccore/MN996532.1
SARS-CoV civets	DQ514528.1	QLTPAWR/TY	0.12	76.0%	0	1	0	cag ctc act cca gct tgg cgt ata tat	46	1	https://www.ncbi.nlm.nih.gov/nuccore/DQ514528.1
					[illegible]	[illegible]	[illegible]	[illegible]	736	34	
										[illegible] excluding CoV-2	[illegible] excluding CoV-2

Furin Score https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3281273/

Page 29 has an incomplete reference claiming that WIV has inserted a similar sequence into another CoV spike protein.

I did not find this error.

The argument regarding optimization of binding to ACE2 has essentially become invalidated by the recent evolution of the "variant" that has higher binding than the original. I'll have to dig up the reference.

I disagree with this comment. This variant actually supports the optimized quality of CoV-2 in the initial human infection because it validates a yeast expression experiment showing CoV-2 is 99.45% optimized with real world data.

The recent variant that has higher binding than Reference Sequence CoV-2 and has become the dominant variant has a non-synonymous mutation in the Spike Protein, N501Y.

What is the evidence CoV-2 was optimized and how does the new N501Y fit in?

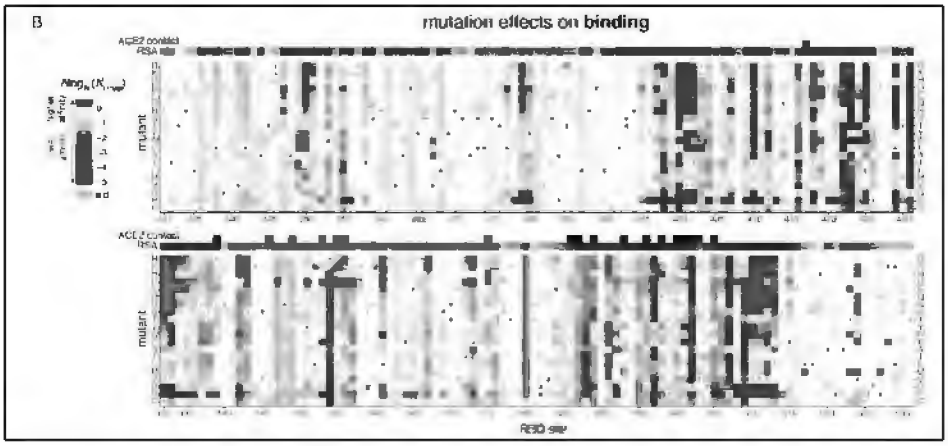
The following is from my analysis.

The receptor binding domain (RBD) of the CoV-2 SP is included in residues 331 to 531, a 201 amino acid sequence, of the SP. To examine the effect of each and every amino acid in each and every position, all 19 different amino acids were changed into all 201 positions of the RBD to the extent possible. Out of a total potential of 3819 different single amino acid variants, the scientists were able to create 3804 of the potential variants or 99.6% of the possible variants. It is probably that the variants with the 0.4% amino acid substitutions could not be made for one reason or another. These 3804 were then tested for binding to the human ACE2. Finally, the RBD from SARS-CoV-1 was also tested.

The Figure below is the result of the experiment. Starting with amino acid 331 and ending with amino acid 531, the amino acids that were changed are in vertical columns and are color coded. Shades of brown are amino acid substitutions that reduce ACE2 binding affinity and blue are amino acid substitutions that improve binding, in all cases compared to the 'native' CoV-2 SP

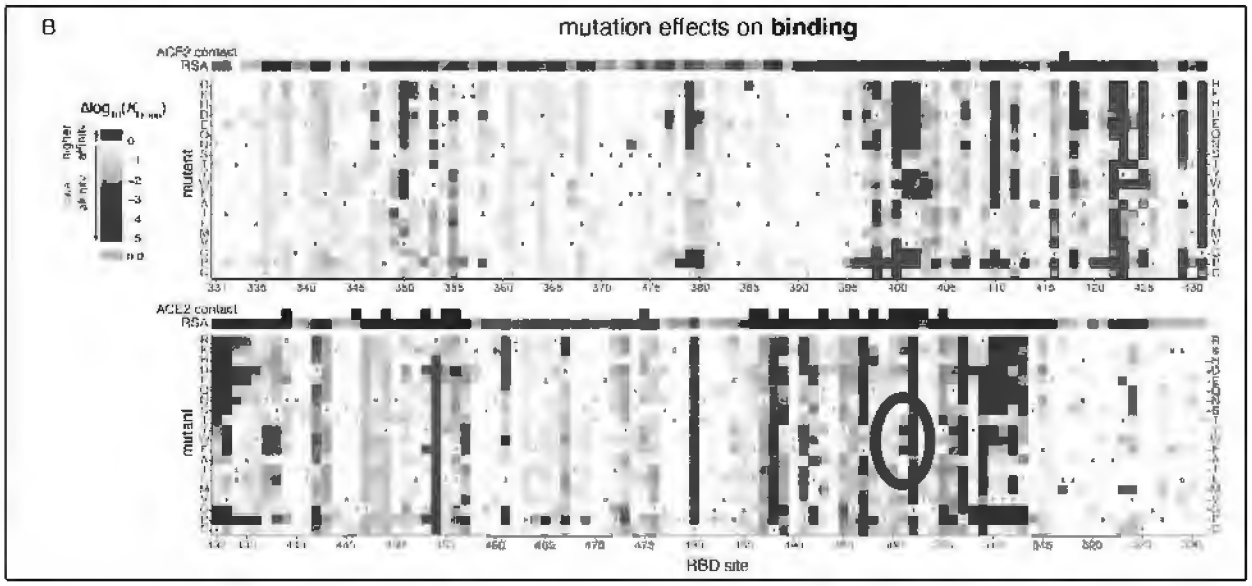
sequence. White is the color of a neutral substitution which neither enhances nor diminishes binding. Only the dark blue substitutions provide a strong improvement in ACE2 binding. There is a black square along the top row that denotes amino acids in the SP that interact with the ACE2 protein. Unlike in the Baric analysis above, in which only five amino acids were considered, this group of 19 amino acids provide a more complete interaction picture.

The first overarching observation is that most amino acid substitutions among the 201 amino acids are negative, while most of the remainder are neutral. The fact that the vast majority of amino acid substitutions do not provide an improved ACE2 interaction is clear evidence that the CoV-2 SP interaction region is not newly evolved to the human ACE2.



There are three levels of potentially improved binding as designated by dark blue, medium blue, and pale blue. Out of the 3804 variants tested, there are 4 dark blue substitutions or 0.11% and 17 medium blue or 0.45%. According to the paper, the binding effect of the light blue could not be measured as different from the native sequence.

What is the impact of N501Y? As shown in the green circle below, this is one of the 4 dark blue circles, the 0.11%, that significantly improves ACE2 binding.



I also had seen an earlier preprint of his with his hypothesis about cases spreading from Wuhan Central Hospital (PLA) via subway line to trains/planes ("line 2 transmission conduit").

The pre-print found the first patient cluster with genome data at the "General Hospital of Central Theater Command of People's Liberation Army of China, located at 627 Wulon Road, Wuchang District, Wuhan" not Wuhan Central Hospital.

The pre-print focused on the first patient "cluster" not the first patient per se. The earliest patient was December 1, 2019 as reported in the *Lancet*.

He says that all patients in December were seen at hospitals served by line 2, but I don't know how he can know this. The Chinese have not been open about where and when cases first arose, and where they were first seen.

I agree with the lack of this information. Included here was the process I undertook to infer the hospital of first admission.

"Unfortunately, the few published reports of early patients in Wuhan in late 2019 and early 2020 are conspicuous in the absence of information of the name of the hospitals where patients were first seen or were transferred between. Vague statements like "(w)e report the epidemiological data of nine inpatients, from at least three hospitals in Wuhan " make it nearly impossible to use early patient demographic data and epidemiologically-useful metadata to contribute to finding the source of CoV-2.

A Lancet paper from Wuhan indicates that there was an effort to consolidate patients in one hospital later in December, but the details are not available. I also was perplexed as was he about the ENA sequence registrations, and asked a colleague with connections at ENA make some inquiries. The long and short of it was that ENA claimed this to be explainable because of the way in which they pre-reserve and time-stamp sequence submission records. It remains not clear to me, and somewhat irregular. But it is even less likely to me that his "first 4 cases" were the first cases. In fact, I think there is reasonable evidence that there were cases in October and early November."

Because in most cases the hospital of admission was not clearly stated for the early patients in Wuhan the hospital was inferred from secondary data. The basis for the inference and a URL link to the primary data are given in the Text-Table below.

Hospital or Institution	Basis for Including in early institutions	URL Source
Wuhan Jinyintan Hospital (designated hospital for COVID)	"Near the end of 2019, a group of strange patients were admitted to Jinyintan's ICU wards."	Life and death at Wuhan's Jinyintan Hospital
Xinhua Hospital	06 Jan 2020 a physician gets sick with COVID-19	BBC China News Feb 1, 2020

Wuhan CDC	Discussed in a Wall Street Journal opinion article 21 April 2020	WSJ article 'Coronavirus and the Laboratories in Wuhan
Tongji Hospital	A Lancet paper with first 41 patients before 02 Jan 2020 has one or more author from this hospital	Lancet paper describing first 41 patients in Wuhan before 02 Jan 2020
Wuhan Asia Heart disease Hospital	Early Jan thoracic surgery outcomes	Clinical course after thoracic surgery
The Central Hospital of Wuhan	A Lancet paper with first 41 patients before 02 Jan 2020 has one or more author from this hospital	Lancet paper describing first 41 patients in Wuhan before 02 Jan 2020
Zhongnan Hospital	A Lancet paper with first 41 patients before 02 Jan 2020 has one or more author from this hospital	Lancet paper describing first 41 patients in Wuhan before 02 Jan 2020
PLA Military Hospital	This paper	NA
Wuhan Institute of Virology	Discussed in a Wall Street Journal opinion article 21 April 2020	WSJ article 'Coronavirus and the Laboratories in Wuhan
Hubei Maternity and Child Health Care Hospital	"From December 8, 2019, to March 20, 2020, we identified 118 pregnant women with Covid-19"	New J of Med Correspondence

I would be cautious in trying to quantify likelihoods among the various scenarios, for a few reasons. Most importantly, there are relatively few numbers on which to base priors regarding known natural and lab-based outbreaks of disease. And each virus and past event tends to be a distinct story, e.g. in terms of transmissibility, distinctness of illness, and host susceptibility. I'm not sure it makes sense to treat them all equally in an attempt to pool and acquire reasonable numbers for the Bayesian analysis.

The analysis includes papers by Daszak and other who are beginning to collect and aggregate data from decades of zoonosis diseases to begin to see patterns that can be used to predict future events.

Furthermore, nucleotide frequencies cannot be treated as independent, equally likely events. There are constraints in nature, as well as dependencies and selective pressures, all of which are uncharacterized; thus, one cannot calculate likelihoods based on a priori equal likelihoods for all occurrences. However, I have not looked at Quay's analysis of codon usage, so don't want to dismiss that necessarily.

The field of relative codon usage bias is well developed with 1247 PubMed reference[4] at the time of this writing. It was these kinds of data that were used for comparisons of unique feature of, for example CoV-2 furin site codon usage.

Furthermore, sampling cannot be assumed to be representative. For example, Quay suggests that the 520 and 1271 negative serological test results in Wuhan and Shanghai can be used, in combination with positive data about SARS and MERS, to refine probabilities about natural versus lab accident. But these numbers are tiny and we have no idea about whether these are representative of the overall population or those at greatest risk in Wuhan and Shanghai.

I cannot agree more that these are small data sets but they are the only ones I have been able to obtain. The size of the data set provides a certain power to the conclusion; the more data, the more power. In the Bayesian analysis this power is reflected in the quantitative correction. So, the reduced weighing because of the sample size is proper accounted for in the analysis, I think.

The data set that established the prior seroconversion for SARS-CoV-1 and MERS at 0.6% was four studies with a total of 12,700 patients.

With respect to Wuhan, the 520 patients were seen with an influenza-like illness in local 'fever clinics' between October 6, 2019 and January 2020. Until the first week of January no PCR-detectable CoV-2 was found. The 1271 in Shanghai were hospitalized with an influenza-like illness from late 2018 to May 2020. The first CoV-2 was seen on January 20, 2020.

I have an unconfirmed report that the China medical system has >100,000 archived specimens that could be used for a robust seroconversion study. This should be one of the 'asks' in the upcoming international investigations.

The lack of SARS-CoV-2 RBD adaptation to the bat ACE2 is something that does need to be addressed: maybe another receptor is used in bats?

In the report I discuss the several orthogonal data which indicate CoV-2 probably doesn't infect most bat species. This seems to reflect an unnecessary assumption of a need for CoV-2 to infect bats. I don't see the need.

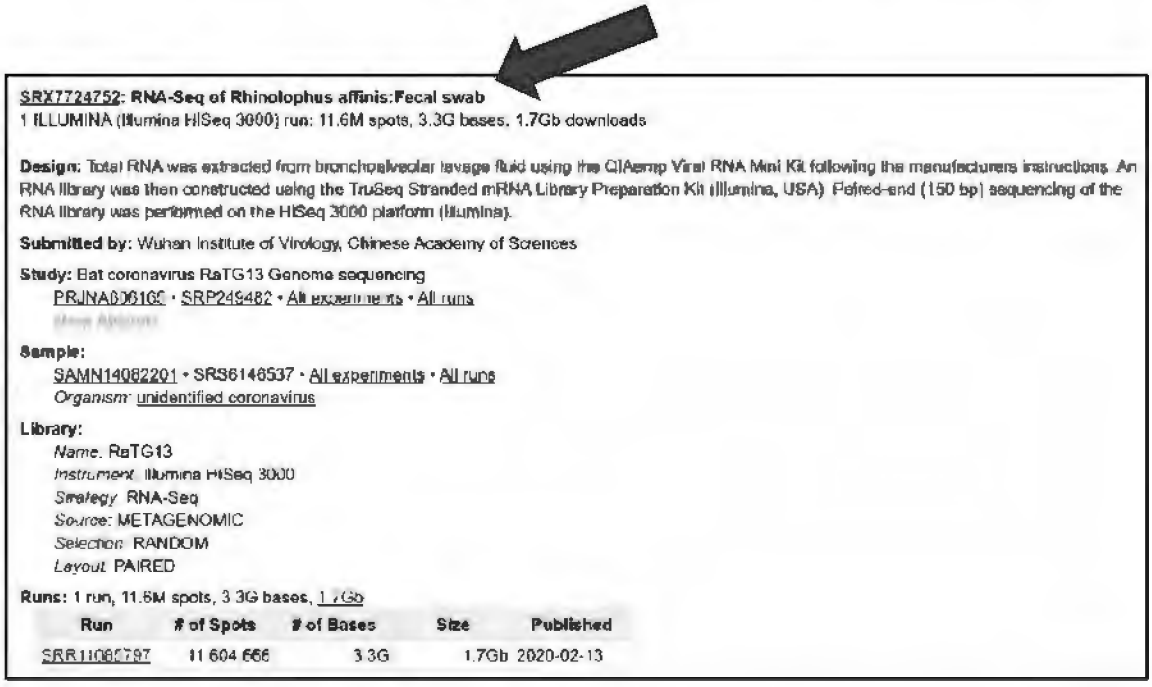
The RaTG13 genome and how it has emerged is quite troubling to me. Quay's analysis bears independent confirmation.

As this information is primarily directed to the credibility of Dr. Shi and secondarily to the origin it has been moved to the Appendix. But I agree it is weighty and should be verified.

As a minor note, he fails to address the possibility that instead of the original sample being a true fecal sample, it was a rectal or anal swab sample from a bat (which WIV describes as part of their sampling protocol). The latter are known to have dramatically increased fractions of host reads versus bacterial/viral reads.

[4] https://pubmed.ncbi.nlm.nih.gov/?term=relative+codon+usage+bias&sort=pubdate

In the GenBank listing, below red arrow, the WIV scientists called the specimen a fecal sample:



SRX7724752: RNA-Seq of Rhinolophus affinis:Fecal swab
1 ILLUMINA (Illumina HiSeq 3000) run: 11.6M spots, 3.3G bases, 1.7Gb downloads

Design: Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit following the manufacturers instructions. An RNA library was then constructed using the TruSeq Stranded mRNA Library Preparation Kit (Illumina, USA). Paired-end (150 bp) sequencing of the RNA library was performed on the HiSeq 3000 platform (Illumina).

Submitted by: Wuhan Institute of Virology, Chinese Academy of Sciences

Study: Bat coronavirus RaTG13 Genome sequencing
PRJNA630169 • SRP249482 • All experiments • All runs

Sample:
SAMN14082201 • SRS6146537 • All experiments • All runs
Organism: unidentified coronavirus

Library:
Name: RaTG13
Instrument: Illumina HiSeq 3000
Strategy: RNA-Seq
Source: METAGENOMIC
Selection: RANDOM
Layout: PAIRED

Runs: 1 run, 11.6M spots, 3.3G bases, 1.7Gb

Run	# of Spots	# of Bases	Size	Published
SRR11085797	11,604,666	3.3G	1.7Gb	2020-02-13

However, the sequences from non-bat animals and primate sequences are very concerning for this not being a bat sample, as advertised. In addition, the region of very high synonymous to nonsynonymous substitutions in comparing RaTG13 to SARS-CoV-2 is not well explained by natural processes.

These comments are appreciated but the RaTG13 treatment has been moved to the Appendix as it does not directly address the origin question.

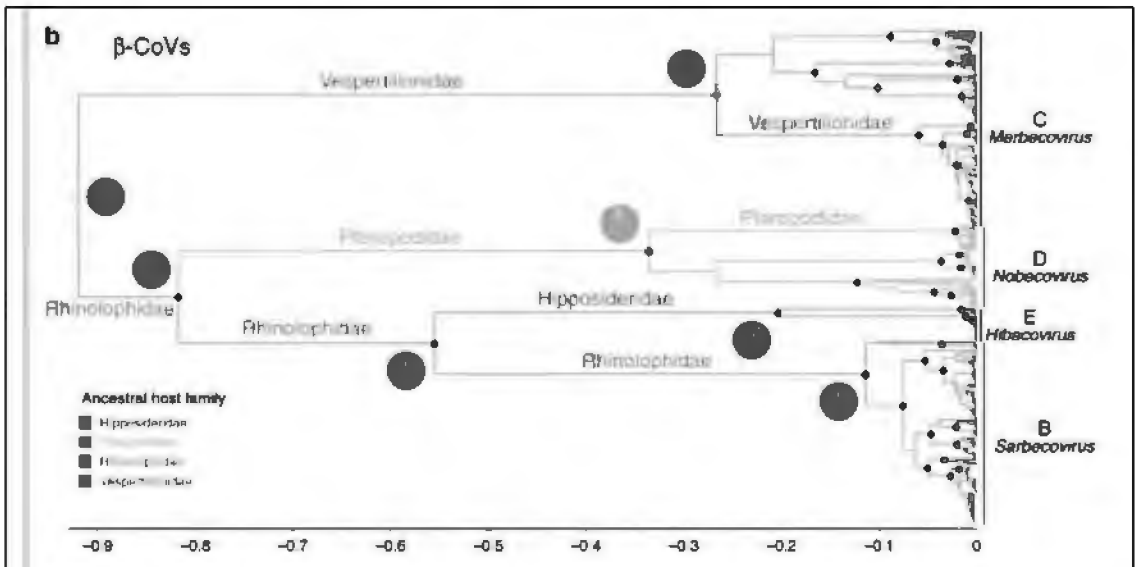
The furin cleavage site story seems to me to have been played up too much. It turns out that FCS's have turned up repeatedly among coronaviruses in nature, so even if it is missing in the closest known relatives of SARS-CoV-2, these relatives are not that close, and other more distant relatives do have an FCS.

(See Yiran Wu, Suwen Zhao, Furin cleavage sites naturally occur in coronaviruses. Stem Cell Research, Volume 50, 2021, 102115, ISSN 1873-5061, https://doi.org/10.1016/j.scr.2020.102115.) All this means is that it could have arisen in SARS-CoV-2 naturally, or one could have had multiple natural examples from which to engineer it into SARS-CoV-2. This doesn't argue it either way.

I disagree with the ease of this happening in nature. The above cited paper of findings related to universal furin site is dealt with in the analysis.

One of the things people seem to forget in looking for ways to get a furin site into a Sarbecovirus, like CoV-2, is that finding a site in another subgenera and hoping for recombination makes things significantly worse.

Remember recombination happens when two viruses infect the same host at the same time. But the four subgenera of the beta coronaviruses have evolved to use different bat hosts for their infection. Daszak of all people gives us the best data on why getting a furin site by recombination is so hard. Here below, from page 58 of my analysis, is the phylogeny tree for which bat species hosts are infected by which viruses.



α-CoV (**a**) and β-CoV (**b**) maximum clade credibility annotated trees using complete datasets of *RdRp* sequences and bat host family as discrete character state. Pie charts located at the root and close to the deepest nodes show the state posterior probabilities for each bat family. Branch color correspond to the inferred ancestral family with the highest probability. Branch lengths are scaled according to relative time units (clock rate = 1.0). Well-supported nodes (posterior probability > 0.95) are indicated with a black dot. The ICTV approved CoV subgenera were highlighted: *Rhinacovirus* (L1), *Decacovirus* (L2), *Myotacovirus* (L3), *Pedacovirus* (L5), *Nyctacovirus* (L6), *Minunacovirus* (L7), and an unidentified lineage (L4) for α-CoVs; and *Merbecovirus* (Lineage C), *Nobecovirus* (lineage D), *Hibecovirus* (lineage E), and *Sarbecovirus* (Lineage B) for β-CoVs.

Note that the bat host family for CoV2 (Sarbecovirus) is Rhinolophidae and for MERS (Merbecovirus) is Vespertilionidae and these are in fact the farthest apart of all the subgenera. So these two virus subgenera have spent a long time learning to live in different bat hosts.

This greatly reduces (eliminates?) the co-infection recombination theory with data from Daszak himself.

The current analysis highlights a new finding (adenovirus sequences in COVID patients at the end of December). Again, intriguing. But I need to make clear that I have not independently looked at the sequence data or tried to verify his sequence similarity hit. But there are some important caveats and cautions needed here. Unless one has a contiguous sequence read across adenovirus and payload (immunogen), one cannot know that one is not looking at a naturally-occurring respiratory adenovirus infection.

Furthermore, the Chinese vaccine adenovirus vectors with which I am familiar are replication-defective (E1/E3 mutants), so they cannot propagate for more than one round of replication in the host. To find them in the throat would have to mean that they were delivered there quite recently.

I find contiguous reads of about 2000 nts from the Expression vector pShuttle-SN" (Genbank AY862402.1). These are not wildtype adenovirus sequences but the 'synthetic sequences' shown in the above GenBank reference.

These include the 1-989 which are the vector and then the reads into the immunogen. Looks like some have the SARS-CoV-1 spike protein gene as well as the synthetic H7N9 influenza sequence. It was suggested by a collaborator it might have been a kind of 'universal vaccine.'[5]

In addition, there are hundreds of reads with 150/150 nt identity in these patients. Seven patients from the same hospital, sampled on the same day, December 30, 2019, have been examined. The five patients whose samples were sent to the WIV have the pShuttle sequences and the two sent to the Hubei CDC do not.

This could be a smoking gun but I need help to finish this adenovirus work. I would enjoy collaborating with someone with legitimate Blast, bio-IT experience who wants to help me.

Bottom line: Both origin hypotheses/scenarios (natural spillover and lab accident) remain 'on the table' and plausible. (So does the third scenario, deliberate release, although it would appear much less tenable in terms of logic.) I don't see how one can dismiss either of these 2 hypotheses with currently available information, nor can I see how one can currently arrive at precise likelihoods for the two with open source information and whatever the mathematical method. The amount of data relevant to a more refined understanding about each, is miserably poor. I personally do feel that the lab accident scenario is likely enough to warrant investigation and a deliberate, open, global discussion. The strongest arguments for the lab accident scenario include co-localization of what is probably the world's largest collection of bat coronavirus-containing samples and lab activity to characterize and understand them, with the first known cases of COVID, while the known reservoirs of the closest related viruses reside 1000 miles away; plus the plausibility of a an accidental lab release, especially with this virus; plus the deliberate efforts by the Chinese to conceal relevant and useful data, or release only partial data, or release confusing data, about the origins of disease and the virus in China.

Agreed.

We don't need fancy mathematics or statistics. We need hard, verified, new information and data "from the ground": samples from nature, samples from labs, data from labs—including lab notebooks, communications, sequencing data, all from the earliest time points, as well as case surveillance data, blood samples and serologies, all of which is time-

[5] Personal communication from H. Lawrence Remmel, Department of Pathology, University Medical Center Utrecht, Utrecht University, Utrecht, The Netherlands.

stamped with provenance verified. Will we get all of this? Probably not. But it doesn't mean that we shouldn't try.

Agree with the higher-level evidence value of primary data from the WIV laboratories but we simply don't have it.

The report appears to dismiss other contending theories of viral origin, it alludes to GOF genomic manipulation, and discounts conventional zoonotic spread theories.

I would need more details of the conventional zoonotic spread theories spoken of to respond.

The cumulative circumstantial evidence that SARS-CoV-2 came from a laboratory is beyond a reasonable doubt

Evidence of adenovirus vaccine experimentation by the Wuhan Institute of Virology in hospitalized COVID-19 patients in December 2019 is documented

Executive Summary.

The one-year anniversary of the COVID-19 pandemic records 1.85 million deaths, 85.5 million confirmed cases, and trillions of dollars of economic damage. Although there is universal agreement that a coronavirus identified as Severe Acute Respiratory Syndrome Coronavirus 2 or SARS-CoV-2 (abbreviated CoV-2 henceforth) causes the disease COVID-19, there is no public understanding and consensus of the origin of the disease.

The Chinese government, WHO, media, and many academic virologists have stated with strong conviction that the coronavirus came from nature, either directly from bats or indirectly from bats through another species. Transmission of a virus from animals to humans is called a zoonosis.

A small but growing number of scientists have considered another hypothesis; that an ancestral bat coronavirus was collected in the wild, genetically manipulated in a laboratory to allow it to infect human cells and to make it more infectious, and then it was released, probably accidentally, in Wuhan, China. For most of 2019 this theory was considered a crackpot idea but in the last few weeks there has been more media attention on the possibility that the Wuhan Institute of Virology, in central Wuhan, may have been the source of the laboratory genetic manipulation and subsequent leak.

Given the majority bias in favor of a zoonosis and the massive effort undertaken by China to find an animal source, for political reasons, one can assume that any evidence in favor of a natural origin, no matter how trivial, would be widely disseminated. This provides a potential evidence bias in favor of a natural origin which isn't quantified but should be kept in mind.

This also becomes important when evidence can be used to support a laboratory origin that has been directly provided by leading Chinese scientists themselves, like Dr. Zhengli Shi, head of coronavirus research at the Wuhan Institute of Virology, by the Chinese government, or by powerful and vocal, pro-natural origin scientists, like Dr. Peter Daszak, of the NYC-based NGO, EcoHealth Alliance.

The report uses Bayesian inference, a common statistical tool in which Bayes' theorem, a well-known statistical equation, is used to update the likelihood for a particular hypothesis as more evidence or information becomes available. It is widely used in the sciences and has begun to be used in the law.

The starting probability for the zoonotic or natural hypothesis was set at 98.8% with the laboratory origin set at 1.2%. Each piece of new evidence for or against each hypothesis is then

used to adjust the probabilities. If evidence favors a natural origin the math adjusts upward the probability of a natural origin, and so on.

The final probability in this report of a laboratory origin for CoV-2 was 98.9% with a corresponding probability of zoonotic origin as 1.1%. This exceeds most academic law school discussions of quantifying 'beyond a reasonable doubt' in legal terms. The report contains the detailed quantitative basis for the statistics and can be referred to if necessary.

The following Text-Table summarizes the 21 pieces of evidence that were examined in this analysis and the change in probabilities of the origin for each step:

Evidence	Zoonotic Origin	Laboratory Origin
Initial State	98.8%	1.2%
Lack of evidence of prior seroconversion in China	95.0%	5.0%
Lack of posterior diversity	66.0%	34.0%
Lack of furin cleavage sites in any other sarbecovirus	17.7%	82.3%
Rare useage of -CGG- single codons & no CGG-CGG pairs	2.6%	96.9%
Routine use of CGG in laboratory codon optimization, including Daszak & Shi	1.1%	98.8%
Spike Protein receptor binging region (200 amino acids) optimized for humans	1.1%	98.9%
Whole genome analysis shows pre-adaption of CoV-2	1.1%	98.9%
The finding of CoV-2 in Barcelona wastewater in early 2019 was an artifact	1.1%	98.9%
Shi and the WHO comment early on that CoV-2 seemed to begin with a single patient	1.1%	98.9%
Mammalian biodiversity between Yunnan and Hubei is limited, reducing candidates for intermediate host	1.1%	98.9%
The ancestor of CoV-2 can only obtain a furin site from other subgenera viruses but recombination is limited/non-existent between subgenera	1.1%	98.9%
Canvas of 410 animals shows humans and primates are the best, bats are the worst, for ACE2-Spike Protein interaction	1.1%	98.9%
A government requested review of samples collected from a mineshaft may have caused the COVID-19 pandemic	1.1%	98.9%
The Hunan Seafood Market was not the source of the pandemic	1.1%	98.9%
Line 2 of the Wuhan Metro System is the likely conduit of the pandemic and is the subway line used by WIV employees	1.1%	98.9%
Feral and domestic cats are not the intermediate host	1.1%	98.9%
Extraodinary pre-adaption for the use of human tRNA is observed	1.1%	98.9%
Evidence of Lax and disregard of laboratory safety protocols and regulations in China	1.1%	98.9%
Previous SARS-CoV-1 laboratory accidents	1.1%	98.9%
Shi and Daszak use Wuhan residents as negative control for zoonotic coronavirus exposure	1.1%	98.9%
Appendix Information		
Evidence that Dr. Shi has published contrived data, making the credibility of everything she says suspect		
Evidence for and against RaTG13 as the direct precursor of CoV-2, I have not made up my mind on this important		
Remarkable evidence of the synthetic Adenovirus vector vaccine in patients sequenced at the WIV		

The summary which follows will simply be a review and discussion of the evidence in the context of the two hypotheses.

A zoonosis has at least three elements, a host, a virus, and the human population. With some viruses there is often a 'reservoir host' where the virus can live for years or even decades in a relatively stable relationship. The reservoir host is never decimated by the virus and the virus is never burned out by the reservoir host, disappearing completely. For coronaviruses the reservoir host is always one or more kinds of bat species.

For two prior human coronavirus epidemics, an intermediate or proximate host was identified. For SARS-CoV-1 in 2003-4 it was the civet cat while for Middle Eastern Respiratory Syndrome (MERS) in 2012-4 it was the camel. In both of these human epidemics the intermediate host was identified within four to ten months of the first clinically identified human infection. With CoV-2 we are at 12 months and still waiting, despite a much larger effort inside China. For both of these pandemics a bat species reservoir host was also identified.

Based on the genome sequence of CoV-2, Dr. Shi and Daszak have proposed that the reservoir host for CoV-2 is the intermediate horseshoe bat (*Rhinolophus affinis*), which lives in Yunnan Province. Yunnan Province is in southern, rural China and about 1900 km from the north central province of Hubei, where the 11 million people of Wuhan live. In the US it would be the distance and difference between the Everglades of Florida and New York City. The intermediate horseshow bat isn't found in Hubei province making a direct bat-to-human transmission improbable. Experiments in three independent laboratories also demonstrate that CoV-2 has changed genetically so much that it can no longer infect any bat species tested. So, while the leading US coronavirus expert, Dr. Ralph Baric of The University of North Carolina stated in early 2020 that CoV-2 may have jumped into the human population directly from bats without an intermediate host, this hypothesis is no longer viable.

For the zoonosis hypothesis to be advanced, it is now required to find an intermediate host. In December 2019 a theory was proposed that CoV-2 arose in the Huanan Seafood Market, a traditional Chinese "wet market" where live animals are butchered and sold. This theory was based on the observation that about 40% of early patients worked or shopped there. This was reminiscent of the wet market sources for civet cats for SARS-CoV-1 or the camel markets for MERS. The Chinese authorities closed the market on December 31, 2019 after performing extensive environmental sampling and sanitation.

But by May, 2020 Gao Fu, Director of the Chinese CDC, announced that the market was not the source of CoV-2 as all of the animal specimens were negative for CoV-2. And while SARS-CoV-1 was found in 100% of farmed civets when tested, CoV-2 was different. In July 2020 Dr. Shi reported that extensive testing of farmed animals in Hubei Province failed to find CoV-2. For about six months the pangolin, a scaly anteater, was suspected to be the intermediate host but finally Dr. Daszak had to report that CoV-2 was not found in pangolins in the wild or from the (illegal) market trade. Domestic and feral cats were also ruled out as a possible source. A comprehensive computer-based screen of 410 different animals reported the remarkable finding that the best hosts were primates (or primate cells) and included the favorite laboratory coronavirus host, the VERO monkey cell culture, and that all bats were the worst host. At the time of the writing of this report there is not even a working hypothesis of what is the intermediate host.

A zoonosis has a number of characteristic properties that can allow identification as a zoonotic infection even in the absence of finding an intermediate host. None of these properties are found for CoV-2.

They all have in common the principle that when nature uses evolution to allow a virus to move from, for example, a bat host to a camel host to a human host, it is a hit and miss, slow process. After all, evolution is random genetic changes, mutations, and then enrichment of the ones that are helpful by amplification during reproduction. With both SARS-CoV-1 and MERS, the virus spent months and years jumping from the intermediate host into humans, not having all of the best mutations needed to be aggressive, grow, and then spread, but enough to cause an infection and an immune response.

The hallmark evidence of this 'practice' in host jumping is in the stored or archived human blood specimens from before the epidemic, where one can find antibodies to the eventual epidemic virus. For SARS-CoV-1 and MERS, about 0.6% of people in the region where the epidemic began show signs of an infection in archived blood. With CoV-2, this seroconversion, as it is called, has never been found, including in over 500 specimens reported by the WHO. Because this is such a potent signal of a zoonosis and because we believe that China has over 100,000 stored specimens from Wuhan taken before 2020, the lack of reports of seroconversion, the silence from China on this, speaks volumes.

Another hallmark of this same, slow natural process can be found in the virus. In SARS-CoV-1 and MERS the coronavirus spent years in the intermediate host, passing back and forth among the hosts living in close proximity. During this time, they would accumulate a background of genetic mistakes, mutations. Usually about one mistake every two weeks. When the final chip falls and a mutation happens allowing the jump into humans, the virus with that new mutation also jumps around in the intermediate host population. The consequence of this latter behavior for a true zoonosis is that the genome sequences found in humans don't all descend from a single jump into a single human but show jumps from viruses that are only cousins of each other, not direct descendants. In a true zoonosis the family tree doesn't pass back through the first patient but instead meets together in an ancestor months or years earlier. This is called posterior diversity and is an easy genetic test to perform. With CoV-2, every one of the more than 200,000 virus genomes sequenced an be traced back to the first genomic cluster and patient, who was seen at the People's Liberation Army (PLA) Hospital about one mile from the Wuhan Institute of Virology. CoV-2 has the genetic signature of one pure virus sequence infecting one human; that is the one and only jump into the human population ever seen. This lack of posterior diversity has been reported by Dr. Shi, the WHO, and other prominent virologists; they just never take the evidence to the proper inference.

The virus in a zoonosis also contains the signatures of the gradual changes and adaptions it made in the protein key, the Spike Protein, it uses to unlock our cells and cause infection. With SARS-CoV-1 the first jump into humans had less than one-third of all the changes it would develop by the time it became an epidemic. With CoV-2 it was almost perfectly adapted to the human lock, with only a 0.5% improvement possible. The new strain that began in the UK was one of the 0.5% improvements for the virus.

Since with CoV-2 we have no evidence from stored blood that it was quietly practicing on humans in the community it is surprising that when it finds its first person, it has perfected to 99.5% its human attack ability. If this adaption couldn't have happened in the community, the only place it could have done this adaption work is in a laboratory, by what is called serial passage, repeatedly giving the virus a chance to practice on humanized mice or VERO cells. A related study of which of dozens of protein manufacturing tools CoV-2 uses (called tRNAs) shows the same uncanny adaption to the human tools with no evidence that the tools from other potential intermediate hosts would be suitable.

The evidence presented makes a strong case that CoV-2 did not come from nature but is there affirmative evidence that it came from a laboratory? The answer is yes.

The spike protein that gives the coronavirus its name, corona or crown, is the key to match with the lock found in host cells. But before it can inject its genetic material in the host cell, the spike protein needs to be cut, to loosen it in preparation for infection. The host cell has the scissors or enzymes that do the cutting. The singular unique feature of CoV-2 is that it requires a host enzyme called furin to activate it. No other coronavirus in the same subgenera have a furin cleavage site, as they are called. This is of course a major problem for the zoonosis theory, but it gets worse. Since 1992 the virology community has known that the one sure way to make a virus more deadly is to give it a furin site in the laboratory. At least eleven gain-of-function experiments, adding a furin site to make a virus more deadly, are published in the open literature. This has caused a flurry of Chinese papers trying to show a natural furin site in a related virus (later shown to be an error in interpretation) or to show that furin sites from distant cousins of CoV-2 might be the source through a process called recombination, where two viruses infect the same host and then make a mistake in copying their genetic material, and swap sequences. These hypothetical methods fail because the viruses that have furin sites are found in different host bats, in different regions of China, and even with these barriers, in the lab they are too far apart to recombine.

But it gets worse for the zoonosis theory. The gene sequence for the furin site in CoV-2 is a very rare set of codons, three letter words, that are never used together by coronaviruses in nature but are always used together by scientists in the laboratory when they want to add amino acids that code for the furin site. When scientists want to add an arginine codon to a coronavirus, they invariably use the word, CGG, but coronaviruses in nature rarely (<1%) use this codon.

So, there is no example of a furin protein site in nature that could be introduced into CoV-2 by recombination, there is no example of the particular gene sequence for the furin protein site of CoV-2 being used to code for anything in nature, but this particular coding is exactly what Dr. Shi and others have used in published experiments to insert genetic material.

It is telling that when Dr. Shi introduced the world to CoV-2 for the first time in January 2020 she showed hundreds of gene sequences of this novel virus but stopped short of showing the furin site, the one she had introduced, seemingly not wanting to call attention to her handywork. She apparently failed to realize that an accomplished but innocent virologist, finding the first furin site in this class of viruses apparently coming from nature, would have featured the

presence of the furin site prominently and would also predict from her experience what it would foretell for the world due to its aggressive nature.

Dr. Shi has denied the virus came from her lab, but she now created a record of multiple examples of obfuscation, half-truths, contrived specimens, genetic sequences taken from thin air, etc. that her veracity is deeply damaged. Perhaps her words and actions on December 30, 2019 show the truth. Her very first response when told there was an unknown outbreak in Wuhan and to return back quickly from a meeting in Shanghai was, "Could this have come from our lab?" Her other action on December 30 was to alter WIV computer databases of novel coronaviruses used by the world's virologists for research to make it more difficult to search for coronaviruses she had in her building. So the day the pandemic began in Wuhan she chose to cover up her work at the expense of transparency and cooperation.

The notion that CoV-2 was a laboratory creation, designed for maximum virulence, that escaped the laboratory accidentally has additional rings of evidence. From President Xi announcing in February new laws about laboratory security, to abundant evidence that the WIV was closed in October, to the top military medical research doctor, General Chen Wei, being placed in charge of the WIV, and many more, it is clear an event occurred sometime in late 2019 that is most consistent with a laboratory escape.

The Asian region has a two-decade record of a little over one laboratory-acquired infection per year. After the first SARS-CoV-1 patient and the epidemic was ended, SARS-CoV-2 jumped six more times into the human population, all from laboratories, with two in China. The last smallpox death was a secretary two floors above a research lab in England, who contracted it through the ventilation system. Over and over again there is a history and record of laboratory acquired infections that provides the background for considering what happened here.

But was SARS-CoV-2 more than just a gain-of-function experiment that escaped a laboratory? Could it have been one part of a two-part novel virus-vaccine bioweapons program?

General Ben Wei has been involved in vaccine research since joining the PLA after college. In a 2017 internal speech at the AMMS (Academy of Military Medical Sciences) she said: *"只要有矛. 才能研究盾."* which translates roughly as, "you need to have an arrow to study a shield."

In this context, genetic sequence evidence of an adenovirus vaccine used and developed by the Chinese has been found in five ICU patients from a Wuhan hospital in December 2019 who also had SARS-CoV-2 in their throat swab specimens. The Wuhan Institute of Virology conducted the sequencing on these specimens. This would be consistent with a vaccine challenge trial. There is evidence of an emerging H7N9 influenza component as well, as if this was a universal vaccine program.

I believe a Rubicon has been crossed by the world with this pandemic and framing the proper understanding of how we got here and the proper response will be the critical next steps.

When Oppenheimer saw the application of Einstein's physics in the embodiment of the atomic bomb he is said to have quoted a line from the Hindu scripture, the Bhagavad Gita, which reads: 'Now I am become Death, the destroyer of worlds.' The contribution of physics' research to human killing would total less than 300,000 people in two ten-square mile zones in Japan but would lead the world to regulate the raw materials of such bombs and to sanction sovereign nations who attempted to violate the rules.

This had followed on the contribution of chemistry to human killing in the form of chemical warfare during World War I, in which 100,000 were killed, and which led the nations of the world to an historic agreement to never use chemical warfare again. It is now only 'rogue' operators who violate the norms civilized nations have agreed to.

It seems to be biology's turn to show its dark arts. If it is generally understood that biology/biotechnology has been harnessed to create a pandemic that has killed more people than either physics or chemistry research combined and to be a weapon where no place on earth is safe from its effects (SARS-CoV-2 has been detected in the deepest Amazon jungles and at research stations in Antarctica), there needs to be developed a new set of regulations, rules, etc. to both honor the 1.8 million innocent people who died from COVID-19 and to protect the world so this never happens again. It is also urgent to gather further data to support or refute if this was a Chinese bioweapons program, as the consequences of that would be significant.

The cumulative circumstantial evidence that SARS-CoV-2 came from a laboratory is beyond a reasonable doubt

A two-hypothesis, Bayesian analysis was conducted to determine the origin of the SARS-CoV-2. The conclusion was that it was created in a laboratory with synthetic biology tools from a bat beta coronavirus, subgenera sarbecovirus backbone (98.9% probability) and not from a natural, zoonotic transmission (1.1%).

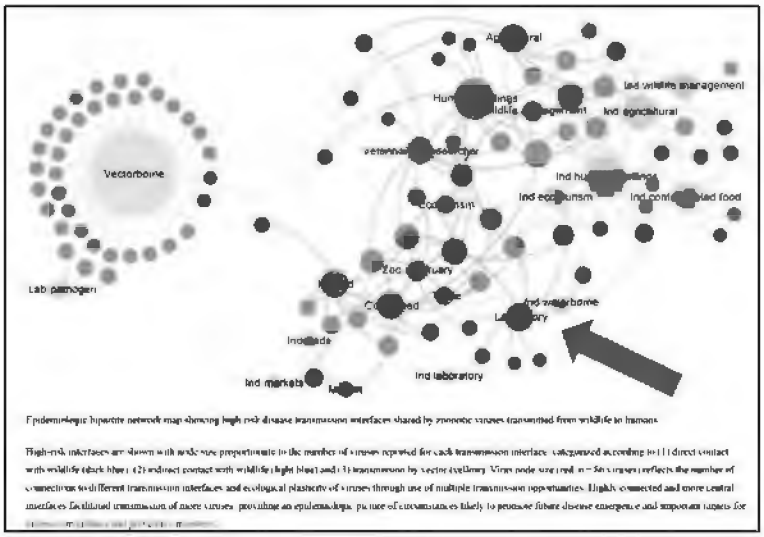
There is no direct evidence of whether the release was accidental or deliberate but circumstantial evidence makes it is highly likely it was accidental.

The most unusual evidence presented, which has not been fully reconciled, is the finding of adenovirus vaccine vector sequence data in human nasopharyngeal lavage specimens taken the end of December from ICU patients at Wuhan Jinyintan Hospital and sequenced at the Wuhan institute of Virology. A high priority of current research is understanding why these patients had vaccine vector sequences, as if from a nasally administered vaccine, and what the vaccine was directed against (it is not directed to Spike Protein from SARS-CoV-1 nor from the codon optimized SARS-Cov-2 Spike Protein). This data is contained in the Appendix.

Introduction. At the one-year anniversary of the first cases of COVID-19, the coronavirus pandemic caused by the SARS-CoV-2 virus, the origin of the virus remains unknown. While leading institutions and experts have been consistently adamant that it is a zoonotic disease which jumped from a bat reservoir host to humans directly or through an intermediate host the alternative possibility that it escaped from a laboratory conducting research remains a viable option.

In fact, in 2015 Peter Daszak, a leading zoonotic proponent of CoV-2 origin, wrote in, "Spillover and pandemic properties of zoonotic viruses with high host plasticity,"[1] that transmission from laboratories was a major source of zoonotic disease. The Figure below from the Daszak paper shows this important relationship (green arrow):

[1] https://www.nature.com/articles/srep14830

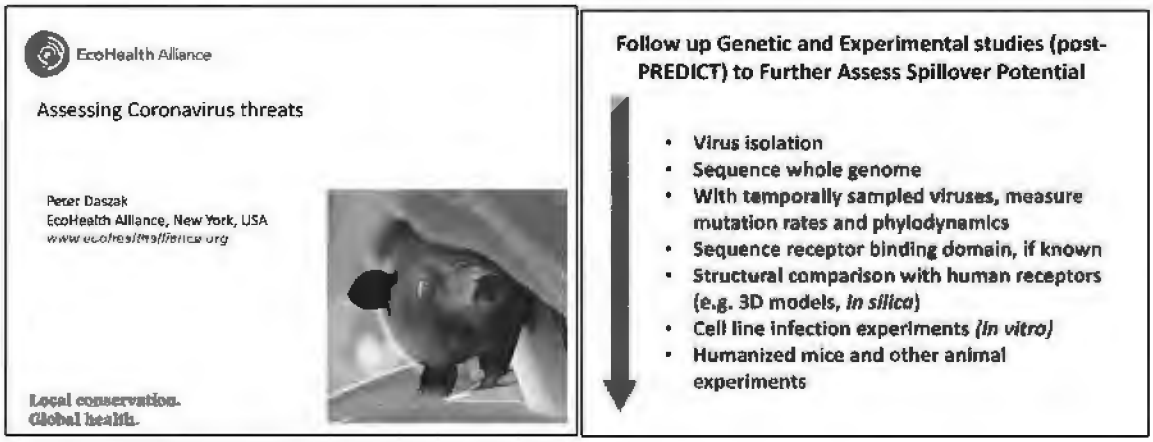


Epidemiologic hypernetwork map showing high-risk disease transmission interfaces shared by zoonotic viruses transmitted from wildlife to humans

High-risk interfaces are shown with node size proportionate to the number of viruses reported for each transmission interface, categorized according to (1) direct contact with wildlife (dark blue), (2) indirect contact with wildlife (light blue) and (3) transmission by vector (yellow). Virus node size (red; n = 56 viruses) reflects the number of connections to different transmission interfaces and ecological plasticity of viruses through use of multiple transmission opportunities. Highly connected and more central interfaces facilitated transmission of more viruses, providing an epidemiologic picture of circumstances likely to perpetuate future disease emergence and important targets for

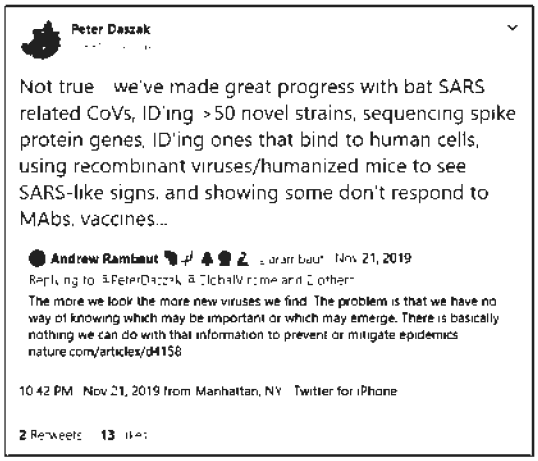
Daszak et al. also writes: "**Zoonotic virus spillover** from wildlife was most frequent in and around human dwellings and in agricultural fields, as well as **at interfaces with occupational exposure to animals** (hunters, laboratory workers, veterinarians, researchers, wildlife management, zoo and sanctuary staff). **Primate hosts were most frequently cited as the source of viruses transmitted by direct contact** during hunting (exact P = 0.051) and **in laboratories** (exact P = 0.009)." [Emphasis added]. Primate "hosts" can presumably include monkey cell culture, such as the ubiquitous VERO cell used in all virology laboratories, including the WIV.

In 2015 Dr. Daszak spoke of the spillover danger of certain types of laboratory research:



He writes: "with each step, increased risk possible" with "Humanized mice and other animal experiments" the highest risk work.

In a prescient Twitter post in November 2019, he highlights the work he is doing using recombinant viruses with humanized mice and making viruses that "**don't respond to MAbs, vaccines…**" in response to criticism his work is of limited value:



Clearly, before the beginning of the pandemic, Daszak, a member of both the WHO and Lancet teams being sent to China to explore the origin of CoV-2, could entertain the possibility of a laboratory created virus escaping into the human population/community.

The purpose of this analysis is to use a Bayesian Network approach to the collected evidence that is available to provide likelihoods of the alternative hypotheses as to the origin of SARS-CoV-2. The analysis will also include certain prior probabilistic conclusions to help set the initial state before the proprietary evidence is used.

Origin hypotheses: Initial States to establish the posterior probabilities.

Two published Bayesian analyses and two independent studies of zoonotic spillover from nature and laboratory-acquired infections in Asia will be used to establish the posterior probabilities for this analysis.

Zoonotic spillover frequency versus laboratory acquired infection frequency based on two published papers, one by Daszak et al.

In 2015 Daszak et al. published a paper entitled, "Spillover and pandemic properties of zoonotic viruses with high host plasticity,"[1] in which they identified 162 zoonotic viruses with naturally occurring animal-to-human transmission from 1990-2010. This is a frequency of 162/20 = 8.1 events per year.

They also note: "The majority (94%) of zoonotic viruses described to date (n = 162) are RNA viruses, which is 28 times higher (95% CI 13.9–62.5, exact P < 0.001) than the proportion of RNA viruses among all vertebrate viruses recognized, indicating that RNA viruses are far more likely to be zoonotic than DNA viruses." CoV-2 is an RNA virus.

Finally, they note that: "In general, wild animals were suggested as the source of zoonotic transmission for 91% (86/95) of zoonotic viruses compared to 34% (32/95) of viruses transmitted from domestic animals and 25% (24/95) with transmission described from both wild and domestic animals."

One of the caveats of the Daszak data is that it categorizes a laboratory-acquired infection (LAI) from an animal acquired in the wild as a zoonotic spillover. There is no data in the paper to assess this issue and leaving it uncorrected is a conservative approach since it only inflates the zoonotic frequency.

In 2018 a paper by Siengsanan-Lamont entitled, "A Review of Laboratory-Acquired Infections in the Asia-Pacific: Understanding Risk and the Need for Improved Biosafety for Veterinary and Zoonotic Diseases," was published.[2] They reported 27 LAIs between 1982 and 2016, a frequency of 27/(2016 – 1982) = 0.8 events per year.

Using these historical frequencies of zoonotic spillover versus LAI to predict a future event can be calculated in the following manner:

Evidence	Zoonotic Origin	Laboratory Origin
Frequency per year from Daszak paper	8.1	NA
Frequency per year from Siengsanan-Lamont paper	NA	0.8
Total events per year	8.1 + 0.8 = 8.9	8.1 + 0.8 = 8.9
Likelihood of future event based on historical frequency	8.1/8.9 X 100 = 0.91	0.8/8.9 X 100 = 0.9

Initial state analysis. This evidence sets the likelihood that CoV-2 was a zoonotic origin event at 91% and a laboratory origin event at 9%.

[2] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6073996/

Independent prior analyses: Rootclaim.

The next data that will be used is a recent analysis published on the Rootclaim website.[3] Three hypotheses below were analyzed through a series of evidence statements and the probabilities that each was the origin of SARS-CoV-2 determined:

Hypothesis	Calculated Probability
Lab escape: The virus was the subject of genetic research, including gain-of-function, and was released by accident	81%
Zoonotic: The virus evolved in nature and was transmitted to humans from a non-human vertebrate animal	16%
Bioweapon: The virus was genetically engineered as a bioweapon and was deliberately released	3%

As can be seen, the highest likelihood probability is a lab escape. The details of the evidence used to arrive at this conclusion is contained in Appendix 1. A summary of the changes in probability at each level of evidence analysis is shown in this table:

Evidence	Laboratory	Zoonosis	Bioweapon
Starting point	1.2%	82%	16%
Contagion and mortality	1.4%	97%	1.9%
Outbreak location: Wuhan	42%	56%	2.8%
Virus sources near Wuhan	16%	83%	1.0%
Chimera	37%	60%	2.5%
Furin cleavage	72%	23%	4.8%
WIV lab procedures	80%	17%	3.5%
WIV disassociation	89%	9%	2.0%
Chinese response	90%	8%	1.7%
No reported infections at WIV	86%	11%	2.4%
No whistleblowers	81%	16%	2.8%

As can be seen, the starting point assumed an 82% probability of a zoonotic origin. This starting point is a reasonable value.

For purposes of this analysis only the Rootclaim initial state will be used since much of their evidence is also covered in the analysis here.

In a paper by Daszak and colleagues it states: "In general, wild animals were suggested as the source of zoonotic transmission for 91% (86/95) of zoonotic viruses compared to 34% (32/95) of viruses transmitted from domestic animals and 25% (24/95) with transmission described from both wild and domestic animals."[1]

[3] https://www.rootclaim.com/analysis/what-is-the-source-of-covid-19-sars-cov-2

On the other hand, domestic animals seem to have been ruled out for SARS-CoV-2. In an interview for *Science* in July 2020, Dr. Zhengli Shi, head of coronavirus research at the Wuhan Institute of Virology, stated: "Under the deployment of the Hubei Provincial Government, our team and researchers from Huazhong Agricultural University collected samples of farmed animals and livestock from farms around Wuhan and in other places in Hubei Province. We did not detect any SARS-CoV-2 nucleic acids in these samples."[4]

Reanalysis of Rootclaim initial state to remove Bioweapons option.

The US government uses the following definitions:

"Gain-of-function (GOF) studies, or research that improves the ability of a pathogen to cause disease, help define the fundamental nature of human-pathogen interactions, thereby enabling assessment of the pandemic potential of emerging infectious agents, informing public health and preparedness efforts, and furthering medical countermeasure development.

Gain-of-function studies may entail biosafety and biosecurity risks; therefore, the risks and benefits of gain-of function research must be evaluated, both in the context of recent U.S. biosafety incidents and to keep pace with new technological developments, in order to determine which types of studies should go forward and under what conditions."[5]

"Dual use research of concern (DURC) is life sciences research that, based on current understanding, can be reasonably anticipated to provide knowledge, information, products, or technologies that could be directly misapplied to pose a significant threat with broad potential consequences to public health and safety, agricultural crops and other plants, animals, the environment, materiel, or national security. "[6]

For this analysis, the assumption is made that GOF and DURC are largely the same processes and techniques in the laboratory and thus can only be distinguished by direct, documentary evidence of the intent of the research from administers in the facilities conducting the work.

In the absence of any such documentary evidence that bioweapon research was being conducted or that SARS-CoV-2 is a bioweapon and to take the least inflammatory posture, the initial state for the above prior analysis will be recalculated by eliminating the hypothesis, and its accompanying probability, that SARS-CoV-2 was created as a bioweapon. The revised initial state calculation is shown in this table:[7]

Evidence	Zoonotic Origin	Laboratory Origin	Bioweapons Origin
Rootclaim initial state	0.86	0.012	0.16
Remove bioweapons	NA	NA	0
Normalize remaining hypotheses	0.86/(0.86 + 0.012) = 0.986	0.012/(0.86 + 0.012) = 0.014	NA

[4] https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf
[5] https://www.phe.gov/s3/dualuse/Pages/GainOfFunction.aspx
[6] https://www.phe.gov/s3/dualuse/Pages/default.aspx
[7] For clarity, the 3% bioweapon probability was simply dropped and the remaining likelihoods, 81% and 16%, were normalized.

Rootclaim Initial state analysis, adjusted. This evidence sets the likelihood that CoV-2 was a zoonotic origin event at 98.6% and a laboratory origin event at 1.4%.

Additional Prior Evidence by Demaneuf and De Maistre. A second prior Bayesian analysis was performed by professionally educated risk assessment personnel and Chinese-language speaking professionals[8] and is included herein in its entirety. For the sake of brevity, the zoonotic origin evidence was based primarily of population size, distribution, and geographic distribution of bat populations relative to Wuhan. With respect to a lab accident, they separately analyze probabilities of a virus escape during collection, transport, and direct lab accidents and then separately the probability of a community outbreak following a lab escape. They also use primary Mandarin-language sources for Chinese estimates of the same events, showing corroboration of the probabilities. Their conclusion is that the probability of a lab escape ranges from 6% to 55% with a zoonotic origin a zoonotic origin probability being 45% to 94%.

Second Bayesian analysis. Using the most conservative probabilities, this evidence sets the likelihood that CoV-2 was a zoonotic origin event at 94% and a laboratory origin event at 6%.

Selection of initial state for Bayesian analysis.

The Text-Table below summarizes the three approaches to an initial state as to the origin of CoV-2. While the Demaneuf and De Maistre analyses set a range for the zoonotic origin of 45% to 94%, I have used the top of the range of their probability of a zoonotic origin to be conservative.

Prior Analysis	Zoonotic Origin	Laboratory Origin
Daszak et al. paper	91%	9%
Rootclaim Bayesian analysis	98.6%	1.4%
Demaneuf and De Maistre Bayesian analysis	94%	6%

Using a simple online calculator[9] the mean of these three value sets is 94.5%, the standard deviation is ± 3.8%, and the 95% confidence interval is ± 4.3%. Using these data, the upper bound of the 95% confidence interval is 98.8% and, to be most conservative, this will be used as the starting probability of a zoonotic origin.

Initial state for this analysis. The likelihood that SARS-CoV-2 began as a zoonotic event is 98.8% and the likelihood it began as a laboratory event is 1.2%.

[8] https://zenodo.org/record/4067919#.X-qIm9gzbOj . For reference purposes, this paper comes with a spreadsheet listing 112 individual BSL-3 labs in China across 62 lab-complexes.

[9] https://www.calculator.net/standard-deviation-calculator.html?numberinputs=91%2C+94%2C+98.6&ctype=s&x=48&y=19

1. General approach of this analysis[10]

This analysis is intended to examine two competing and mutually exclusive theories of the origin of the coronavirus, SARS-CoV-2 (CoV-2), and the pandemic it has caused, COVID-19.

At the time of this writing there have been 83 million confirmed cases and 1.8 million deaths.[11] Some sources place the economic damage at $21 trillion USD.

Theory One. The zoonotic theory is that a vertebrate animal was infected with CoV-2 or an ancestor (Index Host) and that a human was infected with contact to that Index Host in some manner. Human-to-human spread then followed.

Theory Two. The laboratory origin theory is that CoV-2 or an ancestor was being used in laboratory experiments and that it 'escaped' from the lab via an infected person, lab animal, experimental waste, etc.

I have found no evidence of a deliberate release and early firsthand accounts of local officials and scientists suggest surprise and consternation. If this was a deliberate release, such evidence would be extremely local, limited in distribution, and highly compartmentalized. It is beyond the scope of this analysis.

Weight of the evidence. For purposes of the calculation of posterior probabilities in the Bayesian analysis, evidence which has a statistical basis will be used directly to adjust the probabilities.

Since some of the probability calculations have astronomical values which would make a single such evidence statement, if inputted directly, swamp any further calculation and make their later contribution mute, a decision was made to simply treat quantitative probabilities as significant at the p = 0.05 level, no matter how much 'more significant' the calculation suggested.

So, for example, a probability of certain codon usage coming from nature may be one in 440 or p = 0.002, the contribution of this evidence to the input to the posterior probability adjustment would be set at a p-value of 0.05. In such cases the adjustment would be to change the 'winning' hypothesis by multiplying by 19, since a p = 0.05 is the same as a 19 out of 20 likelihood event. This is a conservative treatment of what would be highly significant data.

For evidence that cannot be quantified, the decision was made to treat these as quantitative outcomes with a 51% to 49% value with respect to the 'winning' hypothesis. This has the effect of increasing that hypothesis by 1.04. This is related to the legal standard of the 'preponderance of the evidence.'

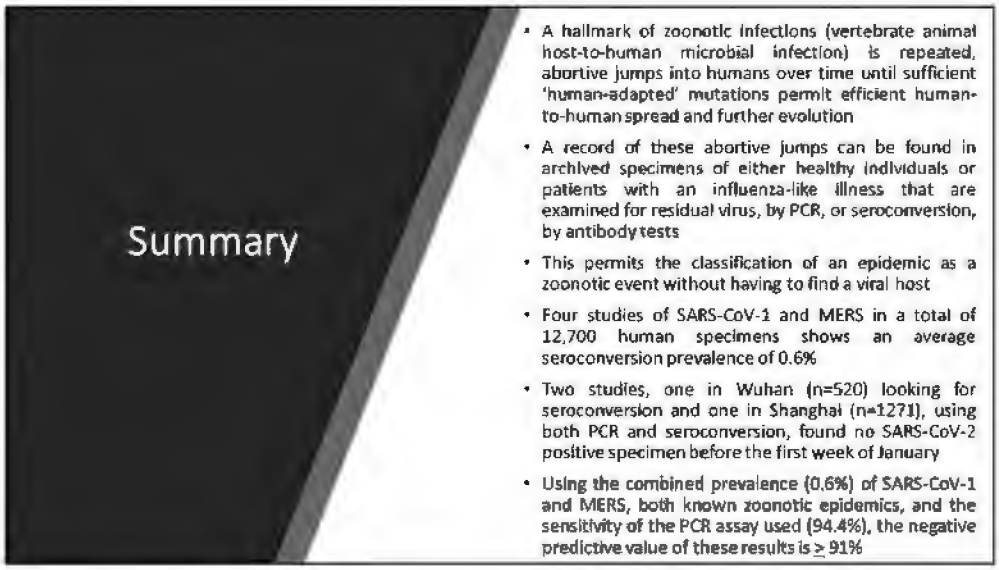
Because of the overall nature of the analyses here, all likelihoods are carried forward at the 'one significant figure' level, with standard rounding rules applied.

[10] The statistical approach and many of the individual statistical analyses were performed by Dr. Martin Lee, PhD, Adjunct Professor of Biostatistics, UCLA. https://ph.ucla.edu/faculty/lee The likelihood adjustments to the Bayesian analysis, which you can see are routine math, were conducted by the author.

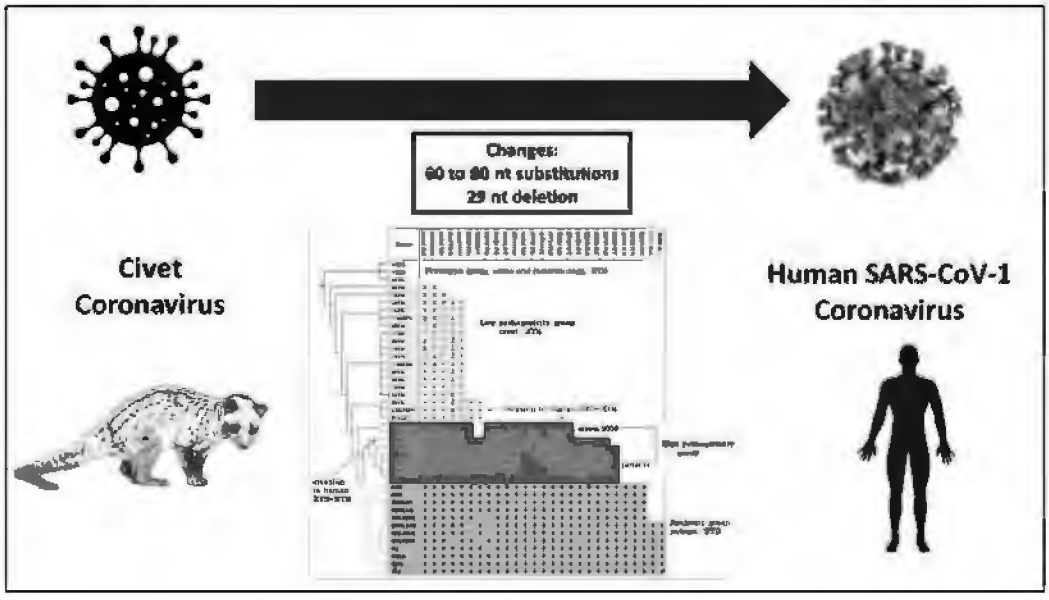
[11] https://www.worldometers.info/coronavirus/coronavirus-cases/

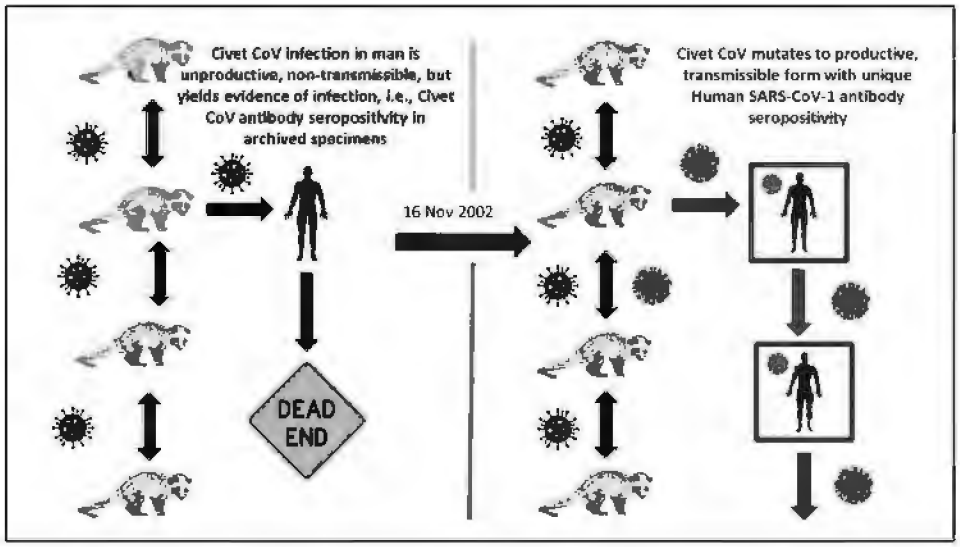
Evidence: Lack of seroconversion in Wuhan and Shanghai. Summary of evidence:

- A hallmark of zoonotic infections (vertebrate animal host-to-human microbial infection) is repeated, abortive jumps into humans over time until sufficient 'human-adapted' mutations permit efficient human-to-human spread and further evolution

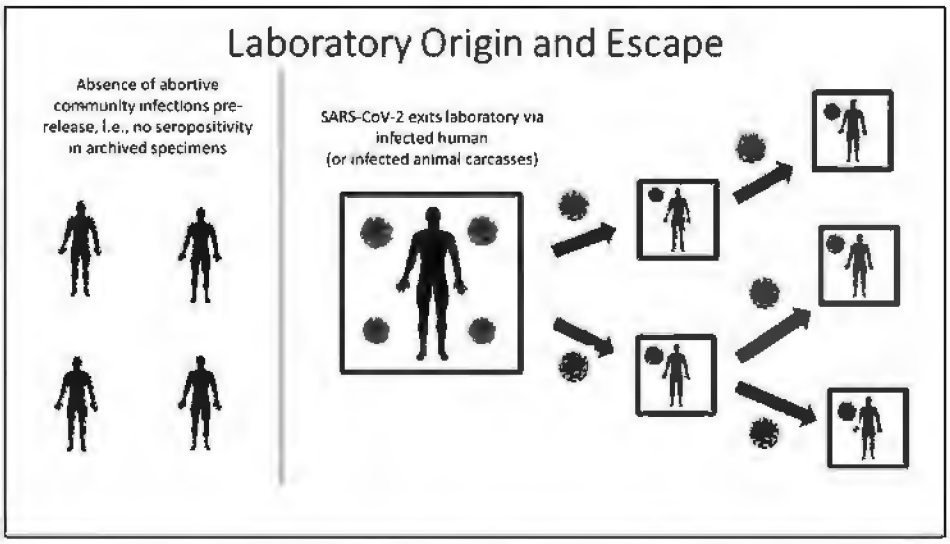


- A record of these abortive jumps can be found in archived specimens of either healthy individuals or patients with an influenza-like illness that are examined for residual virus, by PCR, or seroconversion, by antibody tests





- This permits the classification of an epidemic as a zoonotic event without having to find a viral host
- A laboratory accident is a situation in which there are no prior exposures within the human population as shown in the Figure below:



- Four studies of SARS-CoV-1 and MERS in a total of 12,700 human specimens shows an average seroconversion prevalence of 0.6%

SARS-related Virus Predating SARS Outbreak, Hong Kong

SARS-CoV-1 began in fall of 2002 in southern China

Patient Population	Serum samples collected in May 2001 from 938 healthy adults in Hong Kong	48 confirmed SARS patients diagnosed in February and March 2003 in Guangdong
Civet CoV > SARS-CoV-1 Seropositivity	13	0
SARS-CoV-1 > Civet CoV Seropositivity	4	48
Total	17 out of 938 = 1.8%	48 out of 48 = 100%

Pre-epidemic seroprevalence in the adult community

Prevalence is 0.6% for SARS-CoV-1 and MERS in 12,700 specimens

Epidemic	Nature of the Study	Seropositivity	Reference
SARS-CoV-1	Archived specimens from healthy adults in Hong Kong collected two years before CoV-1 were tested for Ab to civet or human CoV	17/938	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2322899/
MERS	Archived human sera collected in 2011 was tested for MERS-CoV S1-specific antibodies by ELISA	1/90	https://www.sciencedirect.com/science/article/pii/S1876034120300010#fig0010
SARS-CoV-1	Serum specimens collected from military recruits from the People's Republic of China in 2002 were tested for SARS-CoV-1 antibodies.	11/1621	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1074388/
MERS	Between Dec 1, 2012, and Dec 1, 2013, 10,009 individual serum samples were tested for anti-MERS-CoV antibodies in regions without cases.	15/10,009	https://pubmed.ncbi.nlm.nih.gov/25863564/
SARS-CoV-1	Serum samples that were collected from 42 individuals during 2001-2002, before the SARS outbreak, and tested for IgG antibody against SARS-CoV.	28/42	https://arxiv.org/ftp/arxiv/papers/1305/1305.2659.pdf

Pre-epidemic seroprevalence in MERS shepherds and slaughterhouse workers is higher

Prevalence is 2.3% (2/87) in shepherds and 3.6% (5/140) in slaughterhouse workers

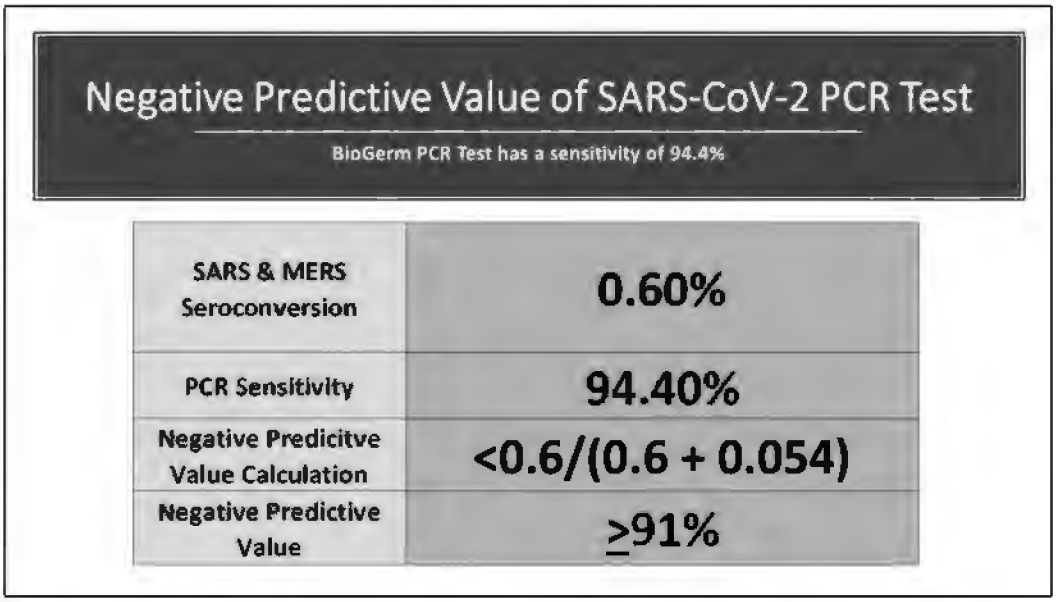
Reference: https://pubmed.ncbi.nlm.nih.gov/25863564/

- Two studies, one in Wuhan (n=520) looking for seroconversion and one in Shanghai (n=1271), using both PCR and seroconversion, found no SARS-CoV-2 positive specimen before the first week of January

Pre-epidemic seroconversion has never been seen for SARS-CoV-2

Epidemic	Nature of the Study	Seropositivity	References
SARS-CoV-2	RNA PCR from 1271 nasopharyngeal swab samples as well as the prevalence of IgM, IgG, and total antibodies against SARS-CoV-2 in 357 matched serum samples collected from hospitalized patients with influenza-like illness between 1 December 2018 and 31 March 2020 in Shanghai Ruijin Hospital. First positive was January 25, 2020.	0/1271	[illegible]
SARS-CoV-2	Re-analysed 5200 throat swabs collected from patients in Wuhan with influenza-like-illness from 6 October 2019 to week one January 2020 and found no positive specimens for SARS-CoV-2 RNA by quantitative PCR.	0/520	https://www.nature.com/articles/s41564-020-0713-1
	CoV-2 Studies Combined	**0/1791**	**Probability is one in 14,881**

- Using the combined prevalence (0.6%) of SARS-CoV-1 and MERS, both known zoonotic epidemics, and the sensitivity of the PCR assay used (94.4%), the negative predictive value of these results is ≥ 91%



Here, the negative predictive value (NPV) represents the probability that a CoV-2 is not a zoonosis, given the negative seroconversion findings.

Confidence: 90% (a one in 10 chance this is wrong). This is a subjective value.

The change in origin likelihoods from this evidence and the calculations are shown in the Text-Table below.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin
Starting likelihood	0.988	0.012
Negative predictive value of lack of seroconversion	0.91	
Reduced by 90% confidence	0.91 x 0.9 = 0.82	
Impact of this evidence	Reduces the likelihood of ZO by 82/18 or 4.6-fold. For every 100 tests, a true ZO would be seen 18 times and a non-ZO would be seen 82 times	
Impact of evidence calculation	0.988/4.6 = 0.215	
Normalize this step of analysis	0.215/(0.215 + 0.012) = 0.947	0.012/(0.215 + 0.012) = 0.053

Adjusted likelihood: Zoonotic origin (95%) and laboratory origin (5%)

[redacted] Lack of posterior diversity for SARS-CoV-2 compared to MERS and SARS-CoV-1

- The earliest stages of human CoV-1 and MERS infections were characterized by viral genome base diversity as expected for multiple, independent jumps from a large and diverse intermediate host population into humans.
- Combining MERS and CoV-1 studies, out of the earliest 255 human infections in which virus genome sequences are available, 137 could not be rooted in a prior human-to-human infection and so are attributed to an independent intermediate host-to-human infection.[12]
- That is about 54% non-human-to-human transmission.
- With CoV-2, there are 249 viral genomes in GISAID from Hubei province, where Wuhan is located, collected between Dec 24, 2019 and Mar 29, 2020.
- From Dec 24, 2019 to November 2020, there are 1001 genomes sequenced from all of China and 198,862 worldwide.
- For CoV-2, every single genome sequence is rooted in the first sequence from the PLA Hospital in Wuhan.
- Not one case of posterior diversity.
- Using the frequency of non-rooted genome diversity seen with MERS and CoV-1, about 50:50 or a coin toss, the probability that CoV-2 is a zoonotic pandemic with 0/249 genomes is the chance of tossing a coin 249 times and getting heads every time!
- Mathematically that is nonexistent; specifically, one in 10 with 84 zeros.
- Since Wuhan had approximately 500,000 cases during the time interval of this sampling, the potential sampling error of testing only 249/500,000 or 0.05% is significant. This sampling error, while large, is unable to obliterate the overwhelming odds that this did not arise from an intermediate host in Wuhan.
- Therefore, to permit continued evidence analysis, this finding will be set at the boundary of customary statistical significance, a p-value of 0.05 or a 1 in 20 likelihood that this is zoonotic.

Detailed explanation

A fundamental difference between a laboratory and a non-laboratory acquired zoonotic disease, the imprint of phylogenetic diversity through pre-human spread within the source population, can be examined by the posterior diversity of human cases with no *a priori* knowledge of an intermediate host.

[12] https://elifesciences.org/articles/31257#abstract ; https://www.researchgate.net/publication/225726653_Molecular_phylogeny_of_coronaviruses_including_human_SARS-CoV ; https://science.sciencemag.org/content/300/5624/1394/tab-pdf ; https://pubmed.ncbi.nlm.nih.gov/14585636/ ; https://www.microbiologyresearch.org/content/journal/jgv/10.1099/vir.0.016378-0?crawler=true ; https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7118731/

MERS. The MERS epidemic has been documented to have arisen from the initial jump from bats to camels, a three to five year expansion within the camel population in which mutational diversity arose by random mistakes, and then a jump into humans. This model of spread predicts that there would, at some point, be additional jumps from other camels into other patients, and a pattern of "posterior diversity," would be found in the human specimens. If the COVID-19 pandemic arose by a similar mechanism the same pattern would be seen. The following Text-Table contains such data.

Phylogenetic Feature	MERS	SARS-CoV-2
Posteriority Diversity	28/30 (93%)	0
No Posteriority Diversity	2/30 (7%)	7666
Time from first patient to first example of posterior diversity	About 60 days	None at >120 days
Depth of posterior diversity to first patient	>365 days	None

The study of MERS noted above was published in 2013 in Lancet[13] in an article entitled, "Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study." Thirty specimens were used in the analysis. The features of a camel-to-human zoonotic epidemic are easily identified. Specimens taken within sixty days of the first patient, "Patient Zero," began to show a background diversity that could not be traced back through Patient Zero. The analysis of all thirty, in fact, documented that 93% were transmitted directly from the camel intermediate reservoir. And looking only at the "background" diversity permitted a calculation of the last common ancestor for the spread within the camel population of over 365 days.

A study of SARS-CoV-2[14] available May 5, 2020 and entitled, "Emergence of genomic diversity and recurrent mutations in SARS-CoV-2," looked at 7666 patient specimens from around the world for phylogenetic diversity. The authors state: "There is a robust temporal signal in the data, captured by a statistically significant correlation between sampling dates and 'root-to-tip' distances for the 7666 SARS-CoV-2 ($R^2 = 0.20$, $p < .001$). Such positive association between sampling time and evolution is expected to arise in the presence of measurable evolution over the timeframe over which the genetic data was collected." This conclusion also argues against a MERS-like pattern of posterior diversity. In fact, the 95% upper bound for the probability of no posterior diversity being seen in SARS-CoV-2, given the data in MERS, is 3.9×10^{-4}.

The finding of posterior diversity in MERS was seen quickly, that is, within 60 days of the first patient and in only 30 specimens. In this study of COVID-19 the cutoff date of the 7666 specimens was April 19, 2020 or approximately 140 days after the first documented case. The

[13] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3898949/
[14] https://www.sciencedirect.com/science/article/pii/S1567134820301829

lack of posterior diversity in COVID-19 at a much later date than what was seen with MERS also argues against a non-laboratory source for this pandemic.

A useful avenue of future research for those working to find an animal source for COVID-19 would be new mathematical models or statistical methods that might find a "hidden" signal of posterior diversity in the current data set which shows none. And given access to the unprecedented quantity of human data for COVID-19 which can be mined via bioinformatics, efforts to find the "missing link" in the wild through search and sample should be a second priority to mining the human specimen data set.

SARS-CoV-1. A similar pattern of clinical cases that do not show a common ancestor in the human population but instead is evidence of posterior diversity is shown in the Text-Table on the left for SARS-CoV-1[15] compared to CoV-2 on the right[16]. SARS-CoV-1 shows clusters of cases in humans that are connected only by phylogenetic branches that reach back in time (all of the branches inside the purple box. This is because of the extensive mutational background created while being in the intermediate host, the civet. With CoV-2 on the right, every clinical case descends from the first clinical case, in the 19A clade. There are no background mutations to account for. I will show elsewhere that the first Clade A patient was at the PLA Hospital about 3 km from the WIV.

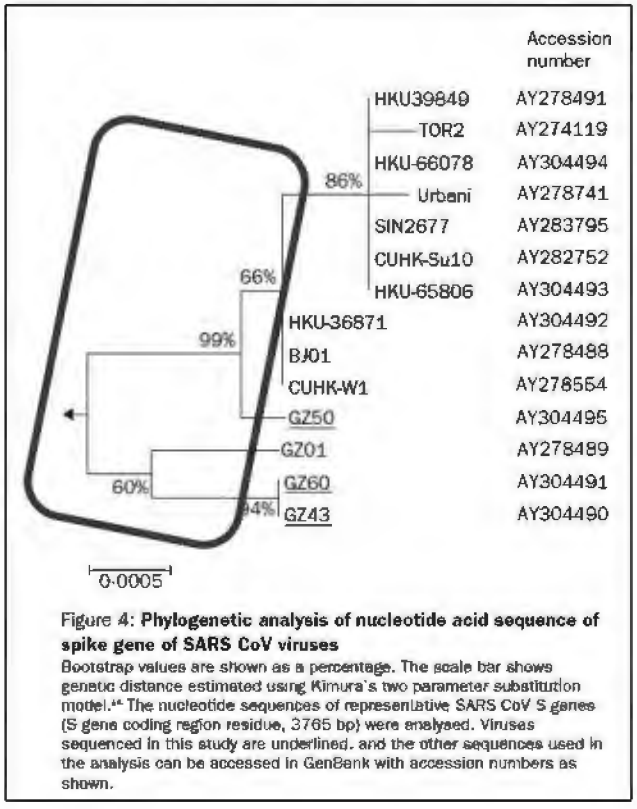
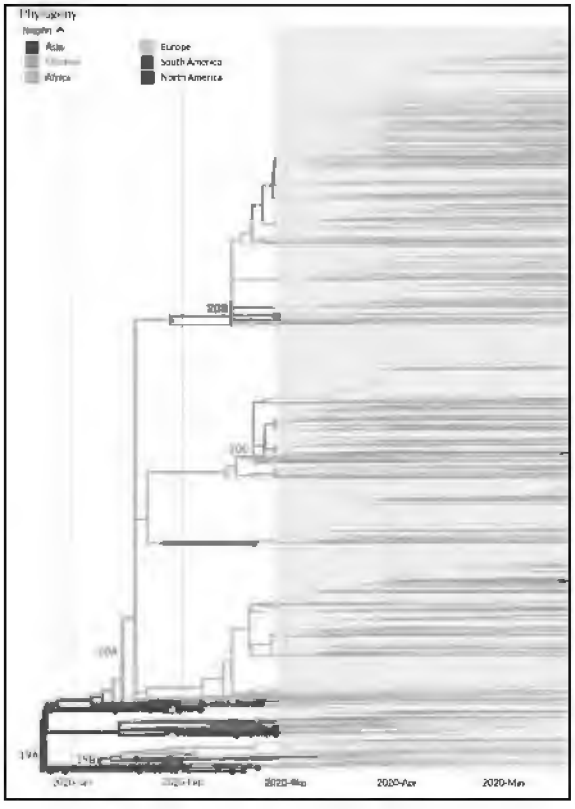
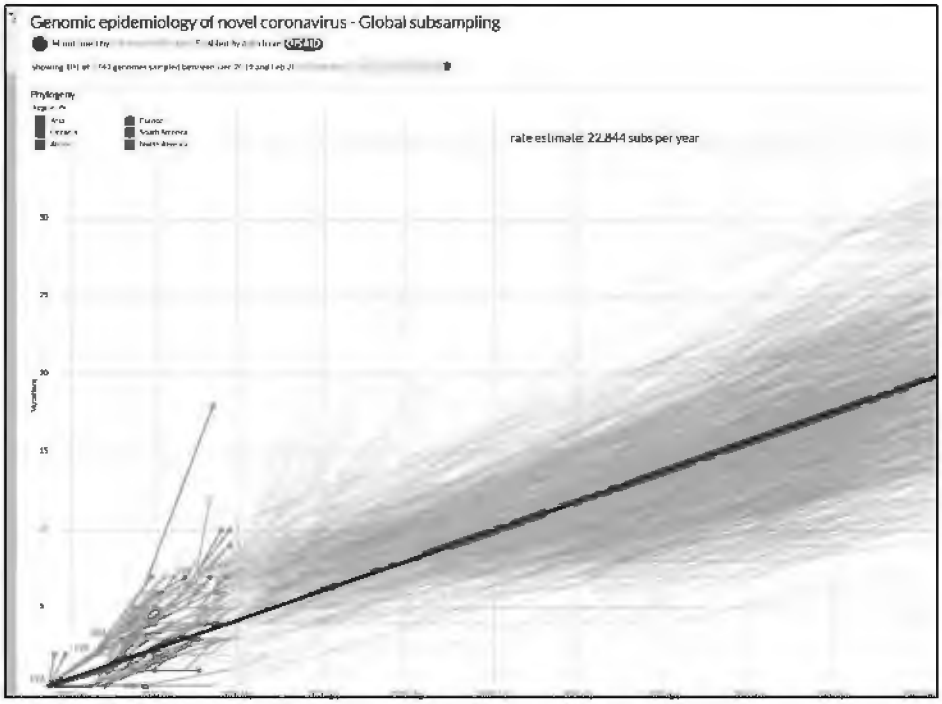


Figure 4: **Phylogenetic analysis of nucleotide acid sequence of spike gene of SARS CoV viruses**
Bootstrap values are shown as a percentage. The scale bar shows genetic distance estimated using Kimura's two parameter substitution model.[14] The nucleotide sequences of representative SARS CoV S genes (S gene coding region residue, 3765 bp) were analysed. Viruses sequenced in this study are underlined, and the other sequences used in the analysis can be accessed in GenBank with accession numbers as shown.



[15] https://pubmed.ncbi.nlm.nih.gov/14585636/
[16] https://nextstrain.org/

Given the rate of mutations of 22.8 per year for CoV-2 as shown in the Nextstrain graph below and a sequencing accuracy of about two calls per genome, CoV-2 could not have spent more than a few weeks in an intermediate host before a pattern of background mutations would be identified as posterior diversity. In the laboratory a pure culture on a single genome is used and the CoV-2 pattern is most consistent with a single pure culture infection a first human.

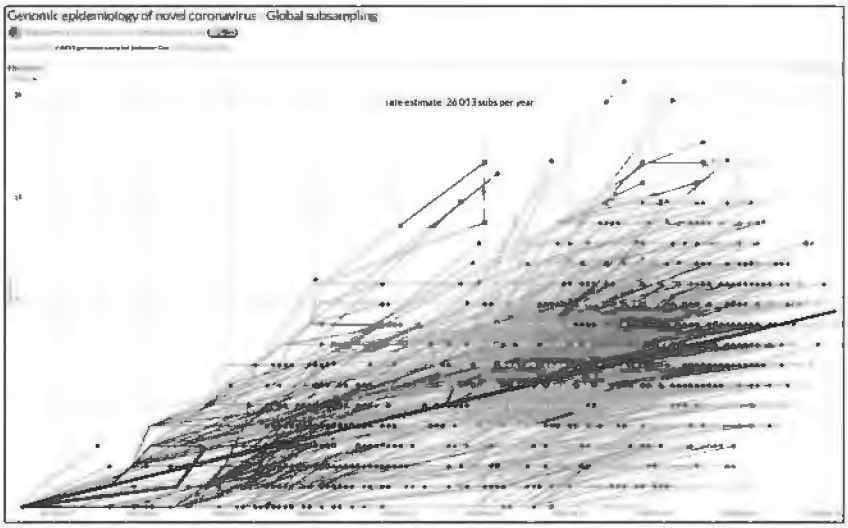


Non-zoonotic evolution. In a hypothetical in which there was a singular event in which one genetically pure virus infected one person and then the epidemic grow the development of the genetic diversity would have a clear, identifiable pattern: every new mutation would only appear on a background of the previous mutations.

The mutations in this virus are literally a personal tag. The general mutation rate leads to one mutation per patient. So by definition, Patient Zero will have just one mutation. And then the 2-4 people that patient passes it to will have that mutation and then will add a new one, and so on. As time goes by two things happen: each patient gets a new mutation of their own and they pass on all the mutations of the past.

Since the virus has 29,900 nt and the mutation rate, as shown in this graph prepared by NextStrain is 26 mutations per year, there is very little chance a mutation will appear and then later get undone. By carefully going back in time it is possible to literally name each person at each generation by the one (on average) new mutation they have and all of those that went before.

This graph of mutations on the Y-axis shows them gradually increasing and the color coding shows where they came from. In this infection, they only came from a previous patient and from the next previous patient and so on.



A NextStrain graphic.

How is that different from MERS, which was passed from camels to humans in a true zoonotic process?

In a true zoonotic spread to humans there is usually an initiating species (in MERS it is bats), and then an intermediate species (in MERS it is camels), and then it moves to man, either because of a new "enabling mutation" or for a non-domestic species, a chance encounter, and Source Zero and Patient Zero met and a cross species event occurs. But "Source Zero" doesn't stop there with one infection in one human; the virus also transmits itself vertically into the intermediate species. Source Zero also creates a vertical infection in the camels. Whether it is mild or not doesn't matter. The new human jumping gene is moving into a very diverse population of viruses, who have themselves been evolving since the first bat to camel transmission.

What is the outcome in terms of a test to show this is happening?

The diversity of the virus in humans begins to be so great and the spots where the mutations occur don't match up to MERS Patient Zero like they do in COVID-19. In MERS, the virus in Patient Zero and the virus in a later infection are not directly descendants but cousins and only descended from an earlier virus, who spent time in another camel population, collecting random mutations until it got the one it needed to infect humans and then it begins again.

The chart below, from Lancet. 2013 Dec 14; 382(9909): 1993–2002, shows just how this works. The patient at Bisha is the earliest case in this chart (Patient Zero in the red circle). But notice, no other case comes from that patient. They have such a diverse genetic background they appear to only be related to the Bisha virus with a posterior timeline of about one year. Their background is in the green boxes and it skips Patient Zero.

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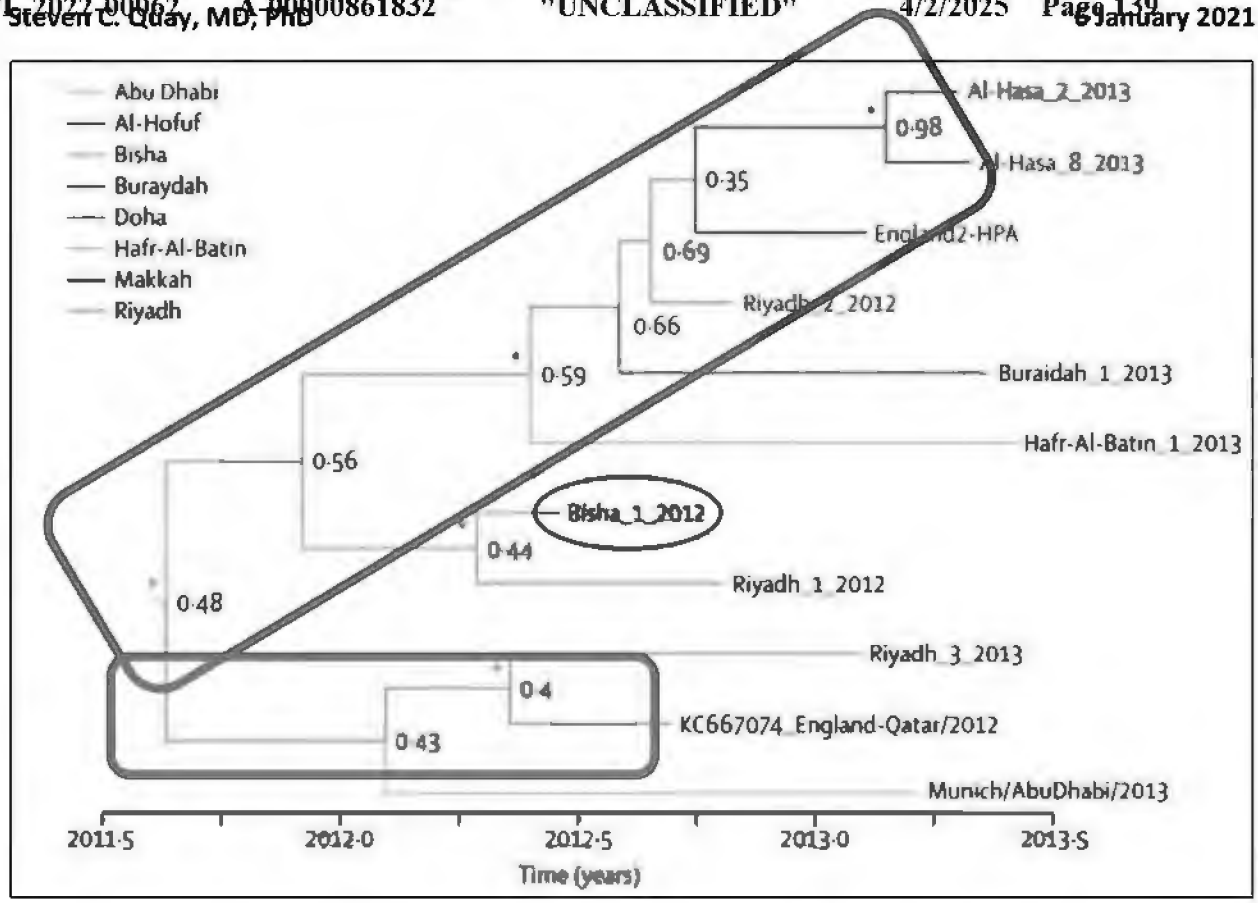


Even without knowing that camels are the zoonotic source for MERS, this data, from clinical sample only and without any field work in cave or camels, is all you need to know that this arose in the wild.

A paper just appeared with this analysis for a region of China and the posterior genomic diversity indicated a single starting point on December 1, 2019 for all cases. There was no posterior diversity. At this point with over 322,000 full genomes sequenced[17] and all showing an additive pattern of mutations and with none showing background diversity before the known appearance in Wuhan, the only conclusion is that there is no reservoir of genetic diversity.

On January 26, 2020 in an article in *Science* written by Jon Cohen, Kristian Andersen, an evolutionary biologist at the Scripps Research Institute who had analyzed sequences of 2019-nCoV to try to clarify its origin said: "The scenario of somebody being infected outside the market and then later bringing it to the market is one of the three scenarios we have considered that is still consistent with the data. It's entirely plausible given our current data and knowledge."

The negative predictive value of finding no posterior diversity in CoV-2 with 322,000 total infections sequenced, over 1000 in China, is 95%

Confidence: 95% (a one in 20 chance this is wrong)

[17] https://www.gisaid.org/

Below is the impact of the pack of posterior diversity on the likelihood of a zoonotic versus laboratory origin

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin
Starting likelihood	0.947	0.053
Negative predictive value of lack of posterior diversity	0.95	
Reduced by 95% confidence	0.95 x 0.95 = 0.90	
Impact of this evidence	Reduces the likelihood of ZO by 90/10 or 9-fold. For every 100 tests, a true ZO would be seen 10 times and a non-ZO would be seen 90 times	
Impact of evidence calculation	0.947/9 = 0.105	
Normalize this step of analysis	0.105/(0.105 + 0.053) = 0.66	0.053/(0.105 + 0.053) = 0.34

Adjusted likelihood: Zoonotic origin (66%) and lahoratory origin (34%)

Evidence and Motive for laboratory genetic insertion:

A key to infectivity of coronaviruses is the addition, in nature or the laboratory, of a furin cleavage site (FCS) at the S1/S2 junction of the Spike Protein.

Furin cleavage sites (FCS) have been widely understood to be important for many viral infections, including HIV, influenza, and others. It has also been widely understood before now that lineage B coronaviruses do not have FCS.

It was therefore surprising when an examination of SARS-CoV-2 Spike Protein found an insertion of a 12-nt, 4-AA sequence near the junction of the S1/S2 subunits which creates a furin site which is essential to human infectivity and transmission. As expected from previous work, no lineage B (sarbecovirus) coronavirus has this feature. This is the most difficult "molecular fingerprint" of SARS-CoV-2 to explain having been acquired in the wild and for that reason there are no even passingly feasible theories.

One database of whole genome sequences of 386 coronaviruses was devoid of furin cleavage sites.[18] Another database of 2956 genomes of sarbecovirus strains sequences shows that none have a furin site.[19] This is a highly significant finding with a probability that sarbecovirus has a furin site in the wild of one in about 985.[20]

It has been known since 1994 that viral glycoproteins can be cleaved by secreted proteases, including furin.[21] Even before that, in 1992, it was known the peptide sequence R-X-K/R-R in surface glycoproteins was required for avian influenza viruses of Serotype H7 pathogenesis.[22] The first paper using furin inhibitors to define a role for an FCS in coronavirus-cell fusion was published in 2004.[23]

Since that time it has become common practice to insert FCS during laboratory gain-of-function experiments to increase infectivity. The following Text-Table illustrates the scope of just a few of the experiments conducted, with the hyperlink to the paper in column one.

URL for Paper	Title of Paper
One	Characterization of a panel of insertion mutants in human cytomegalovirus glycoprotein B.
Two	Insertion of the two cleavage sites of the respiratory syncytial virus fusion protein in Sendai virus fusion protein leads to enhanced cell-cell fusion and a decreased dependency on the HN attachment protein for activity.

[18] https://academic.oup.com/bioinformatics/article/36/11/3552/5766118

[19] https://academic.oup.com/database/advance-article/doi/10.1093/database/baaa070/5909701

[20] When a series of samples are taken and none produce the result expected, the probability that this is a false negative finding can be estimated by taking the number of samples and dividing by three. Here, 2956 sarbecoviruses without a single furin site is a probability of one in 2956/3 or 985.

[21] https://www.ncbi.nlm.nih.gov/pubmed/8162439

[22] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7172898/pdf/main.pdf

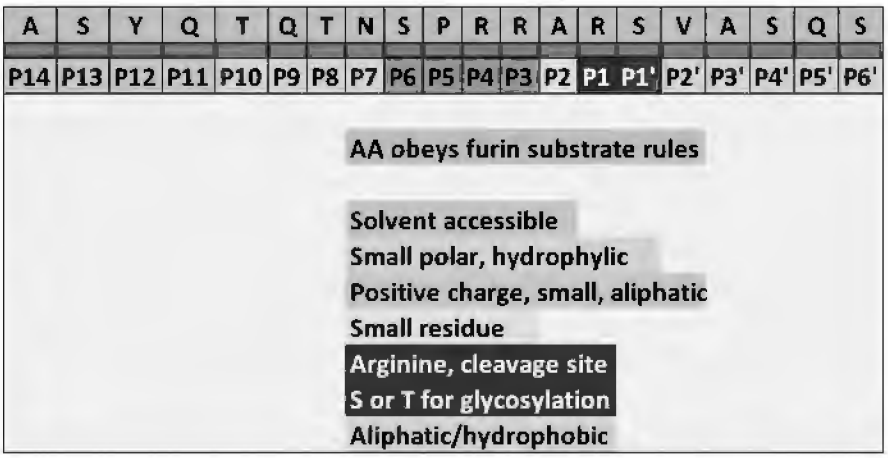
[23] https://www.ncbi.nlm.nih.gov/pubmed/15141003

Three	Recombinant Sendai viruses expressing fusion proteins with two furin cleavage sites mimic the syncytial and receptor-independent infection properties of respiratory syncytial virus.
Four	Amino acid substitutions and an insertion in the spike glycoprotein extend the host range of the murine coronavirus MHV-A59
Five	Induction of IL-8 release in lung cells via activator protein-1 by recombinant baculovirus displaying severe acute respiratory syndrome-coronavirus spike proteins: identification of two functional regions.
Six	Coronaviruses as vectors: stability of foreign gene expression.
Seven	Experimental infection of a US spike-insertion deletion porcine epidemic diarrhea virus in conventional nursing piglets and cross-protection to the original US PEDV infection.
Eight	Minimum Determinants of Transmissible Gastroenteritis Virus Enteric Tropism Are Located in the N-Terminus of Spike Protein.
Nine	Reverse genetics with a full-length infectious cDNA of the Middle East respiratory syndrome coronavirus.
Ten	Construction of a non-infectious SARS coronavirus replicon for application in drug screening and analysis of viral protein function
Eleven	A severe acute respiratory syndrome coronavirus that lacks the E gene is attenuated in vitro and in vivo.

The creation in the wild of a coronavirus FCS that is used as an example of what might have happened in SARS-CoV-2 is uninformative. In this case a strain of influenza, in which a new polybasic site appears spontaneously leads to increased infectivity and lethality,[24] was reported by Tse *et al.* 2014. The mechanism of the FCS acquisition here was an RNA polymerase dependent stuttering at a small, constrained loop in which one or more A nt were inserted, removing the strain in the loop and inserting an AAA codon which represents the basic amino acid lysine. No such method was described for the insertion of arginine.

The insert generates a canonical 20 AA furin site sequence. In 2011 Tian et al.[25] published an analysis of 126 furin cleavage sites from three species: mammals, bacteria and viruses. The analysis showed that when the furin sites are recorded as a 20-residue motif, a canonical structure emerges. It includes one core cationic region (eight amino acids, P6–P2′) and two flanking solvent accessible regions (eight amino acids, P7–P14, and four amino acids, P3′–P6′).

[24] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3911587/
[25] https://www.nature.com/articles/srep00261



This figure above shows the 20-AA of the furin motif in SARS-CoV-2 (in green) with the P14 to P6' AA positions marked with the cleavage site being the amide bond between P1-R and the P1' residue. The motif is color coded with the requirements (in most cases, except for the positively charged AA requirements, most position requirements can be relaxed).

With the insertion, all 20 residues obey the rules as established by Tian. Since there are 20^4 different 4-AA peptides or 160,000 choices, it is remarkable that the 4 AA insert created a sequence that contained a small or cationic AA (8 AA/20 qualify), a cationic AA (3/20), another cationic AA (3/20), and a small AA (5/20) in that order. In fact, there are only 360 or the total or about 0.2% of all four amino acid inserts that would be expected to follow the exact rules for furin substrates. Of course, given the increase in infectivity SARS-CoV-2 has over other coronaviruses that do not have a well-designed furin cleavage site, selection pressure would drive this rare mutational event once it happened randomly. It would also be a likely choice for a laboratory designed furin cleavage site created *de novo*.

Based on the evidence that there are no furin cleavage sites in 2956 sarbecovirus (beta coronavirus) genome sequences[26], the likelihood that CoV-2 acquired the furin site from a wild sarbecovirus is one in 985 or 0.001. Because this is highly significant, we will use the conservative rule established in the beginning and use a likelihood of 0.05 for this evidence.

Confidence. 95% confidence (only a one in 20 chance this is wrong). Below is the calculation of the Bayesian adjustment.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin
Starting likelihood	0.66	0.34
Negative predictive value of a lack of furin sites in sarbecovirus genomes	0.95	
Reduced by 95% confidence	0.95 x 0.95 = 0.90	
Impact of this evidence	Reduces the likelihood of ZO by 90/10 or 9-fold. For every 100 tests, a true ZO would be seen 10 times and a non-ZO would be seen 90 times	
Impact of evidence calculation	0.66/9 = 0.073	
Normalize this step of analysis	0.073/(0.073 + 0.34) = 0.177	0.34/(0.34 + 0.073) = 0.823

Adjusted likelihood. Zoonotic origin (17.7%), laboratory origin (82.3%).

[26] https://academic.oup.com/database/advance-article/doi/10.1093/database/baaa070/5909701

Evidence: Codon usage can distinguish insertion events in the wild from those created in the laboratory.

Not only is the insertion of an FCS peptide unique among lineage B coronaviruses, the nt sequence used for the process is more broadly unique among coronaviruses in general, regardless of lineage:

-CCT-**CGG-CGG**-GCA-

I will now use synonymous codon bias methods to try to inform the question of the origin of SARS-CoV-2.

Because of the redundancy of the genetic code, more than one 3-nt sequence specifies any given amino acid. For example, there are six codons that specify arginine, R. The frequencies with which such synonymous codons are used are unequal and have coevolved with the cell's translation machinery to avoid excessive use of suboptimal codons that often correspond to rare or otherwise disadvantaged tRNAs. This results in a phenomenon termed "synonymous codon bias," which varies greatly between evolutionarily distant species and possibly even between different tissues in the same species.

Decades of research has identified that all life forms, viruses, bacteria, and humans, use the codons in a signature pattern of frequency which can be used to identify a particular sequence of RNA or DNA as human or non-human; viral or non-viral.

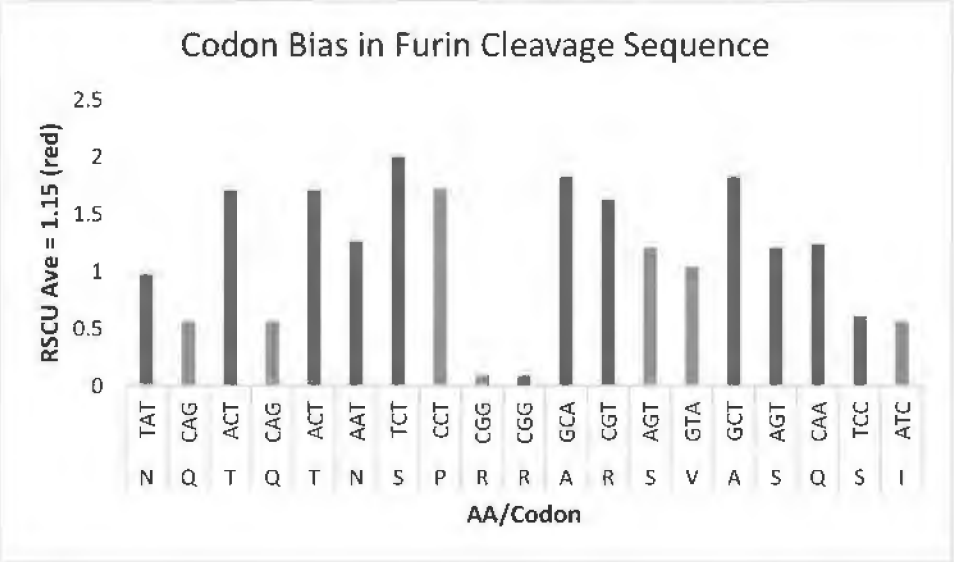
In this way, viruses in nature and scientists in the laboratory, with different goals and motivations, make distinguishing codon usage decisions which can sometimes be used as a fingerprint of their source.

The Text-Table below contains the arginine codon usage for two populations, pooled data for SARS-CoV 2003 and related viruses and 13 Sars-CoV-2 human specimens from widely dispersed locations.

Codon	SARS-CoV 2003 and ten other evolutionary related viruses in the Nidovirales	SARS-CoV-2 from 13 Geo-locations
CGG	0.09	0.09
CGA	0.44	0.37
CGC	0.72	0.37
AGG	0.9	1.07
CGU	1.77	1.63
AGA	2.08	2.48

Since these values are of a type of multiplicative scale, they were fit using a log-normal distribution, which appears appropriate (although the sample size is small). Using the log mean and standard deviation and this distribution, the probability of finding a CGG codon is about 0.024. Assuming they are independent the probability of finding a CCG-CCG codon pair is effectively 0.024^2 or 0.00058. This is a likelihood of about one in 1700.

The following Figure shows the RSCU for the amino acids that comprise the new furin cleavage site in SARS-CoV-2. As one can see, the RSCU values are similar to each other with the exception of the RR dimer insert, which have a very low RSCU of 0.09.



The RSCU value for the CGG codon for R of 0.09 was taken from a 2004 paper of the RSCU for SARS-CoV 2003 and ten other evolutionary related viruses in the *Nidovirales* and is confirmed by 13 SARS-CoV-2 specimens obtained from diverse geographic locations. If one assumes that the RSCU observations are independent and that the probability distribution of these measurements is Gaussian (normal; a reasonable assumption), then one can calculate the probability of obtaining a result as small as 0.09. Removing the two 0.09 values, then the mean and standard deviation of the remaining values are 1.275 and 0.4992, respectively. Then the probability of a single 0.09 value is 0.0088. However, there are two 0.09 values. If we assume that these are independent findings, then the probability of both values being seen is 0.0088^2 or 7.7×10^{-5}. Using the RSCU of 0.2 from the Table above does not change the immense improbability of the usage of a CGGCGG codon pair in the wild.

Single Arginine CGG codon usage analysis suggests this will not be found in the wild.

The codon usage for SARS-CoV-2, like most coronaviruses studied, has a bias toward AT and away from GC nucleotides. The frequency of third position G use in CoV-2, for example, is 13%, 21%, 17%, and 16% for the spike protein, envelope, membrane, and nucleocapsid protein, respectively.

In that context, the scarcity of the CGG genome in SARS-CoV-2 and related coronaviruses, the relative synonymous codon usage, determined by the method of Behura and Severson,[27] was calculated and tabulated below. The color coding is blue for underutilized codons (RSCU < 1.0) and red for overutilized codons (RSCU > 1.0); light blue for RSCU values of 0.60 to 0.99 and

[27] https://www.ncbi.nlm.nih.gov/pubmed/22889422

light red for RSCU of 1.01 to 1.60. The highest RSCU usage of CGG is 1.21 in the membrane protein in the MERS virus but zero in SARS-CoV-2.

RSCU	SARS-CoV-2	Beta CoV Pangolin	SARS CoV	Bat SARS CoV	MERS CoV
Spike	0.29	0	0.19	0.08	0.25
Envelope	0	0	0	0	0
Membrane	0	0.35	0.74	0.24	1.21
Nucleocapsid	0.41	0.16	0.03	0.04	0.8

Looking at these five coronaviruses:

The largest structural protein of the coronaviruses is the spike protein, with 1273 amino acids. In SARS-CoV-2 there are 42 R residues, with only one RR dimer, the one in the insert that created SARS-CoV-2.

As a reminder none of these related coronaviruses have the 12 nucleotide insertion that forms the putative furin site in CoV-2. Interestingly, the pangolin coronavirus has no CGG residues in the spike protein. The significance of this is it makes the acquisition of this insert from pangolin by recombination impossible.

The smallest structural protein, the envelope protein, has 75 amino acids, including three R residues, but has no CGG codons in any of the related coronaviruses examined.

The SARS-CoV-2 membrane protein has 441 amino acids, 14 R residues and no CGG codons. Among related coronaviruses, this is the most unique finding of the four proteins for SARS-CoV-2 since the other four coronaviruses all utilize CGG to some extent in this protein. In the case of the MERS virus, this protein is the only occurrence in which this codon is overutilized.

The nucleocapsid protein has 418 amino acids and is responsible for packing the RNA genome. As expected for the role of R in protein-RNA interactions, it has 29 R residues and four RR dimers. None of the dimers use the CGGCGG sequence.

The nt usage of the 12-nt insert which forms the FCS cleavage site has a probability this sequence was selected for in the wild of one in 129,870.

A blast search was performed for the 12-nt inserted sequence and adjacent extensions and only the SARS-CoV-2 sequences were identified.

Shortening the search to just the two CGG-CGG codons was only slightly more fruitful. The Text-Table below shows the frequency of the middle half of the insert, CGGCGG, across the genomes of all seven known human coronaviruses, as well as a specimen bovine coronavirus and the bat and pangolin coronaviruses with greatest homology to SARS-CoV-2. Only a single example, outside of the Spike Protein gene, has been found.

Furin PBCS sequence	Beta Coronavirus	Total Arginine Dimers Anywhere	CGGCGG in Spike Protein *	CGGCGG Anywhere in genome *	CCGCCG Anywhere in genome
SRRKRRS	Human CoV-HKU1 GenBank: KF686346.1	12	0	0	0
KRRSRRA	Bovine CoV-Quebec GenBank: AF220295.1	12	0	0	0
PRRARSV	**SARS-CoV-2 Wuhan reference sequence GenBank: NC_045512.2**	**16**	**1; nt 23,606**	0	0
PRSVRS	MERS-CoV NCBI Reference Sequence: NC_019843.3	21	0	0	0
NRRSRGA	Human CoV-OC43 London/2011 GenBank: KU131570.1	16	0	0	0
None	Human CoV-229E GeneBank: KF514433.1	15	0	0	0
None	Human CoV NL63 NCBI Reference Sequence: NC_005831.2	9	0	0	0
None	SARS-CoV 2003 ZJ0301 from China GenBank: DQ182595.1	17	0	0	0
None	Bat coronavirus RaTG13 GeneBank: MN996532.1	11	0	1; nt 9394	0
None	Pangolin PCoV_GX-P4L GenBank: MT040333.1	10	0	0	0
	Total	139	1	0	0

* - Includes both in phase codons as well as out of phase, frameshift codons.

To understand what this means for the search for the zoonotic source for SARS-CoV-2, a statistical approach was taken. Using the data from the nine viruses other than SARS-COV-2 there was a single incidence of the CGGCGG found in the bat coronavirus. Assuming 10,000 codons per genome, the frequency of CGGCGG in coronaviruses can be estimated at 2 per 45,000 codons or 4×10^{-5}. Therefore, the frequency of finding the center half of the SARS-CoV-2 insert is very small. This is consistent with the strong bias in all coronaviruses to place an A/U nt in the third codon position.

The last column above, the presence of -CCG-CCG- in these coronaviruses was included because it is the hybridization sequence partner for the negative strand sequence, which arises during genome replication. This eliminates the possibility of a strand jumping event to generate a CGGCGG codon dimer.

A similar analysis for the spike protein gene can be done. Since there are no instances of CGGCGG in the spike protein genome, and the gene is 3819 nucleotides long, there are 636 pairs of codons Thus, over the 9 other viruses, there are 5724 pairs of codons and no cases of the CGGCGG pair. To calculate the upper bound on the probability of such a pair from these data, one can use the Poisson "Rule of Three", which yields a value of 3/5724 or 0.00052 with 95% confidence. Now examining the SARS-COV-2 genome, there was 1 instance of the pair in question out of 636 pairs. The probability of this happening if the true rate of this occurrence for a beta coronavirus is 0.00052 is 0.044. Obviously for smaller assumed rates of this occurrence, this would result in probabilities less than 0.044.

Since the 12-nt insert has been found nowhere in the coronavirus genomic universe, examining over 300,000 sequences and using the Poisson "Rule of Three" again, the upper bound on the frequency that it exists in nature is less than one in 100,000 with 95% confidence.

This observation in conjunction with the lack of finding the 12-nt sequence in any candidate zoonotic species makes unlikely a natural source for the virus. One line of investigation to establish a wild source for this infection would be to find a coronavirus strain with the 12-nt sequence in the wild somewhere. The fact that 10 of the 12 nts are either G or C coupled with the documented bias against GC suggests this search will futile.

Based on these analyses that demonstrate that the finding of a -CGG-CGG- codon pair in the furin site of CoV-2 is a highly improbable event and using the conservative value of a one in 20 chance (the value for a p-value of 0.05) one can recalculate the likelihood of the choice between a zoonotic origin and a laboratory origin.

Confidence. 95% confidence (only a one in 20 chance this is wrong). Below is the calculation of the Bayesian adjustment.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin
Starting likelihood	0.177	0.823
Negative predictive value of the absence of the -CGG-CGG- pair in any coronavirus in nature	0.95	
Reduced by 95% confidence	0.95 x 0.95 = 0.90	
Impact of this evidence	Reduces the likelihood of ZO by 90/10 or 9-fold. For every 100 tests, a true ZO would be seen 10 times and a non-ZO would be seen 90 times	
Impact of evidence calculation	0.177/9 = 0.022	
Normalize this step of analysis	0.022/(0.022 + 0.823) = 0.026	0.823/(0.823 + 0.026) = 0.969

Adjusted likelihood. Zoonotic origin (2.6%), laboratory origin (96.9%).

Evidence. Laboratory codon optimization uses CGG for laboratory insertions 50% of the time.

Codon optimization by recombinant methods (that is, to bring a gene's synonymous codon use into correspondence with the host cell's codon bias) has been widely used to improve cross-species expression of protein.

Though the opposite objective of reducing expression by intentional introduction of suboptimal synonymous codons has not been extensively investigated, isolated reports indicate that replacement of natural codons by rare codons can reduce the level of gene expression in different organisms. For example, one approach to vaccine development is to create an attenuated virus which comprises a modified viral genome containing nucleotide substitutions engineered in multiple locations in the genome, wherein the substitutions introduce synonymous de-optimized codons.

In US Patent 9,476,032[28] titled, "Attenuated viruses useful for vaccines," they state: "In one high-priority redesigned virus, most or all Arg codons are changed to CGC or **CGG** (the top two frequent human codons). This does not negatively affect translation." The patent contains numerous codon usages optimized for vaccine production, including the SARS-CoV virus, and in fact they use the CGG-CGG codon pair 45 times.

Beginning with a paper in 2004,[29] one motivation for codon-optimized SARS genomes is stated here: "The gene encoding the S protein of SARS-CoV contains many codons used infrequently in mammalian genes for efficiently expressed proteins. We therefore generated a codon-optimized form of the S-protein gene and compared its expression with the S-protein gene of the native viral sequence. S protein was readily detected in HEK293T cells transfected with a plasmid encoding the codon-optimized S protein."

Since that time human optimized codons have been frequently used for coronavirus research, mostly in gain-of-function experiments. In that context the "molecular fingerprint" of CGG for R is one of those common laboratory reagent gene manipulators.

Other examples:

Examples of the use of CGG codon for arginine in coronavirus research	**Reference**
SARS was genetically modified to improve ACE2 binding using "human optimized" codons, like CGG for arginine, to grow better in the laboratory. The strains were more infective.Preparation of SARS-CoV S protein pseudotyped virus. "The full-length cDNA of	Wu, K. et al. Mechanisms of Host Receptor Adaptation by Severe Acute Respiratory Syndrome

[28] http://patft.uspto.gov/netacgi/nph-Parser?Sect1=PTO1&Sect2=HITOFF&d=PALL&p=1&u=%2Fnetahtml%2FPTO%2Fsrchnum.htm&r=1&f=G&l=50&s1=9476032.PN.&OS=PN/9476032&RS=PN/9476032

[29] https://www.ncbi.nlm.nih.gov/pubmed/15367630

the SARS-CoV S gene was optimized according to human codon usage and cloned into the pCDNA3.1(+) vector (Invitrogen). The resulting "humanized" S sequence was identical with that of strain BJ01 at the amino acid level."	Coronavirus. J Biol Chem. 2012 Mar 16; 287(12): 8904–8911.
Predictions of future evolution of a virus are a difficult, if not completely impossible, task. However, our detailed structural analysis of the host receptor adaptation mutations in SARS-CoV RBD has allowed us to predict, design, and test optimized SARS-CoV RBDs that may resemble future evolved forms of the virus. "RBD might evolve into the human-optimized form by acquiring two mutations at the 442 and 472 position." SARS-CoV-2 acquired the mutation at position 472.	Fang Li. Receptor recognition and cross-species infections of SARS coronavirus. Antiviral Res. 2013 Oct; 100(1): 246–254.
Plasmid encoding a codon-optimized form of the SARS-CoV S protein of the TOR2 i	Wenhui Li, Chengsheng Z, et al., Receptor and viral determinants of SARS-coronavirus adaptation to human ACE2. EMBO J. 2005 Apr 20; 24(8): 1634–1643.
The gene encoding the S protein of SARS-CoV contains many codons used infrequently in mammalian genes for efficiently expressed proteins. We therefore generated a codon-optimized form of the S-protein gene and compared its expression with the S-protein gene of the native viral sequence. S protein was readily detected in HEK293T cells transfected with a plasmid encoding the codon-optimized S protein (Fig. (Fig.1).1). No S protein was detected in cells transfected with a plasmid encoding the native S-protein gene.	Moore, MJ, Dorfman, T. Retroviruses Pseudotyped with the Severe Acute Respiratory Syndrome Coronavirus Spike Protein Efficiently Infect Cells Expressing Angiotensin-Converting Enzyme 2. J Virol. 2004 Oct; 78(19): 10628–10635.
Published in 2019 by **Dr. Zhengl-Li Shi,** entitled "Origin and evolution of pathogenic coronaviruses," reviews genetic optimized SARS viruses using human codons	Cui, J, Fang, L. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019; 17(3): 181–192.
In 2006, Montana scientists put a synthetic furin cleavage site into a SARS coronavirus by adding an R residue at position R667. They write: "We show that furin cleavage at the modified R667 position generates discrete S1 and S2 subunits and potentiates membrane fusion activity." Mutations were introduced by using	Follis, KE, York, J, Nunberg, JH. Furin cleavage of the SARS coronavirus spike glycoprotein enhances cell–cell fusion but does not affect virion entry. Virology 350 (2006) 358–369

QuikChange mutagenesis (Stratagene)[30]	
Identification of murine CD8 T cell epitopes in codon-optimized SARS-associated coronavirus spike protein is the title of a paper that shows that the expression of spike protein in vitro was greatly increased by expression cassette optimization.	Zhia, Y, Kobinger, GP, Jordan, H, et al. Identification of murine CD8 T cell epitopes in codon-optimized SARS-associated coronavirus spike protein
As for the human clec4C_1 and mouse clec14A, they showed very similar profiles with spike genes, especially with bat SARS-CoV, in the arginine coding groups, showing the high RSCU values over 2.50 in AGA.	Ahn,I, Jeong, B-J, Son, HS. Comparative study of synonymous codon usage variations between the nucleocapsid and spike genes of coronavirus, and C-type lectin domain genes of human and mouse. Experimental & Molecular Medicine volume 41, pages746–756, 2009.

One relevant paper,[31] in which arginine residues were being inserted into bovine herpesvirus-1, used primers to create RR dimers with nine separate -CGG-CGG- codon pairs. as testament to their broad use in the Wuhan Institute of Virology laboratory.

Scientists from the Wuhan Institute of Virology provided the scientific community with a technical bulletin on how to make genetic inserts in coronaviruses and proposed using the very tool that would insert this CGGCGG codon.

A Technical Appendix[32] entitled, "Detailed methods and primer sequences used in a study of genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015, by Yang, Xinglou & Zhang, Yunzhi & Jiang, Ren-Di & Guo, Hua & Zhang, Wei & Li, Bei & Wang, Ning & Wang, Li & Rumberia, Cecilia & Zhou, Ji-Hua & Li, Shi-Yue & **Daszak, Peter** & Wang, Lin-Fa & **Shi, Zheng-Li.** (2017), from the Wuhan Institute of Virology identifies primer sequences for doing genetic experiments in coronaviruses and identifies CGG containing primers when a R amino acid is being inserted.

[30] Since the codon usage here was not reported I contacted Professor Nunberg to inquire which arginine codons were used. He replied: "Unfortunately, those files have all been archived and access to the nt sequences would involve considerable digging. If it is useful to you, I typically choose codons that are more frequent in highly expressed human proteins."

[31] From the Wuhan Institute of Virology; https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7125963/

[32] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5382765/

Given that there are two codons of six possibilities that are used in codon optimization, CGG and CGC, the finding of a CGG pair would have a likelihood of happening by chance of (2/6) times (2/6) or one in nine.

Confidence: 80% (this has a probability of being wrong one in five times). This is arbitrary. The calculation to make this adjustment in likelihood is shown here:

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.026	0.969
This is the outcome expected 8 of 9 times if this is codon optimization		0.88
Reduced by 80% confidence		0.88 x 0.8 = 0.704
Impact of this evidence		Increases the likelihood of LO by 70.4 divided by 29.6 or 2.378.
Impact of evidence calculation		0.969 x 2.378 = 2.304
Normalize this step of analysis	0.026/(2.304 + 0.026) = 0.011	2.303/(0.026 + 2.304) = 0.988

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.8%).

[redacted] SARS-CoV-2 Spike Protein is Highly Optimized for ACE2 Binding and Human Cell Infectivity, a Finding that is Inconsistent with Natural Selection but is Consistent with Laboratory Creation

Summary:

- Andersen et al.[33] hypothesized that if the CoV-2 interaction with the human ACE2 was apparently "not ideal," it was evidence that CoV-2 arose by natural selection.

- The alternative hypothesis would be that a finding that CoV-2 was optimized for ACE2 binding and human infection from the initial infection would be evidence of laboratory creation.

- Andersen relied on a paper for the "not ideal" interaction that relied on a computer algorithm rather than laboratory data, was qualitative in nature, sampled only five amino acids or 0.45% of the interaction region, and was over-interpreted.

- The analysis of the Baric et al. paper cited by Andersen as evidence the interaction was not ideal was reexamined and it was concluded that Andersen had over-interpreted the paper. The paper was a computer simulation study of only 5 of 201 amino acids in the CoV-2-ACE2 interaction region. Only one of the five amino acids discussed was said to be inferior to the equivalent amino acid in SARS-CoV-1; the remainder were either positive or neutral with respect to binding.

- A comprehensive, laboratory-based, and quantitative paper by Starr et al. of all 201 amino acids in the receptor binding region, not just five amino acids, was examined. Fully 99.6% of all of the possible 3819[34] amino acid substitutions were tested for their effect on CoV-2 binding to ACE2. Only 21 substitutions of the 3819 improved ACE2 binding. Therefore, CoV-2 has been optimized for human ACE2 binding in 99.45% of the possible amino acids in its Spike Protein interaction region.

- To support this finding, Starr also made an examination of 31,570 CoV-2 sequences from human infections, looking for the 21 substitutions that had been show to improve CoV-2 binding in the above in vitro laboratory experiments. Among the 31, 570 CoV-2 cases, they failed to find even a single case in which there was an amino acid substitution that improved binding at the time of writing this analysis.[35]

[33] https://www.nature.com/articles/s41591-020-0820-9

[34] There are 201 amino acids in the residue 331 to 531 interaction region and so 201 times the 19 possible alternative amino acids not found in CoV-2 equals 3819.

[35] The recent finding of the N501Y variant, first in the UK, and now spreading globally, is evidence of the power of this analysis. N501Y is one of only five potential substitutions in the Starr analysis that had a major effect in improving ACE2 binding.

- Based on Andersen's hypothesis and its alternative, SARS-CoV-2 is fully optimized for interaction with the human ACE2 receptor and was at the time of the first patient. There is no evidence of an evolving SP binding region, as was seen with SARS-CoV-1. This is consistent with a laboratory optimized coronavirus which entered the human population fully evolved.

Analysis

Quote from Andersen: 'While the analyses above suggest that SARS-CoV-2 may bind human ACE2 with high affinity, computational analyses predict that the interaction is not ideal (reference 7) and that the RBD sequence is different from those shown in SARS-CoV to be optimal for receptor binding (references 7,11).

Thus, the high-affinity binding of the SARS-CoV-2 spike protein to human ACE2 is most likely the result of natural selection on a human or human-like ACE2 that permits another optimal binding solution to arise. This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation."

The apparent **hypothesis** for the above conclusion is:

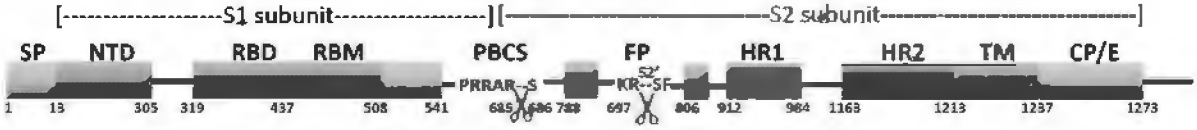
"If the SARS-CoV-2 (CoV-2) Spike Protein interaction with the ACE2 receptor is not maximized, then it is evidence that the interaction is the product of natural selection and not purposeful (laboratory) manipulation."

This would lead to an **alternative hypothesis**:

"If the CoV-2 Spike Protein interaction with the ACE2 receptor is maximized, then it is evidence that the interaction was the product of purposeful (laboratory) manipulation."

Background.

The Spike Protein (SP) structure and its functional domains are shown in this Figure. The S1 subunit is the initial host interaction portion while the S2 is the post-binding portion responsible for initiating host cell entry, with HR1, HR2, and TM being responsible for breaching the host cell membrane. Allowing viral RNA to enter the cell.



The interaction of the SP portions which interact with the ACE2 of the host cell, which begins the internalization, infectious process, are contained in the Receptor Binding Domain (RBD) and to a lesser extent the Receptor Binding Motif (RBM), specifically residues 331 to 531. Herein, residues 331 to 531 are called the "interaction region."

Evidence given by Andersen:

Reference 7 in the Andersen paper above is a Ralph Baric paper[36] from early in the pandemic (submitted January 22, 2020) and examines five key residues in the receptor binding domain of the Spike Protein (SP) and whether they are "ideal" for interacting with the ACE2 of human cells. The entire paper is based on computer calculations or prior laboratory work but importantly does not do any new "wet" lab work with CoV-2.

Baric et al. had previously identified five amino acid residues that are important for SP-ACE2 interaction. Using the amino acid numbers of CoV-2 these amino acids are: 455, 486, 493, 494, and 501. Baric opines that the most critical residues are 493 and 501 and the next most important residues are 455, 486, and 494. The authors then discuss each amino acid in turn:

Residue 493: "Gln493 in 2019-nCoV RBD is compatible with hot spot 31, suggesting that 2019-nCoV is capable of recognizing human ACE2 and infecting human cells." In this analysis 4 of the 20 amino acids are probed.

Residue 501: "This analysis suggests that 2019-nCoV recognizes human ACE2 less efficiently than human SARS-CoV (year 2002) but more efficiently than human SARS-CoV (year 2003). Hence, at least when considering the ACE2-RBD interactions, 2019-nCoV has gained some capability to transmit from human to human."

Direct binding evidence has shown that this statement is wrong, and CoV-2 binds the ACE2 receptor about ten-times better than SARS-CoV (year 2002).[37] In this analysis 3 of the 20 amino acids are probed.

Residues 455, 486, and 494: First, Baric et al. state: "Leu455 of 2019-nCoV RBD provides favorable interactions with hot spot 31, hence enhancing viral binding to human ACE2."

Next, they state: "Phe486 of 2019-nCoV RBD provides even more support for hot spot 31, hence also enhancing viral binding to human ACE2." Importantly, they also talk about their own laboratory work on an "optimized" receptor binding domain and state: "Leu472 of human and civet SARS-CoV RBDs provides favorable support for hot spot 31 on human ACE2 through hydrophobic interactions with ACE2 residue Met82 and several other hydrophobic residues (**this residue has been mutated to Phe472 in the optimized RBD**)." [emphasis added.]

Finally, they state: Ser494 in 2019-nCoV RBD still provides positive support for hot spot 353, but the support is not as favorable as that provided by Asp480. Overall, Leu455, Phe486, and Ser494 of 2019-nCoV RBD support the idea that 2019-nCoV recognizes human ACE2 and infects human cells."

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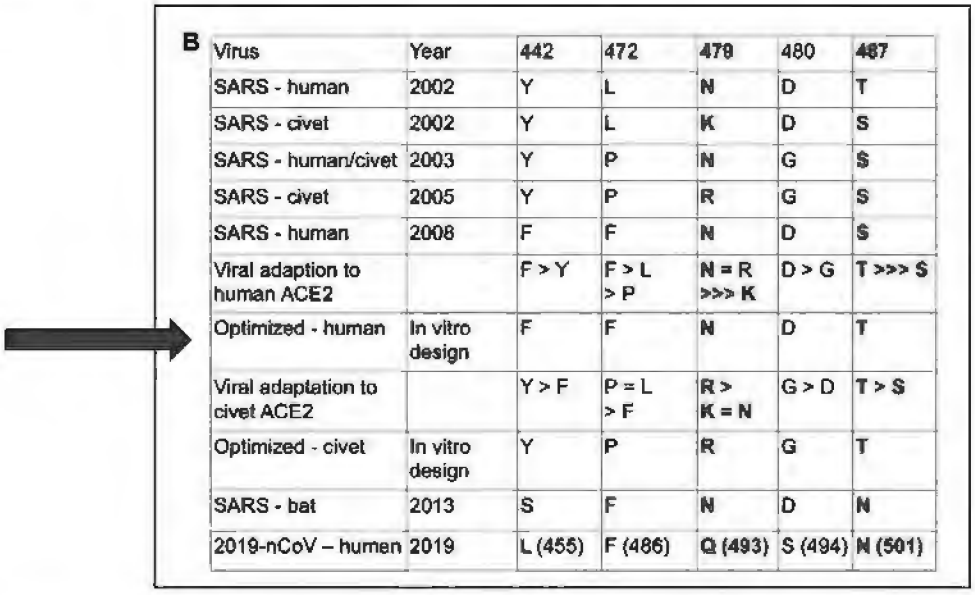
[36] https://jvi.asm.org/content/94/7/e00127-20

[37] https://www.cell.com/action/showPdf?pii=S0092-8674%2820%2931003-5 ; https://www.nature.com/articles/s41586-020-2179-y ; https://www.sciencedirect.com/science/article/pii/S0092867420302622 ; https://science.sciencemag.org/content/367/6483/1260

In this analysis they probe 3 of 20 amino acid residues for position 480, 4 of 20 for position 486, and 4 of 20 for position 442.

As shown in the Figure below from the Baric paper, the in vitro designed, optimized human SP (red arrow) had the amino acid residues F, F, N, D, and T at these five key residues. Since CoV-2 was identical in only one of these five it was not "optimal" and, according to Andersen, it therefore was not laboratory derived.



B

Virus	Year	442	472	479	480	487
SARS - human	2002	Y	L	N	D	T
SARS - civet	2002	Y	L	K	D	S
SARS - human/civet	2003	Y	P	N	G	S
SARS - civet	2005	Y	P	R	G	S
SARS - human	2008	F	F	N	D	S
Viral adaption to human ACE2		F > Y	F > L > P	N = R >>> K	D > G	T >>> S
Optimized - human	In vitro design	F	F	N	D	T
Viral adaptation to civet ACE2		Y > F	P = L > F	R > K = N	G > D	T > S
Optimized - civet	In vitro design	Y	P	R	G	T
SARS - bat	2013	S	F	N	D	N
2019-nCoV – humen	2019	L (455)	F (486)	Q (493)	S (494)	N (501)

Conclusion from the above paper: by examining five amino acid residues of the 200 residues encompassing the interaction region, and calculating the expected interaction of a total of 18 of the 4000 possible residues or 0.45% of all possibilities, they conclude CoV-2 can infect human cells but is not optimized to do so. This data was twisted by Andersen to be 'strong evidence' of natural selection.

An alternative and comprehensive analysis in another paper:[38]

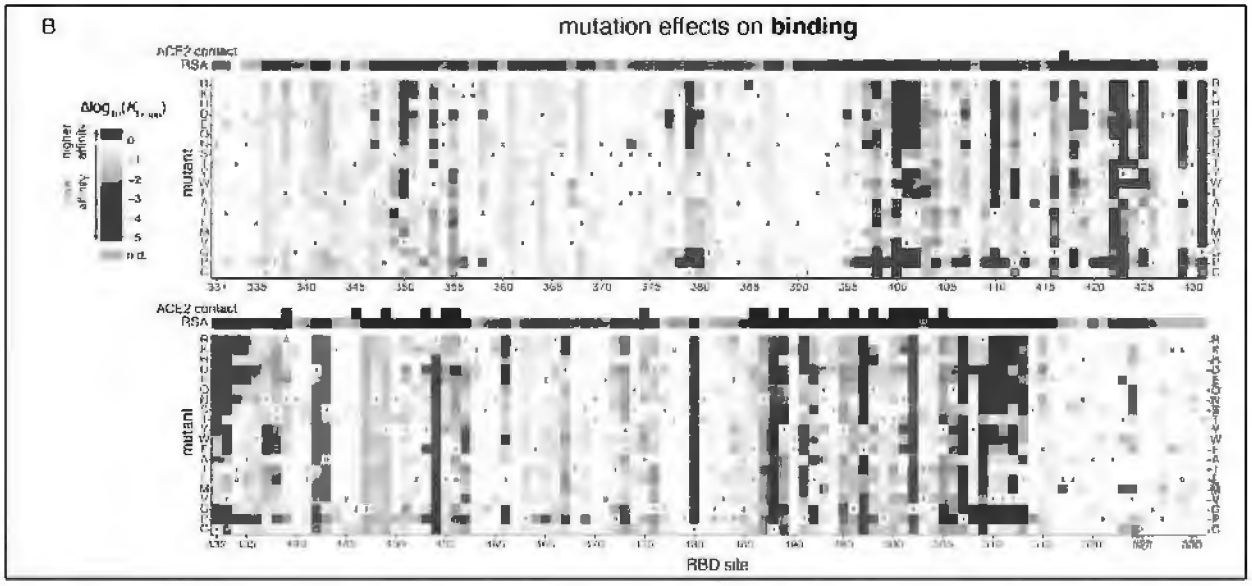
The receptor binding domain (RBD) of the CoV-2 SP is included in residues 331 to 531, a 201 amino acid sequence, of the SP. To examine the effect of each and every amino acid in each and every position, all 19 different amino acids were changed into all 201 positions of the RBD to the extent possible. Out of a total potential of 3819 different single amino acid variants, the scientists were able to create 3804 of the potential variants or 99.6% of the possible variants. It is probably that the variants with the 0.4% amino acid substitutions could not be made for one reason or another. These 3804 were then tested for binding to the human ACE2. Finally, the RBD from SARS-CoV-1 was also tested.

The Figure below is the result of the experiment. Starting with amino acid 331 and ending with amino acid 531, the amino acids that were changed are in vertical columns and are color coded. Shades of brown are amino acid substitutions that reduce ACE2 binding affinity and blue are

[38] https://www.cell.com/action/showPdf?pii=S0092-8674%2820%2931003-5

amino acid substitutions that improve binding, in all cases compared to the 'native' CoV-2 SP sequence. White is the color of a neutral substitution which neither enhances nor diminishes binding. Only the dark blue substitutions provide a strong improvement in ACE2 binding. There is a black square along the top row that denotes amino acids in the SP that interact with the ACE2 protein. Unlike in the Baric analysis above, in which only five amino acids were considered, this group of 19 amino acids provide a more complete interaction picture.

The first overarching observation is that most amino acid substitutions among the 201 amino acids are negative; while a large number are neutral. The fact that the vast majority of amino acid substitutions do not provide an improved ACE2 interaction is clear evidence that the CoV-2 SP interaction region is not newly evolved to the human ACE2.

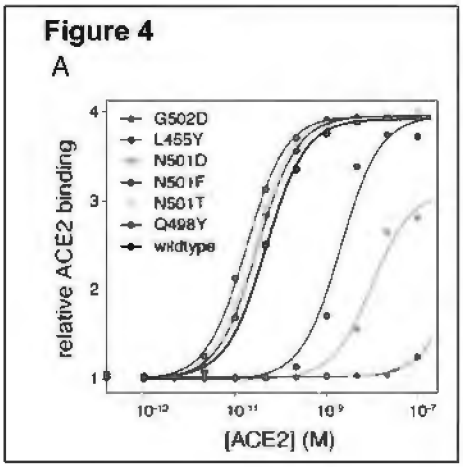


There are three levels of improved binding as designated by dark blue, medium blue, and pale blue. Out of the 3804 variants tested, there are 4 dark blue substitutions or 0.11% and 17 medium blue or 0.45%. According to the paper, the binding effect of the light blue could not be measured as different from the native sequence.

The conclusion of this comprehensive work is the demonstration that for 99.45% of the amino acids in the 201 amino acid interaction region, the CoV-2 choice is optimized, where any substitution is either detrimental or, at best, neutral.

How much could CoV-2 binding be improved or made worse by substitutions during the human-to-human transmission of the pandemic?

The Figure 4 below, taken from the paper, shows that the three best amino acid substitutions have only a slight effect on the binding curve (Black is wildtype; curves to the left are better binding; curves to the right are worse binding). This is further evidence that CoV-2 is optimized as the original virus.



The authors also concluded that Anderson et al was wrong: "An initially surprising feature of SARS-CoV-2 was that its RBD tightly binds ACE2 despite differing in sequence from SARS-CoV-1 at many residues that had been defined as important for ACE2 binding by that virus (Andersen et al., 2020; Wan et al., 2020)."

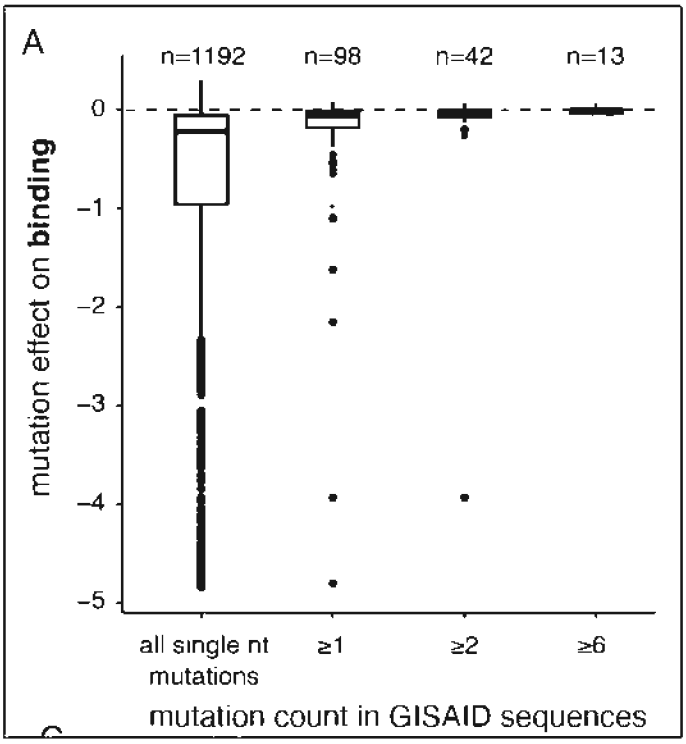
In fact, multiple studies have shown that CoV-2 binds ACE2 better than SARS-CoV-1, contradicting Andersen.

Is there evidence that CoV-2 in human circulation has mutations that enhance ACE2 binding?

Another measure of whether CoV-2 is optimized for human infection is to see if Spike Protein mutations have arisen during the pandemic that improve binding of the virus to the ACE2 receptor or if the SP amino acids are ideal from the very first human patient.

The Starr paper addressed this issue as well. A total of 31,570 human sequences were analyzed to see if any of the 21 amino acid substitutions from the binding experiments (or any other fir that matter) were being selected for.

Below is Figure 8 of the Starr paper. Of the 31,570 sequences, all mutations in the receptor interaction region were analyzed for their effect on ACE2 binding. The data below are for all examples of a single nt mutation (1192), two mutations (98), 3-5 mutations (42), and six or more (13) and the effect the mutation would have on ACE2 binding. The logarithmic scale has the wildtype CoV-2 as 0 and each negative integer is a 10-fold reduction in affinity. Shockingly, there is not a single mutation that is above the 0 line, which would be an improved affinity for the ACE2 receptor. All of the mutations lower the receptor affinity.



Here are the results, in the words of Starr:

"Our discovery of multiple strong affinity-enhancing mutations to the SARS-CoV-2 RBD raises the question of whether positive selection will favor such mutations, since the relationship between receptor affinity and fitness can be complex for viruses that are well-adapted to their hosts (Callaway et al., 2018; Hensley et al., 2009; Lang et al., 2020). Strong affinity-enhancing mutations are accessible via single-nucleotide mutation from SARS-CoV-2 (Figure S8C), but **none are observed among circulating viral sequences in GISAID** (Figure 8A), and **there is no significant trend for actual observed mutations to enhance ACE2 affinity more than randomly drawn samples of all single nucleotide mutations** (see permutation tests in Figure S8D). **Taken together, we see no clear evidence of selection for stronger ACE2 binding, consistent with SARS-CoV-2 already possessing adequate ACE2 affinity at the beginning of the pandemic."** [emphasis added.]

It is striking that the authors, in observing the complete absence of any evidence for stronger ACE2 binding in over thirty thousand cases, would describe this as evidence of "adequate ACE2 affinity" and not as an exceptional finding of "optimized ACE2 affinity." Of course, calling the SP affinity exceptional from the beginning of the pandemic would beg the question of a laboratory derived virus.

Returning to the initial hypotheses, since the 3804 possible amino acids at the receptor interaction region of CoV-2 are 99.45% optimized for ACE2 binding and there is not a single example in 31,570 human CoV-2 genomes of a substitution that enhances ACE2 binding, the CoV-2 interaction with ACE-2 is maximized.

Therefore, the hypothesis, "If the SARS-CoV-2 (CoV-2) Spike Protein interaction with the ACE2 receptor is not maximized, then it is evidence that the interaction is the product of natural selection and not purposeful (laboratory) manipulation," is **rejected**.

The alternative hypothesis, "If the CoV-2 Spike Protein interaction with the ACE2 receptor is maximized, then it is evidence that the interaction was the product of purposeful (laboratory) manipulation," is thus **accepted**.

At the time of this writing, a new RBD mutant N501Y has been observed. It is one of the five potential mutations that could be expected to increase RBD-ACE2 affinity.

This is the first example of evidence that will not be statistically quantified. The evidence is more consistent with having been optimized by various methods used in the laboratory than with the slow natural process as seen with SARS-CoV-1 and so the conservative rule that this is consistent with a laboratory origin (51%) versus zoonotic origin (49%) will be used. There will be no confidence adjustment.

The adjusted likelihoods are shown in the following table.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.988
This is the outcome favors LO over ZO at 51% versus 49%		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.988 = 1.028
Normalize this step of analysis	0.011/(0.011 + 1.028) = 0.011	1.028/(0.011 + 1.028) = 0.989

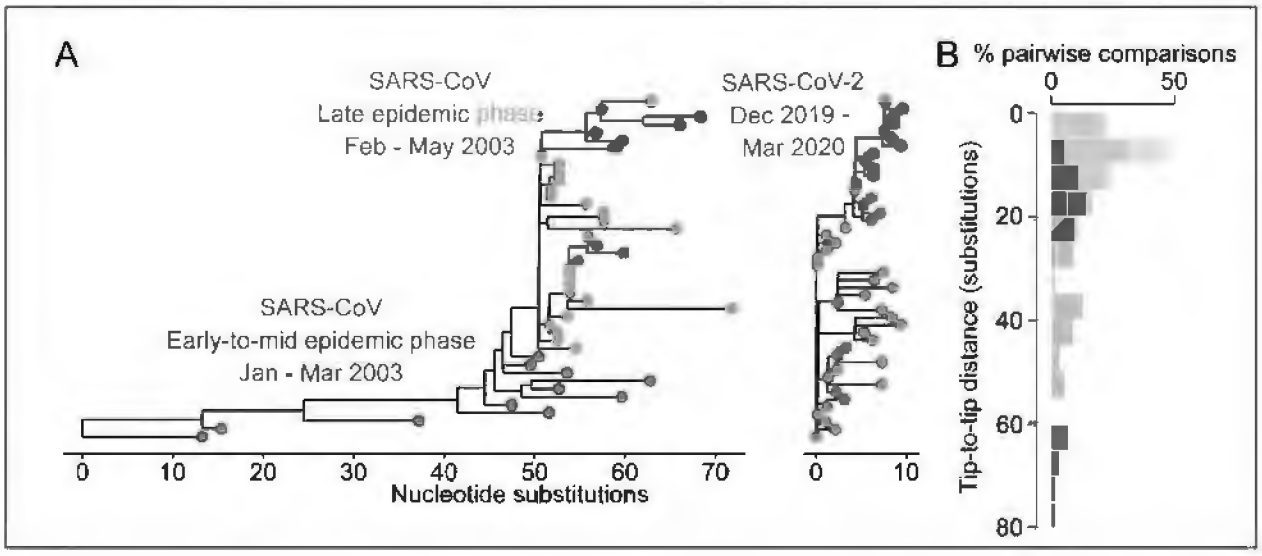
Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

Evidence. Whole genome comparison of human adaption of CoV-2 compared to SARS-CoV-1 is consistent with a "pre-adaption" of CoV-2 to the human host

A paper[39] entitled, "SARS-CoV-2 is well adapted for humans. What does this mean for re-emergence?" by Shing Hei Zhan, Benjamin E. Deverman, and Yujia Alina Chan states in the abstract:

"In a side-by-side comparison of evolutionary dynamics between the 2019/2020 SARS-CoV-2 and the 2003 SARS-CoV, we were surprised to find that SARS-CoV-2 resembles SARS-CoV in the late phase of the 2003 epidemic after SARS-CoV had developed several advantageous adaptations for human transmission. Our observations suggest that **by the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission to an extent similar to late epidemic SARS-CoV. However, no precursors or branches of evolution stemming from a less human-adapted SARS-CoV-2-like virus have been detected.** The sudden appearance of a highly infectious SARS-CoV-2 presents a major cause for concern that should motivate stronger international efforts to identify the source and prevent near future re-emergence. [Emphasis added.]

The following Figure from the paper best illustrates the relative SNV adaption for SARS-CoV-1 versus CoV-2.



The paper also makes a tangential comment about posterior diversity: "It would be curious if no precursors or branches of SARS-CoV-2 evolution are discovered in humans or animals."

This is another example of evidence that will not be statistically quantified. The evidence is more consistent with having been adapted by various known methods used in a laboratory than with the slow natural process as seen with SARS-CoV-1 and so the conservative rule that this is consistent with a laboratory origin (51%) versus zoonotic origin (49%) will be used. There will be no confidence adjustment.

[39] https://www.biorxiv.org/content/10.1101/2020.05.01.073262v1

The adjusted likelihoods are shown in the following table.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
This is outcome favors LO over ZO at 51% versus 49%		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

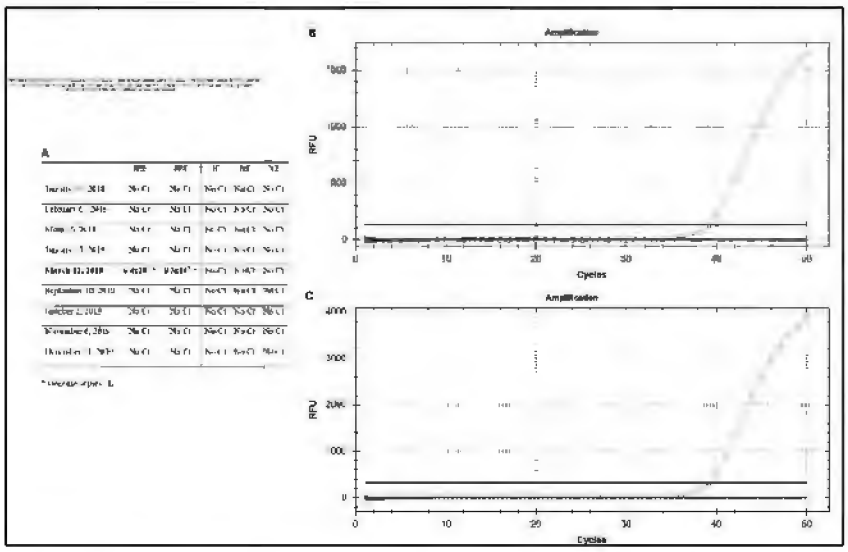
Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

Evidence: Evidence of CoV-2 during early 2019 in wastewater from Barcelona, Spain is a false positive artifact

A paper entitled "Sentinel surveillance of SARS-CoV-2 in wastewater anticipates the occurrence of COVID-19 cases"[40] claims CoV-2 was present in Barcelona, Spain in March 2019. Specifically they state:

"This possibility prompted us to analyze some archival WWTP samples from January 2018 to December 2019 (Figure 2). All samples came out to be negative for the presence of SARS-CoV-2 genomes with the exception of March 12, 2019, in which both IP2 and IP4 target assays were positive. This striking finding indicates circulation of the virus in Barcelona long before the report of any COVID-19 case worldwide."

This is a false positive



As shown above from the paper, they found 43/45 runs with zero and two runs had only 600-800 CoV-2 copies/L

But the limit of detection (LoD) of their assay is 1,000,000 CoV-2/L.

According to the Promega PCR assay FDA clearance package, the Ct at the LoD is 33-34 for the N1 and N2, respectively (Table 17, page 51).[41] Here the LoD is listed as 1 RNA/μL.

In the paper the Ct is 40 or 6-7 above the LoD.

This evidence is neutral as to origin and will not be used to adjust the likelihoods. It does reduce the credibility of some of the new origin theories coming out of China.

[40] https://www.medrxiv.org/content/10.1101/2020.06.13.20129627v1.full.pdf
[41] https://twitter.com/quay_dr/status/1340572543548227585/photo/1

[redacted] WHO and Dr. Shi have spoken of the singular nature the beginning of COVID-19

On January 23, 2020 Dr. Shi wrote in the draft of her paper: "The almost identical sequences of this virus in different patients imply a probably recent introduction in humans…"[42] By February 3, 2020, when the final version of this paper was published, this sentence had been **deleted**.[43]

On April 23, 2020 the WHO stated: "All the published genetic sequences of SARS-CoV-2 isolated from human cases are very similar. This suggests that the start of the outbreak resulted from a single point introduction in the human population around the time that the virus was first reported in humans in Wuhan, China in December 2019."[44]

The evidence is more consistent with a single introduction in a laboratory accident like the lack of posterior diversity and seroconversion reported earlier. This evidence will not be used to adjust probabilities but is included because it could be a form of party admissions of unfavorable facts.

[42] RaTG13 paper as a preprint
[43] RaTG13 final Nature paper
[44] WHO document page 2 of 12

[redacted] Mammalian biodiversity and bat species differences between Yunnan and Hubei Provence are significant and are not supportive of a zoonotic origin

Summary. SARS-CoV-2 is most closely related to bat coronaviruses from Yunnan, a rural province in South West China. Wuhan, where the pandemic began, is a large urban city of 11 million inhabitants in north central China. They are approximately 1900 km apart.

This is the US equivalent of the difference between New York City (population 8.4 million) and the Everglades in Florida, 2000 km away. The incongruent image of a bat or intermediate host in the Everglades somehow finding their way to New York City is a clear demonstration of the difficulty in this hypothetical transmission process. Nonetheless, a strict literature-based analysis will be conducted.

If COVID-19 is a zoonotic disease it must have travelled from bats to humans or from bats to an intermediate species to humans. Therefore, an examination of mammalian biodiversity differences and commonalities between Yunnan and Wuhan might provide useful information about the intermediate host or the particular bat species.

Peter Daszak, Zhengli-li Shi and colleagues published an August 2020 paper entitled, "Origin and cross-species transmission of bat coronaviruses in China,"[45] in which they make a number of observations that are relevant to this analysis. It should be remembered that multiple, strong, public statements over many months by both lead authors that SARS-CoV-2 is a natural zoonosis have been made.

Yunnan and Hubei Provinces have very dissimilar mammalian diversity

Quoting from the Methods section of the paper:

"Defining zoogeographic regions in China

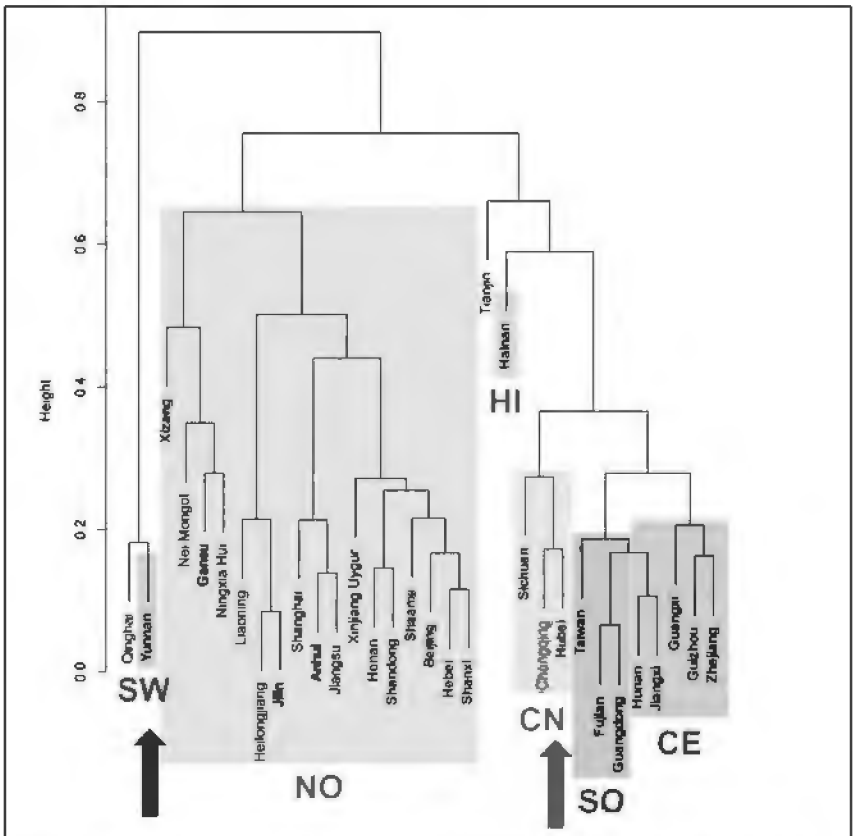
Hierachical clustering was used to define zoogeographic regions within China by clustering provinces with similar mammalian diversity45. Hierarchical cluster analysis classifies several objects into small groups based on similarities between them. To do this, we created a presence/absence matrix of all extant terrestrial mammals present in China using data from the IUCN spatial database84 and generated a cluster dendrogram using the function *hclust* with average method of the R package stats. Hong Kong and Macau were included within the neighboring Guangdong province. We then visually identified geographically contiguous clusters of provinces for which CoV sequences are available (Fig. 1 and Supplementary Fig. 1).

We identified six zoogeographic regions within China based on the similarity of the mammal community in these provinces: **SW (Yunnan province)**, NO (Xizang, Gansu, Jilin, Anhui, Henan, Shandong, Shaanxi, Hebei, and Shanxi provinces and Beijing municipality), **CN (Sichuan and Hubei provinces)**, CE (Guangxi, Guizhou, Hunan, Jiangxi, and Zhejiang provinces), SO (Guangdong and Fujian provinces, Hong Kong, Macau, and Taiwan), and HI. Hunan and Jiangxi, clustering with the SO provinces in our dendrogram, were included within

[45] https://www.nature.com/articles/s41467-020-17687-3#Sec19

the central region to create a geographically contiguous Central cluster (Supplementary Fig. 1). These six zoogeographic regions are very similar to the biogeographic regions traditionally recognized in China85. The three β-CoV sequences from HI were included in the SO region to avoid creating a cluster with a very small number of sequences."

Below is a cluster dendrogram of Chinese provinces based on similarities between their mammalian diversity (hierarchical clustering). Provinces with CoV sequences available in this study are highlighted in bold.



Supplementary Figure 1: Cluster dendrogram of Chinese provinces based on similarities between their mammalian diversity (hierarchical clustering). Provinces with CoV sequences available in this study are highlighted in bold.

The y-axis height is a measure of the biodiversity with 1.0 being complete similarity and 0.0 being no similarity. As expected for the geography and location of the two provinces, Yunnan (red arrow above) and Hubei (green arrow above) have a height score of about 0.1, with seven branches and six nodes separating them. This is close to the biggest different in mammalian biodiversity of any two locations in all of China.

In conclusion, Daszak and Shi et al. demonstrate that the mammalian biodiversity between Yunnan and Hubei is very significant, reducing the options for a common intermediate host to be the natural conduit between bats and humans.

Shi and Daszak statement: "SARS-CoV-2 is likely derived from a clade of viruses originating in horseshoe bats (*Rhinolophus* spp.). The geographic location of this origin appears to be Yunnan province."

This is evidence will not be statistically quantified. The evidence reduces the biodiversity overlap needed to create a common intermediate species between the two provinces and so the conservative rule that this is consistent with a laboratory origin (51%) versus zoonotic origin (49%) will be used. There will be no confidence adjustment.

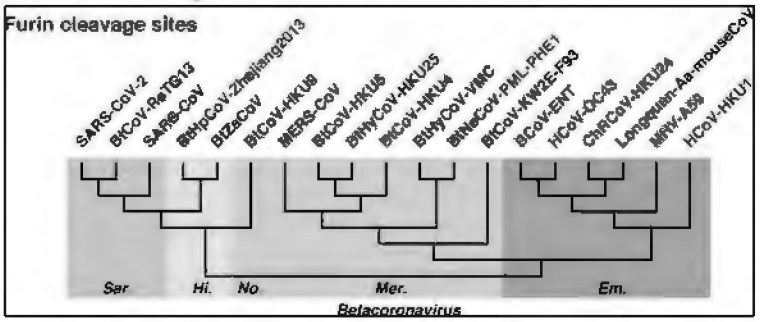
Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
This data from Shi & Daszak disfavors a ZO		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

Because of the rule on the use of significant figures, the likelihood does not change.

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

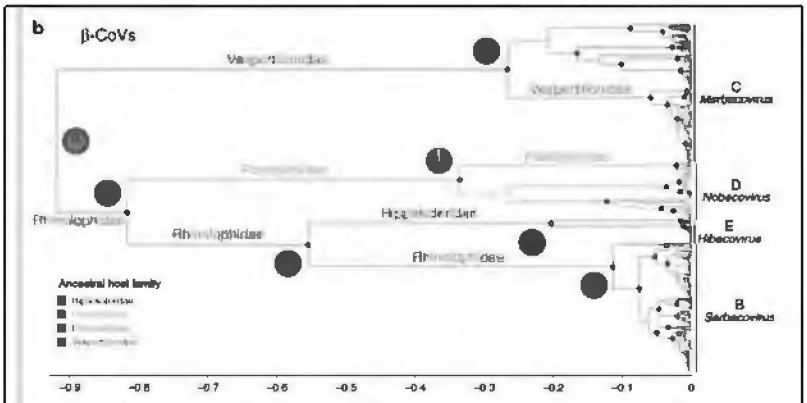
Evidence: The ancestor of SARS-CoV-2 can only obtain a furin site by recombination outside of the sarbecovirus subgenera but there is strong evidence that coronavirus recombination is largely limited to the clade level, with limited evidence of sub-genera or genera recombination

- SARS-CoV-2 is a beta coronavirus, subgenera sarbecovirus and is the only sarbecovirus with a furin site.[46]
- Furin sites can be found in either alpha or gamma coronaviruses or the other beta coronavirus subgenera. The following Figure from reference 66 shows examples of such coronaviruses (furin containing viruses are shown in red):



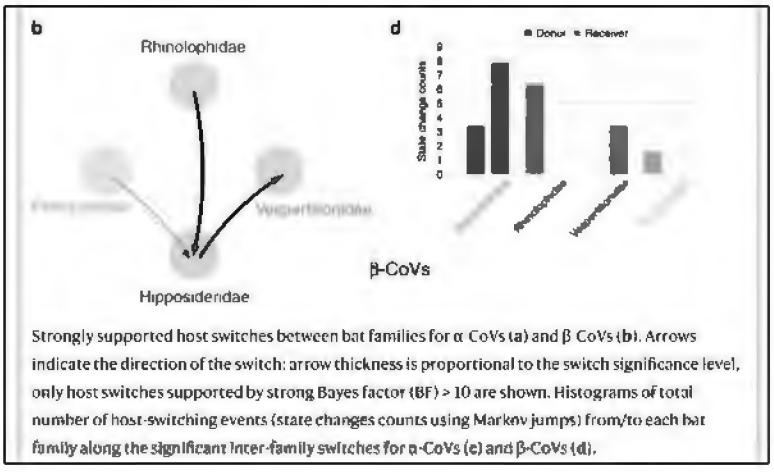
- To acquire a furin site in nature would require a co-infection between the CoV-2 sarbecovirus ancestor and a furin-containing non-sarbecovirus as shown above.
- However, there is no evidence of recombination in coronaviruses at either the genus level or the subgenus level; only at the clade level.[47][48]
- There is also evidence from Daszak and Shi that within the subgenera of the beta coronaviruses, there is bat host specificity. So each subgenera of coronaviruses has a preferred bat host species. This reduces the opportunities for a co-host event to permit recombination.[49] The phylogeny below shows the problem of host incompatibility for beta coronaviruses (from reference 69):

[46] https://www.sciencedirect.com/science/article/pii/S1873506120304165#f0015
[47] file:///C:/Users/Steven%20Quay/Desktop/journal.pgen.1009272.pdf
[48] https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msaa281/5955840
[49] https://www.nature.com/articles/s41467-020-17687-3#Sec2



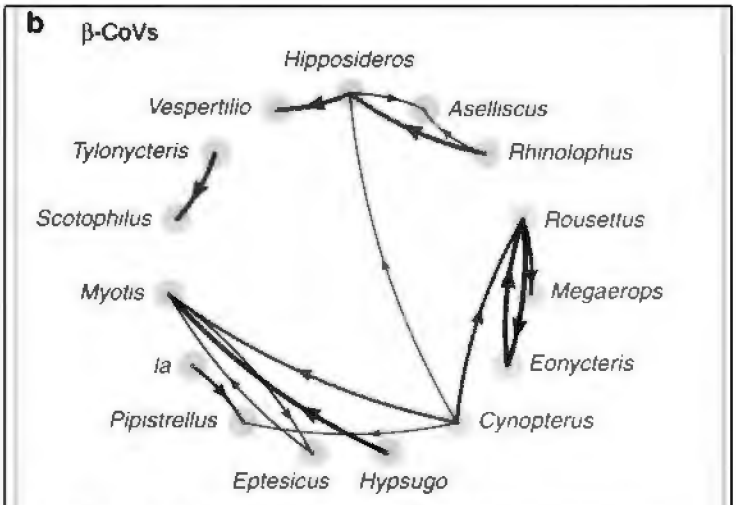
α-CoV (a) and β-CoV (b) maximum clade credibility annotated trees using complete datasets of *RdRp* sequences and bat host family as discrete character state. Pie charts located at the root and close to the deepest nodes show the state posterior probabilities for each bat family. Branch color correspond to the inferred ancestral family with the highest probability. Branch lengths are scaled according to relative time units (clock rate = 1.0). Well-supported nodes (posterior probability > 0.95) are indicated with a black dot. The ICTV approved CoV subgenera were highlighted: *Rhinacovirus* (L1), *Decacovirus* (L2), *Myotacovirus* (L3), *Pedacovirus* (L5), *Nyctacovirus* (L6), *Minunacovirus* (L7), and an unidentified lineage (L4) for α-CoVs; and *Merbecovirus* (Lineage C), *Nobecovirus* (lineage D), *Hibecovirus* (lineage E), and *Sarbecovirus* (Lineage B) for β-CoVs.

- Daszak and Shi also identified preferred directions of host switching. Since RaTG13, the closest coronavirus to SARS-CoV-2, is most closely related to viruses with bat hosts from the family, Rhinolophidae, it would be reasonable to expect furin-containing viruses from other bat hosts to migrate into Rhinolophidae, recombine by methods which have not been identified, and then the furin-containing sarbecovirus could evolve into the ancestor of SARS-CoV-2. Unexpectedly, Daszak et al. found host migration for the Rhinolophidae bats only outward and not inward, as required by the above, admittedly, convoluted process. The data Figure is shown here:



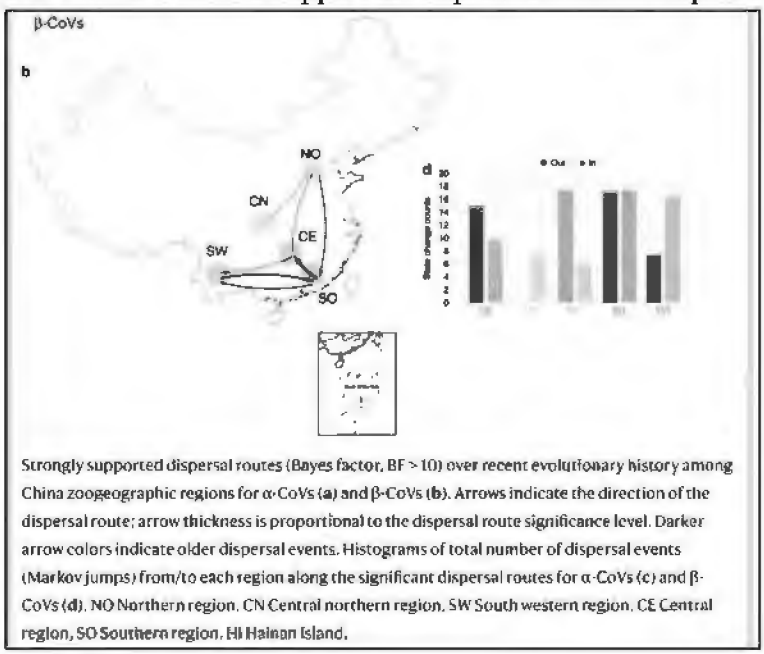
Strongly supported host switches between bat families for α CoVs (a) and β CoVs (b). Arrows indicate the direction of the switch: arrow thickness is proportional to the switch significance level, only host switches supported by strong Bayes factor (BF) > 10 are shown. Histograms of total number of host-switching events (state changes counts using Markov jumps) from/to each bat family along the significant inter-family switches for α-CoVs (c) and β-CoVs (d).

- Daszak and Shi also observed outward host switches from *Rhinolophus* at the genera level as well, also against a hypothesis for furin-site acquisition:



Strongly supported host switches between bat genera for α-CoVs (a) and β-CoVs (b) and their significance level (Bayes factor, BF). Only host switches supported by strong BF values >10 are shown. Line thickness is proportional to the switch significance level. Red lines correspond to host switches among bat genera belonging to different families, and black lines correspond to host switches among bat genera from the same family. Arrows indicate the direction of the switch. Genus names are colored according to the family they belong to using the same colors as in Figs. 2 and 3.

- Finally, this paper by Daszak and Shi states: "We used our Bayesian discrete phylogeographic model with zoogeographic regions as character states to reconstruct the spatiotemporal dynamics of CoV dispersal in China." If SARS-CoV-2 began in Yunnan and first crossed over into humans in Wuhan, this analysis should support a northernly spatiotemporal dispersal of beta coronaviruses. Unfortunately, Daszak and Shi cannot catch a break; their own data do not support the expected route of dispersion:



Strongly supported dispersal routes (Bayes factor, BF > 10) over recent evolutionary history among China zoogeographic regions for α-CoVs (a) and β-CoVs (b). Arrows indicate the direction of the dispersal route; arrow thickness is proportional to the dispersal route significance level. Darker arrow colors indicate older dispersal events. Histograms of total number of dispersal events (Markov jumps) from/to each region along the significant dispersal routes for α-CoVs (c) and β-CoVs (d). NO Northern region, CN Central northern region, SW South western region, CE Central region, SO Southern region, HI Hainan Island.

As shown in the above Figure the only dispersal routes into Wuhan, which is in the CN region, are from the northern region. And the northern region has no inward dispersals from the SW, southwest region, where Yunnan and the origin of the ancestor of SARS-CoV-2, is located.

- Independent evidence documents that Hubei province does not have the bat species needed for SARS-CoV-2 reservoir host[50]

While statistical models of this data could be interesting and informative for general research about future spillovers, this is evidence will not be statistically quantified for this analysis. The evidence reduces the opportunities for subgenera co-infection and furin-site recombination into the CoV-2 ancestor and so the conservative rule that this is less consistent with a zoonotic origin (49%) versus laboratory origin (49%) will be used. There will be no confidence adjustment.

The results from the calculations are shown below.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
This data from Shi & Daszak and the 'furin sites are everywhere' paper are disfavored		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

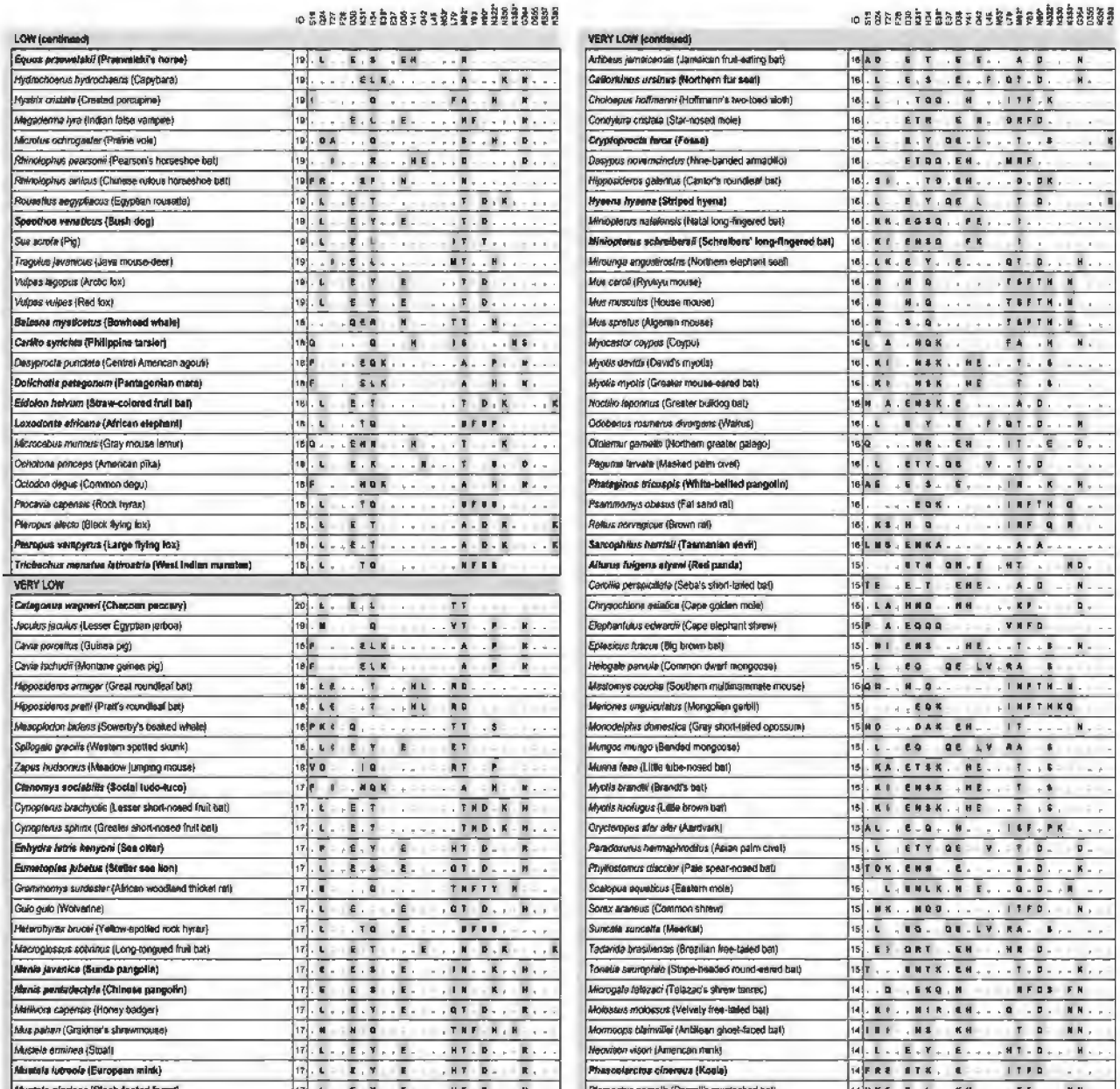
[50] file:///C:/Users/Steven%20Quay/Desktop/Zhangetal2009.pdf

[redacted] Of 410 vertebrate species tested for affinity to CoV-2 Spike Protein binding domain, primate ACE2 receptor, including human and VERO monkey cells, are the best at binding and bat species ACE2 are the worse, making direct bat-to-human host jumping extremely unlikely

- An examination of the ACE2 receptor binding domain amino acid sequences and their suitability for interacting with SARS-CoV-2 was performed in 410 vertebrates, including 252 mammals.[51]
- A five-category binding score was developed based on the conservation properties of 25 amino acids important for the binding between ACE2 and the SARS-CoV-2 spike protein.
- Only mammals fell into the medium to very high categories and only primates scored 25/25 for binding.
- This implies that SARS-CoV-2 is optimized for human ACE2-bearing cells from the first introduction into the human population, an observation that contradicts a zoonotic origin.
- It also suggests that other primates may be the proximate species from which SARS-CoV-2 entered the human population.
- Both VERO monkey kidney cells and ACE2 humanized mice would quality as an intermediate species by this criterion.
- Surprisingly, "all chiropterans (bats) scored low (n = 8) or very low (n = 29), including the Chinese rufous horseshoe bat, from which a coronavirus (SARSr-CoV ZC45) related to SARS-CoV-2 was identified."
- This is evidence that bats are probably not a reservoir host for SARS-CoV-2.
- A separate study observed: "Severe acute respiratory syndrome coronavirus 2 did not replicate efficiently in 13 bat cell lines."[52]
- The following two Tables are taken from the paper and are organized according to ACE2 SARS-CoV-2 affinity, from highest to lowest:

[51] https://www.pnas.org/content/117/36/22311
[52] https://wwwnc.cdc.gov/eid/article/26/12/20-2308_article

Species	ID	S19	Q24	T27	F28	D30	K31	H34	E35	E37	D38	Y41	Q42	L45	N53	L79	M82	Y83	N90	N322	N330	K353	G354	D355	R357	R393
VERY HIGH																										
Homo sapiens (Human)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Gorilla gorilla gorilla* (Western lowland gorilla)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Nomascus leucogenys* (Northern white-cheeked gibbon)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Pongo abelii* (Sumatran orangutan)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Macaca fascicularis (Crab-eating macaque)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Mandrillus leucophaeus* (Drill)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Nasalis larvatus* (Proboscis monkey)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Pan paniscus* (Bonobo)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Pan troglodytes* (Chimpanzee)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Piliocolobus tephrosceles* (Ugandan red colobus)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Pygathrix nemaeus* (Red-shanked douc)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Rhinopithecus roxellana* (Golden snub-nosed monkey)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Chlorocebus sabaeus (Green monkey)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Erythrocebus patas (Patas monkey)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Macaca mulatta (Rhesus macaque)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Papio anubis (Olive baboon)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Theropithecus gelada (Gelada)	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Cercocebus atys* (Sooty mangabey)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
***Macaca nemestrina* (Southern pig-tailed macaque)**	25	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
HIGH																										
***Colobus angolensis* (Angola colobus)**	24	.	.	.	.	.	.	.	.	.	.	.	.	.	.	N	.	.	.	.	.	.	.	.	.	.
***Propithecus coquereli* (Coquerel's sifaka)**	24	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Cricetomys gambianus (Gambian pouched rat)	22	.	.	A	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	.	.	.	.	.	.	.	.
Cricetulus griseus (Chinese hamster)	22	.	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	.	H	.	.	.	.	.	.
Ctenodactylus gundi (Common gundi)	22	.	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	T	.	.	.	.	.	.	.
Delphinapterus leucas (Beluga whale)	22	.	.	.	.	Q	.	.	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
***Eulemur flavifrons* (Blue-eyed black lemur)**	22	.	E	A	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Indri indri* (Indri)**	22	.	.	.	.	.	N	Q	.	.	.	.	.	.	.	.	N	.	.	.	.	.	.	.	.	.
Monodon monoceros (Narwhal)	22	.	.	.	.	Q	.	.	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
***Neophocaena asiaeorientalis* (Narrow-ridged finless porpoise)**	22	.	.	.	.	Q	.	.	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
Phocoena phocoena (Harbour porpoise)	22	.	.	.	.	Q	.	.	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
Balaenoptera acutorostrata scammoni (Minke whale)	21	.	.	.	.	Q	.	.	.	.	.	.	R	.	.	I	T	.	.	.	.	.	.	.	.	.
Balaenoptera bonaerensis (Antarctic minke whale)	21	.	.	.	.	Q	.	.	.	.	.	.	R	.	.	I	T	.	.	.	.	.	.	.	.	.
Eschrichtius robustus (Gray whale)	21	.	.	.	.	Q	.	.	.	.	.	.	E	.	.	I	T	.	.	.	.	.	.	.	.	.
Nannospalax galili (Spalax)	21	.	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	K	.	D	Q	.	.	.	.	.	.
Odocoileus virginianus texanus (White-tailed deer)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	H	.	.	.	.	.	.
***Rangifer tarandus* (Reindeer)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	H	.	.	.	.	.	.
Tamandua tetradactyla (Southern tamandua)	21	.	.	.	.	E	.	Q	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
***Dipodomys stephensi* (Stephens's kangaroo rat)**	20	.	L	.	.	.	N	Q	.	.	.	.	.	.	.	.	I	.	.	K	.	.	.	.	.	.
***Elaphurus davidianus* (Pere David's deer)**	20	.	.	.	.	E	N	.	.	.	.	.	.	.	.	M	T	.	.	H	.	.	.	.	.	.
Ellobius lutescens (Transcaucasian mole vole)	20	.	D	.	.	.	.	Q	.	.	.	.	.	.	.	.	S	.	.	H	.	.	Q	.	.	.
Globicephala melas (Long-finned pilot whale)	20	.	R	.	.	Q	.	R	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
Lagenorhynchus obliquidens (Pacific white-sided dolphin)	20	.	R	.	.	Q	.	R	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
***Lipotes vexillifer* (Baiji)**	20	.	R	.	.	Q	.	.	.	.	.	.	.	.	.	I	T	F	.	.	.	.	.	.	.	.
***Myrmecophaga tridactyla* (Giant anteater)**	20	.	.	.	.	E	.	Q	.	.	N	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
Ondatra zibethicus (Muskrat)	20	.	.	.	.	E	.	Q	.	.	.	.	.	.	.	.	N	.	.	H	.	.	Q	.	.	.
Orcinus orca (Killer whale)	20	.	R	.	.	Q	.	R	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
Tursiops truncatus (Common bottlenose dolphin)	20	.	R	.	.	Q	.	R	.	.	.	.	.	.	.	I	T	.	.	.	.	.	.	.	.	.
MEDIUM																										
***Daubentonia madagascariensis* (Aye-aye)**	23	P	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Cheirogaleus medius (Fat-tailed dwarf lemur)	22	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	K	Q	.	.	.	.	.
Ictidomys tridecemlineatus (Thirteen-lined ground squirrel)	22	.	L	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.
Marmota flaviventris (Yellow-bellied marmot)	22	.	L	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.
Marmota marmota marmota (Alpine marmot)	22	.	L	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.
***Mesocricetus auratus* (Golden hamster)**	22	.	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	.	Y	.	.	.	.	.	.
***Physeter catodon* (Sperm whale)**	22	.	.	.	.	Q	.	.	.	.	.	.	.	.	.	T	T	.	.	.	.	.	.	.	.	.
Spermophilus dauricus (Daurian ground squirrel)	22	.	L	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.
Allactaga bullata (Gobi jerboa)	21	.	T	.	.	.	.	Q	.	.	.	.	.	.	.	.	T	.	.	H	.	.	.	.	.	.
***Ammotragus lervia* (Barbary sheep)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Antilocapra americana (Pronghorn)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Aotus nancymaae* (Nancy Ma's night monkey)**	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
***Beatragus hunteri* (Hirola)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Bison bison bison* (American bison)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Bos indicus (Zebu)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Bos mutus* (Wild yak)**	21	.	.	.	.	.	.	K	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
MEDIUM (continued)																										
Bos taurus (Cattle)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Bubalus bubalis (Water buffalo)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Callicebus donacophilus (White-eared titi)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Callithrix jacchus (Common marmoset)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
***Capra aegagrus* (Wild goat)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Capra hircus (Goat)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Cebus capucinus imitator (Panamanian white-faced capuchin)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Felis catus (Cat)	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Giraffa tippelskirchi* (Masai giraffe)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Hemitragus hylocrius* (Nilgiri tahr)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Lynx canadensis (Canadian lynx)	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Mirza coquereli* (Coquerel's giant mouse lemur)**	21	.	.	I	.	.	.	N	.	.	.	.	.	.	.	.	T	.	.	.	R	.	.	.	.	.
***Moschus moschiferus* (Siberian musk deer)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Neofelis diardi* (Sunda clouded leopard)**	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Neofelis nebulosa* (Clouded leopard)**	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Okapia johnstoni* (Okapi)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Ovis aries (Sheep)	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Panthera onca* (Jaguar)**	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Panthera pardus* (Leopard)**	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Panthera tigris altaica* (Siberian tiger)**	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Pantholops hodgsonii* (Tibetan antelope)**	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Perognathus longimembris (Little pocket mouse)	21	.	V	.	.	.	.	Q	.	.	.	.	.	.	.	.	T	.	.	K	.	.	.	.	.	.
Peromyscus maniculatus bairdii (Deer mouse)	21	.	.	I	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	.	H	.	.	.	.	.	.
Pithecia pithecia (White-faced saki)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Puma concolor (Cougar)	21	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Saimiri boliviensis boliviensis (Black-capped squirrel monkey)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Sapajus apella (Tufted capuchin)	21	.	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Urocitellus parryii (Arctic ground squirrel)	21	.	L	.	.	.	.	Q	.	.	.	N	.	.	.	.	Q	.	.	.	.	.	.	.	.	.
Bos indicus x Bos taurus	21	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
***Acinonyx jubatus* (Cheetah)**	20	.	L	.	.	E	.	.	.	.	E	.	.	.	.	.	T	.	.	.	K	.	.	.	.	.
***Alouatta palliata* (Mantled howler)**	20	.	.	.	.	.	E	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
***Ateles geoffroyi* (Geoffroy's spider monkey)**	20	A	.	.	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Fukomys damarensis (Damaraland mole-rat)	20	L	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	H	.	.	N	.	.	.
Heterocephalus glaber (Naked mole-rat)	20	L	.	.	.	.	.	Q	.	.	.	.	.	.	.	.	A	.	.	H	.	.	D	.	.	.
***Hippopotamus amphibius* (Hippopotamus)**	20	.	.	.	.	L	.	.	Q	.	.	.	.	.	.	A	.	F	Q	.	.	.	.	.	.	.
Lepus americanus (Snowshoe hare)	20	.	L	.	.	E	.	Q	.	.	.	.	.	.	.	.	T	.	.	S	.	.	.	.	.	.
***Nanger dama* (Dama gazelle)**	20	.	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	F	.	Y	.	.	.	.	.	.
***Oryctolagus cuniculus* (European rabbit)**	20	.	L	.	.	E	.	Y	.	.	.	.	.	.	.	.	T	.	.	S	.	.	.	.	.	.
***Oryx dammah* (Scimitar oryx)**	20	[illegible]	.	.	.	E	.	.	.	.	.	.	.	.	.	M	T	.	.	Y	.	.	.	.	.	.
Saguinus imperator (Emperor tamarin)	20	.	.	A	.	.	.	.	.	.	.	H	E	.	.	.	T	.	.	.	.	.	Q	.	.	.
Vicugna pacos (Alpaca)	20	.	L	.	.	K	E	.	.	.	.	.	.	.	.	A	I	.	.	.	.	.	.	.	.	.
LOW																										
***Ceratotherium simum cottoni* (Northern white rhinoceros)**	21	.	L	.	.	E	.	P	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Ceratotherium simum simum* (Southern white rhinoceros)**	21	.	L	.	.	E	.	P	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Diceros bicornis* (Black rhinoceros)**	21	.	L	.	.	E	.	P	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Galeopterus variegatus (Sunda flying lemur)	21	F	L	.	.	.	.	.	.	.	.	.	E	.	.	.	N	.	.	.	.	.	.	.	.	.
Peromyscus leucopus (White-footed mouse)	21	.	.	I	.	.	.	Q	.	.	.	.	.	.	.	.	N	.	.	F	.	.	.	.	.	.
***Ailuropoda melanoleuca* (Giant panda)**	20	.	L	.	.	E	.	Y	.	.	.	.	.	.	.	N	T	.	.	.	.	.	.	.	.	.
Camelus bactrianus (Bactrian camel)	20	.	L	.	.	E	Q	.	.	.	.	.	.	.	.	T	T	.	.	.	.	.	.	.	.	.
Camelus dromedarius (Dromedary)	20	.	L	.	.	E	Q	.	.	.	.	.	.	.	.	T	T	.	.	.	.	.	.	.	.	.
***Camelus ferus* (Wild bactrian camel)**	20	.	L	.	.	E	E	.	.	.	.	.	.	.	.	T	T	.	.	.	.	.	.	.	.	.
***Dicerorhinus sumatrensis* (Sumatran rhinoceros)**	20	.	L	.	.	E	.	P	.	.	.	H	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Graphiurus murinus (Woodland dormouse)	20	.	T	.	.	.	N	R	.	.	.	.	.	.	.	N	N	.	.	.	.	.	.	.	.	.
***Tapirus indicus* (Malayan tapir)**	20	.	L	.	.	E	.	P	.	.	.	H	.	.	.	.	T	.	.	.	.	.	.	.	.	.
***Tapirus terrestris* (South American tapir)**	20	.	L	.	.	E	.	P	.	.	.	H	.	.	.	.	T	.	.	.	.	.	.	.	.	.
Ursus arctos horribilis (Grizzly bear)	20	.	L	.	.	E	.	Y	.	.	.	.	.	.	.	N	T	.	.	.	.	.	.	.	.	.
***Ursus maritimus* (Polar bear)**	20	.	L	.	.	E	.	Y	.	.	.	.	.	.	.	N	T	.	.	.	.	.	.	.	.	.
***Canis lupus dingo* (Dingo)**	19	.	L	.	.	E	.	Y	.	.	E	.	.	.	.	.	T	.	Q	.	.	.	.	.	.	.
Canis lupus familiaris (Dog)	19	.	L	.	.	E	.	Y	.	.	E	.	.	.	.	.	T	.	Q	.	.	.	.	.	.	.
***Chinchilla lanigera* (Long-tailed chinchilla)**	19	.	.	.	.	.	N	E	K	.	.	.	.	.	.	.	A	.	.	H	.	.	D	.	.	.
***Chrysocyon brachyurus* (Maned wolf)**	19	.	L	.	.	E	.	Y	.	.	E	.	.	.	.	.	T	.	Q	.	.	.	.	.	.	.
Dipodomys ordii (Ord's kangaroo rat)	19	Q	L	.	.	.	N	Q	.	.	.	.	.	.	.	.	I	.	.	K	.	.	.	.	.	.
Eonycteris spelaea (Lesser dawn bat)	19	.	L	.	.	E	.	T	.	.	.	.	.	.	.	.	T	.	Q	.	R	.	.	.	.	.
Equus asinus (Donkey)	19	.	L	.	.	E	.	S	.	.	E	H	.	.	.	.	N	.	.	.	.	.	.	.	.	.
Equus caballus (Horse)	19	.	L	.	.	E	.	S	.	.	E	H	.	.	.	.	N	.	.	.	.	.	.	.	.	.



While statistical models of this data could be interesting and informative this is evidence will not be statistically quantified for this analysis. The evidence is another way of looking at the pre-adapted state of the CoV-2 for humans and suggests that primate animals, monkey cell cultures like the VERO cell, and humanized mice could be likely laboratory models that were used by the

WIV in GoF research. This will contribute a 51%/49% contribution in favor of laboratory compared to zoonotic origin. There will be no confidence adjustment.

The results from the calculations are shown below.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
A study of 410 animal ACE2 receptors shows CoV2 binds best to humans and other primates and worst to bat species		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

Evidence: Did a Review of Samples Collected from a Mineshaft Cause the COVID-19 Pandemic?[53]

Abstract. The origin of the COVID-19 pandemic caused by SARS-CoV-2 has been hotly debated. Proponents of the natural spillover theory allege that the virus jumped species, possibly via an intermediary host, to cross over to humans via the wildlife trade or by other means. Proponents of a rival theory allege that the virus escaped from a laboratory in Wuhan. This research presents circumstantial evidence of a transmission route via a late 2019 review of samples collected from a mineshaft in Mojiang, Yunnan Province, China. It examines the activity at the Wuhan Institute of Virology in late 2019, when samples from a mineshaft associated with a suspected SARS outbreak were being reviewed. It proposes that spillover occurred during this review of samples including of a virus (BtCoV/4991) only 1% different to SARS-CoV-2 in its RNA-dependent RNA polymerase (RdRp). It also proposes that the chance of identifying the outbreak may have been reduced by the issuance of new influenza guidance in November 2019.

It is a meticulous sourced analysis. It purposely avoids the question of whether SARS-CoV-2 was being grown or manipulated in the laboratory.

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[53] https://zenodo.org/record/4029545#.X-x_f9gzbOg. Author anonymous. A meticulously documented analysis that concludes an accident occurred at the Wuhan Institute of Virology during the fall of 2019. Includes many primary documents from Mandarin. No direct evidence of 'what' was the nature of the accident or if it was SARS-CoV-2.

Evidence: The Hunan market was not the source of SARS-CoV-2

From the WHO Terms of Reference for the investigation of the origin of SARS-CoV-2:[54]

"The Huanan wholesale market is a large market (653 stalls and more than 1180 employees) mainly supplying seafood products but also fresh fruits and vegetables, meat, and live animals. In late December 2019, 10 stalls operators were trading live wild animals including chipmunks, foxes, racoons, wild boar, giant salamanders, hedgehogs, sika deer, among others. Farmed, wild and domestic animals were also traded at the market including snakes, frogs, quails, bamboo rats, rabbits, crocodiles, and badgers. The market was closed on 1 January 2020, and several investigations followed, including environmental sampling in the market, as well as sampling of frozen animal carcasses at the market. **Of the 336 samples collected from animals, none were PCR positive for SARS-CoV-2**, whereas 69 out of 842 environmental samples were positive by PCR for SARS-CoV-2. Sixty- one of those (88%) were from the western wing of the market. Of these, 22 samples were from 8 different drains and sewage, and 3 viruses were isolated, sequenced and shared on GISAID. These were virtually identical to the patient samples collected at the same time (>99.9 % homology)."

For contrast, with SARS-CoV-1 91 civets & 15 raccoon dogs in wet markets were tested with 106/106, 100% positive.[55]

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[54] https://drive.google.com/file/d/1rx0W2efbE0R1Aq-lALWTqD22VsWbTlO-/view
[55] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1212604/

[redacted] Analysis of the hospital of admission for COVID-19 patients during December 2019 places "ground zero" for the outbreak somewhere along Line 2 of the Wuhan Metro System.

Line 2 carries 500,000 people per day and services the Wuhan Institute of Virology, the Hunan Seafood Market, the high-speed rail system, and the Wuhan International Airport

A preprint manuscript[56] reported that the earliest genomic cluster of SARS-CoV-2 patients is a group of four individuals associated with the General Hospital of Central Theater Command of People's Liberation Army (PLA) of China in Wuhan. This cluster contains the "Founder Patients" of both Clade A and Clade B, from which every SARS-CoV-2 coronavirus that has infected every patient with COVID-19 anywhere in the world has arisen.

The PLA Hospital is about one mile from the Wuhan Institute of Virology (WIV) and the closest hospital to WIV. Both the PLA Hospital and WIV are serviced by Line 2 of the Wuhan Metro System. The Hunan Seafood Market is also located adjacent to Line 2. All patients between December 1st, 2019 and early January 2020 were first seen at hospitals that are also serviced by Line 2 of the Metro system.

With 40 hospitals located near seven of the nine Metro Lines, the likelihood that all early patients were seen at hospitals only near Line 2 by chance is about 1 in 68,500 (p-value = 0.0000146). The inference then would be that the early spread of SARS-CoV-2 was through human-to human transmission on Line 2.

Line 2 carries one million passengers per day and assuming most are round trip business workers going to and from work in the morning and evening, represents 500,000 riders or about 5% of the Wuhan population. A very recent publication determined that, in fact, 500,000 residents of Wuhan contracted COVID-19, a ten-fold upper estimate.[57] The coincidence of my prediction that 500,000 riders on Line 2 were likely exposed to SARS-CoV-2 in late 2019 and the recent admission from Chinese CDC that Wuhan had 500,000 COVID-19 cases is duly noted!

Line 2 connects to all eight other lines of the Wuhan Metro System (1, 3, 4, 6, 7, 8, 11, and Yanglu) facilitating rapid spread in Wuhan and Hubei Province, and also services both the high-speed rail station (Hankou Railway Station), facilitating rapid spread throughout China, and the Wuhan International Airport (Tianhe International Airport), facilitating rapid spread throughout Asia, Europe, and to the United States. In fact, direct human-to-human spread from the Reference Sequence patient to patients around the world is suggested by an unexpectedly reduced genome base substitution rate seen in patient specimens in cities with direct flights from Wuhan.

[56] https://zenodo.org/record/4119263#.X-rszNgzbOg

[57] https://mp.weixin.qq.com/s/LXTfDmsQLf3qZnu_S_MxcA ; https://thehill.com/policy/international/china/531935-study-shows-wuhan-coronavirus-cases-may-have-been-10-times-higher

In a separate paper by Quay and Lee from May 2020, now accepted for publication in *Epidemics*,[58] they provide evidence that COVID-19 was appearing in California as early as the first week of 2020. This is likely due to direct flights connecting Line 2 to the Wuhan airport and then to San Francisco.

While of little probative value, this 50-second video[59] from Rep. Steven Smith's (R-GA) Twitter account is a concise summation of this evidence: the speaker is Peter Daszak, at 17-seconds it shows a crowded Wuhan Metro Station with a Line 2 sign overhead, and then at 25-seconds it shows Drs. Daszak and Shi looking at a computer screen inside the Wuhan Institute of Virology.

In conclusion, Line 2 of the Wuhan Metro System services the PLA Hospital with the first genomic cluster of patients with COVID-19, the hospitals where patients first went in December 2019 and early January 2020 and is the likely conduit for human-to-human spread throughout Wuhan, China, and the world.

The Hunan Seafood Market, Wuhan Institute of Virology, and the Wuhan CDC, all locations suggested to be the possible source of SARS-CoV-2 in Wuhan, are also all serviced by Line 2 of the Metro system, suggesting this public transit line should become the focus for further investigations into the origin of this pandemic.

Given that the Hunan Seafood Market has been removed as a source for the origin of CoV-2, this evidence will contribute a 51%/49% contribution in favor of laboratory compared to zoonotic origin. There will be no confidence adjustment.

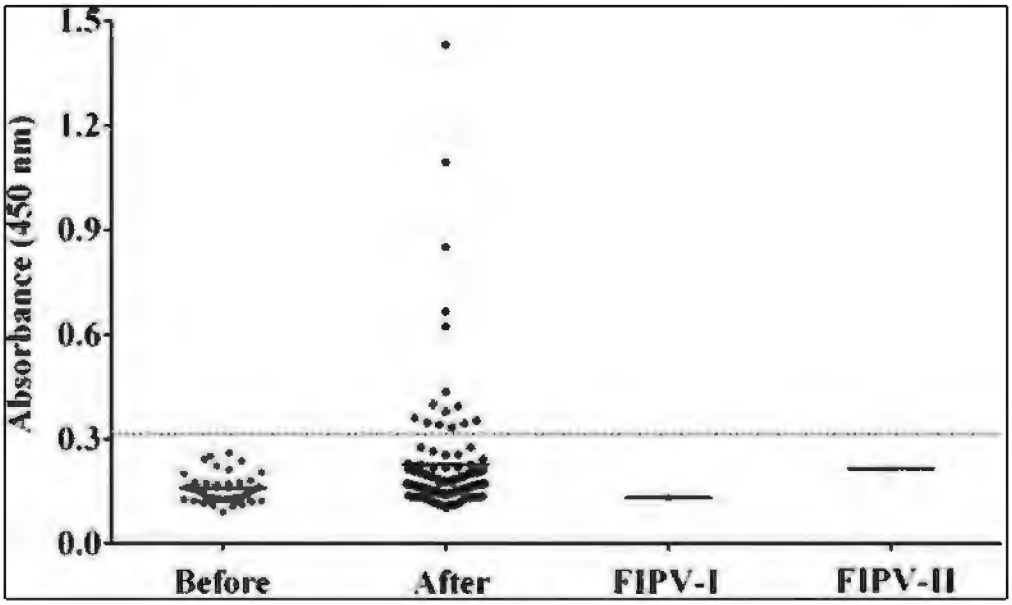
The results from the calculations are shown below.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
The finding of Line 2 as the likely geoorigin for CoV-2 and the fact it services the WIV this evidence favors a LO		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[58] https://www.researchgate.net/publication/341742303_COVID-19_May_Have_Have_Reached_United_States_in_January_2020_05272020
[59] https://twitter.com/i/status/1264742199754756097

Evidence: SARS-CoV-2 infection, based on antibody seroconversion, was not found in 39 archived specimens taken from cats (1/3 feral) between March and May 2019[60]



Based on these results, the prevalence of SARS-CoV-2 in domestic and feral cats prior to January 2020 is less than 8% with a 90% confidence interval.

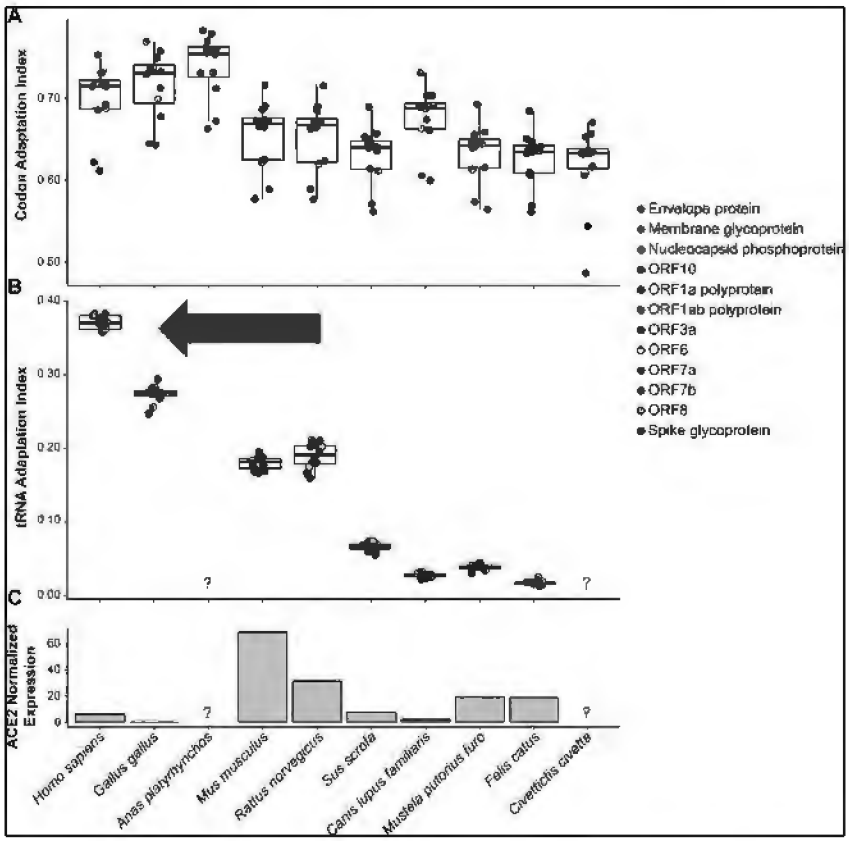
This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[60] https://www.tandfonline.com/doi/full/10.1080/22221751.2020.1817796

Evidence: The extraordinary pre-adaption of SARS-CoV-2 for human cells is demonstrated by a paper looking at a tRNA adaption index.[61]

"The proteome of SARS-CoV-2 is mainly composed of the replicase polyprotein (ORF1ab) and of structural proteins: the spike glycoprotein, the membrane and envelope proteins, and the nucleoprotein [41]. Based on the genomic codon usage of each of the possible host species, we compute the codon adaptation index (CAI) and the tRNA adaptation index (tAI) to estimate the translational efficiency of SARS-CoV-2 proteins in each host (Fig 3A and 3B and S2 Table). Humans are among the top three species whose CAIs are mostly over 0.70, together with ducks and and chicken. In terms of the tAI, humans show the highest translational adaptation among all others, followed by chicken, and, to some extent, mice and rats. On the other hand, cats, ferrets, pigs, and dogs are less translationally adapted than humans both by CAI and tAI."



As shown in panel B above, the tRNA Adaption Index is highest, by far, for humans (blue arrow) followed by the red junglefowl. This is additional evidence of the extraordinary adaption to humans of SARS-CoV-2 from the very beginning. This also is the first evidence of a reasonable intermediate host but based only on these *in silico* data.

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[61] https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1008450#pcbi.1008450.s004

[redacted] Evidence of Lax and disregard of laboratory safety protocols and regulations in China

A collection[62] from the Chinese Q&A website, https://www.zhihu.com/ , of first-hand documentation of laboratory safety breaches and incidents within a large number of laboratories with diverse research subjects and purposes in the People's Republic of China (PRC). The laboratories involved including Chemistry labs, Biolabs, Computer labs as well as Physics and Engineering labs.

From these first-handed documentation, we obtained evidence of relaxed safety regulations and frequent breach of such regulations, with reasons ranging from poor training/education on lab safety, chronic ignorance of safety rules to intentional breach of protocols for purposes other than the research projects of the lab(s) of which the breach was documented in.

Such breaches often resulted in safety accidents ranging from physical injury, chemical burns, chemical leaks, damage to property to lab-acquired infection and escape of in-lab pathogens. With consequences from personal-level to institution-level.

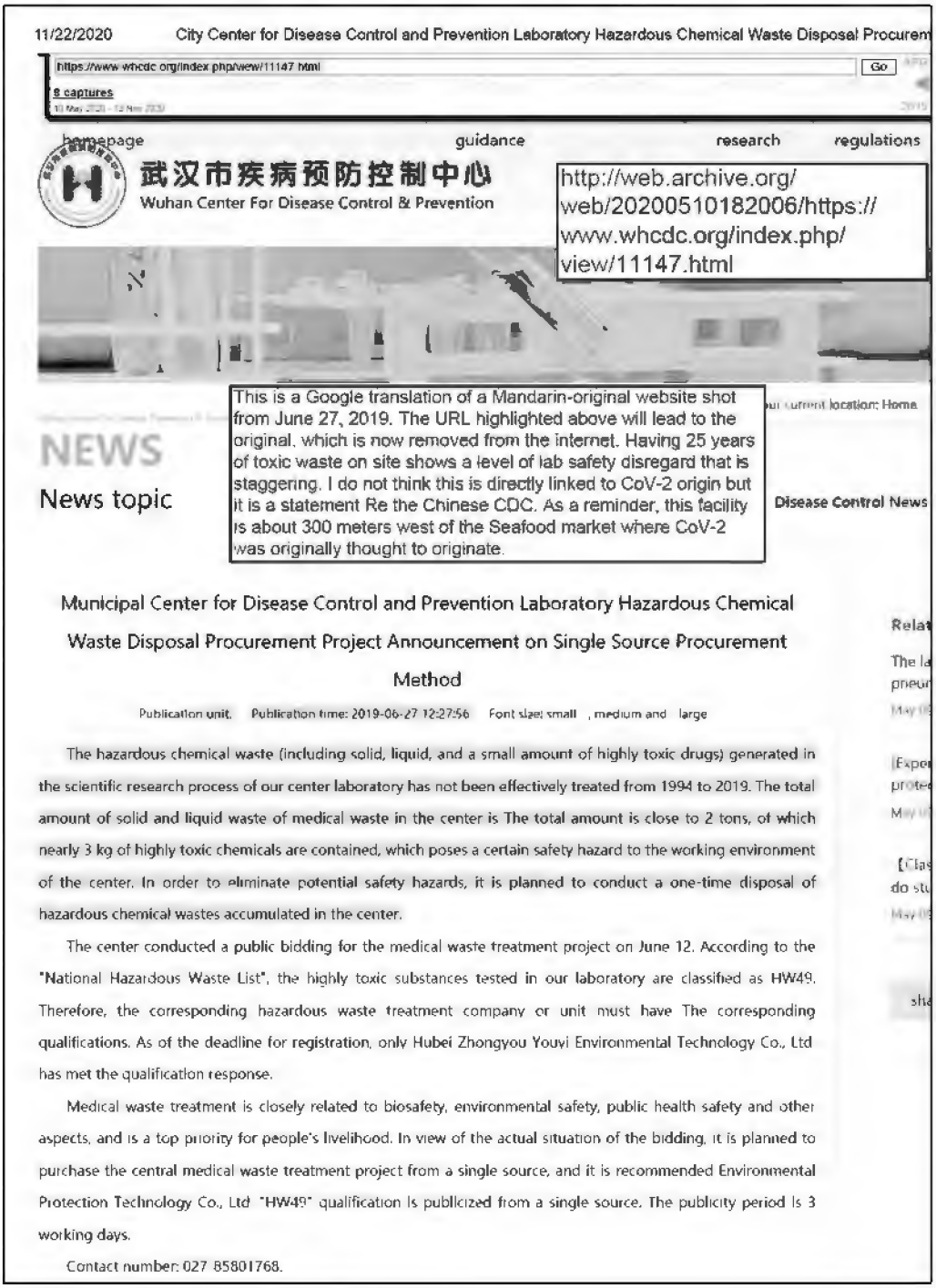
Here is the reference to the State Department cables concerning safety concerns at the WIV.[63]

The following document shows that in June 2019, the Chinese CDC was soliciting for the removal of 25-years of solid and liquid medical waste. The total is close to two tons including three kg of highly toxic waste.

This is a Google translation of a Mandarin-original website shot from June 27, 2019. The URL highlighted above will lead to the original, which is now removed from the internet. Having 25 years of toxic waste on site shows a level of lab safety disregard that is staggering.

I do not think this is directly linked to CoV-2 origin but is a statement about the Chinese CDC. As a reminder, this facility is about 300 meters west of the Seafood market where CoV-2 was originally thought to originate.

[62] https://zenodo.org/record/4307879#.X-yUo9gzbOh
[63] https://foia.state.gov/Search/Results.aspx?caseNumber=F-2020-05255



11/22/2020 City Center for Disease Control and Prevention Laboratory Hazardous Chemical Waste Disposal Procurem

https://www.whcdc.org/index.php/view/11147.html Go

8 captures

homepage guidance research regulations

武汉市疾病预防控制中心
Wuhan Center For Disease Control & Prevention

http://web.archive.org/web/20200510182006/https://www.whcdc.org/index.php/view/11147.html

This is a Google translation of a Mandarin-original website shot from June 27, 2019. The URL highlighted above will lead to the original, which is now removed from the internet. Having 25 years of toxic waste on site shows a level of lab safety disregard that is staggering. I do not think this is directly linked to CoV-2 origin but it is a statement Re the Chinese CDC. As a reminder, this facility is about 300 meters west of the Seafood market where CoV-2 was originally thought to originate.

NEWS

News topic

Disease Control News

Municipal Center for Disease Control and Prevention Laboratory Hazardous Chemical Waste Disposal Procurement Project Announcement on Single Source Procurement Method

Publication unit: Publication time: 2019-06-27 12:27:56 Font size: small , medium and large

The hazardous chemical waste (including solid, liquid, and a small amount of highly toxic drugs) generated in the scientific research process of our center laboratory has not been effectively treated from 1994 to 2019. The total amount of solid and liquid waste of medical waste in the center is The total amount is close to 2 tons, of which nearly 3 kg of highly toxic chemicals are contained, which poses a certain safety hazard to the working environment of the center. In order to eliminate potential safety hazards, it is planned to conduct a one-time disposal of hazardous chemical wastes accumulated in the center.

The center conducted a public bidding for the medical waste treatment project on June 12. According to the "National Hazardous Waste List", the highly toxic substances tested in our laboratory are classified as HW49. Therefore, the corresponding hazardous waste treatment company or unit must have The corresponding qualifications. As of the deadline for registration, only Hubei Zhongyou Youyi Environmental Technology Co., Ltd has met the qualification response.

Medical waste treatment is closely related to biosafety, environmental safety, public health safety and other aspects, and is a top priority for people's livelihood. In view of the actual situation of the bidding, it is planned to purchase the central medical waste treatment project from a single source, and it is recommended Environmental Protection Technology Co., Ltd "HW49" qualification is publicized from a single source. The publicity period is 3 working days.

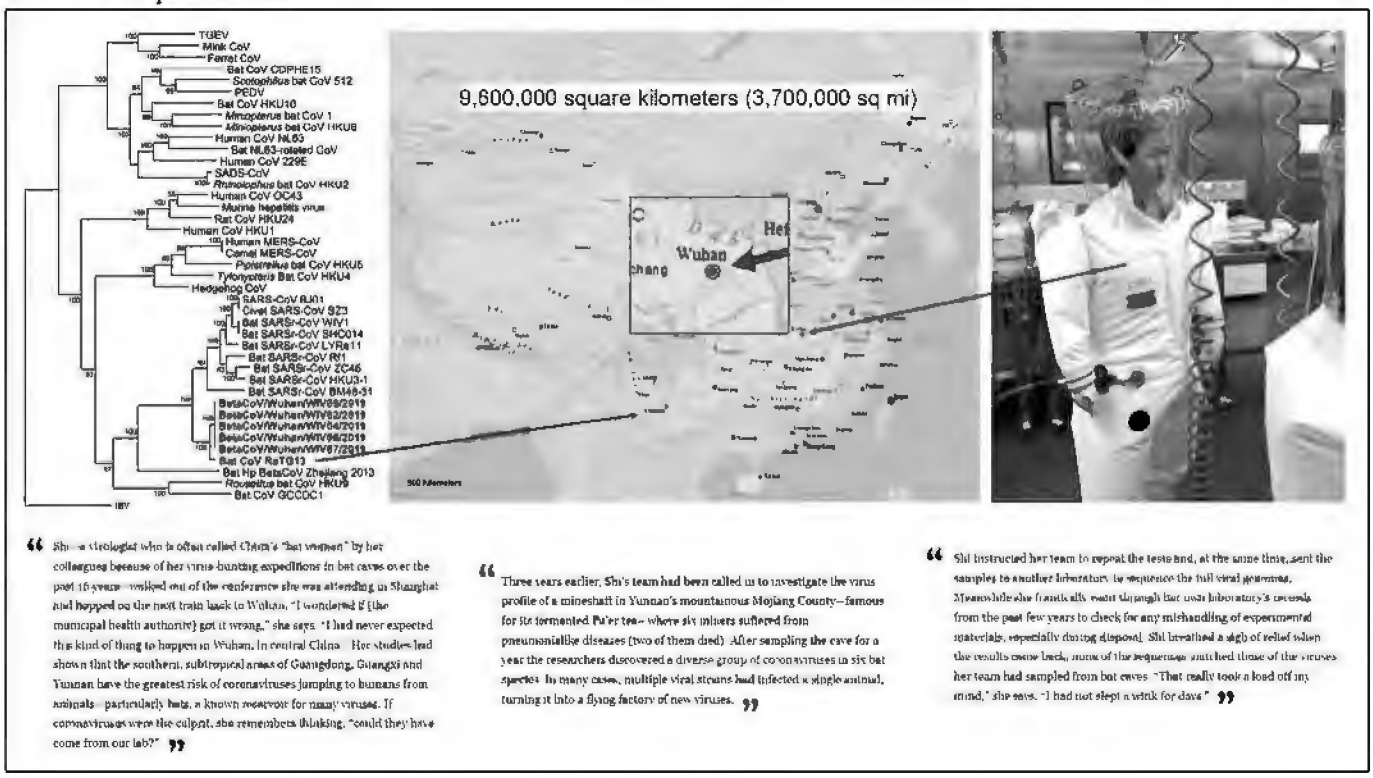
Contact number: 027 85801768.

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

Evidence: The careful words of Dr. Shi do NOT say she did not have SARS-CoV-2 at the WIV.

This Figure contains quotes from an article about Dr. Shi and her reaction to the beginning of the COVID-19 pandemic.



Notice in the last frame Dr. Shi says two strange sentences:

Sentence 1: "…she frantically went through her own laboratory's records from the past few years to check for any mishandling of experimental materials, **especially during disposal**."

If you don't know what you are looking for this, "especially during disposal," is a bit of an odd qualifier. Other evidence elsewhere suggests that, in fact, disposal may have been a likely source of the accidental lab release.

Sentence 2: "She breathed a sigh of relief when the results came back: none of the sequences matched those of the viruses her team had sampled from bat caves."

If Dr. Shi had created SARS-CoV-2 as a chimera, perhaps starting with one of those cave viruses, of course you would no longer have a sequence match. This is a probably truthful statement that leaves open the question of lab creation.

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

Evidence: The Good, the Bad and the Ugly: a review of SARS Lab Escapes[64]

In 2003–04, in the wake of the SARS epidemics, there were multiple cases of laboratory acquired infection (LAI) with SARS in just a few months: first in a P3 in Singapore, then in a military P4 in Taipei and last a protracted case in a P3 in Beijing. The 'WHO SARS Risk Assessment and Preparedness Framework' has a good summary of these lab accidents:

Since July 2003, there have been four occasions when SARS has reappeared. Three of these incidents [note: Singapore, Taipei and Beijing] were attributed to breaches in laboratory biosafety and resulted in one or more cases of SARS. The most recent laboratory incident [note: in Beijing] resulted in 9 cases, 7 of which were associated with one chain of transmission and with hospital spread. Two additional cases at the same laboratory with a history of illness compatible with SARS in February 2004 were detected as part of a survey of contacts at the facility.[i.1]

This article reviews some of these cases and discusses briefly some of the insights that were gained from these at the time.

Another article along the same lines is, "10 incidents discovered at the nation's biolabs"[65] This included Dr. Baric's laboratory in which "(b)etween April 2013 and September 2014, eight individual mouse escapes were reported at the University of North Carolina-Chapel Hill. Several of the mice were infected with either SARS or the H1N1 flu virus."

Dozens of holes in BSL-4 'spacesuits'

As a key protection against the world's most deadly pathogens, including the Ebola virus, scientists in the BSL-4 labs at the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID) at Fort Detrick in Maryland wear pressurized, full-body spacesuit-like gear and breathe purified air. Yet those suits ruptured or developed holes in at least 37 incidents during a 20-month period in 2013 and 2014, according to lab incident reports obtained by USA TODAY under the federal Freedom of Information Act.

This will contribute a 51%/49% contribution in favor of laboratory compared to zoonotic origin. There will be no confidence adjustment. The results from the calculations are shown below.

Evidence or process	Zoonotic Origin (ZO)	Laboratory Origin (LO)
Starting likelihood	0.011	0.989
The history of SARS laboratory accidents is consistent with the laboratory origin hypothesis		0.51
Impact of this evidence		Increases the likelihood of LO by 51/49 = 1.041
Impact of evidence calculation		1.041 x 0.989 = 1.030
Normalize this step of analysis	0.011/(0.011 + 1.030) = 0.011	1.030/(0.011 + 1.030) = 0.989

Adjusted likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[64] https://gillesdemaneuf.medium.com/the-good-the-bad-and-the-ugly-a-review-of-sars-lab-escapes-898d203d175d

[65] https://www.usatoday.com/story/news/2015/05/29/some-recent-us-lab-incidents/25258237/

Evidence: Drs. Shi and Daszak use Wuhan residents as negative controls for zoonotic coronavirus seroconversion[66]

"As a control, we collected 240 serum samples from random blood donors in **Wuhan >1000 km away from Jinning & where inhabitants have a much lower likelihood of contact with bats due to its urban setting**" [emphasis added]. As expected, 0/240 had a positive serological evidence of prior coronavirus infection.

"The 2.7% seropositivity for the high risk group of residents living in close proximity to bat colonies suggests that spillover is a **relatively rare event**, however this depends on how long antibodies persist in people, since other individuals may have been exposed and antibodies waned."

In this paper from 2018, Drs. Shi and Daszak conclude that bat-to-human transfer is relatively rare for high risk people living in close proximity to bat colonies and much less likely in Wuhan, a conclusion that does not support a hypothesis of bat-to-human transmission.

This will not be used to adjust the likelihoods.

Current likelihood: Zoonotic origin (1.1%), laboratory origin (98.9%).

[66] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6178078/

The Appendix contains the following information which was determined to be important to the overall investigation into the origin of CoV-2 but which did not become part of the Bayesian analysis:

- Evidence that Dr. Shi has published contrived data, making the credibility of everything she says suspect. Specifically:
    - The seminal paper from the Wuhan Institute of Virology claiming SARS-CoV-2 probably originated in bats appears to contain a contrived specimen, an incomplete and inaccurate genomic assembly, and the signature of laboratory-derived synthetic biology
    - *The coronavirus RaTG13 was purportedly identified in a bat "fecal" specimen that is probably not feces, has significant unresolved method-dependent genome sequence errors and an incomplete assembly with significant gaps, and has an anomalous base substitution pattern that has never been seen in nature but is routinely used in codon-optimized synthetic genome constructions performed in the laboratory*
- Evidence for and against RaTG13 as the direct precursor of CoV-2. I have not made up my mind on this important hypothesis
    - To establish a precursor-product relationship for RaTG13 and CoV-2 a relative simple process must be proposed to make approximately 1140 nt changes in the 30,000 nt genome
    - Evidence in favor of the hypothesis:
        - While the nucleotide sequence data show these coronaviruses are only 96.2% homologous a comparison of their amino acid homology indicates they are 98.8% identical and as similar as the Civet SARS-CoV-1 and human SARS-CoV-1
        - About 26% of the entire genomes contain only synonymous mutations without any non-synonymous mutations, a highly improbably outcome in nature but an easy exercise in the laboratory to introduce. The motivation would be to obscure the closeness of the two genomes without worrying about introducing detrimental mutations. This represents about 200 of the nt differences
        - There are two restriction enzyme sites in RaTG13 that begin at the receptor binding domain and end 3' to the furin cleavage site that use the 'No See 'Em' technology developed and patented by Ralph Baric, a Dr. Shi and WIV collaborator. Shi has used these enzymes herself. As expected for the technology, the sites are lost in CoV-2. However, they are not the "pure-form" of the Baric technology, are less hidden, and so I would be surprised if Shi did this less robust approach. Nonetheless, the likelihood these sites are there by chance is infinitesimal.

- CoV-2 and RaTG13 share a >100 nt insertion in the ORF1ab gene found no where else in sarbecoviruses. A very strange fact and significantly greater than the 12-nt furin site that has caught so much attention. I spent a day or so probing the function of the site, I believe it is nsp3 (from memory), but didn't find a smoking gun to warrant deeper work. Should be returned to.
- It is part of the nine viruses found in the Yunnan cave where miners died of a coronavirus-like illness.

o Evidence against RaTG13
- My proof that it did not come from the bat feces specimen as reported by Shi is troublesome for an hypothesis it is the critical precursor virus
- To my knowledge no has grown it and examination of its Spike Protein by numerous groups comes to the unlikely conclusion it will bind to ACE2 of most species or grow in a lab culture.
- Peter Daszak, who has said many things proven to be false, nonetheless has described RaTG13 as a "composite sequence" a term used for a really mixed specimen where metagenomics are used to obtain a "genome sequence" which in reality was pieced together artificially by the computers running the analysis
- I can reduce the 1140 nt difference to about 600 with two steps, the No See 'Em insertion of the CoV-2 RBD in the Spike Protein and using a synonymous mutation algorithm to create artificial phylogenetic distance. But a simple method of closing that 600 nt, mostly non-synonymous mutations, has not been identified.
- Shi collected nine beta coronaviruses in the mine but has published the sequence of only RaTG13. She voluntarily published RaTG13. It seems more likely that she would publish a virus close to CoV-2 to establish the bat origin in the medical field (the RaTG13 paper title was "A pneumonia outbreak associated with a new coronavirus of probable bat origin) but not publish the actual virus she used for the construction of CoV-2, in the unlikely event a 'bullet proof' connection that she hadn't thought of could be found.

- Remarkable evidence of the synthetic Adenovirus vector vaccine in patients sequenced at the WIV
  - More work will be focused on this to establish what the immunogen is and to further this proof.

Tracking the intermediate host of SARS-CoV-2: how the pangolin became suspect

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Abstract

We review the current knowledge of SARS-CoV-2-like viruses, including the controversy surrounding the most closely related genome from bat coronavirus RaTG13, and the results of our investigation into the cluster of papers describing the same pangolin CoV with a SARS-CoV-2-like Spike receptor-binding domain. How did SARS-CoV-2 traverse a thousand miles from bats in South China to break out in Wuhan? Was an intermediate host required or did the virus spillover directly from bats into humans?

It has been more than a year since the detected emergence of COVID-19 in Wuhan in late 2019. With the urgent objective of preventing future pandemics, the search continues for the origins of SARS-CoV-2 and the animal that originally transmitted the virus into humans (1). According to reports, the virus has not been detected in the animal samples from the initially suspected site of natural spillover, the Wuhan Huanan Seafood market, or any farmed animals and livestock around Wuhan city and elsewhere in Hubei province (2 , 3). The available epidemiological data describing the initial outbreak do not support the hypothesis that the Huanan market was the site where SARS-CoV-2 had first spilled over from an animal into humans (4 –7). The lack of leads as to the possible animal source of SARS-CoV-2 has led experts to speculate that the zoonosis of the virus into humans did not occur in Wuhan or even Hubei province (3). Furthermore, despite years of bat virus surveillance in Hubei, CoVs closely

related to SARS-CoV-2 have not been detected in the province (3). Instead, the viruses known to be most closely related to SARS-CoV-2 were collected from bats in Yunnan province, approximately one thousand miles away from Wuhan: RaTG13 (96.2% genome identity with SARS-CoV-2) and RmYN02, sampled in 2013 and 2019, respectively (8 –10). This leaves us with two major questions: How did SARS-CoV-2 get from bats proximal to Yunnan all the way to Wuhan? Was an intermediate host required for transmission of SARS-CoV-2 into humans, or did the virus spill over directly from bats into humans?

Lessons from the original SARS outbreaks

The first SARS-CoV broke out twice in Guangdong province, in late 2002 and again in late 2003. Based on the genetic data, each outbreak was determined to have emerged from separate spillover events (11). In both outbreaks, a considerable portion of the index patients were restaurant employees or other food handlers (12). This spurred investigators to sample animals at live animal markets or restaurants, which successfully identified a variety of SARS-CoV-positive animals (13–16). In the first outbreak, animals carrying SARS-CoV were rapidly detected and reported by May, 2003 (13). In the second outbreak, palm civets carrying SARS-CoV were even more swiftly detected at the workplace (a restaurant) of an index patient and at an animal market (14–16). In addition, a May, 2003 survey of 508 market traders in Guangdong exhibited higher seroprevalence (13%) against SARS-CoV compared to control populations (1.2% in healthy adults at a clinic for routine physical examinations, 2.9% in healthcare workers involved with SARS control), despite none of the traders being among the detected SARS cases (12 , 17); of the 1,511 clinically confirmed Guangdong SARS cases, up to Jun 15, 2003, only 2 were identified as animal sellers (17 , 18). These findings collectively suggested an animal origin for SARS-CoV and indicated that SARS-related CoVs
(SARSr-CoVs) were prevalent in the Guangdong animal trading community (11 , 19, 20). By mid-2005, scientists had traced SARSr-CoVs to bats, which were determined to be the natural reservoir (11 , 21).

Investigators now face the reverse situation for tracing the origins of SARS-CoV-2. None of the tested market animals carried SARS-CoV-2 and there is still no sign of an intermediate host one year post-outbreak. Market workers, rather than restaurant workers, were highly represented among index cases (9), suggesting that market workers may not have had a high level of pre-existing immunity against SARS-CoV-2. Furthermore, a 2015 survey of 240 blood donors in Wuhan found that none had antibodies against SARSr-CoVs, in comparison to the 2.7% seropositivity observed in 218 Yunnan residents living close to bat colonies (22). A survey of 640 throat swabs collected between October, 2019 to January, 2020 from patients in Wuhan presenting influenza-like illness found that only samples in January tested positive for SARS-CoV-2 (23). These suggest that SARSr-CoVs were unlikely to have been circulating in Wuhan and its animal trading community prior to SARS-CoV-2's emergence. Yet, even in the absence of a known intermediate host, the available genetic evidence suggests that the natural reservoir of SARS-CoV-2-like viruses is likely bats located in or proximal to Yunnan.

The EcoHealth Alliance and Wuhan Institute of Virology (WIV) recently reported 97 new SARS-related CoV (SARSr-CoV) sequences discovered from their 2010 to 2015 bat CoV sampling expeditions in China (24). A November 17, 2020 addendum to Zhou et al. *Nature* by the WIV (published on February 3, 2020) provided new details about the origins of RaTG13 (the virus genome most closely related to SARS-CoV-2) as well as when and how it had been characterized in the laboratory (25). Concerningly, the addendum revealed that RaTG13 was only one of nine SARSr-CoVs collected between 2012 and 2015 by the WIV from a Yunnan mine, where, in 2012, workers developed severe pneumonia suspected to be due to infection by unknown virus (25–28). It is unclear when the data describing these novel SARSr-CoVs will be published to clarify whether these are closely related to SARS-CoV-2. Nonetheless, SARS-CoV-2 origins investigations have now turned to countries on Yunnan's border: Myanmar, Vietnam, and Laos to see if they can find other closely related viruses (29 , 30). One prevailing hypothesis is that the trafficking of exotic animals, such as pangolins from South East Asia, brought SARS-CoV-2 into Wuhan.

How the pangolin became suspect

On January 22, 2020, the director of the China Center for Disease Control and Prevention announced that they had "*confirmed (SARS-CoV-2) was transmitted via wild animals illegally sold at a seafood market in Wuhan*" (31). In February, it was revealed that smuggled pangolins had been found carrying viruses related to SARS-CoV-2. Specifically, a Guangdong pangolin CoV shared ~90% genome sequence identity with SARS-CoV-2 and possessed the most similar known Spike receptor-binding domain (RBD) to that of SARS-CoV-2 (97% Spike RBD amino acid identity). In comparison, RaTG13, which shared 96% genome identity with SARS-CoV-2, only shared 90% amino acid identity at the RBD. This was significant because the Spike RBD plays a major role in determining the host specificity of the CoV. Four *bioRxiv* preprints describing the Guangdong pangolin CoV were released on February 18 [(32); later published as Lam et al. *Nature (33)*] and February 20 [(34–36); later published as Xiao et al. *Nature*, Liu et al. *PLoS Pathogens*, and Zhang et al. *Current Biology (37–39)*] (**see Timeline in Fig. 1**). Lam et al. *Nature* additionally described a less closely related Guangxi pangolin CoV that shared ~85% genome and ~86% Spike RBD amino acid identity with SARS-CoV-2 (33). These preprints stimulated speculation that pangolins were a likely intermediate host that transmitted SARS-CoV-2 into humans, possibly at the Huanan Seafood market.

As the four manuscripts were published alongside supporting data by mid-May, 2020 (33, 37–39), we realized that each publication had described the same Guangdong pangolin CoV derived from a single batch of 21 smuggled pangolins confiscated in March, 2019 (40). Moreover, the four studies had assembled their Guangdong pangolin CoV sequence primarily using the same dataset (BioProject PRJNA573298; deposited to NCBI on September 23, 2019) published earlier on October 24, 2019 by Liu et al. *Viruses* (which shares senior authors with Xiao et al. *Nature* and Liu et al. 2020 *PLoS Pathogens*). Strikingly, the 2019 Liu et al. *Viruses* dataset had only been released ~3 months post-publication, on January 22, 2020 (41).

The Guangdong pangolin CoV genomes published by Xiao et al. *Nature* and Liu et al. *PLoS Pathogens* (99.95% identical to each other) have since been used and cited by numerous studies on SARS-CoV-2 evolution and origins. To independently assemble these genomes, we contacted both journals in May to seek the metagenomic and/or amplicon trace data that had not been made available by the time of publication. Although Xiao et al. claimed to have isolated pangolin CoV particles in Vero E6 cell culture, they decided to assemble their genome by amplifying sequences across multiple frozen pangolin samples rather than sequencing from the cultured viruses (37). Upon closer inspection, we observed that Xiao et al. *Nature* had re-published samples under different names without proper attribution to the original 2019 Liu et al. *Viruses* paper, and used an inconsistent definition of "total reads" in their sample description that made it difficult to match their samples with those from Liu et al. *Viruses* . After uncovering this inconsistency, we confirmed that Xiao et al. had re-published the samples lung02, lung07, lung08, and lung11 from Liu et al. *Viruses* under different names: M3, M2, M4, and M8, respectively (**Supplementary Table 1**). Furthermore, the only sample profile shown in Xiao et al.'s publication resembled the combined profiles of lung08 from Liu et al. *Viruses* and pangolin_9 (sample M1) (**Fig. 2A**). However, Xiao et al. described their profile as that of a single unspecified sample: "*For one sample, higher genome coverage was obtained by remapping the total reads to the reference genome (Extended Data Fig. 4)*" (37). It is important to note that most of the pangolin_9 reads map onto a single Ort1a region, and that the vast majority of metagenomic sequencing reads covering the pangolin CoV genome are from the Liu et al. *Viruses* 2019 dataset (**Fig. 2B**).

To compound the confusion surrounding the samples and datasets, on June 22, 2020, Xiao et al. added a new sample, pangolin_10 to their *Nature* paper's BioProject (PRJNA607174). This

sample was not described in the text, figures, tables, or extended materials of their paper published on May 7, 2020. Their paper stated that "*Illumina RNAseq was used to identify viruses in the lung from nine pangolins*" (37). All nine pangolins are accounted for in their Extended Data Table 3. Instead, the pangolin_10 read coverage profile resembles that of a sample in their June 22 Li et al. *bioRxiv* preprint (42). Li et al. did not attribute this pangolin_10-like sample to the *Nature* paper or BioProject in which the pangolin_10 data was released (42). It is unclear whether pangolin_10 data was used to assemble the Xiao et al. genome and one of the Li et al. genomes. Yet, pangolin CoV genomes from both Xiao et al. *Nature* (EPI_ISL_410721) and Li et al. *bioRxiv* (EPI_ISL_471467-471470) have been deposited into the GISAID database (alongside six other Guangdong pangolin CoV sequences from Li et al., EPI_ISL_471461-471466). It is challenging, based on the publicly available information, to correctly determine which sequences came from which samples, and which samples came from which animals. In November, Xiao et al. finally released their amplicon sequencing trace data (**see Timeline in Fig. 1**). However, Liu et al. *PLoS Pathogens*, despite repeated requests, still have not released the raw metagenomic sequencing data or amplicon trace data described in their paper.

The challenges we faced in trying to verify the Guangdong pangolin CoV genome highlights the urgency and importance of journals requiring authors to publish their detailed genome assembly pipeline and immediately release all raw sequence data — particularly when the genomes are used by a growing number of studies to support COVID-19 epidemiological investigations. For genome assembly, the sequencing trace data describing base quality in addition to the bases called are vital, and, importantly, do not require extra labor or time for the authors to share. If authors are unable to accurately recount sample histories and/or produce original data in a timely manner, notices of concern should be immediately published to inform other researchers so that they can decide whether to trust and use these data. In response to our persistent inquiry since May, *Nature* recently added an Editor's Note to Xiao et al. *Nature* on November 11, stating that "*concerns have been raised about the identity of the pangolin samples reported in this paper and their relationship to previously published pangolin samples. Appropriate editorial action will be*

taken once this matter is resolved." Recently published emails from *Nature* and *PLoS Pathogens* show that both journals are looking into the issues raised with each pangolin CoV paper (43).

A study of 334 smuggled pangolins confiscated in Malaysia, between 2009 to 2019, found that none were positive for coronaviruses (44). Xiao et al. *Nature* had also noted that they did not detect CoVs in a second batch of smuggled pangolins from the same Guangdong wildlife rescue center in August, 2019 (37). In comparison, the CoV-positive pangolins from March, 2019 rapidly perished with signs of respiratory distress and did not appear to transmit the CoV to any of the 20+ humans who had close contact with the pangolins (37 , 45). These suggest that pangolins are not natural hosts or reservoirs of SARSr-CoVs in the wild, and that the smuggled pangolins, in both Guangdong and Guangxi, were likely incidental hosts that were infected during transport closer to the point of sale in China (45 , 46). Furthermore, we do not know how many pangolins in China have been tested and found to be CoV-negative, but not published. We also do not know which other smuggled species have been tested. This sampling bias could make it difficult to interpret whether pangolins are more likely to carry SARSr-CoVs as compared to other smuggled species, and whether the pangolins may have been infected by a co-captive species. Further scrutiny of the March, 2019 Guangdong pangolins in terms of their trafficking route, other animals in the same confiscated batch, how the sequencing data was generated and shared in 2019, and how the pangolin samples and/or virus can be independently verified today, could yield insights to the source of the SARS-CoV-2-like CoV and where it may continue to circulate.

Back to square one, the bat CoV RaTG13 from Yunnan

Despite reports of SARSr-CoVs in Japan and Cambodia (47), the strongest lead to the origins of SARS-CoV-2 remains the RaTG13 bat CoV that was collected by the WIV in 2013. Extensive research and characterization of SARSr-CoVs by the WIV, EcoHealth Alliance, and collaborators have suggested that some varieties of SARSr-CoV, which are capable of utilizing the human ACE2 receptor to infect cells, may be able to transmit directly from bats to humans (22, 48–50). In September, 2019, the EcoHealth Alliance and WIV reported serological evidence of bat CoV

spillover in South China rural communities, albeit seroprevalence was low (0.6%) and they deduced that spillover is rare (51). Based on the possibility that SARS-CoV-2 could have spilled over directly from bats into humans in rural settings before being transported undetected to Wuhan city, it is worthwhile to revisit the circumstances under which RaTG13 was first revealed, in Zhou et al. *Nature* , as the most closely related virus genome to SARS-CoV-2.

Shortly after the first SARS-CoV-2 genome was released on January 12, 2020 (52), Chen et al. *Emerging Microbes & Infections* pointed out, on February 5, that the virus exhibited 98.7% nucleotide identity to the partial RNA-dependent RNA polymerase (*RdRp*) gene of a bat coronavirus BtCoV/4991 published by the WIV in 2016 (53 , 54). BtCoV/4991 was described as the only SARSr-CoV sequence of 152 *RdRp* coronavirus sequences discovered in an abandoned mineshaft in the town of Tong Guan in Mojiang county, Yunnan, 2012–2013 (54). Chen et al. expressed regret that the rest of the BtCoV/4991 genome was not available for comparison (only that short *RdRp* fragment was published in 2016). However, they noted that SARS-CoV-2 also shared 87.9% nucleotide identity with two SARSr-CoVs, ZXC21 and ZC45 published in 2018 (55). In particular, that 2018 study had demonstrated that, although neither

SARSr-CoV could be isolated via conventional Vero E6 cell culture, ZC45 could replicate and cause disease in suckling rats that had been intracerebrally inoculated with ZC45-positive bat intestinal tissue grinding supernatant; despite the route of virus introduction, the highest viral loads were still observed in the lung tissues (55).

In parallel, on February 3, Zhou et al. *Nature* (the WIV study) reported that SARS-CoV-2 shared high sequence identity in a short *RdRp* region with a bat CoV RaTG13, which, similar to BtCoV/4991, was sampled from an *Rhinolophus affinis* bat in Yunnan (9). Zhou et al. said that full genome sequencing of the RaTG13 sample revealed 96.2% genome sequence identity with SARS-CoV-2. Notably, RaTG13 shared 100% nucleotide identity with the BtCoV/4991 *RdRp*

fragment. With no prior citation provided by Zhou et al. *Nature* for RaTG13, this led to speculation that BtCoV/4991 and RaTG13 could be the same virus, or, at the very least, closely related viruses with proximal origins in Yunnan (26, 28, 56). The deposition of RaTG13 amplicon sequencing data onto NCBI in May, 2020 added to the confusion because the metadata suggested that the sample had been repeatedly sequenced in 2017 and 2018; this would have yielded sequences aside from the *RdRp* fragment that would have been found to closely match SARS-CoV-2 when initially queried by Zhou et al. *Nature*.

In response to inquiries by a growing number of scientists and journalists, on July 24, the WIV told Science Magazine that RaTG13 was indeed BtCoV/4991, and that its full genome had been sequenced in 2018 and not post-COVID as some readers had thought based on the text in Zhou et al. *Nature* (26, 56, 57). Furthermore, although the RaTG13 raw sequence data were of sufficient quality for genome assembly (58), scientists observed an inexplicable mismatch between the sequencing data and published genome: on September 17, Eldholm & Brynildsrud noted "*Positions 18797-18798, which were called as TG rather than GC in our pileups*" (58); all of the sequence reads at that region showed TG, in contradiction of the GC in the published RaTG13 genome. By October 13, the WIV updated the RaTG13 genome, which corrected this mismatch and other bases, and even produced sequences at the 5' end of the genome when they had previously claimed that they "*obtained the full-length genome sequence of RaTG13 except the 15 nucleotides at the 5' end. As the sample was used many times for the purpose of viral nucleic acid extraction, there was no more sample after we finished genome sequencing*" (57). The November addendum to Zhou et al. *Nature* birthed even more questions about the connection to unresolved viral infections and severe pneumonia in workers from the mine where RaTG13 and eight other SARSr-CoVs had been later collected by the WIV. Needless to say, these revelations have resulted in considerable concerns regarding the sample history of RaTG13 (26–28), with potential effects on the dozens of studies that have incorporated RaTG13 in their analysis of SARS-CoV-2 evolution and origins.

Conclusions

As the World Health Organization (WHO) reported on November 5, 2020, "*there is no evidence to demonstrate the possible route of transmission from a bat reservoir to human through one or several intermediary animal species*" (29). In other words, despite international efforts throughout 2020 to find a proximal animal source or recent SARS-CoV-2 precursor or sibling viruses, no evidence has yet been unearthed to show that SARS-CoV-2 spilled over naturally into humans. The announcement by China on January 22, 2020 that SARS-CoV-2 was likely from animals sold at the Huanan Seafood market; the release of the Liu et al. *Viruses* Guangdong pangolin CoV datasets that same day; and the rapid release of four preprints describing Guangdong pangolin CoV sequences, with a SARS-CoV-2-like spike RBD, each assembled primarily using the same Liu et al. *Viruses* dataset, fuelled speculation for a time that SARS-CoV-2 had spilled over from the wildlife trade (**Fig. 1**) . Yet, no definitive evidence has emerged to support this hypothesis. Instead, the market has been largely exonerated (4), more recently described as merely an amplification site for the early outbreak and not the location of the original zoonosis. Issues regarding the sample histories and data representation in key pangolin CoV papers have confounded the role of the pangolin in SARS-CoV-2's origins. Even the most closely related virus genome, RaTG13 has been a topic of great contention, surrounded by numerous questions as to its own origins and identity. We propose that elucidating the still evolving stories of RaTG13 and the Guangdong pangolin CoV could offer important insights to SARS-CoV-2-like viruses collected and studied by scientists over the years, and ultimately point us in the correct direction for the investigation of the origins of SARS-CoV-2.

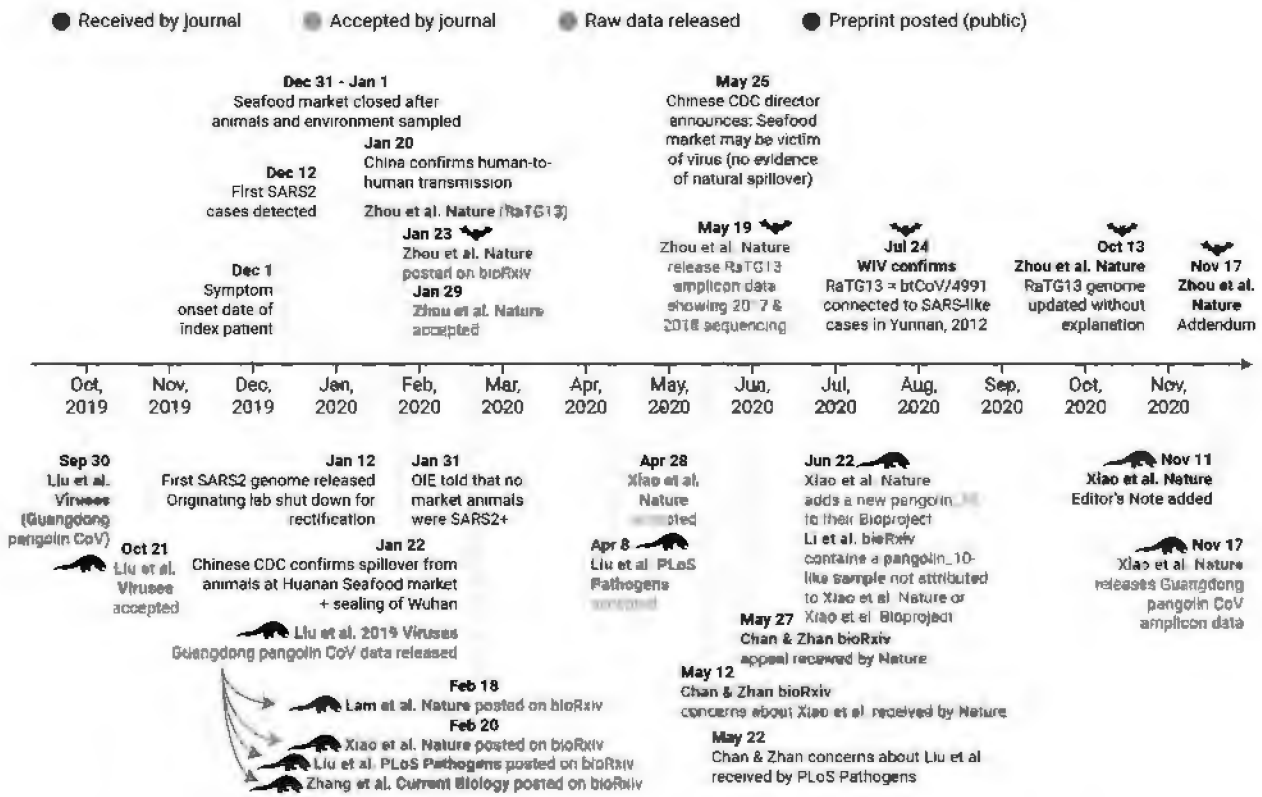

Figure 1. Timeline of select early COVID events and SARS-CoV-2 and related virus publications.

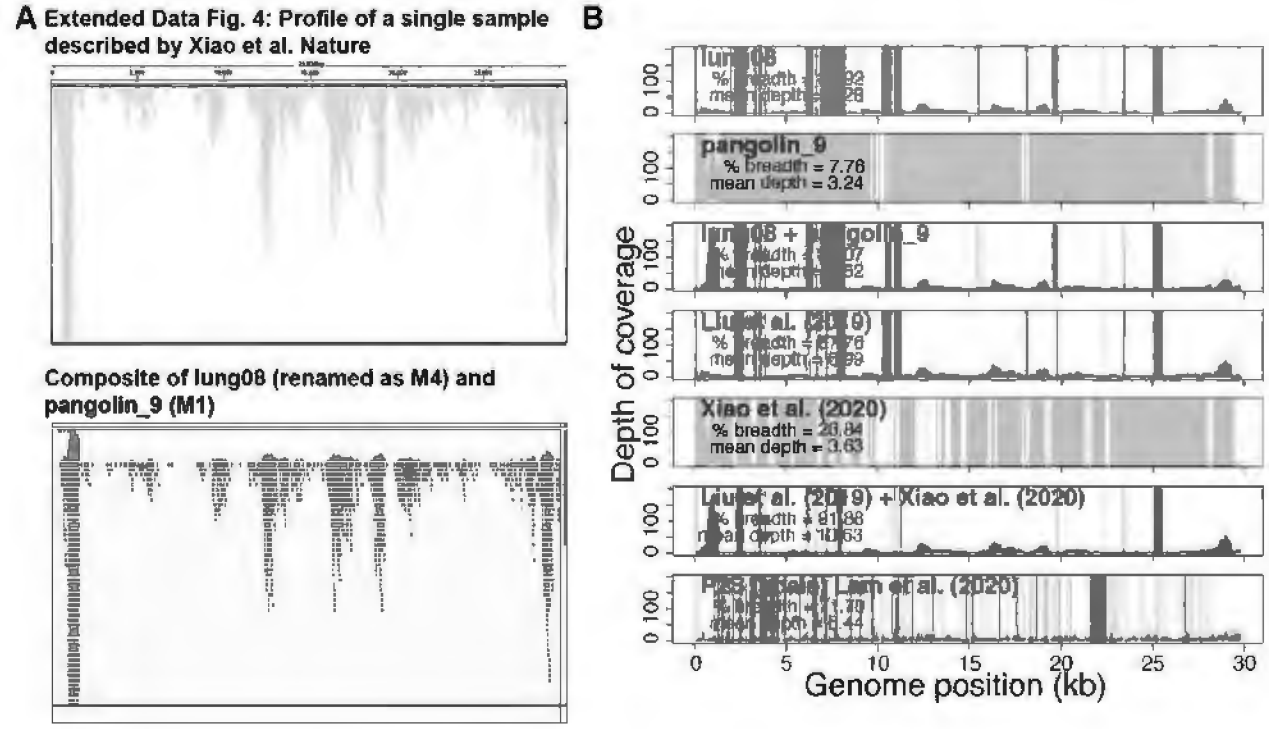

Figure 2. Read profiles of the metagenomic data sets from Liu et al. 2019 *Viruses*, Xiao et al. 2020 *Nature*, and Lam et al. 2020 *Nature* mapped to the Xiao et al. pangolin CoV genome GD_1. Lung08 and pangolin_9 contained the highest number of pangolin CoV reads in their respective datasets, Liu et al. 2019 *Viruses* and Xiao et al. *Nature* (before pangolin_10 was added to the Xiao et al. BioProject). **(A)** The profile in Xiao et al.'s Extended Figure 4 (top panel) resembles the composite profile of sample lung08 (Liu et al. *Viruses*; named differently as sample M4 in Xiao et al. *Nature*) and pangolin_9 (sample M1 in Xiao et al. *Nature*) (bottom panel). **(B)** The "lung08 + pangolin_9" track shows the combined read coverage of both samples, which largely reflects the read coverage of lung08. The "Liu et al. (2019)" track indicates the read coverage pooled from all samples in BioProject PRJNA573298 with mapped reads. The "Xiao et al. (2020)" track reveals the read coverage pooled from all samples unique to Xiao et al. *Nature* with mapped reads. The "Liu et al. (2019) + Xiao et al. (2020)" track combines the read coverage from both studies. The "P2S Lam et al. (2020)" track shows the read coverage from the scale sample that was sequenced by Lam et al. *Nature*. Regions with zero read coverage are highlighted in blue. The estimated mean depth of coverage with all mapped reads are shown.

Materials and Methods

Guangdong pangolin CoV sequences

Liu et al. *Viruses* data: NCBI SRA BioProject PRJNA573298 (also accession: SRP223042) and Genome Warehouse BioProject PRJCA002224 (also accession: GWHABKW00000000). Liu et al. *PLoS Pathogen* pangolin CoV sequence: NCBI GenBank MT121216. Xiao et al. *Nature* data: NCBI SRA BioProject PRJNA607174. Lam et al. *Nature* data: NCBI SRA BioProject PRJNA606875. Reads were filtered and cleaned using *fastp* version 0.20.0, default settings (59) . Clean reads were mapped to the Xiao et al. GD_1 sequence (GISAID: EPI_ISL_410721) using *minimap2* version 2.17, default settings (60). Duplicate reads were marked. Clean reads were

coordinate-sorted using *samtools* version 1.10 (sub-commands *markdup* and *sort*, respectively) (61). We computed read coverage statistics using *bedtools* version 2.29.2 (62). Read coverage profiles and alignments were visualized using IGV version 2.8.2 (63).

RaTG13 sequences

There are two RaTG13 datasets associated with Zhou et al. *Nature* BioProject PRJNA606165. The first, SRX7724752, released on February 13, 2020 comprises ~11 million paired-end 150 nt NGS reads generated via Illumina HiSeq 3000; the description mistakenly indicates that the data was derived as follows: "*Total RNA was extracted from bronchoalveolar lavage fluid...*" The second, released on May 19, comprises 33 amplicon sequences obtained in 2017 and 2018 via Applied BioSystems 310 Genetic Analyzer; we heard that scientists had requested this data to attempt assembly of RaTG13's genome. We aligned the NGS and amplicon reads to the RaTG13 genome (MN996532.1). The amplicon reads appear to bridge the contigs reconstructed via *de novo* genome assembly.

Acknowledgements

We thank the GISAID CoV genome contributors (**Supplementary Table 2**).

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Perspectives on the emergence of the Spike S1/S2 furin cleavage site in SARS-CoV-2

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In comparison to other SARS-related coronaviruses (SARSr-CoVs), SARS-CoV-2 possesses a unique four-residue PRRA (681-684) insertion at the S1/S2 junction in its Spike, resulting in a furin cleavage site (FCS). This S1/S2 FCS was first identified in the literature on February 10, 2020 by Coutard et al., who noted that the cleavage of viral envelope glycoproteins, such as the Spike protein, by furin proteases can enhance viral fusion with host cells, and speculated that the novel FCS could have "*significant functional implications for virus entry*" (*1*). Since then, independent groups have tested SARS-CoV-2 FCS deletion mutants in hamster infection models and discovered that FCS deletion significantly attenuated viral infection (*2, 3*). Mutations in the PRRA(R) motif have been rare among the 260,000+ high quality human SARS-CoV-2 genomes deposited on the GISAID database; <0.01% have mutations at R682 or R683, and essentially none have mutations at R685 (*4, 5*). These observations have led scientists to speculate that the FCS may be under strong selective pressure in humans (*2*) or animals (*6*). Additional studies have demonstrated that the FCS confers on SARS-CoV-2 the enhanced ability to efficiently enter and replicate in Calu-3 (human lung) cells and induce efficient cell-cell fusion, suggesting "*a critical role for the furin cleavage site insertion in SARS-CoV-2 replication and pathogenesis*" (*3, 7*). Due to the unique presence and abilities conferred by the FCS in SARS-CoV-2 within its clade, there has been considerable discussion on whether the FCS insertion arose naturally.

How does the SARS-CoV-2 Spike compare to those of other SARSr-CoVs?

On January 20, 2020, the Wuhan Institute of Virology (WIV) submitted two manuscripts to *Nature (8)* and *Emerging Microbes & Infections (9)*: Zhou et al. stated that "*the major differences in the sequence of the S gene of 2019-nCoV are the three short insertions in the N-terminal domain as well as changes in four out of five of the key residues in the receptor-binding motif compared with the sequence of SARS-CoV*" (*8*). Jiang et al. said "*we predicted that the cleavage site for generating S1 and S2 subunits is located at R694/S695*" (*9*). To put this in context, the 2003 SARS-CoV has been reported to have a likely S1/S2 cleavage site at R667 in the Spike (*10*); an R667S mutant exhibited 60% of the wild type virus ability to promote cell-cell fusion in cells expressing human ACE2 (*11*). Notably, both WIV papers did not describe the novel four-residue insertion of the S1/S2 FCS (residues P681-R685) despite their close analysis of the SARS-CoV-2 genome and Spike.

Since January, 2020, other SARS-CoV-2-like viruses sampled from bats and pangolins have been published. However, none have been reported to have an FCS insertion at this S1/S2 junction. One study reported that a close relative of SARS-CoV-2, named RmYN02, collected in Yunnan province in 2019, may have a natural S1/S2 insertion (but not an FCS) in its Spike (74% Spike gene identity with SARS-CoV-2) (*12*). The authors presented an alignment over the S1/S2 region between RmYN02 and other SARSr-CoVs that represents one hypothesis among others, and could be refuted or supported in light of new sequences discovered in the future. In particular, SARS virus sequences are under sampled and the alignment over the flexible S1/S2 region is not supported by structural information, resulting in difficulty determining whether there is a bona fide natural insertion in this region in RmYN02. In comparison, the more closely related Spikes of RaTG13 (93% Spike gene identity with SARS-CoV-2) and the Guangdong and Guangxi pangolin CoVs (~84% Spike gene identity with SARS-CoV-2) all do not have an apparent S1/S2 insertion, FCS or otherwise. These suggest that within lineage b betacoronaviruses, an S1/S2 FCS either emerged in SARS-CoV-2 or was lost from several other viruses in the same clade, including those sharing high Spike gene identity with SARS-CoV-2. The latter scenario is less parsimonious, especially in consideration of the enhanced functionalities conferred by the FCS on SARS-CoV-2, and hypothesis generation has been generally focused on mechanisms by which the FCS could have naturally emerged in SARS-CoV-2 (*13–15*). There is an instance in the literature where an S1/S2 FCS was lost in a singular

coronavirus, while its close relatives with highly similar Spikes (up to 96% Spike gene identity) retained the FCS (*16*). However, this is the reverse scenario to that of SARS-CoV-2, which appears to have gained a highly advantageous FCS compared to the rest of its clade.

Will we ever find the answer to whether the SARS-CoV-2 FCS emerged in nature or in a lab?

Jack Nunberg, whose group first inserted an FCS into the Spike of SARS-CoV, was quoted in 2020 by *Nature News* as saying, "*there is no way to know whether humans or nature inserted the site*" in SARS-CoV-2 (*17*). In 2006, Follis et al. (Nunberg's group) investigated whether SARS-CoV-1's fusion activity could benefit from proteolytic cleavage, similar to other coronaviruses characterized at the time. They inserted a synthetic furin recognition sequence at the putative R667 S1/S2 cleavage site, and demonstrated that an FCS insertion (as compared to a substitution mutation) significantly increased the ability of the SARS-CoV Spike to mediate cell-cell fusion (*11*). A different group later showed that a substitution was sufficient when combined with the introduction of another FCS at the S2' region (*10*). Later, when MERS emerged, it was determined that the S1/S2 FCS is required for efficient entry into cells expressing TMPRSS2 protease, such as human lung and intestine cells, and influences the cell tropism of the virus (*18*, *19*). These experiments on the S1/S2 FCS in SARS and MERS have led to speculation that the FCS in SARS-CoV-2 could have been similarly inserted to test for enhanced infectivity in different cell types or animal models. There have also been guesses as to how a scientific team would design and modify their cloning, codon optimization, and gene synthesis strategy, based on whether there are restriction sites proximal to the FCS and whether the insertion is in- or out-of-frame; however, it will be challenging to find evidence supporting or disproving specific hypotheses of how the FCS emerged in nature or in a lab.

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MDRNA, Inc. (MRNA)
Member, Board of Directors and Scientific Advisory Board; formerly, Chairman of Board of Directors and SAB, CEO, and Chief Scientific Officer
'Founder" of the RNA interference effort within Nastech, inventor of the core company RNAi IP and in-licensed key patents from MIT, City of Hope, and University of Southern Denmark, and architect of the company re-branding as MDRNA (ticker symbol mRNA), and hiring the CEO and President, Scientific Advisory Board, and key members of the Board of Directors.

2000-08
Nastech Pharmaceuticals Company (NSTK)
Chairman, CEO and President
Invented (15 patents; 45 applications) nasal drug delivery technology with one FDA approved drug (Nascobal Nasal Spray) and successful Phase 1 and Phase 2 clinical trials on triptans (migraine pain), morphine (breakthrough cancer pain), Interferon beta (multiple sclerosis), Interferon alpha (hepatitis), PYY (obesity), parathyroid hormone (osteoporosis), apomorphine (erectile dysfunction), insulin and exenatide (diabetes), and cyanocobalamin (anemia).

1998-2000
Atossa HealthCare, Inc.
Founder and CEO
Invented and obtained FDA approval for MASCT, the mammary aspirate specimen cytology test, a "Pap Smear" test for early breast cancer

1995-1998
Food & Drug Administration
Member, Advisory Panel for Radiological Products
Assisted medical device manufacturers, including digital mammography suppliers, before the FDA.

1991-1999
SONUS Pharmaceuticals, Inc. (SNUS)
Founder, Chairman of Board, President & CEO
Invented (19 US patents) the use of fluorocarbon gases in ultrasound contrast agents such as Optison (Perflutren) which is marketed by GE Healthcare and used in suboptimal echocardiograms.

1983-1990
Salutar and Nycomed Salutar, Inc.
Founder, President & CEO, Chairman of Board of Directors
Invented (21 US patents) Omniscan® (Gadodiamide), the leading nonionic MRI contrast agent for use in brain, spine and body imaging in pediatrics and adults (36 million patients worldwide) and Teslascan® (Mangafodipir), the first positive organ-specific MP contrast agent for staging cancer patients.

1988-1991
University of Kentucky
Associate Professor, College of Pharmacy
Taught MRI imaging and the role of contrast agents in diagnostic medicine to pharmacy students.

1988-1990
National Institute of Health
Member, SBIR, Proposal Review Committee
Reviewed third party grant applications within the SBIR program.

1980-1991
Stanford University School of Medicine
Staff Physician; Assistant Professor; Chairman, Curriculum Committee of School of Medicine; Senator, Faculty Senate; Member, Admission Committee
From 1980 to 1991 taught the "Human Genetics and Genetic Diseases" course to second year medical students. From 1981 to 1986 was Chairman of the Curriculum for the Stanford School of Medicine. Committee was responsible for all curricular issues for the first two years of the medical schools four year curriculum.

1980-1986
Palo Alto VAMC
Staff Physician; Member, Research & Development Committee

1977-1980
Massachusetts General Hospital, Harvard Medical School
Instructor; Research Fellow; Clinical Fellow; Resident, Department of Pathology; Intern, department of Pathology

1976-1979
Massachusetts Institute of Technology
Postdoctoral Fellow, H. Gobind Khorana's Laboratory (Nobel Lauerate), Chemistry

Department

1976-1977
University of Michigan
Research Associate

1971-1972
West Michigan University
Waldo-Sangren Scholar

BIOGRAPHICAL SUMMARY

Steven C. Quay, M.D., Ph.D. is a physician scientist and biotechnology entrepreneur who has founded six companies and rebranded a seventh over a 25+ year career. He has received 87 US patents and has seven drugs and one medical device FDA approved that he invented.

In 1984, while on the faculty of Stanford University School of Medicine, Dr. Quay founded Salutar, Inc. in Sunnyvale, CA to develop contrast agents for magnetic resonance imaging (MRI). Arthur Rock, William Hambrecht, and Mohr-Davidow Ventures financed the Series A round and received a 27.5-fold return five years later upon acquisition. Follow-on investors included Sequoia Ventures, Interwest Partners, Oak Investments, and Merrill Pickard. Dr. Quay has been awarded 21 patents covering MRI technology. In 1989 Salutar was acquired for $55 million by Hafslund Nycomed, a Norwegian pharmaceutical company, world leader in contrast agents and the prior company to Nycomed Amersham, later acquired by GE Healthcare. Two pharmaceuticals, OmniScan® and TeslaScan®, were invented by Dr. Quay at Salutar and are now FDA-approved for sale in the United States, Japan, and Europe. Omniscan has been used with over 36 million patients worldwide generating total sales in excess of $3.5 billion US.

In 1991, Dr. Quay founded SONUS Pharmaceuticals, Inc. (NASDAQ: SNUS). Dr. Quay invented the use of fluorocarbon gases in ultrasound contrast agents, solving a 30 year problem of stability of micron-sized gas dispersions in the bloodstream. These inventions have lead to 19 patents directed to ultrasound contrast agents. Enterprise Partners, Versant Ventures, Utah Ventures, and Horsley Bridge financed the Series A for $3.0 MM ($1.00/sh) and the company never raised private money again. The company went public with H&Q, UBS, and Montgomery Securities at $7.00/sh in 1995 and the VCs distributed their position at between $42-44/sh in 1997. The first fluorocarbon ultrasound contrast FDA approved, Optison™, is based on Dr. Quay's patents. From 1991 until June 1999, he served as Chief Executive Officer, President, and a director of SONUS. EchoGen®, an ultrasound contrast agent he invented was approved for sale in Europe. In 1997, he was awarded the Ernst & Young Entrepreneur of the Year Award for the Northwest as CEO of Sonus Pharmaceuticals.

In 1996, Dr. Quay founded Atossa HealthCare, Inc. ("Atossa") to commercialize the Mammary Aspirate Specimen Cytology Test (a "Pap" smear for breast cancer) that he had invented. The first US patent on this technology was awarded in 1998. In August 2000, Dr. Quay merged

Atossa with Nastech Pharmaceuticals Company, Inc., a public company in Hauppauge, NY (NASDAQ: NSTK), and became its major shareholder as well as Chairman, CEO and President. At Nastech he invented (15 patents; 45 applications) nasal drug delivery technology with one FDA approved drug (Nascobal Nasal Spray) and successful Phase 1 and Phase 2 clinical trials on triptans (migraine pain), Morphine (breakthrough cancer pain), Interferon beta (multiple sclerosis), Interferon alpha (hepatitis), PYY (obesity), parathyroid hormone (osteoporosis), apomorphine (erectile dysfunction), insulin and exenatide (diabetes), and cyanocobalamin (anemia).

In 1977, Dr. Quay was awarded the Dean's Research Award upon graduation from the University of Michigan Medical School, where he also received a M.A. and Ph.D. in Biological Chemistry (in 1974 and 1975, respectively). He did post-graduate research in the chemistry department at Massachusetts Institute of Technology under H. Gobind Khorana, a Nobel Laureate, and received his residency training at the Massachusetts General Hospital, Harvard Medical School from 1977 to 1980. From 1980 to 1986 he was a faculty member at Stanford University School of Medicine, where in addition to his research and clinical duties he served on the medical school admissions committee and the University Facility Senate. From 1988 to 1991 he was appointed as Associate Professor, School of Pharmacy, at The University of Kentucky.

Dr. Quay has authored more than 130 papers in RNA interference, diagnostic imaging, oncology and biochemistry. He is a member of the American Society for Biochemistry and Molecular Biology and the American Society for Investigative Pathology. From 1995 to 1998, he was the industrial representative to the FDA Advisory Panel for Radiological Products, the committee that oversees radiological machines, such as ultrasound machines, MRI machines, and mammography equipment.

PUBLICATIONS AND ABSTRACTS

PROFESSIONAL ACHIEVEMENTS

Steven Quay

CEO and President, Atossa Genetics, Inc.

Medicine
Molecular Biology
and Retrogeria

	All	Since 2015
Citations	9696	2209
h-index	51	23
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Development of an intranasal formulation of the Y2R agonist peptide YY3-36: Multivariate statistical analysis of in vitro human primary epithelial cell culture studies M Kleppe, A Deshpande, Z Go, G Brandt, M Lee, S Quay OBESITY RESEARCH 11, A109-A109		2003
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5219553 Composition of a N-carboxymethylated tetraazacyclododecane chelating agent, a paramagnetic metal and excess calcium ions for MRI KF Kraft, SC Quay, SM Rocklage, D Worah Magnetic Resonance Imaging 12 (3), VIII-IX		1994
5039512 NMR imaging with paramagnetic polyvalent metal salts of poly-(acid-alkylene-amino)-alkanes KF Kraft, SC Quay, S Rocklage, D Worah Magnetic Resonance Imaging 11 (1), II		1993
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MR hepatobiliary imaging KO Lim, D Worah, M O'Tool, M Van Wagoner, P Leese, A Pfefferbaum, ... Proceedings of the 75th anniversary scientific assembly and annual meeting …		1989
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4687658 Metal chelates of die thylene triamine pentaacetic acid partial esters for NMR imaging SC Quay Magnetic Resonance Imaging 6 (1), I		1988
4687659 Diamide-DTPA-paramagnetic contrast agents for MR imaging SC Quay Magnetic Resonance Imaging 6 (1), II		1988
DELINEATION OF ISCHEMIC MYOCARDIUM BY CONTRAST ENHANCED INVIVO MAGNETIC-RESONANCE-IMAGING PW PFLUGFELDER, WW HOLT, MF WENDLAND, S QUAY, N DERUGIN, ... CIRCULATION 76 (4), 159-159		1987
4637929 Ferrioxamine-paramagnetic contrast agents for MR imaging, composition, apparatus and use SC Quay Magnetic Resonance Imaging 5 (6), II		1987
Delineation of ischemic myocardium by contrast-enhanced in vivo MR imaging PW Pflugfelder, WW Holt, MF Wendland, SC Quay, N Derugin, ... Radiological Society of North America 73rd scientific assembly and annual …		1987
EFFECTS OF METABOLIC-INHIBITORS ON CALCIUM FLUX AND RELAXATION PROPERTIES IN VENTRICULAR MUSCLE-CELLS S BIEDERT, DS MIURA, SC QUAY BIOPHYSICAL JOURNAL 47 (2), A459-A459		1985
VISUALIZATION OF ATHEROSCLEROTIC PLAQUE USING PARAMAGNETIC TETRACYCLINE AND MAGNETIC-RESONANCE IMAGING D MURPHYCHUTORIAN, SC QUAY, PM SELZER, R GINSBURG, ... CIRCULATION 72 (4), 301-301		1985

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MOLECULAR STUDIES OF PROTEIN-LIPID INTERACTIONS. 3. CONFORMATIONAL STUDIES OF AQUEOUS MELITTIN-CHARACTERISTICS OF A FLUORESCENT-PROBE BINDING-SITE CC CONDIE, SC QUAY JOURNAL OF BIOLOGICAL CHEMISTRY 258 (13), 8231-8234		1983
Reaction of Immune Complexes With Hodgkin's Disease Tissue Cultures JC Long, AM Dvorak, SC Quay, C Stamatos, SY Chi Journal of the National Cancer Institute 67 (1), 3-3		1981
VOLTAGE-DEPENDENT CONDUCTANCE IS INDUCED BY AN ALAMETHICINPHOSPHOLIPID CONJUGATE IN LIPID BILAYERS CG MILLER, R LATORRE, SC QUAY FEDERATION PROCEEDINGS 40 (6), 1771-1771		1981
MOLECULAR MECHANISMS OF ALAMETHICIN CHANNEL GATING AND FORMATION R LATORRE, S QUAY ARCHIVOS DE BIOLOGIA Y MEDICINA EXPERIMENTALES 13 (1), 158-158		1980
Regulation of Amino Acid Transport SC QUAY Microorganisms and Nitrogen Sources: Transport and Utilization of Amino ...		1980
DALE L. OXENDER SC QUAY Biological regulation and development 2, 421		1979
LEUCINE TRANSPORT MUTANTS AND REGULATION OF LEUCINE TRANSPORT IN ESCHERICHIA-COLI JJ ANDERSON, MM MAYO, SC QUAY FEDERATION PROCEEDINGS 36 (3), 827-827		1977
REGULATION OF LEUCINE, ISOLEUCINE, AND VALINE TRANSPORT ACTIVITY IN ESCHERICHIA-COLI SC QUAY, JJ ANDERSON FEDERATION PROCEEDINGS 34 (3), 492-492		1975
LEUCINE TRANSPORT IN AZALEUCINE RESISTANT MUTANTS OF ESCHERICHIA-COLI SC QUAY, RAHMANIA. M, DL OXENDER FEDERATION PROCEEDINGS 33 (5), 1394-1394		1974
The Role of D-Gluconic Acid in the Regulation of the Synthesis of the Enzymes of the Entner-Doudoroff Pathway in Pseudomonas fluorescens SC Quay Honors College Thesis, Western Michigan University		1971
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(IN/quay AND IN/steven): 87 patents.
*Hits **1** through **50** out of **87***

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	PAT. NO.		Title
1	9,731,016	T	Tyrosine-based lipids for delivery of therapeutics
2	9,415,007	T	Cyanocobalamin low viscosity aqueous formulations for intranasal delivery
3	9,339,461	T	Arginine-based lipids for delivery of therapeutics
4	9,295,658	T	Second generation fatty acid compositions, formulations, and methods of use and synthesis thereof
5	9,074,205	T	Nicked or gapped nucleic acid molecules and uses thereof
6	9,052,318	T	Absorbent paper and use thereof for breast cancer detection
7	9,023,793	T	Intranasal carbetocin formulations and methods for the treatment of autism
8	8,940,714	T	Cyanocobalamin low viscosity aqueous formulations for intranasal delivery
9	8,877,729	T	Amino acid lipids and uses thereof
10	8,501,824	T	Amino acid lipids and uses thereof
11	8,486,891	T	Nasal calcitonin formulations containing chlorobutanol
12	8,138,149	T	Nasal calcitonin formulations containing chlorobutanol
13	8,063,178	T	Phage displayed Trp cage ligands
14	8,003,353	T	Cyanocobalamin low viscosity aqueous formulations for intranasal delivery
15	7,939,505	T	Amino acid lipids and uses thereof
16	7,879,349	T	Cyanocobalamin low viscosity aqueous formulations for intranasal delivery
17	7,863,245	T	Compositions for enhanced epithelial permeation of neuropeptide Y for treating obesity
18	7,812,120	T	Nasal calcitonin formulations containing chlorobutanol
19	7,560,572	T	Production and use of derivatized homoserine lactones
20	7,435,720	T	Compositions and methods for enhanced mucosal delivery of parathyroid hormone
21	7,404,489	T	Cyanocobalamin low viscosity aqueous formulations for intranasal delivery
22	7,329,725	T	Phage displayed Trp cage ligands

23 7,244,709 T Compositions and methods for enhanced mucosal delivery of parathyroid hormone

24 7,129,062 T Compositions and methods for enhanced mucosal delivery of Y2 receptor-binding peptides and methods for treating and preventing obesity

25 7,229,636 T Cyanocobalamin low viscosity aqueous formulations for intranasal delivery

26 7,186,692 T Compositions and methods for enhanced mucosal delivery and non-infused administration of Y2 receptor-binding peptides and methods for treating and preventing obesity

27 7,186,691 T Compositions and methods for enhanced mucosal delivery of Y2 receptor-binding peptides and methods for treating and preventing obesity

28 7,166,575 T Compositions and methods for enhanced mucosal delivery of peptide YY and methods for treating and preventing obesity

29 7,157,426 T Compositions and methods for enhanced mucosal delivery of Y2 receptor-binding peptides and methods for treating and preventing obesity

30 7,128,877 T Methods and devices for obtaining and assaying mammary fluid samples for evaluating breast diseases, including cancer

31 7,036,104 T Method of and system for buffer insertion, layer assignment, and wire sizing using wire codes

32 7,030,155 T Emulsion vehicle for poorly soluble drugs

33 6,982,282 T Emulsion vehicle for poorly soluble drugs

34 6,894,026 T Long-acting oxytocin analogues for the treatment and prevention of breast cancer and psychiatric disorders

35 6,887,210 T Devices and methods for obtaining mammary fluid samples for evaluating breast diseases, including cancer

36 6,875,420 T Method of ultrasound imaging

37 6,727,280 T Method for treating colorectal carcinoma using a taxane/tocopherol formulation

38 6,723,303 T Ultrasound contrast agents including protein stabilized microspheres of perfluoropropane, perfluorobutane or perfluoropentane

39 6,703,513 T Production and use of derivatized homoserine lactones

40 6,689,073 T Methods and devices for collecting, handling and processing mammary fluid samples for evaluating breast diseases, including cancer

41 6,667,048 T Emulsion vehicle for poorly soluble drugs

42 6,660,286 T Emulsion vehicle for poorly soluble drugs

43 6,620,404 T Gaseous ultrasound contrast media and method for selecting gases for use as ultrasound contrast media

44 6,569,404 T Phase shift colloids as ultrasound contrast agents

45 6,458,373 T Emulsion vehicle for poorly soluble drugs

46 6,444,791 T Methods and compositions for the treatment of keratoconus using protease inhibitors

47 6,287,521 T Methods and devices for obtaining and assaying mammary fluid samples for evaluating breast diseases, including cancer

48 6,274,713 T Polychelants

49 6,245,319 T Colloidal dispersions of perfluoropentane

50 6,156,292 T Gaseous ultrasound contrast media and method for selecting gases for use as ultrasound contrast media

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Refine Search in/quay and in/steven

PAT. NO.		Title
51	5,897,851 T	Nucleation and activation of a liquid-in-liquid emulsion for use in ultrasound imaging
52	5,876,696 T	Composition comprising a fluorine containing surfactant and perfluoropentane for ultrasound
53	5,798,266 T	Methods and kits for obtaining and assaying mammary fluid samples for breast diseases, including cancer
54	5,707,607 T	Phase shift colloids as ultrasound contrast agents
55	5,707,606 T	Phase shift colloids as ultrasound contrast agents
56	5,595,723 T	Method for preparing storage stable colloids
57	5,573,751 T	Persistent gaseous bubbles as ultrasound contrast media
58	5,558,855 T	Phase shift colloids as ultrasound contrast agents
59	5,558,854 T	Ultrasound contrast media comprising perfluoropentane and perfluorohexane gas
60	5,558,853 T	Phase shift colloids as ultrasound contrast agents
61	5,558,094 T	Methods for using persistent gases as ultrasound contrast media
62	5,409,688 T	Gaseous ultrasound contrast media
63	5,393,524 T	Methods for selecting and using gases as ultrasound contrast media
64	5,364,613 T	Polychelants containing macrocyclic chelant moieties
65	5,223,243 T	Dipyridoxyl phosphate chelating compound intermediates useful as NMRI contrast agents
66	5,219,553 T	Composition of a n-carboxymethylated tetraazacyclododecane chelating agent, a paramagnetic metal and excess calcium ions for MRI
67	5,130,437 T	N,N'-bis-(pyridoxal)ethylenediamine-N,N'-diacetic acid derivatives
68	5,130,431 T	Dipyriodoxyl phosphate chelating compound intermediates
69	5,091,169 T	Dipyridoxyl phosphate NMRI contrast agent compositions
70	5,089,644 T	Preparation of oxamine complexes
71	5,087,439 T	Paramagnetic metal-diethylenetriamine-pentaacetic acid partial amide complexes for magnetic

resonance imaging

72 5,039,512 T NMR imaging with paramagnetic [illegible] salts of poly(2-[omega-alkylene-amino)-alkanes

73 5,039,511 T Amyloidosis and alzheimer's disease diagnostic assay and reagents therefor

74 5,008,099 T Amyloidosis and Alzheimer's disease diagnostic assay and reagents therefor

75 4,994,259 T Improvement in the method of NMR imaging employing a manganese II chelates of N,N'-bis[pyridoxal-alkylene (or cycloalkylene) (or arylene)]-N,N'-diacetic acid derivatives

76 4,992,555 T Certain dipyridylphosphate chelatable compounds capable of forming metal ion chelates

77 4,992,554 T Dipyridoxyl phosphate chelating compounds

78 4,935,518 T Manganese(II), chelate contrast agents derived from N,N'-bis-(pyridoxal ethylene diamine-N,N')-diacetic acid and derivatives thereof

79 4,933,456 T Dipyridoxyl phosphate NMRI contrast agents

80 4,933,156 T Amyloidosis and Alzheimer's disease diagnostic assay and reagents therefor

81 4,863,716 T Determination of fallopian tubal patency by magnetic resonance imaging

82 4,859,451 T Paramagnetic contrast agents for MR imaging

83 4,842,845 T Radioactive metal chelates for dipyridoxyl phosphate

84 4,758,422 T Ferrioxamine paramagnetic contrast agents for MR imaging

85 4,687,659 T Diamide-DTPA-paramagnetic contrast agents for MR imaging

86 4,687,658 T Metal chelates of diethylenetriaminepentaacetic acid partial esters for NMR imaging

87 4,637,929 T Ferrioxamine-paramagnetic contrast agents for MR imaging, composition, apparatus and use

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Prev. List | Top | View Cart

Home | Quick | Advanced | Pat Num | Help

Dr. Alina Chan

Dr. Alina Chan is a recent Human Frontier Science Program fellow with 12+ years of research training in medical genetics, biochemistry, synthetic biology, and vector engineering. Dr. Chan previously prototyped human artificial chromosomes (HACs) at the Harvard Medical School, presented in plenaries at 4 international conferences, and is now consulting a startup, Centaura, on the development of HACs for medical applications. At the Broad Institute of MIT & Harvard, Dr. Chan is currently creating next generation AAV vectors for human gene therapy. Her work promises to transform current genome engineering practices and widen the breadth of its biomedical applications towards more complex human diseases and traits. During the COVID-19 pandemic, Dr. Chan began to investigate problems relevant to finding the origins of the SARS-CoV-2 virus and in parallel spearheaded the development of the COVID-19 CoV Genetics (covidcg.org) browser for scientists worldwide to rapidly track virus lineages and mutations by locations and date ranges of interest.

Joshua Santarpia, Ph.D.

Research Director, Chem/Bio Programs

Dr. Joshua L. Santarpia is the Research Director for Chem/Bio programs at the National Strategic Research Institute.

He is also associate professor of microbiology and pathology and program director for the biodefense and health security graduate programs at the University of Nebraska Medical Center.

Dr. Santarpia has held past positions at Edgewood Chemical and Biological Center and Johns Hopkins University Applied Physics Laboratory. He was most recently a distinguished staff member at Sandia National Laboratories.

Dr. Santarpia is trained in aerosol physics, atmospheric chemistry, and microbiology. His peer reviewed research focuses largely on the fate biological aerosols in the atmosphere, detection of biological aerosols and atmospheric chemistry of biological and anthropogenic particles. He has contributed to several books on the characterization and measurement of biological aerosols in the environment.

Dr. Santarpia's work is aimed at understanding and countering threats from biological organisms, especially those that pose a threat when dispersed in aerosols. He has worked extensively on RDT&E and OT&E efforts for biological sensors for both Department of Defense and Department of Homeland Security.

Much of Dr. Santarpia's current work involves understanding the factors related to aerosol/airborne transmission of the SARS-CoV-2 virus.

Highlights of his accomplishments include:

- Developed building and facility sensing networks for biological detection in numerous facilities.
- Developed aerosol measurement tools, including those for unmanned aerial vehicles, for biodetection/collection activities.

- Worked extensively to understand optical and other signatures that can be used to detect and identify biological aerosol and studied how those signatures change over time.
- Developed novel methods to study bioaerosol hazard in medical environments, including the Containerized Biological Containment System (CBCS) for the Department of State, the Nebraska Biocontainment Unit and studies for private companies to determine potential aerosol hazards of medical devices in operating rooms.
- Supported several U.S. government operational units in missions to interdict biological hazards through training, directed research and development and assessment of training, tactics and procedures for biological interdiction and disablement.

News Highlights

- **Scientists Urge WHO To Update Guidance On Airborne Transmission Of The Coronavirus** | NPR | 6 July 2020
- **The Difference Between Terms Like 'Airborne Spread' And 'Droplet Spread'** | NPR | 17 May 2020
- **How Coronavirus Spreads through the Air: What We Know So Far | Scientific America** | 12 May 2020
- **Can the novel coronavirus be transmitted through the air? UNMC study suggests it can** | Omaha World Herald | 3 August 2020
- **Aircraft airflow tested in Nebraska to reduce COVID-19 spread** | Air Force News | 15 April 2020

Recent Publications

- **Aerosol and surface contamination of SARS-CoV-2 observed in quarantine and isolation care**. Joshua L. Santarpia, Danielle N. Rivera, Vicki L. Herrera, M. Jane Morwitzer, Hannah M. Creager, George W. Santarpia, Kevin K. Crown, David M. Brett-Major, Elizabeth R. Schnaubelt, M. Jana Broadhurst, James V. Lawler, St. Patrick Reid & John J. Lowe. 29 July 2020.

- **The Infectious Nature of Patient-Generated SARS-CoV-2 Aerosol**. Joshua L Santarpia, Vicki L Herrera, Danielle N Rivera, Shanna Ratnesar-Shumate, St. Patrick Reid, Paul W Denton, Jacob W.S. Martens, Ying Fang, Nicholas Conoan, Michael V Callahan, James V Lawler, David M Brett-Major, John J Lowe. 21 July 2020.

Neal Woollen, DVM, Ph.D., MSS

Senior Research Strategy Officer

Dr. Neal Woollen is the Senior Research Strategy Officer for the National Strategic Research Institute at the University of Nebraska, a University Affiliated Research Center sponsored by U.S. Strategic Command.

Dr. Woollen retired from the U.S. Army Veterinary Corps in May 2018 after more than 29 years of military service.

He earned his doctor of veterinary medicine as well as doctorate degree in veterinary pathology from Kansas State University. He earned his master's degree in strategic studies from the U.S. Army War College.

Prior to his active duty military service, Dr. Woollen was engaged in production animal health research for the United States Department of Agriculture, Agricultural Research Service and received training in foreign animal disease diagnostics.

Throughout his military career, Dr. Woollen's work focused primarily on managing consequences associated with zoonotic diseases and high consequence pathogens that may cause endemic disease or be used as biological weapons.

Dr. Woollen is experienced in laboratory studies, field work with outbreak investigations and mobile platform diagnostics and response to accidental and intentional release of pathogens.

Prior to military retirement he stood up a new office in the Department of Defense focused on managing risk associated with biological select agents and toxins (BSAT), the BSAT Biorisk Program Office, that merged the disciplines of biosafety and biosecurity.

Current committees and working groups

- Member of the Centers for Disease Control and Prevention Office of Public Health Preparedness and Response Board of Scientific Counselors Biological Agent Containment Working Group
- Member of the leadership committee for the Coalition for Epi Response, Engagement, and Science

Highlighted publications

- Neal E. Woollen and Gary W. Carter. "Consequence Management: The Local and National Response." In: Medical Aspects of Biological Warfare. Office of the Surgeon General Borden Institute, Fort Sam Houston, Texas. 2018.
- Samuel S. Edwin, Virginia I. Roxas-Duncan, America M. Ceralde, Shelley C. Jorgensen, and Neal E. Woollen. "Biological Surety, In: Medical Aspects of Biological Warfare." Office of the Surgeon General Borden Institute, Fort Sam Houston, Texas. 2018.
- Dragon DC, Bader DE, Mitchell J, Woollen N. "Natural dissemination of Bacillus anthracis spores in northern Canada." Appl Environ Microbiol. 2005 Mar;71(3):1610-5.
- Pavlin JA, Gilchrist MJ, Osweiler GD, Woollen N. "Diagnostic analyses of biological agent-caused syndromes: laboratory and technical assistance." Emerg Med Clin North Am. 2002 May;20(2):331-50.
- Leirs H, Mills JN, Krebs JW, Childs JE, Akaibe D, Woollen N, Ludwig G, Peters CJ, Ksiazek TG. "Search for the Ebola virus reservoir in Kikwit, Democratic Republic of the Congo: reflections on a vertebrate collection." J Infect Dis. 1999 Feb;179 Suppl 1:S155-63.

David A. Relman is the Thomas C. and Joan M. Merigan Professor in Medicine, and a Professor of Microbiology & Immunology at Stanford University, and Chief of Infectious Diseases at the Veterans Affairs Palo Alto Health Care System. He is also Senior Fellow at the Freeman Spogli Institute for International Studies (FSI), and served as science Co-Director at the Center for International Security and Cooperation (2013-2017), at Stanford. Relman trained at MIT and then Harvard Medical School, followed by clinical training in internal medicine and infectious diseases at the Massachusetts General Hospital in Boston, and a postdoctoral fellowship in microbiology at Stanford.

Relman was an early pioneer in the modern study of the human indigenous microbiota (microbiome). His current research work focuses on assembly, diversity, stability and resilience of human microbial communities. Previous work included pathogen discovery, and bacterial pathogenesis. Among policy-relevant activities in biological security Relman served as vice-chair of the National Research Council Committee that reviewed the science performed for the FBI 2001 Anthrax Letters investigation, chair of the Forum on Microbial Threats (2007-2017), chair of the Standing Committee that examined illnesses in U.S. State Department employees stationed in Cuba and China (2019-2020), and currently serves on the Intelligence Community Studies Board, all at the U.S. National Academies of Science, Engineering, and Medicine. He was a founding member of the National Science Advisory Board on Biosecurity (2005-2014), a member of the Working Group on Biodefense for the President's Council of Advisors on Science and Technology (The White House) (2016), and President of the Infectious Diseases Society of America (2012-2013). He currently serves on the Senior Advisory Group, for the NTI-Bio Initiative at Nuclear Threat Initiative. He was elected to the National Academy of Medicine in 2011.

RICHARD A. MULLER

Personal Information

Birthdate: January 6, 1944

Married, two children, 2 grandchildren. Wife is architect and structural engineer

Education

A.B.	1964, Columbia University, New York
Ph.D.	1969, University of California, Berkeley, Physics

Professional positions

1969-1975	Assistant Research Physicist, Space Sciences Laboratory
1971-1974	Lecturer, Department of Physics, U.C. Berkeley
1975-1978	Associate Research Physicist, Joint Appointment at Lawrence Berkeley Laboratory and Space Sciences Laboratory
1978-1980	Associate Professor of Physics, U.C. Berkeley
1979-2010	Faculty Senior Scientist, Lawrence Berkeley Laboratory Group Leader, LBL Astrophysics.
1980-2010	Professor of Physics, University of California, Berkeley
2008-present	Muller and Associates, consulting firm; cofounded with daughter Elizabeth Muller.
2010-present	Emeritus Professor, U. Calif. Berkeley
2010-present	Berkeley Earth co-founder, Scientific Director, Board member
2016-present	Deep Isolation Inc., co-founder and CTO

Research

1965-1969	Cosmic-ray studies with balloon-borne superconducting magnet.
1968-1973	Nuclear interactions and decay of cascade hyperon Liquid proportional counters for high-energy physics and medicine. Gravity wave detection. Cosmic ray measurements.
1973-1977	Discovered cosine anisotropy in cosmic microwave background and high peculiar velocity (600 km/sec) of Milky Way. "Image sharpness" theorem. Experimental adaptive optics. Search for heavy charge +1 particles in terrestrial matter.
1976-1991	Accelerator Mass Spectrometry: Invented and first to use method for direct detection of natural radioisotopes. Design and construction of table-top "cyclotrino" for dating.
1980-1992	Automated system for supernovae; discovered 20. Work continued by Saul Perlmutter, awarded Nobel Prize for the discoveries.
1984-present	Nemesis theory, and experimental program to find Nemesis. Periodicities in crater ages. Theory of the effect of galactic tides on comet orbits.
1986	Geomagnetic reversals: theory, and association with climate events.
1988	Origin of meteorites in comet showers.
1993-2004	Radioisotope dating of lunar spherules for crater rates
1993-2003	Glacial cycles and Earth orbit perturbations (Milankovitch cycles)

1999-2009	Fossil extinctions Extraterrestrial accretion Climate-Astrophysics links Deep Earth geophysics
2010-present	Berkeley Earth, founder and scientific director. Study of global warming, air pollution.
2014-present	Analysis of air pollution in China
2016-present	Geologic isolation of spent nuclear fuel in horizontal boreholes

Awards and Honors

1977 Texas Instruments Foundation Founders' Prize "for outstanding achievement in the physical sciences."
1978 National Science Foundation Alan T. Waterman Award "for highly original and innovative research which has led to important discoveries and inventions in diverse areas of physics, including astrophysics, radioisotope dating, and optics."
1982 MacArthur Foundation Prize Fellowship
1984 Science Digest list of 100 Outstanding Scientists Under Age 40
1985 Fellow, American Physical Society
1989 Honorary Doctor of Humane Letters, American University of Switzerland
1989 Newsweek citation as one of 25 Innovators in United States
1990 Miller Professorship, University of California, Berkeley
1991 Fellow, American Association for the Advancement of Science
1999 Distinguished Teaching Award, University of California at Berkeley
1999 Fellow, California Academy of Arts and Sciences
2005 "Unsung Hero" citation, UC Berkeley Students
2008 Donald Sterling Noyce Prize for Excellence in Undergraduate Teaching
2010 Fellow, American Academy of Arts and Sciences
2009 "Best Course on Campus", rated #1 by poll by student newspaper
2010 "Best Course on Campus", again rated #1 by poll by student newspaper
2011 *Brave Thinker*, one of 21 cited by the Atlantic Magazine
2012 *Global Thinker*, citation by Foreign Policy Magazine
2012 *Courage Award*, citation by Poder Business Magazine
2014 *Breakthrough Prize for Fundamental Physics*, shared with Saul Perlmutter and others, "For the most unexpected discovery that the expansion of the universe is accelerating, rather than slowing as had been long assumed."

Honorary lectures

1988 Vaden Miles Memorial Lecture, Wayne State University
1990 Maria Goeppert Mayer Memorial Lecture, U.Calif. La Jolla
1990 Distinguished Lecturer, Mitre Institute, Bedford Massachusetts
1990 Wright Science Colloquium speaker, Geneva Switzerland
2003 Jim Arnold Lecture
2011 Arthur Compton Lecture, U. Washington
2013 Freshman Address, U. Mississippi

Keynote addresses and Colloquia 2012 to present:

2012: California Institute of Technology; University of Shanghai; NKH; Power Association of Northern California; Common Core distinguished lecture at Hong Kong University; Commenius; University of Kentucky; Stanford Linear Accelerator Center; IVP; University of Sweden at Stockholm.

2013: University of Hong Kong; RIPED Beijing; KPMG Chicago, Nuclear Engineering (UC Berkeley); Future of Science (Geneva), Monterey Conference, General Electric, NY; WAVE Equity Partners Boston; Pacific Union Club; Shell (Houston); Apache (Houston); Future 500; Commenius; DNV

2014: 7th Fleet Admirals Meeting in Japan; Govt. of Korea (President Park); UK House of Lords; Liquefied Natural Gas Conference Vancouver; GSR (Beijing); Kaidi (Wuhan, China); Commenius; DNV.

Physics Courses Taught

for physics majors: H7a, 105 (Mechanics); 49 (Thermodynamics); H5c, H7b, 7b, 110a,b (Electricity and Magnetism, Special Relativity); 110C (Optics); 5e, H5e, 7c, 137a,b,c (Quantum Mechanics); 129a,b (Nuclear Physics) 199, H190 (honors seminar), 295, 299 (Research), H195 (senior honors thesis), 111 (Advanced Laboratory); Graduate Seminar on Physics and U.S. Defense.

for non-majors: 10 (Qualitative Physics), 39 (Freshman Seminars); 106 (Optics for optometrists); 121, 132 (Modern Physics).

Geology & Geophysics: Seminar

New Course created

Physics for future Presidents. This is a complete overhaul for Physics 10. Wrote textbook; now used at over 40 other universities, ranked by NYTimes as the 3rd most popular of all lectures on YouTube; appreciatory email from 92 countries and 49 states.

Ph. D. thesis students supervised:

Marc Gorenstein, A Measurement of Anisotropy in the Cosmic Background Radiation on a Large Angular Scale at 33 GHz (1978)

Jordin Kare, Automated Search for Supernovae, LBL-19340 (1984)

James J. Welch, A Low Energy Cyclotron for Radiocarbon Dating (1984)

M. Shane Burns, Development of a CCD Camera for an Automated Supernova Search, and Observations of a Supernova in NGC 5033 (1985)

Saul Perlmutter, An Astrometric Search for a Stellar Companion to the Sun LBL-23187 (November 1986); Saul won Nobel Prize.

Peter G. Friedman, A Low Background-Rate Detector for Ions in the 5 to 50 keV Energy Range to be used for Radioisotope Dating with a Small Cyclotron, LBL-17804 (1986)

Kirk Bertsche, A Small Low Energy Cyclotron for Radioisotope Measurements, LBL-28106, November 1989.

Timothy Sasseen, An Optical and Near Infrared Search for a Pulsar in Supernova 1987A, LBL-29992, December 1990.

Li Ping Wang (Mechanical Engineering), "Development of the 30" Remote-Operating Robotic Telescope System for the Berkeley Automated Supernova Search." July 1991.

Heidi Marvin Newberg, "Measuring q_0 using Supernovae at $z \approx 0.3$," July 1992, LBL-32634.

Craig Kenton Smith, Supernova Rates for the Berkeley Automated Supernova Search Using V and R Band Light Curve Templates (1995)

Alex Kim, 1997.

Matthew Kim, High Redshift Supernova Light Curves (1999)

Timothy Culler 1999 (Geophysics)

Jonathan Levine 2004. Lunar Glass Spherules as Probes of the Meteoroid Impact History of the Moon.

Robert A. Rohde (shared with P. Buford Price) 2010

Consulting, Advisory boards, National Committees

1972-1973	Oximetrix, San Francisco, Biomedical instrumentation.
1972-1973	Unimark, Livermore. Electrostatic printing.
1974-1975	American Physical Society. Nuclear reactor safety.
1973-2007	JASON consultant to U.S. Government on energy and U.S. security. Member of steering committee 1980 to 1982.
1979	NASA: member of Innovation Study group. NSF: consultant on basic/applied research concepts.
1979-1980	White House Office of Science and Technology Policy: member of committee to analyze putative South African nuclear test.
1981-1987	Lawrence Livermore Laboratory. Consultant fusion, U.S. security.
1982-1986	Advisory Board, Institute of Theoretical Physics, Santa Barbara.
1983	Accelerator Mass Spectroscopy committee, Geological Survey.
1986-1987	Panel to Explore New Directions, Lawrence Berkeley Laboratory
1990-preseent	Many others
2010-presebt	consultant to various venture capital and private equity firms
1984-1987	National Academy of Sciences Committee on International Security and Arms Control. Met twice yearly with Soviet delegation.
1989-1990	Board of Overseers, American College of Switzerland, Leysin
1989-2002	Institute for Defense Analyses, CRD, Princeton N.J.
1989-1990	FAS Committee to study possible ASAT treaty
1990-present	Fellow of the Committee for the Scientific Investigation of Claims of the Paranormal
1990-1998	Sponsor, Federation of American Scientists

1991	Helped organize the Kuwaiti Oil Fire Symposium, sponsored by the Union of Concerned Scientists
1990-1992	Organizing committee, NSF Symposium on Frontiers of Science
1991-1992	NRC Committee on Special Operations and Low Intensity Conflict
1991- 1999	Lawrence Livermore Laboratory -- advisory committee for Laboratory Directed Research and Development
1992-2006	Institute for Nuclear and Particle Astrophysics, founding committee, Board of Advisors
2000-present	Berkeley Geochronology Center (BCG). Member, Board of Directors
2005-present	Advanced Ignition Facility, Lawrence Livermore National Laboratory, member of the scientific advisory board
2009-present	Consultant on energy technology, many VC and private equity firms; delivered keynote address before the President of Korea.
2011-2013	BP (enhanced oil recovery; methane hydrates; cementing)
2013-2015	World Economic Forum, Sustainability

Professional societies

American Physical Society (fellow), American Astronomical Society, American Association for the Advancement of Science (fellow); International Astronomical Union, Sigma Xi, American Geophysical Union, American Academy of Arts and Sciences

Publications

1. Production and decay of cascade hyperon, with P. Dauber, J. Berge, J. Hubbard, D. Merrill, Phys. Rev. 179, 1262 (1969).
2. Study of the reaction K-N to -K from threshold to 2.7 GeV/c (Ph.D. thesis), UCRL-19372 (August 8, 1969).
3. Prospect of high spatial resolution for counter experiments: a new particle detector using electron multiplication in liquid Argon, with S. Derenzo, R. Smits, L. Alvarez, UCRL-19254, NAL Summer Study Report, 79-102, Aspen, Colorado (July 1969).
4. Liquid-filled proportional counter, with S. Derenzo, G. Smadja, D. Smith, R. Smits, H. Zaklad, L. Alvarez, Phys. Rev. Lett. 27, 532 (1971).
5. Twin paradox in special relativity, Am. J. Phys. 40, 966 (1972).
6. High precision charged particle detector using Noble liquids, with S. Derenzo, G. Smadja, R. Smits, H. Zakland, L. Alvarez, Nature 233, 617 (1971).
7. Observation of cascade hyperon interactions, Phys. Lett. 38B, 123 (1972).
8. Search for seismic signals from gravitational radiation of pulsar CP1133, with T. Mast, J. Nelson, J. Saarloos, B. Bolt, Nature 240, 140 (1972).
9. High energy particle astronomy, with A. Buffington, L. Smith, G. Smoot, in "Astronomy from a Space Platform," Am. Astronaut. Soc. Sci. Tech. 28, 289 (1972).

10. Recent developments in high resolution noble liquid counters, with S. Derenzo, D. Smith, R. Smits, H. Zaklad, L. Alvarez, UCRL-20118, NAL Summer Study Report, 45-74, Batavia, Illinois (December 1970).
11. Particle detectors based on noble liquids, with S. Derenzo, R. Smits, H. Zaklad, Proc. Int. Conf. Instr. for High Energy Physics, Dubna USSR (December 1971).
12. Source of alpha particle collimated to 35 microns, with 7 other authors, UCRL-20857, UC-37 Instruments, TID-4500 58th edition (June 1971).
13. Liquid Xenon radioisotope camera, with H. Zaklad, S. Derenzo, G. Smadja, R. Smits, L. Alvarez, IEEE Trans. Nucl. Sci. NS-19, 206 (1972).
14. Measurements of geomagnetic cutoff rigidities, with C. Pennypacker, G. Smoot, A. Buffington, L. Smith, Jour. Geophys. Res. 78, 1515 (1973).
15. Liquid-filled multi-wire proportional counter, with S. Derenzo, et al., Fourth Hawaii Topical Conf., U. Hawaii UH-511-109, 109-111 (August 1971).
16. Preliminary images in a 24 wire liquid Xenon gamma ray camera, with H. Zaklad, S. Derenzo, R. Smits, L. Alvarez, IEEE Trans, Nuc. Sci. NS-20, 429 (1973).
17. Liquid Xenon filled wire chambers, with S. Derenzo, et al., LBL-1321, Proc. XVI Int. Conf. High Energy Physics, U. Chicago (September 1972).
18. Liquid Xenon Compton telescope: a new technique for gamma-ray astronomy, with 7 other authors, UCBSSL report series 14, issue 17.
19. Electronic processes in liquid Xenon, with S. Derenzo, T. Mast, H. Zaklad, Nucl. Inst. & Meth. 118, 611 (1974).
20. Real-time correction of atmospherically degraded telescope images through sharpening, R. A. Muller and A. Buffington, J. Opt. Soc. Am. 64, 1200 (1974).
21. Light-water reactor safety, H. Lewis and 11 other authors, Rev. Mod. Phys. 47 Suppl 1 (1975). Summary section published separately in Physics Today 28, 38 (July 1975); Nuclear Safety (October 1975).
22. Image, optical, R. A. Muller and A. Buffington, 1976 McGraw-Hill Yearbook of Science and Technology.
23. Active image restoration with a flexible mirror, with 4 other authors, Topical Meeting on Imaging in Astronomy, Cambridge, MA (June 18-21, 1975).
24. Active image restoration with a flexible mirror, with 4 other authors, SPIE/SPSE Tech. Symp. East, 75 (March 23, 1976).
25. Correction of atmospheric distortion with an image sharpening telescope, A. Buffington, F. Crawford, R. Muller, A. Schwemin, R. Smits, Jour. Opt. Soc. Am. 67, 298 (1977).
26. First observatory results with an image-sharpening telescope, A. Buffington, F. Crawford, R. Muller, and C. Orth, Jour. Opt. Soc. Am. 67, 304 (1977).
27. Aether Drift and the Isotropy of the Universe: Proposal to NASA for a search for anisotropy in the primordial blackbody radiation (1976). Principal Investigator.
28. Quarks with unit charge: a search for anomalous Hydrogen, R.A. Muller, L. Alvarez, W. Holley, E. Stephenson, Science 196, 521 (1977).
29. Radioisotope dating with a cyclotron, Science 196, 489 (1977).
30. Anisotropy of the cosmic microwave background radiation, M. Gorenstein, R.A. Muller, G. Smoot, Bulletin of Am. Astron. Soc. 9, 431 (1977).

31. Detection of anisotropy in the cosmic blackbody radiation, G. Smoot, M. Gorenstein and R.A. Muller, Phys. Rev. Lett. 39, 898 (1977).
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33. Sharpening Stellar Images, A. Buffington, F. Crawford, R.A. Muller, S. Pollaine, C. Orth, Science 200, 489 (1978).
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75. Submillisecond optical pulsar in supernova 1987A, J. Kristian, C. R. Pennypacker, J. Middleditch, M.A. Hamuy, J.N. Imamura, W.E. Kunkel, D.E. Morris, R.A. Muller, S. Perlmutter, S.J. Rawlings, T.P. Sasseen, I.K. Shelton, T.Y. Steiman-Cameron, I.R. Tuohy, Nature 338, 234-236 (16 March 1989).
76. A Search for Nemesis: Current Status and Review of Theory. S. Perlmutter, R A. Muller, C. R. Pennypacker, C. K. Smith, L. P. Wang, S. White, H. S. Yang, to be published in the proceedings of the Second Snowbird Conference on Mass Extinctions (1989).
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78. Recent Advances in the Berkeley Automated Supernova Search: The Introduction of a Real-Time System, C. K. Smith, F. Crawford, R. A. Muller, C. Pennypacker, S. Perlmutter, T. Sasseen, R. Williams, R. Treffers, in Automatic

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100. High-resolution spectral analysis of glacial cycles: eccentricity is ruled out, G. J. MacDonald and R. A. Muller, Lawrence Berkeley Laboratory report LBL-35666.
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From: "Paulopol, Andreea I" (b)(6) @state.gov>
To: AVC-CBW-DL <AVC-CBW-DL2@state.gov>
Subject: FW: MX2 paper clearance Friday 7/17
Date: Fri, 17 Jul 2020 18:08:16 +0000

(b)(5) Deliberative Process

Please let me know if anyone has any issues with the attached version. Due COB today.

Thanks,
Andreea

From (b)(6); (b)(7)(C)
Sent: Friday, July 17, 2020 11:06 AM
To: (b)(6) @state.gov>; ATL Treaties Team (b)(6) (b)(6) AVC-CBW-DL <AVC-CBW-DL2@state.gov>; (b)(6) (b)(6) (b)(6) ; (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (Geneva) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) hafin, Kelly (b)(6) (b)(6) (b)(6) (b)(6) ; (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) Ferro, Philip (b)(6) (b)(6) ; Geneva CD <GenevaCD@state.gov>; GHSA-State-OES-IHB <GHSA-State-OES-IHB@state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) ; (b)(6) (b)(6) (b)(6) (b)(6) ; (b)(6) @state.gov>; (b)(6): (b)(7)(C) (b)(6); (b)(7)(C) ISN-BPS-DL <ISN-BPS-DL@STATE.GOV>; ISN-CTR-BioSecurity-DL <ISN-CTR-BioSecurity-DL@state.gov>; (b)(6) (b)(6) (b)(6); (b)(7)(C) (b)(6); (b)(7)(C) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) @usaid.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (GH/HIDN/ID) (b)(6) @usaid.gov>; (b)(6) (b)(6) (b)(6) (b)(6) ; (b)(6) @state.gov>; (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) Waterman, Page (b)(6) (b)(6)
Subject: Re: MX2 paper clearance Friday 7/17

(b)(6)

FBI appreciates the opportunity to review and provide comments on the latest iteration of the 2020 MX2 working paper. Please refer to the attached file for proposed edits and comments. We look forward to the next steps as State adjudicates interagency submissions prior to providing clearance.

Regards,

(b)(6); (b)(7)(C)

Management and Program Analyst

Federal Bureau of Investigation

Weapons of Mass Destruction Directorate

Policy & Strategy Unit

(b)(6); (b)(7)(C)

From: (b)(6) @state.gov>
Sent: Tuesday, July 14, 2020 4:45 PM
To: ATL Treaties Team <osd.pentagon.ousd-atl.list.treaties-team-trac@mail.mil>; AVC-CBW-DL <AVC-CBW-DL2@state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) Seoul) (b)(6) @state.gov>; (b)(6) (b)(6) Chafin, Kelly (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>(b)(6) (b)(6) (b)(6) (b)(6) ; (b)(6) (b)(6) Ferro, Philip (b)(6) (b)(6) Geneva CD <GenevaCD@state.gov>; GHSA-State-OES-IHB <GHSA-State-OES-IHB@state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6); (b)(7)(C) ISN-BPS-DL <ISN-BPS-DL@STATE.GOV>; ISN-CTR-BioSecurity-DL <ISN-CTR-BioSecurity-DL@state.gov>; (b)(6) (b)(6) (b)(6) (b)(6); (b)(7)(C) (b)(6); (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) @state.gov>; (b)(6) @state.gov>; (b)(6) (b)(6) (b)(6) (b)(6) (b)(6) (b)(6)

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(b)(6) (b)(6) (b)(6)
Cc: ISN-BPS-DL <ISN-BPS-DL@STATE.GOV>
Subject: MX2 paper clearance Friday 7/17

Dear BWC Backstoppers,

Thank you all for Friday's discussion on the MX2 paper. I am seeking Department clearances by **COB Friday July 17th** on the revised paper attached. To aid your review, I highlighted areas where there were substantial changes or additions from the previous version (though I left out the many minor editorial changes).

Please feel free to reach out with any questions or concerns (b)(6)

Thank you,

(b)(6)
(b)(6)
Foreign Affairs / Science Officer | AAAS S&T Policy Fellow
Biological Policy Staff | Bureau of International Security and Nonproliferation
U.S. Department of State
Office: (b)(6)
I anticipate frequent telework - please feel free to call my cell phone (b)(6)

Sender: "Paulopol, Andreea I" (b)(6) @state.gov>
Recipient: AVC-CBW-DL <AVC-CBW-DL2@state.gov>

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Subject: Fw: Federal Grants and Contracts Awarded to EcoHealth Alliance

Date: Thu, 17 Dec 2020 23:57:37 +0000

recipient_parent_name awarding_agency_name awarding_sub_agency_name period_of_performance_start_date period_of_performance_current_end_date federal_action_obligation total_obligated_amount primary_place_of_performance_country_name cfda_title award_description assistance_transaction_unique_key ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/18/2013 10/14/2016 1999203 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS LAND USE CHANGE & DISEASE EMERGENCE 7200_AID486A1300005_AID-486-A-13-00005-00_98.001_0000 ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/20/2013 05/30/2018 499944 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS LAND USE CHANGE & DISEASE EMERGENCE 7200_AID486A1300005_AID-486-A-13-00005-02_98.001_0002 ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/20/2013 11/30/2016 0 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS LAND USE CHANGE & DISEASE EMERGENCE 7200_AID486A1300005_AID-486-A-13-00005-01_98.001_0001 ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/20/2013 05/30/2018 0 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS LAND USE CHANGE & DISEASE EMERGENCE 7200_AID486A1300005_AID-486-A-13-00005-03_98.001_0003 ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/20/2013 11/30/2018 0 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS LAND USE CHANGE & DISEASE EMERGENCE 7200_AID486A1300005_AID-486-A-13-00005-04_98.001_0004 ECOHEALTH ALLIANCE INC. AGENCY FOR INTERNATIONAL DEVELOPMENT (USAID) AGENCY FOR INTERNATIONAL DEVELOPMENT 09/20/2013 02/28/2019 0 2499147 THAILAND USAID FOREIGN ASSISTANCE FOR PROGRAMS OVERSEAS THE INFECTIOUS DISEASE EMERGENCE AND ECONOMICS OF ALTERED LANDSCAPES (IDEEAL) 7200_AID486A1300005_AID-486-A-13-00005-05_98.001_0005 ECOHEALTH ALLIANCE INC. DEPARTMENT OF AGRICULTURE (USDA) ANIMAL AND PLANT HEALTH INSPECTION SERVICE 09/30/2008 09/29/2009 143000 143000 MEXICO WILDLIFE SERVICES CONDUCT AN AVIAN INFLUENZE SURVEILLANCE PROGRAM TO DETECT THE OCCURRENCE OF HIGHLY PATHOGENIC H5N1 AVIAN INFLUENZA IN MEXICO. 12K3_08-7100-0206-CA_12K30008-7100-0206-CA 12X1600_10.028_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF AGRICULTURE (USDA) ANIMAL AND PLANT HEALTH INSPECTION SERVICE 09/30/2009 09/29/2010 100001 100001 MEXICO WILDLIFE SERVICES CONDUCT AN AVIAN INFLUENZE SURVEILLANCE PROGRAM TO DETECT THE OCCURRENCE OF HIGHLY PATHOGENIC H5N1 AVIAN INFLUENZA IN MEXICO. 12K3_09-7100-0206-CA_12K30009-7100-0206-CA 12X1600_10.028_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE

(DOD) DEPARTMENT OF DEFENSE 05/28/2014 05/27/2019 0 2942019 SOUTH AFRICA BASIC SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA, CHANGE OF ACO TO ONR 9700_HDTRA11410029_2014HDTRA12468_12.351_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEPARTMENT OF DEFENSE 05/28/2014 05/27/2017 970536 2942019 SOUTH AFRICA BASIC SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA, CHANGE OF ACO TO ONR 9700_HDTRA11410029_2016HDTRA12741_12.351_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEPARTMENT OF DEFENSE 05/28/2014 05/27/2019 992699 2942019 SOUTH AFRICA BASIC SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA 9700_HDTRA11410029_2014HDTRA12467_12.351_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEPARTMENT OF DEFENSE 05/28/2014 05/27/2019 978784 2942019 SOUTH AFRICA BASIC SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA, CHANGE OF ACO TO ONR 9700_HDTRA11410029_2015HDTRA12469_12.351_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 05/28/2014 05/27/2017 996147 1994340 SOUTH AFRICA BASIC SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN THE REPUBLIC OF SOUTH AFRICA, CHANGE OF ACO TO ONR 9761_HDTRA11410029_2016HDTRA12741_12.351_04 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 05/01/2017 04/30/2022 565205 1604523 MALAYSIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION SEROLOGICAL BIOSURVEILLANCE FOR SPILLOVER OF HENIPAVIRUSES AND FILOVIRUSES AT AGRICULTURAL AND HUNTING HUMANANIMAL INTERFACES IN PENINSULAR MALAYSIA 9761_HDTRA11710037_2017:HDTRA1:2742_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 05/01/2017 04/30/2022 156044 1604523 MALAYSIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION SEROLOGICAL BIOSURVEILLANCE FOR SPILLOVER OF HENIPAVIRUSES AND FILOVIRUSES AT AGRICULTURAL AND HUNTING HUMANANIMAL INTERFACES IN PENINSULAR MALAYSIA 9761_HDTRA11710037_2018:HDTRA1:4112_12.351_P00002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 10/02/2017 10/01/2022 782330 GEORGIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_2017:HDTRA1:2749_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 10/02/2017 10/01/2022 1101958 GEORGIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_2018:HDTRA1:4133_12.351_P00001 ECOHEALTH ALLIANCE

INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 10/02/2017 10/01/2019 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_-NONE-_12.351_P00001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 10/02/2017 10/01/2020 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_-NONE-_12.351_P00002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 10/02/2017 10/01/2022 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORNE ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_-NONE-_12.351_P00003 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 05/25/2018 04/30/2019 883274 1604523 MALAYSIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION SEROLOGICAL BIOSURVEILLANCE FOR SPILLOVER OF HENIPAVIRUSES AND FILOVIRUSES AT AGRICULTURAL AND HUNTING HUMAN-ANIMAL INTERFACES IN PENINSULAR MALAYSIA 9761_HDTRA11710037_2018:HDTRA1:4125_12.351_P00003 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 05/28/2018 05/27/2019 998193 1994340 SOUTH AFRICA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING RIFT VALLEY FEVER IN SOUTH AFRICA 9761_HDTRA11410029_2018:HDTRA1:4119_12.351_P00006 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 07/30/2019 07/20/2020 997623 GEORGIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION UNDERSTANDING THE RISK OF BAT-BORN ZOONOTIC DISEASE EMERGENCE IN WESTERN ASIA 9761_HDTRA11710064_2019:HDTRA1:4153_12.351_P00002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 08/19/2019 08/18/2024 4988987 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION REDUCING THE THREAT OF RIFT VALLEY FEVER THROUGH ECOLOGY, EPIDEMIOLOGY AND SOCIO-ECONOMICS 9761_HDTRA11910033_-NONE-_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 08/19/2019 08/20/2020 4988987 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION REDUCING THE THREAT OF RIFT VALLEY FEVER THROUGH ECOLOGY, EPIDEMIOLOGY AND SOCIO-ECONOMICS 9761_HDTRA11910033_-NONE-_12.351_P00001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 08/19/2019 08/01/2024 3990550 4988987 UNITED STATES SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION REDUCING THE THREAT OF RIFT VALLEY FEVER THROUGH ECOLOGY, EPIDEMIOLOGY, AND SOCIO-ECONOMICS. 9761_HDTRA11910033_-NONE-_12.351_P00002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 06/01/2020 05/31/2025 LIBERIA

SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION REDUCING THE THREAT FROM HIGH-RISK PATHOGENS CAUSING FEBRILE ILLNESS IN LIBERIA 9761_HDTRA12010016_-NONE-_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 07/01/2020 06/30/2025 TANZANIA SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION CRIMEAN-CONGO HEMORRHAGIC FEVER: REDUCING AN EMERGING HEALTH THREAT IN TANZANIA. 9761_HDTRA12010018_-NONE-_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) UNIFORMED SERVICES UNIVERSITY OF THE HEALTH SCIENCES 09/21/2020 09/20/2022 1360002 1360002 UNITED STATES UNIFORMED SERVICES UNIVERSITY MEDICAL RESEARCH PROJECTS STRATEGIC COORDINATION TO STRENGTHEN AFRICOM ONE HEALTH AND VETERINARY PROGRAMS FOR GLOBAL HEALTH ENGAGEMENT STRENGTHENING MULTI-SECTORAL APPROACHES TO BIODEFENSE AND BIOSURVEILLANCE IN THE CAUCASUS 97HW_HU00012010031_-NONE-_12.750_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF DEFENSE (DOD) DEFENSE THREAT REDUCTION AGENCY 09/29/2020 09/28/2023 JORDAN SCIENTIFIC RESEARCH - COMBATING WEAPONS OF MASS DESTRUCTION REDUCING THE THREAT OF MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS AND AVIAN INFLUENZA IN JORDAN&STRENGTHENING REGIONAL DISEASE SURVEILLANCE CAPACITY 9761_HDTRA12010029_-NONE-_12.351_0 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 6982 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-000-8-2012-93989-75-0819-NON_93.989_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 199992 3725160 UNITED STATES UNKNOWN THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-003-7-2010-93999-75-0140-NON_93.999_003 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 204688 3725160 UNITED STATES TRANS-NIH RECOVERY ACT RESEARCH SUPPORT THE ECOLOGY EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-003-6-2009-93701-75-0818-REC_93.701_003 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 494455 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-001-8-2011-93989-75-0819-NON_93.989_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 499975 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-001-6-2009-93989-75-0819-NON_93.989_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL

INSTITUTES OF HEALTH 08/01/2002 06/30/2013 494455 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-001-9-2012-93989-75-0819-NON_93.989_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 499998 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-001-7-2010-93989-75-0819-NON_93.989_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 51225 3725160 UNITED STATES TRANS-NIH RECOVERY ACT RESEARCH SUPPORT THE ECOLOGY EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-004-6-2009-93701-75-0818-REC_93.701_004 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 46399 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-006-6-2009-93989-75-0140-NON_93.989_006 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 63018 3725160 UNITED STATES UNKNOWN THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-002-7-2010-93999-75-0140-NON_93.999_002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 266919 3725160 UNITED STATES UNKNOWN THE ECOLOGY, EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-002-8-2011-93999-75-0140-NON_93.999_002 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 08/01/2002 06/30/2013 199698 3725160 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING THE ECOLOGY EMERGENCE AND PANDEMIC POTENTIAL OF NIPAH VIRUS IN BANGLADESH 7529_R01TW005869_75-148-R01TW005869-005-6-2009-93989-75-0140-NON_93.989_005 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/18/2008 08/31/2013 510005 2579553 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH RISK OF VIRAL EMERGENCE FROM BATS 7529_R01AI079231_75-104-R01AI079231-000-4-2011-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/18/2008 08/31/2013 518980 2579553 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH RISK OF VIRAL EMERGENCE FROM BATS 7529_R01AI079231_75-104-R01AI079231-000-5-2012-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/18/2008 08/31/2013 535156 2579553 UNITED STATES ALLERGY, IMMUNOLOGY AND

TRANSPLANTATION RESEARCH RISK OF VIRAL EMERGENCE FROM BATS 7529_R01AI079231_75-104-R01AI079231-001-2-2009-93855-75-0885-NON_93.855_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/18/2008 08/31/2013 480423 2579553 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH RISK OF VIRAL EMERGENCE FROM BATS 7529_R01AI079231_75-104-R01AI079231-000-3-2010-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/22/2009 08/31/2011 49994 442844 UNITED STATES TRANS-NIH RECOVERY ACT RESEARCH SUPPORT RISK FOR FUTURE OUTBREAKS OF HENIPAVIRUSES IN SOUTH ASIA 7529_K08AI067549_75-104-K08AI067549-001-3-2009-93701-75-0900-REC_93.701_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/22/2009 08/31/2011 130950 442844 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH RISK FOR FUTURE OUTBREAKS OF HENIPAVIRUSES IN SOUTH ASIA 7529_K08AI067549_75-104-K08AI067549-000-3-2009-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/22/2009 08/31/2011 130950 442844 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH RISK FOR FUTURE OUTBREAKS OF HENIPAVIRUSES IN SOUTH ASIA 7529_K08AI067549_75-104-K08AI067549-000-4-2010-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/17/2012 08/31/2017 300000 300000 UNITED STATES INTERNATIONAL RESEARCH AND RESEARCH TRAINING COMPARATIVE SPILLOVER DYNAMICS OF AVIAN INFLUENZA IN ENDEMIC COUNTRIES 7529_R56TW009502_75-148-R56TW009502-000-1-2012-93989-75-0140-NON_93.989_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 05/31/2019 666442 3748715 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_75-104-R01AI110964-000-1-2014-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 05/31/2019 611090 3748715 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_75-104-R01AI110964-000-3-2016-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 05/31/2019 630445 3748715 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_75-104-R01AI110964-000-2-2015-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 05/31/2019 597112 3748715 UNITED STATES ALLERGY, IMMUNOLOGY AND TRANSPLANTATION RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_7529-104-R01AI110964-000-4-2017-

93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 05/31/2019 581646 3748715 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_7529-104-R01AI110964-000-5-2018-93855-75-0885-NON_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 06/30/2025 733750 3748715 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_R01AI110964-2724294570_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 06/30/2025 -71770 3748715 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_R01AI110964-1667898916_93.855_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 06/30/2025 -369819 3748715 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_R01AI110964-1548787081_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/01/2014 06/30/2025 369819 3748715 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE 7529_R01AI110964_R01AI110964-236927158_93.855_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/17/2020 05/31/2025 1546744 1546744 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING RISK OF ZOONOTIC VIRUS EMERGENCE IN EID HOTSPOTS OF SOUTHEAST ASIA 7529_U01AI151797_U01AI151797-3312009326_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 06/17/2020 05/31/2025 0 1546744 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH UNDERSTANDING RISK OF ZOONOTIC VIRUS EMERGENCE IN EID HOTSPOTS OF SOUTHEAST ASIA 7529_U01AI151797_U01AI151797-4190450196_93.855_001 ECOHEALTH ALLIANCE INC. DEPARTMENT OF HEALTH AND HUMAN SERVICES (HHS) NATIONAL INSTITUTES OF HEALTH 09/15/2020 06/30/2025 580858 580858 UNITED STATES ALLERGY AND INFECTIOUS DISEASES RESEARCH STUDY OF NIPAH VIRUS DYNAMICS AND GENETICS IN ITS BAT RESERVOIR AND OF HUMAN EXPOSURE TO NIV ACROSS BANGLADESH TO UNDERSTAND PATTERNS OF HUMAN OUTBREAKS 7529_U01AI153420_U01AI153420-1871155957_93.855_000 ECOHEALTH ALLIANCE INC. DEPARTMENT OF THE INTERIOR (DOI) U.S. GEOLOGICAL SURVEY 08/15/2008 03/01/2009 -22512 -22512 U.S. GEOLOGICAL SURVEY_ RESEARCH AND DATA COLLECTION SEABIRD ECOLOGICAL ASSESSMENT NETWORK-SEANET 1434_G05AC00002_-NONE-_15.808_0004 ECOHEALTH ALLIANCE INC. DEPARTMENT OF THE INTERIOR (DOI) U.S. FISH AND WILDLIFE SERVICE 09/13/2012 09/13/2014 44499 44499 MALAYSIA GREAT APES CONSERVATION FUND DEVELOPMENT OF A GREAT APE HEALTH UNIT IN SABAH, MALAYSIA 1448_F12AP01117_-NONE-

_15.629_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF THE INTERIOR (DOI) U.S. FISH AND WILDLIFE SERVICE 09/14/2012 03/31/2015 154087 154087 ENDANGERED SPECIES CONSERVATION â€“ RECOVERY IMPLEMENTATION FUNDS ECO HEALTH ALLIANCE - GEOMYCES DESTUCTANS, IMPLICATIONS FOR THE MIGRATION OF WHITE-NOSE SYNDROME BAT 1448_F12AP01208_-NONE-_15.657_-NONE- ECOHEALTH ALLIANCE INC. DEPARTMENT OF THE INTERIOR (DOI) U.S. FISH AND WILDLIFE SERVICE 04/28/2014 06/30/2015 29988 29988 MEXICO WILDLIFE WITHOUT BORDERS-MEXICO ECOSYSTEM APPROACH FOR BIODIVERSITY MONITORING AND CONSERVATION 1448_F14AP00269_-NONE-_15.641_-NONE- ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 10/15/2006 09/30/2008 428794 932085 BIOLOGICAL SCIENCES PREDICTING SPATIAL VARIATION IN WEST NILE VIRUS TRANSMISSION 4900_0622391_-NONE-_47.074_001 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 10/01/2008 03/31/2012 468673 468673 SOCIAL, BEHAVIORAL, AND ECONOMIC SCIENCES HSD: COLLABORATIVE RESEARCH: HUMAN-RELATED FACTORS AFFECTING EMERGING INFECTIOUS DISEASES 4900_0826779_-NONE-_47.075_000 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 07/01/2010 06/30/2015 13948 72002 UNITED STATES BIOLOGICAL SCIENCES COLLABORATIVE RESEARCH: THE COMMUNITY ECOLOGY OF VIRAL PATHOGENS - CAUSES AND CONSEQUENCES OF COINFECTION IN HOSTS AND VECTORS 4900_1015791_NONB201206011015791001_47.074_001 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 07/01/2010 06/30/2015 14293 72002 UNITED STATES BIOLOGICAL SCIENCES COLLABORATIVE RESEARCH: THE COMMUNITY ECOLOGY OF VIRAL PATHOGENS - CAUSES AND CONSEQUENCES OF COINFECTION IN HOSTS AND VECTORS 4900_1015791_NONB201307011015791002_47.074_002 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 07/01/2010 06/30/2012 29109 72002 UNITED STATES BIOLOGICAL SCIENCES COLLABORATIVE RESEARCH: THE COMMUNITY ECOLOGY OF VIRAL PATHOGENS - CAUSES AND CONSEQUENCES OF COINFECTION IN HOSTS AND VECTORS 4900_1015791_NONA201006211015791000_47.074_000 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 07/01/2010 06/30/2015 14652 72002 UNITED STATES BIOLOGICAL SCIENCES COLLABORATIVE RESEARCH: THE COMMUNITY ECOLOGY OF VIRAL PATHOGENS - CAUSES AND CONSEQUENCES OF COINFECTION IN HOSTS AND VECTORS 4900_1015791_-NONE-_47.074_003 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2010 08/31/2012 98673 497121 UNITED STATES BIOLOGICAL SCIENCES ECOHEALTHNET: ECOLOGY, ENVIRONMENTAL SCIENCE AND HEALTH RESEARCH NETWORK 4900_0955897_NONB201108030955897001_47.074_001 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2010 08/31/2015 98992 497121 UNITED STATES BIOLOGICAL SCIENCES ECOHEALTHNET: ECOLOGY, ENVIRONMENTAL SCIENCE AND HEALTH RESEARCH NETWORK 4900_0955897_NONB201306100955897003_47.074_003 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE

FOUNDATION 09/01/2010 08/31/2011 99611 497121 UNITED STATES BIOLOGICAL SCIENCES ECOHEALTHNET: ECOLOGY ENVIRONMENTAL SCIENCE AND HEALTH RESEARCH NETWORK 4900_0955897_NONA201009020955897000_47.074_000 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2010 08/31/2015 99919 497121 UNITED STATES BIOLOGICAL SCIENCES ECOHEALTHNET: ECOLOGY, ENVIRONMENTAL SCIENCE AND HEALTH RESEARCH NETWORK 4900_0955897_NONB201207130955897002_47.074_002 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2010 08/31/2015 99926 497121 UNITED STATES BIOLOGICAL SCIENCES ECOHEALTHNET: ECOLOGY, ENVIRONMENTAL SCIENCE AND HEALTH RESEARCH NETWORK 4900_0955897_-NONE-_47.074_004 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 08/15/2012 07/31/2013 22890 22890 UNITED STATES BIOLOGICAL SCIENCES US-CHINA ECOLOGY AND EVOLUTION OF INFECTIOUS DISEASES COLLABORATIVE WORKSHOP; KUNMING, CHINA - OCTOBER, 2012 4900_1257513_NONA201208061257513000_47.074_000 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2016 08/31/2021 309674 499897 UNITED STATES BIOLOGICAL SCIENCES RCN: ECOHEALTH NET 2.0: A ONE HEALTH APPROACH TO DISEASE ECOLOGY RESEARCH & EDUCATION 4900_1618919_-NONE-_47.074_001 ECOHEALTH ALLIANCE INC. NATIONAL SCIENCE FOUNDATION (NSF) NATIONAL SCIENCE FOUNDATION 09/01/2016 08/31/2021 190223 499897 UNITED STATES BIOLOGICAL SCIENCES RCN: ECOHEALTH NET 2.0: A ONE HEALTH APPROACH TO DISEASE ECOLOGY RESEARCH & EDUCATION 4900_1618919_NONA201608251618919000_47.074_000

From: "Gross, Laura J" (b)(6) @state.gov>
To: AVC-CBW-DL <AVC-CBW-DL2@state.gov>
Subject: FW: Draft cable to China on consultations under Article V of the BWC
Date: Wed, 30 Dec 2020 14:36:35 +0000

FYSA

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6) (b)(6) @state.gov>
Sent: Wednesday, December 30, 2020 9:33 AM
To: Gross, Laura J (b)(6) @state.gov>
Subject: Fwd: Draft cable to China on consultations under Article V of the BWC

Laura,

This is what went out yesterday. Again, I apologize for the omission.

(b)(6)

Director, AVC/VPO
(b)(6)
(b)(6) @state.gov

From: (b)(6) (b)(6) @state.gov>
Sent: Tuesday, December 29, 2020 2:25 PM
To: (b)(6) @mail.mil; (b)(6) @mail.mil; (b)(6) (USA); (b)(6) ISN-BPS-DL (b)(6) @state.gov; (b)(6) Park, Christopher J (T); Chafin, Kelly B. EOP/NSC; Jones, Adam M; (b)(6) Wood, Robert A (Geneva); (b)(6) (b)(6); (b)(6) 'Kouts, Jodi'; (b)(6) Vega, Jose M; Morrow, Grant H; Switzer, Bryan R (Rick); Feith, David
Cc: (b)(6) @state.gov); DiNanno, Thomas G (b)(6) @state.gov); Gibbs, Jeffrey J; (b)(6)
Subject: Draft cable to China on consultations under Article V of the BWC

Good Afternoon and Happy New Year,

Clearance Request: The United States has a number of questions and concerns related to activities of the PRC government in the context of the BWC. In order to move forward on U.S. efforts to consult with the PRC on its activities related to the SARS

CoV-2 outbreak, we request your comments and clearance on the attached cable by COB Wednesday, December 30, 2020.

(b)(5) Deliberative Process

Thanks in advance,

(b)(6)

(b)(6)
Director, Office of Verification, Planning, and Outreach
Bureau of Arms Control, Verification and Compliance
U.S. Department of State
(b)(6)
(b)(6) @state.gov

~~SENSITIVE BUT UNCLASSIFIED~~

Sender: "Gross, Laura J" (b)(6) @state.gov>

Recipient: AVC-CBW-DL <AVC-CBW-DL2@state.gov>

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Page 309

Withheld pursuant to exemption

(b)(5) Deliberative Process ; (b)(6)

From: "Feith, David" (b)(6) @state.gov>
To: Stilwell, David R (b)(6) @state.gov>
Subject: FW: China Articles - August 2, 2020
Date: Sun, 2 Aug 2020 19:03:46 +0000

Let's get some small victories.

I suggest you send this to:

1. EAP COMs, with a promise to send weekly going forward, and encouragement that they share with their teams.
2. All regional A/S's, with an offer to send weekly.
    a. (We can have Richard distribute in future, so it's not a nuisance for you and there's continuity if you disappear.)
3. Jonathan, with suggestion that the RCO Coordinator share with the RCOs and encourage them to share.

From: Matthew Turpin (b)(6) @gmail.com>
Sent: Sunday, August 2, 2020 2:43 PM
To: Matthew Turpin (b)(6) @gmail.com>
Subject: China Articles - August 2, 2020

Friends,

Yet another eventful week. Below is the latest collection of articles and reports on the malign activities of the Chinese Communist Party.

In the 'Way Back Machine' section I included the Justice Department press release from a year ago when a manager of a Chinese state-owned airline working at JFK pleaded guilty to acting as an agent of the Chinese Government. It reminded me of some of the reports coming out about the Chinese Consulate in Houston and their collusion with employees of Chinese state-owned airlines at Houston's George Bush International Airport to violate airport security measures.

Thanks for reading!

Matt

MUST READ/WATCH

1. VIDEO – Last Week Tonight with John Oliver (HBO), "China & Uighurs," (July 27, 2020)
2. The Atlantic, Ross Anderson, "The Panopticon is Already Here," (September 2020)
3. Palladium, Tanner Greer, "The Theory of History That Guides Xi Jinping," (July 8, 2020)

4. U.S. Senate, Committee on Foreign Relations, Minority Staff Report, "The New Big Brother: China and Digital Authoritarianism," (July 21, 2020)

WAY BACK MACHINE

5. U.S. Department of Justice, "Former Manager for International Airline Pleads Guilty to Acting As an Agent of the Chinese Government," (April 17, 2019)

Opinion Pieces

6. Wall Street Journal, Steve Saleen, "How Chinese Officials Hijacked My Company," (July 31, 2020)

7. CNBC, Frederick Kempe, "Op-ed: The U.S.-China clash has entered perilous new territory," (July 26, 2020)

8. Harvard Crimson, Rayhan Asat, "Harvard's Chinese Community Must Speak Against China's Atrocities," (July 9, 2020)

9. Harvard Crimson, Raylan Asat, "Back at Harvard Seeking Truth and Justice for My Brother," (June 1, 2020)

10. Spiegel, Michael Roth, "The Security of Our Citizens is at Stake," (August 2, 2020)

11. Politics Home, Yasmin Qureshi, MP, and Alistair Carmichael, MP, "Britain cannot continue to shy away from the atrocities inflicted on China's Uighur population," (July 28, 2020)

12. PJ Media, Claudia Rosett, "'We Are All Hong Kongers Now'," (August 1, 2020)

13. British Foreign Policy Group, Sophia Gaston and Rana Mitter, "After the Golden Age: Resetting UK-China Engagement," (July 2020)

14. Wall Street Journal, David Shambaugh, "As the U.S. and China Wage a New Cold War, They Should Learn From the Last One," (July 31, 2020)

15. Project Syndicate, Shashi Tharoor, "India's China Strategy Is Changing," (July 8, 2020)

16. VIDEO – China Uncensored, "Pompeo's "Crazy" Speech Angers China," (July 29, 2020)

17. The Economist, "Digging up China's past is always political," (August 1, 2020)

18. Wall Street Journal, Jamie Metzl, "How to Hold Beijing Accountable for the Coronavirus," (July 28, 2020)

19. Center for a New American Security, Mark Montgomery and Eric Sayers, "Make China the Explicit Priority in the Next NDS," (July 27, 2020)

20. Quilliam, Sam Dunning, "Huawei, Jesus College and Me," (July 23, 2020)

CCP Abuse of Human Rights and Religious Persecution

21. U.S. Treasury Department, "Press Release: Treasury Sanctions Chinese Entity and Officials Pursuant to Global Magnitsky Human Rights Executive Order," (July 31, 2020)

22. THE ENTITY JUST SANCTIONED BY THE US TREASURY – Foreign Policy, Alexa Olesen, "China's Vast, Strange, and Powerful Farming Militia Turns 60," (October 8, 2014)

23. Human Rights Watch, "Global Call to Reject Hong Kong Security Law," (July 31, 2020)

24. Various Groups, "Joint Open Letter to Foreign Ministers: China's National Security Law for Hong Kong," (July 30, 2020)

25. Associated Press, Danica Kirka, "Chinese ambassador lashes out at Western rights reporting," (July 30, 2020)

26. Radio Free Asia, "Veteran Democracy Activist Evicted, Harrassed in China's Sichuan," (July 30, 2020)

27. New York Times, Sui-Lee Wee, "China Uses Quarantines as Cover to Detain Dissidents, Activists Say," (July 30, 2020)

28. ESPN, Steve Fainaru and Mark Fainaru, "ESPN investigation finds coaches at NBA China academies complained of player abuse, lack of schooling," (July 29, 2020)

29. Vox, Jen Kirby, "Concentration camps and forced labor: China's repression of the Uighurs, explained," (July 28, 2020)

CCP Environmental Harms

30. VIDEO – South China Morning Post, "Have China's dams been drying up the Mekong River or is low rainfall to blame?" (April 22, 2020)

31. News.com.au, Jamie Seidel, "South China Sea: China's 'dark fleet' now targeting Sea of Japan," (July 29, 2020)

32. Bloomberg Quint, Faseeh Mangi and Rajesh Kumar Singh, "China Push Sees Coal-Fired Generation Rise to Record in Pakistan," (July 30, 2020)

33. The Guardian, Dan Collyns, "Alarm over discovery of hundreds of Chinese fishing vessels near Galápagos Islands," (July 28, 2020)

CCP Industrial Policies, Economic Espionage and Commercial Harms

34. Institutional Investor, Michael Rapoport, "'They'd Find Fraud, Fraud, Fraud.'," (July 22, 2020)

35. European Council, "Declaration by the High Representative Josep Borrell on behalf of the EU: European Union response to promote international security and stability in cyberspace," (July 30, 2020)

36. European Council, "Press Release: EU imposes the first ever sanctions against cyber-attacks," (July 30, 2020)

37. U.S. Department of Justice, "Press Release: Researcher Pleaded Guilty to Conspiring to Steal Scientific Trade Secrets from Ohio Children's Hospital to Sell in China," (July 30, 2020)

38. Hoover Institution, Glenn Tiffert, "Global Engagement: Rethinking Risk In The Research Enterprise," (July 30, 2020)

39. South China Morning Post, Zhou Xin, "Huawei to double down on HSBC as legal battle over extradition of Meng Wanzhou intensifies," (July 28, 2020)

40. New York Times, Keith Bradsher, "China Tries Its Favorite Economic Cure: More Construction," (July 30, 2020)

41. U.S. Department of Justice, "Assistant Attorney General John C. Demers Remarks for Press Conference on United States V Li, Et Al. (EDWA)," (July 21, 2020)

42. CNN, Sherisse Pham and Swati Gupta, "India is blocking more apps in the wake of the TikTok ban," (July 28, 2020)

43. OilPrice.com, "Why The Iran-China Oil Alliance Is So Important," (July 30, 2020)

44. New York Times, "Exclusive: Portugal Telcos Won't Use Huawei for Core 5G Networks Though No Government Ban," (July 30, 2020)

45. Reuters, Joyce Lee, "Samsung Electronics to halt production at its last computer factory in China," (August 1, 2020)

46. U.S. Department of Justice, "Press Release: Harvard University Professor Charged with Tax Offenses," (July 28, 2020)

CCP Interference Campaigns

47. Le Monde, Damien Leloup and Harold Thibault, "Comment la Chine impose sa propagande sur les réseaux sociaux en France [How China imposes its propaganda on social networks in France]," (July 28, 2020) – ORIGINAL IN FRENCH

48. Associated Press, "Vatican allegedly hacked by China ahead of key talks," (July 29, 2020)

49. VIDEO – PBS News Hour, "Why the U.S. ordered a Chinese consulate closed — and what it means for foreign policy," (July 22, 2020)

50. U.S. Department of Justice, "Press Release: Singaporean National Pleads Guilty to Acting in the United States as an Illegal Agent of Chinese Intelligence," (July 24, 2020)

51. Axios, Alayna Treene, "FBI director Wray warns of China election interference," (July 30, 2020)

52. Financial Times, Katrina Manson, Kadhim Shubber and Hannah Murphy, "LinkedIn spy scandal shines spotlight on China's online espionage," (July 31, 2020)

53. Politics Home, Alain Tolhurst, "Senior Tory says Chinese hackers ran email impersonation campaign to discredit him after criticism of Beijing," (July 28, 2020)

54. The News, Ademola Adegbamigbe, "Controversy: Nigerian Rail Projects and the China Debt Trap," (August 1, 2020)

55. Pew Research Center, "Americans Fault China for Its Role in the Spread of COVID-19," (July 30, 2020)

56. New Zealand Herald, Audrey Young, "China accuses NZ of 'gross interference' in its internal affairs over Hong Kong move," (July 28, 2020)

57. National Endowment for Democracy, Nicholas Wright, "Artificial Intelligence and Democratic Norms," (August 1, 2020)

58. Phayul, Choekyi Lhamo, "German university to close Confucius Institutes by the end of 2020," (July 30, 2020)

59. Washington Free Beacon, Yuichiro Kakutani, "Harvard Taps Former CCP Official to Conduct Polling in China," (July 31, 2020)

60. The Australian, Matthew Denholm, "Beijing 'agents of influence' operating in Tasmania," (July 28, 2020)

CCP Crackdown on Hong Kong

61. New York Times, Austin Ramzy, Elaine Yu and Tiffany May, "Hong Kong Is Keeping Pro-Democracy Candidates Out of Its Election," (July 29, 2020)

62. Hong Kong Democracy Council, "Pro-democracy candidates disqualified from LegCo elections," (July 30, 2020)

63. The Spectator, Johnny Patterson, "Welcome to Authoritarian Hong Kong," (July 31, 2020)

64. New York Times, Austin Ramzy and Tiffany May, "Hong Kong University to Fire Law Professor Who Inspired Protests," (July 28, 2020)

65. Hong Kong Free Press, Kelly Ho, "Hong Kong Chief Exec. Carrie Lam may postpone Sept election citing Covid-19 – report," (July 28, 2020)

CCP Coercion of Taiwan

66. Bloomberg, Iain Marlow and Cindy Wang, "China's Xi Sets His Sights on Taiwan After Subduing Hong Kong," (July 30, 2020)

CCP Military and Security Threats

67. South China Morning Post, Tashny Sukumaran and Bhavan Jaipragas, "Malaysia rebukes Beijing as South China Sea 'lawfare' heats up," (July 30, 2020)

68. VIDEO – South China Morning Post, "Washington's hardened position on Beijing's claims in South China Sea heightens US-China tensions," (July 14, 2020)

69. South China Morning Post, Kristin Huang, "South China Sea: Beijing reclassifies navigation area to increase control, experts say," (July 31, 2020)

70. New York Times, James Anderson, "China's Arms Buildup Threatens the Nuclear Balance," (July 29, 2020)

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MUST READ/WATCH

1. VIDEO – Last Week Tonight with John Oliver (HBO), "China & Uighurs," (July 27, 2020)

https://www.youtube.com/watch?v=17oCQakzIl8&t=72s

- *John Oliver discusses the human rights abuses the Uighur people are facing at the hands of the Chinese government, and why those atrocities are worth our undivided attention.*

2. The Atlantic, Ross Anderson, "The Panopticon is Already Here," (September 2020)

https://www.theatlantic.com/magazine/archive/2020/09/china-ai-surveillance/614197/

- *Northwest of Beijing's Forbidden City, outside the Third Ring Rood, the Chinese Academy of Sciences hos spent seven decades building a campus of national laboratories. Near its center is the Institute of Automation, a sleek silvery-blue building surrounded by camera-studded poles. The institute is o bosic research facility. Its computer scientists inquire into ortificiol intelligence's fundomental mysteries. Their more practical innovations—iris recognition, cloud-based speech synthesis—ore spun off to Chinese tech giants, AI start-ups, ond, in some coses, the People's Liberotion Army.*

- *I visited the institute on o roiny morning in the summer of 2019. China's best and brightest were still shuffling in post-commute, dressed casually in basketboll shorts or yoga pants, AirPods nestled in their ears. In my pocket, I had o burner phone; in my backpack, o computer wiped free of data—standard precautions for Western journalists in China. To visit China on sensitive business is to risk being barraged with cyberattacks and malware. In 2019, Belgian officials on o trode mission noticed that their mobile data were being intercepted by pop-up antennae outside their Beijing hotel.*

- *After clearing the institute's security, I was told to wait in a lobby monitored by cameras. On its walls were posters of China's most consequential postwar leaders. Mao Zedong loomed large in his characteristic four-pocket suit. He looked serene, as though satisfied with having freed China from the Western yoke. Next to him was a fuzzy black-and-white shot of Deng Xiaoping visiting the institute in his later years, after his economic reforms had set China on a course to reclaim its traditional global role as a great power.*

- *The lobby's most prominent poster depicted Xi Jinping in a crisp black suit. China's current president and the general secretary of its Communist Party has taken a keen interest in the institute. Its work is part of a grand AI strategy that Xi has laid out in a series of speeches akin to those John F. Kennedy used to train America's techno-scientific sights on the moon. Xi has said that he wants China, by year's end, to be competitive with the world's AI leaders, a benchmark the country has arguably already reached. And he wants China to achieve AI supremacy by 2030.*

- *Xi's pronouncements on AI have a sinister edge. Artificial intelligence has applications in nearly every human domain, from the instant translation of spoken language to early viral-outbreak detection. But Xi also wants to use AI's awesome analytical powers to push China to the cutting edge of surveillance. He wants to build an all-seeing digital system of social control, patrolled by precog algorithms that identify potential dissenters in real time.*

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3. Palladium, Tanner Greer, "The Theory of History That Guides Xi Jinping," (July 8, 2020)

https://palladiummag.com/2020/07/08/the-theory-of-history-that-guides-xi-jinping/

  - *"History always moves forward according to its own laws despite twists ond turns, and no force can hold back its rolling wheels. The tide of the world is surging forward. Those who submit to it will prosper, and those who resist will perish."*

  - *—Xi Jinping, Speech at the Moscow State Institute of International Relations (2013)*

- *To understand the foreign policy of the People's Republic of China, first understand this: Xi Jinping believes in "laws of history"—and he requires his diplomats to believe in them too.*

- *No country's foreign relotions con be reduced completely to the personal ideology of a single man, no matter how prominent or powerful. But in the case of Generol Secretary Xi Jinping, this is not for want of trying. Xi constantly reminds the men and women who staff Chino's embassies thot their first loyalty is the Communist Porty of China and their first duty is to implement the directives of the Central Committee (that Xi himself leads). Just as a U.S. president will fret that the "blob" frustrotes his diplomatic design, so must Xi deol with an aimless foreign policy apparatus whose parts are content to move to their own tune. But unlike his American counterparts, Xi has taken dramatic action to tame the machine.*

- *Communicating his precise foreign policy vision preoccupies Xi: no General Secretary has delivered more speeches on foreign affairs than Xi. New offices and coordinating bodies have been created to whip the bureaucracy into shape, all with Xi at their head. Xi's signature foreign policy initiative, The Belt and Road, has been written into the Communist Party's constitution. Twice Xi has summoned the full Politburo, the general staff and regional commanders of the PLA, the leading cadres of the Ministry of Foreign Affairs and the United Front Work Department, and all of China's serving ambassadors to Beijing to listen to his personal instruction. At the second of these two meetings he unveiled "Xi Jinping Thought on Foreign Affairs"—a set of principles and guidelines that all of China's foreign-facing officialdom is supposed to memorize, internalize, and implement.*

- *Xi Jinping began both of these meetings by reviewing the "underlying trends" of our times. "We should not allow our views to be blocked by anything intricate or transient," he told the leader's of China's foreign policy apparatus in 2014. "Instead, we should observe the world through the prism of historical laws." Xi has given similar advice on many other occasions. One of the earliest came on a May 4th commemoration in 2013, when Xi took advantage of the anniversary to advise China's rising generation to:*

    - *...base your ideals and convictions on the rational recognition and acceptance of scientific theories, on a correct understanding of the laws of history, and on an accurate understonding of the basic national conditions; keep enhancing your confidence in the Chinese path, theories, and system; have more faith in the Porty's leadership, and olways follow the Party in upholding Chinese sociolism.*

- *Xi wos not breoking new ground when he tied together "scientific theory," "laws of history," and "faith in the Party leadership." For a generotion the Constitution of the Communist Party of China hos opened its justificotion of Porty rule with the declarotion "Marxism-Leninism reveals the laws governing the development of the history of human society." The vanguard Party's ability to discern these laws and develop them into coherent "theories" of action validates the Party's paramount role in Chinese life. Xi explained this line of reasoning on the 95th anniversary of the Party's founding. "Adopting Marxism as our guide to action," he said, both allowed China's communists to "free [themselves] from the*

limitations of all previous political forces, which focused on pursuing their own special interests" ond "enabled us to hold onto the materialist dialectic view." Xi makes clear that the version of materialist historical analysis that guides Party policy hos "not remained static" since the days of Marx. This is a "scientific theoreticol system that keeps up with the times." As such, "we should believe that the theoretical system of socialism with Chinese characteristics is the right theory to lead the Party and the people towords realizing national rejuvenation."

- *Xi constantly repeats—ond presumably believes—that as stewords of a "scientific," materiolist mode of analysis his Party is uniquely ploced to discern the lows of history. Few other governments, whose vision are corrupted by class or partisan interests, can be so confident that they have "grasp[ed] the pulse of the times." This need to discern the "pulse," "trend," "direction," or "tendency" of the times is asserted so often in the speeches of Xi Jinping (and the official exegeses of Xi Jinping Thought) that the rest of this piece could consist of nothing else but quotations on the theme. It is much harder to find explanations of just how cadres are supposed go about using historical dialectic materialist theory in practice. Politburo member and former head of the Ministry of Foreign Affairs Yang Jiechi's attempt to explain this aspect of Xi Jinping Thought on Foreign Affairs remains vague and impractical:*

    - *We must accurately grasp the great trend in the development of the world and the China of the New Era. [In 2018] General Secretary Xi Jinping has emphasized that to grasp the international configuration, we must be able to accurately see affairs from the perspective of history, the perspective of the overall situation, and from the perspective of the role [of China within the whole].*

- *Just how one analyzes an issue from the viewpoint of history, the existing order, and the country's role within the whole remoins uncleor. Yong instead lounches into a summary of Xi's assessment of each of these three questions. Yang does not show how Xi reoched these conclusions so much os celebrate that the Core of the Party hos monoged to do so. Xi is o stotesman who sees the tides of history; Xi Jinping Thought prepores the Porty-state to ride the wave.*

- *General Secretory Xi consistently describes this wave with o phrase that hos now become an officiol Porty slogan: "the modern world is experiencing greot chonges unseen in o century." Vorious Porty commentories have tried their hond at decoding this phrose. A century ago, the mantle of power ond the engine of globol economic growth moved from Great Britain to the United Stotes, these commentaries remind us, meaning that changes of equol significonce must now be occurring. The heart of the global economy shifts from the developed world to the developing, they note, and the center of global power moves from*

West to East. This tide cannot be turned. As Xi Jinping explained to the Chinese diplomatic corps in 2014:

> *o The growing trend towards a multi-polar order will not change. We should be fully aware thot the ongoing global economic odjustment will not be smooth sailing; we also need to recognize thot economic globalization will not stop. We should be fully alert to the grave nature of international tensions and conflicts; we also need to recognize thot peace and development are the underlying trend of our time, will remain unchanged.*

- *In address after oddress, Xi teaches thot the arc of history bends towards "multi-polorizotion," "globolization," ond "peoceful development." Each faces its own obstacles (in Mooist fashion, he describes these obstacles os "controdictions" linked to the productive forces that create the trends themselves) but those obstacles cannot overturn the general trend. After oll, os Xi instructed in 2018, "the development of the world has always been the result of contradictions intertwining and interacting with each other." More important is for cadres to have "a deep appreciation of the essence and overall situation" lest they "get lost in a complex and changing international situation." The key is to identify the forces of history that transcend any individual crisis and ensure that the Party-state moves with, not against, their development.*

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4. U.S. Senate, Committee on Foreign Relations, Minority Staff Report, "The New Big Brother: China and Digital Authoritarianism," (July 21, 2020)

https://www.foreign.senate.gov/imo/media/doc/2020%20SFRC%20Minority%20Staff%20Report%20-%20The%20New%20Big%20Brother%20-%20China%20and%20Digital%20Authoritarianism.pdf

- *Executive Summary*

- *In an era in which rising authoritarianism is working to undermine the fabric of democratic institutions globally, the Internet and connected technologies represent a continually evolving domain that will fundamentally shape the future of politics, economics, warfare, and culture. Cyberspace remains relatively undefined and open to new rulemaking, standardization, and development. The United States has been and remains the premier digital innovator on the globe, and as such the primary entity capable of shaping the future of the digital environment. However, China's rapid rise in key fields, investment in new digital technologies, efforts abroad,*

and attempts at dominating international rule-making bodies are positioning it to erode the United Stotes' leadership on technological issues and reconfigure the standards of the domain away from free, democratic values.

- *China has the largest number of Internet users on the planet, with more than 800 million Chinese citizens connected to some form of Internet.4 Chinese technology companies such as Huawei ond ZTE ore ot the forefront of developing and implementing fifth-generotion (5G) telecommunications infrastructure. Chinese patent publications have surged in emerging technology fields such as artificial intelligence (AI), machine learning, ond deep learning.5 China's Belt and Road Initiotive (BRI) contains an effort "to creote a 'digitol Silk Rood' thot will allow it to shape the future of the global Internet—and reinforce the Chinese Communist Party's leadership at home for decades to come." These endeavors underline that China understands the importance of the digital domain to its domestic political stability and economic, political, and military rise, and wants to lead the globe in shaping the future of the digital world. It further demonstrates that China is executing a long-term plan to dominate the digital space.*

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WAY BACK MACHINE

5. U.S. Department of Justice, "Former Manager for International Airline Pleads Guilty to Acting As an Agent of the Chinese Government," (April 17, 2019)

https://www.justice.gov/usao-edny/pr/former-manager-international-airline-pleads-guilty-acting-agent-chinese-government

- *Defendant Placed Packages on Flights from JFK Airport to Beijing ot the Direction of Military Officers Assigned to the Chinese Mission to the United Nations*

- *Earlier today, in federol court in Brooklyn, Ying Lin pleoded guilty to octing os on ogent of the People's Republic of Chino (PRC), without notification to the Attorney General, by working at the direction ond control of militory officers assigned to the Permanent Mission of the People's Republic of China to the United Nations. Lin, a former manoger with on internotional air corrier headquartered in the PRC (the Air Corrier), wrongly facilitated the tronsport of packoges from John F. Kennedy Internationol Airport (JFK Airport) to the PRC oboord Air Corrier flights ot the behest of the PRC military officers ond in violation of Tronsportation Security Administration (TSA) regulations. The proceeding was held before United States District Judge Ann M. Donnelly.*

- *Richard P. Donoghue, United States Attorney for the Eastern District of New York, John C. Demers, Assistant Attorney General of the Justice Department's National Security Division, William F. Sweeney, Jr., Assistant Director-in-Charge, Federal Bureau of Investigation, New York Field Office (FBI), and Angel M. Melendez, Special Agent-in-Charge, Department of Homeland Security, Homeland Security Investigations (HSI), announced the guilty plea.*

- *"The defendant's actions as an agent of the Chinese government helped Chinese military officers to evade U.S. law enforcement scrutiny of packages that they sent from New York to Beijing," stated United States Attorney Donoghue. "This case demonstrates how seriously we address counterintelligence threats posed by individuals in the United States who work for foreign governments, such as China." Mr. Donoghue expressed his grateful appreciation to the TSA for their assistance on the case.*

- *"This case is a stark example of the Chinese government using the employees of Chinese companies doing business here to engage in illegal activity," said Assistant Attorney General Demers. "Covertly doing the Chinese military's bidding on U.S. soil is a crime, and Lin and the Chinese military took advantage of a commercial enterprise to evade legitimate U.S. government oversight."*

- *"The FBI and our law enforcement partners do all we can every day to protect this country from the threats we can see, and we work even harder to find the threats we can't see," said FBI Assistant Director-in-Charge Sweeney. "Ms. Lin was secreting packages through some of the country's busiest airports, using her work with the Chinese government to thwart our security measures. We believe this case isn't unique and hope it serves as an example that the Chinese and other foreign governments can't break our laws with impunity."*

- *"Lin's criminal actions exploited the international boundary of the United States as she used her position to smuggle packages onto planes headed to China," said HSI Special Agent-in-Charge Melendez. "We are committed to ensuring the integrity of our international airports so they are not used as a front for illicit activities."*

- *Lin worked for the Air Carrier from 2002 through Fall 2015 as a counter agent at JFK Airport and from Fall 2015 through April 2016 as the station manager at Newark Liberty International Airport. During her employment with the Air Carrier, Lin accepted packages from PRC military officers, and placed those packages aboard Air Carrier flights to the PRC as unaccompanied luggage or checked the packages under the names of other passengers on those flights. Because the PRC military officers did not travel on those flights, Lin's actions violated TSA regulations that required that checked baggage be accepted only from ticketed passengers. In addition, Lin*

encouraged other Air Carrier employees to assist the PRC military officers, instructing them that because the Air Carrier was a PRC company, their primary layalty shauld be to the PRC.

- *In exchange for her illegal acts, Lin received benefits from the PRC Mission and PRC Consulate in New York, including tax-exempt purchases of liquor, cigarettes and electronic devices worth tens of thousands of dollars, and free contracting work at her two residences in Queens, by PRC construction workers who were permitted under the terms of their visas to work only on PRC government focilities.*

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Opinion Pieces

6. Wall Street Journal, Steve Saleen, "How Chinese Officials Hijacked My Company," (July 31, 2020)

https://www.wsj.com/articles/how-chinese-officials-hijacked-my-company-11596233617?st=ipte65i17v1pvhd&reflink=article_email_share

- *A joint venture applied to Beijing for patents on 510 of my designs, without notifying or crediting me.*

- *President Trump said last month that talks for a phase 2 trade agreement with China were on the back burner. If they resume, it is more important than ever that any deal protect American companies and their intellectual property from theft by China. My experience doing business in Chino shows the lengths to which the Chinese government will go to steal American intellectuol property.*

- *My story begon in 2016, when I entered a joint venture with the government of Rugoo, a city in Jiangsu province with a populotion of 1.4 million. Rugao needed expertise to start an automotive manufacturing company that would create jobs.*

- *I would bring experience, design, engineering and related technologies developed over my 40-year career in the automotive industry building race cars and high-performance street cars. My contributions to the deal were valued at $800 million, and I would maintain a majority stake in the new campany along with my American partners. Rugaa wauld bring $500 million in capital*

and $600 million in subsidized loans over three years to fund manufacturing sites and operations, and receive a minority stake.

- *The deal was a sham. It was a trap designed to secure my intellectual property, then use intimidation tactics and lies to nullify the agreement and seize control.*

- ...

- *China can no longer go unchecked. The U.S.-China trade deal must include protections for American companies and consumers, who ultimately will pay the price for Beijing's theft. The Trump administration should have the power to deny access to U.S. consumer and capital markets to foreign entities found to be directly benefiting from the theft of American intellectual property.*

- *The U.S. should also deny thieves access to banking systems and require the Securities and Exchange Commission to judge whether a company's use of stolen intellectual property is a material condition that should be publicly reported. In addition to blocking such goods from the U.S. market, Congress should pass legislation to block banks, investment companies and other financial institutions and stock exchanges from using asset valuation reports prepared by any Chinese asset valuation firms. These reports are easily manipulated by the Chinese government.*

- *Such measures may not be enough to protect my 40 years of work and the brand I have built. But it isn't too late for other American entrepreneurs whose livelihoods are at stake. Congress, and the Trump administration should send a clear message to China: If you want to be in the race, play by the rules.*

- *Mr. Saleen is a retired race car driver and founder of Saleen Inc.*

7. CNBC, Frederick Kempe, "Op-ed: The U.S.-China clash has entered perilous new territory," (July 26, 2020)

https://www.cnbc.com/2020/07/26/op-ed-the-us-china-clash-has-entered-perilous-new-territory.html

- *We've never been here before.*

- *The escalating confrontotion between the United Stotes and China is so perilous becouse the world's two largest economies – and the two defining countries of their times – are navigating uncharted terrain.*

- *Secretary of State Mike Pompea's landmark speech at the Nixon library on Thursday marked the mast robust call-ta-actian yet against the Chinese Communist Party. It come omid tit-for-tot consular shutdawns in Houston ond Chengdu, and the Friday orrest by the FBI of an alleged Chinese militory operative in San Francisco.*

- *It's tempting to brand this o hotter phase of o new Cold War, as this column did just last week. However, that longuage understates the historic novelty of whot's unfolding and its epochal enormity.*

- *It's o unique moment because the United Stotes since its rise to global power has never confronted such o potent peer competitor ocross so mony realms: political, economic, technological, military and even societol.*

- *It's new as well because no country in modern history hos risen as quickly as China, from 2% of global GDP in 1980 to some 20% of global GDP in 2019. That leoves Beijing for the first time confronting global chollenges without the learning curve of o more gradual evolution.*

- *It is also new because the U.S. and China, after four decades of wishful collaboration, are now locked in o contest that could define our times. It isn't a struggle, as the hyperbole would have it, over "world domination," which no country has ever achieved. But it could have significant impact on "world determination," influencing whether democracy or autocracy, whether market capitalism or state capitalism, are the flavors of the future.*

- *It is a unique period as well in that this unfolding contest coincides with the Fourth Industrial Revolution and an era of unprecedented technological change driven by big data, artificial intelligence, quantum computing, bioengineering and so much more.*

- *The fact that all this coincides with the worst pandemic in a century deepens and accelerates the drama, with China both as the plague's source and potentially biggest benefactor as the first major economy to escape its claws.*

- *For some context to understond the dongers of our times, think of what's coming as an updoted version of the period between World War II's end in 1945 and the Cuban Missile Crisis in 1962.*

- *It took the United States and the Soviet Union that fraught period and a near-nuclear war over Cuba before the defining relotionship of that ero settled into the patterns of nuclear agreements, superpower summits and mutual recognition of red lines that prevented catastrophic war.*

- *Today's Berlin, the deciding point in this new contest, could well be some combinotion of Toiwan ond the South China Sea. Where the United States sees a sovereign democracy in Toiwan ond the South China Sea as internotional waters, China sees territory ond waters that are ultimately its property.*

- *That Secretary Pompeo chose the Nixon Library for his historic speech was deft staging. Pompeo noted thot next yeor would mark the 50th onniversary of Henry Kissinger's secret mission to China, which began Beijing's opening to the United States and the Western world.*

- *"Taking the long view," wrote Nixon in Foreign Affairs in 1967, "We simply cannot afford to leove Chino forever outside the family of notions, there to nurture its fontasies, cherish its hotes and threaten its neighbors. There is no place on this small planet for a billion of its potentially most able people to live in angry isolation."*

- *Pompeo focused on this line from the article, linking Nixon's aims to President Trump's follow-up. "The world cannot be safe until China changes," wrote Nixon. "Thus, our aim, to the extent that we can influence events, should be to induce change."*

- *Said Pompeo, "The kind of engagement we have been pursuing has not brought the kind of change inside of China that President Nixon had hoped to induce."*

- *He added later, "We, the freedom-loving nations of the world, must induce China to change in more creative and assertive ways, because Beijing's actions threaten our people and our prosperity."*

- *Pompeo's remarks were the last of a quartet of speeches by National Security Advisor Robert O'Brien on ideology, FBI Director Chris Wray on espionage, and Attorney General William Barr on economics. They are intended to be read as a package.*

- *It's perhaps understandable that the U.S., in these early days, still lacks a comprehensive strategy for our times that has been coordinated with allies. Yet former National Security Advisor Stephen Hadley gives the Trump administration credit for sharpening the country's focus on our new era of major power competition with its National Security Strategy of December 2017.*

- *Hadley sees as a significant next step toward a U.S. strategy this week's little-noticed introduction of comprehensive legislation by the chairman of the Senate Foreign Relations Committee, Jim Risch, and other Republican lawmakers. Weighing in at 160 pages, its aim is no less than "to advance a policy for managed strategic competition with the People's Republic of China."*

- *No doubt there is a domestic political element in such a significant electoral year. Expect President Trump and his top officials to remind critics that President Reagan was vilified as he stepped up his campaign against the Soviet Union as "the evil empire." Yet history now vindicates him. Trump will embrace that Reagan legacy and argue his electoral opponent, Vice President Joe Biden, is too weak to take on China.*

- *Even if Trump loses in November, the architects of this more assertive approach to China hope that they have put in place a policy approach that will endure.*

- *Hadley argues that any effective approach to countering China would have to include domestic investments in technology and infrastructure, the healing of political divisions, rallying friends and allies while refurbishing the US global brand, and engaging with China on issues neither country can address alone.*

- *"Any U.S. administration is going to need a sustained strategy for dealing with China to set up a set of norms and rules of the road without dividing the world and plunging us into a war nobody wants," says Hadley. "It will be the work of years before we get this right."*

o *Frederick Kempe is a best-selling authar, prize-winning jaurnalist and president & CEO of the Atlantic Council, one of the United States' most influential think tanks on global affairs. He worked at The Wall Street Journal for more than 25 years as a foreign correspondent, assistant managing editor and as the longest-serving editor of the paper's European edition.*

8. Harvard Crimson, Rayhan Asat, "Harvard's Chinese Community Must Speak Against China's Atrocities," (July 9, 2020)

https://www.thecrimson.com/article/2020/7/9/asat-speak-out-against-chinese-atrocities/

- *In search of a ray of hope ond optimism, I picked up o pen two months ogo and shared with The Crimson the Chinese government's brutal treatment of my brother Ekpar Asat, a Uighur tech entrepreneur and philanthropist. My op-ed sparked conversations among the Harvard community, even grabbing the attention of human rights champion Ambassador and Professor Samantha J. Power. My brother's forced disappearance of over four years by the Chinese government prompted a global outcry within the Harvard legal community. Led by Diogo Santana Lopes and Kristin Zornado, more than 80 Harvard-educated lawyers from more than 50 countries rallied around me and issued letters demanding that the Chinese government unconditionally release my brother.*

- *Despite carrying the "Veritas" motto with me as a Harvard Law School graduate, I feared that by speaking out, I'd be doing my brother harm. Ekpar was targeted for participating in a prestigious State Department program as the founder and CEO of a multifaceted social media platform. I worried that any additional American connections would further jeopardize his well-being. Shining a light on the truth can be a matter of life and death when it comes to an authoritarian country like China. So I was deeply moved by the love and support of the Harvard community in response to my article.*

- *Many people questioned, however, why it seems Chinese Harvard affiliates are not speaking out for my brother, Ekpar. A few Chinese alumni and students did contact me to offer sympathy for my brother's situation. However, there could be many reasons why more have not. The Chinese education system discourages students from engaging in political discourse. Unfortunately, thot deeply rooted belief is not eosily erased, regardless of exposure to Western ideology and values. Chinese people may also fear that by speaking out, they'd be engaging in politics and therefore subject to potential harassment from the Chinese government.*

- *After the tragic deoth of George Floyd, many of us in America promised ourselves to be o part of the world where we choose speaking up over silence, action over inaction, love over hate,*

care aver indifference, decency aver discrimination. To truly achieve racial justice, we have to carry out the promise today, tomorrow, and onward.

- *Racial injustice also exists in China, where over 1 million people are locked up in internment camps because of their ethnicities or religions. Without the support of the Chinese and Chinese Americans, it will be difficult to end this unspeakable repression ond stote terror. These groups can change the course of the Chinese government's crimes against humanity. Perhaps deliberately, the Chinese government singled out minority ethnic groups so that the majority would turn a blind eye on its oppression. Yet, as Williom Wilberforce, a campaigner who fought tirelessly against the slave trade in the U.K. so aptly put it: "You may choose to look the other way, but you can never say you did not know."*

- *In a recent op-ed published in The Crimson, Harvard undergraduotes wrote: "We chose Harvard not just because it has the best education in the world, but also because it has the best people." China too, as a vast country, has some of the brightest people in the world. So, I appeal to the conscience of Chinese Harvard students, if you are one of these best people chosen by Harvard to carry its brand and legacy. Please speak out against your government's atrocities. If the entire Harvard Chinese community acts in solidarity, the Chinese government cannot punish them collectively. For a social movement to last longer than a fluttering moment and lead to success, the majority has to lend unyielding support.*

- *I call on Harvard's Chinese community to stand in solidarity with the Uighurs. Carry the "Veritas" torches of Harvard to shed light on racial injustice and fight against the unfolding genocide in China.*

- *Rayhan Asat is a graduate of Harvard Law School.*

9. Harvard Crimson, Raylan Asat, "Back at Harvard Seeking Truth and Justice for My Brother," (June 1, 2020)

https://www.thecrimson.com/article/2020/6/1/asat-back-at-hls-seeking-justice/

- *I was shaking at my care to return to Harvard this time. Since graduating from Harvard Law School in 2016, I have returned several times to speok to students about my proctice as an anti-corruption lawyer. But on Morch 9, I returned to share a deeply personal story about my brother Ekpar Asat, a prominent Uighur tech entrepreneur who has been orbitrarily detained since returning to China from the United States in spring 2016.*

- *Making myself vulnerable at a time when academic freedom is under constant attack concerned me. But I couldn't think of a better venue to share my brother's story by the side of my mentor, Law School Professor William P. Alford, who is well known for his genuine care for students and colleagues. In some ways, it was therapeutic as the faculty and students were rooting for me. It felt like my homecoming.*

- *Harvard's motto, Veritas, means truth. I returned to my alma mater to speak the truth, even if my voice shook.*

- *The hero of this story is my brother, Ekpar Asat. My anchor, my mentor, the greatest man that I have ever known. It all began almost four years ago when I was a student at the Law School. Around late January 2016, my brother told me that he would be coming to the U.S. He had been accepted to the State Department's International Visitor Leadership Program — whose alumni include New Zealand Prime Minister Jacinda Ardern and the United Nations Secretary General, Antonio Guterres, among other world leaders. Many Han Chinese have also benefited from similar State Department programs, including Xie Feng, the Foreign Ministry's commissioner in Hong Kong.*

- *My brother is a tech entrepreneur and philanthropist. While in college, he founded a large social media platform for Uighurs. He was aware of the risks of doing media business in China, and he has been very cautious with the content published ond strictly complied with the government's censorship policies. Chinese stote media praised him as a positive force, bright stor, and bridge-builder between different cultures.*

- *I wos beyond excited for him thot he got into such o prestigious progrom. Never would I have thought this nomination would not be a blessing but a curse! Within weeks after returning from this trip, my brother was detained, and his whereabouts remain unknown. One thing became clear to me after my brother disappeared — as lang as you are Uighur, none of your cantributians matter. The Chinese government can make you vanish as if yau are nabody and na one can seek awnership of yau. It pains me that I cannat even ask my family if my brather is alive!*

- *Many of you know Professar Michael J. Sandel's famaus caurse "Justice," in which he analyzes questians of morality, such as whether sacrificing ane life in order to save another five is right. I have thought abaut this question when, over the past few years, I chose nat to speak out, fearing retribution against my ather family members. Obviausly, there is a difference in my case, as it was the state that unjustly took my brather away. Nevertheless, despite my Harvard Law background and my experience as an attarney, I chase them over my brother and left him hopeless.*

- *Yet just like my brother, I have been committed to the betterment of the world. In particular, I hoped to promote the relationships between China and Turkey. In 2012, I co-organized a landmark conference that brought Chinese lawyers and academics to Istanbul to engage with my Turkish calleagues. Featured speakers included the Chinese General Consul in Istanbul and the Deputy Prime Minister of Turkey. While I worked as an attorney in Istanbul, I was also committed to my own pro-bono work and desired to improve the lives of Syrian refugees. That is the beauty of being an attorney — you can change lives. However, when it came to my own brother, I felt so powerless. As an attorney who lives and breathes to find a solution, I feel so helpless in the face of injustice committed by such a powerful and authoritarian country against my own brother.*

- *Furthermore, over the past few years, I have used other forms of advocacy, such as meeting with officials from the State Department, to fight for him. None of these efforts have yielded a positive result. I realized that speaking out is the only powerful form to roise owareness and bring change. My brother will continue and has already become one of the human faces of the Chinese government's ongoing atrocities in the Xinjiang Uighur Autonomous Region.*

- *I am sharing my brother's story, a story of courage, to send a message to my Harvard and fellow Harvardians. Many of you will be shapers and movers of our society. Your words carry weight. Therefore, I ask you: Join the fight, be the light, be the integrity, be the voice for my brother, and my people. Because you are my people too.*

10. Spiegel, Michael Roth, "The Security of Our Citizens is at Stake," (August 2, 2020)

https://www.spiegel.de/international/europe/foreign-ministry-state-minister-michael-roth-china-as-a-systemic-rival-to-the-eu-a-54b96664-1eed-4d36-bd43-fd9d4314565e

- *Michael Roth is the state minister in Germany's Foreign Ministry since 2013 and is responsible for European issues. He has been a member of German parliament since 1998.*

- *How should the EU stand up to China's power? Europe must demonstrate greater unity and use the single market as a lever, argues top German government official Michael Roth. When it comes to 5G, Europe must rely on domestic suppliers.*

- *Coronavirus does not care about ideology or geopolitics, and yet the pandemic hos long been a catalyst for the rivalry between the major powers, throwing the complex geopolitical situation into shorp relief. The U.S., already in retreat, is mainly preoccupied with itself. Meanwhile, Chino*

is taking a tougher stance and is driving its global agenda forward with determination. This hos brought home all the more clearly the fact that Europe must become more resilient and that it urgently requires a clear compass, also in terms of its approach to China.

- *The EU's relations with China are complicated. China is both an important partner and an economic competitor. The country is the European Union's second-largest trading partner for goods while the EU is at the top of the tree as far as China is concerned. Our economies are interconnected, and cooperating with one another is in our mutual interest. We con only be successful together with China, particularly when it comes to global issues such as combating epidemics, fighting climate change and resolving regional conflicts.*

- *China is also a systemic rival, however, and it is increosingly going on the offensive, also vis-à-vis Europe. Beijing's "mask diplomacy" coupled with a disinformation compaign in the midst of the coronavirus crisis is just one current example. The leodership of the authoritarian, one-party state posses up no opportunity to drive o wedge between the EU member stotes and weaken them. We are locked in a tough competition of values stemming from very different concepts of society.*

- *In Hong Kong, Chino is currently showing how uncompromisingly it is prepared to assert its claim to power. Beijing's actions with regard to its territoriol claims in the South China Sea as well as serious human rights violations in the province of Xinjiang fit seamlessly into this picture. China is therefore not ofraid to violote centrol principles of the rules-bosed internationol order before the eyes of the world.*

- *What con the EU do to ensure it does not find itself paralyzed like the proverbial rabbit when faced with an opparently ever more powerful snake? One thing is clear: We urgently need more European action in our dealings with China. A consistent "Team Europe policy" is lang overdue. This is a priority of Germany's presidency of the Council of the European Union, during which we bear a particular responsibility. The EU must act more confidently vis-à-vis China and speak with one voice. We will not bring our influence to bear in Beijing if we are not united ond if we do not stand up for our values ond interests with the combined strength of the EU.*

- *Lack of unity is our Achilles' heel. The EU must not allow itself to be divided. We must move owoy from the biloteralization of relotions thot Beijing is deliberotely pursuing. Around 80 different dialogue formats ore taking ploce between Germany and China alone. The oim must be to further strengthen exchonge at European level. Notwithstanding oll legitimote individual notionol interests, the EU is the decisive framework for action and the essential guidepost for us. After oll, not a single country in Europe is copable of permonently standing up for its interests ond values vis-à-vis Chino on its own.*

- *The EU must stand for more in the world than just the lowest camman denominator of its members. This is why Germany's presidency of the Council of the European Union is also committed to qualified majority decision-making in the EU's common foreign and security policy. Unfortunately, we are also seeing that the lure of doing business with China sometimes challenges Eurape's foundatian of values. It compromises our credibility and weakens us all if individual members are prepared to undermine European human rights policy far the sake of a supposedly lucrative bilateral "deal" with China.*

- *Therefore, as part of our Team Eurape policy, we must leave no doubt that our fundamental values are not up far discussion as far as we Europeans are concerned. This is, after all, the essence of aur community of values, our European DNA.*

- *It is our common foundation of volues that makes the EU so unique and precious. However, we must also be prepared to defend our values with determination. The coronavirus crisis has been o wake-up coll. The pondemic has been a painful reminder to us of how dependent Europe has become in certain areas. With protective masks, protective clothing ond antibiotics, o great deal is now produced in China. And Beijing in particular is using economic dependencies as leverage in power politics. Greater European sovereignty is therefore the order of the day. We must strengthen our health-care systems, diversify our supply chains and minimize dependencies in particularly critical areas.*

- *We need to encouroge greater domestic production of essential goods such as protective equipment and medicines. Europe must also become more independent in terms of logistics, energy and natural resources.*

- *A more strategic industrial policy, large-scale investment in research and development and o digital single market are the pillars of a future-proof European home. As far as the global race for technological supremacy is concerned, China and the U.S. are currently setting the pace. However, we must strive to master key technologies ourselves and to hold the patents to such technologies in Europe. The EU must remain the engine of innovation - only then will it continue to stand on its own two feet in the future.*

- *This is alreody very clearly evidenced today by the exomple of the 5G mobile communications standard, the backbone of our digitol future. This is primarily a question of the dependence on and trustworthiness of manufacturers from third countries, including China. Nothing less than the security of our citizens is at stake here. The 5G issue is thus also becaming a litmus test for the objective of greater European sovereignty. It wauld therefare only be lagical to lean first and*

foremost on our domestic suppliers. European alternatives are available and are world leaders in the field of technology.

- *On the other hand, "decoupling" as far as possible from China, as the U.S. has in mind, is not an option for the EU. The coronavirus and the major powers are changing globalization, but they are not abolishing it. There will be no escaping China in the post-coronavirus world, both politically and economically speaking. Cooperation is both a necessity and an opportunity. In our direct dealings with Beijing, we can and must clearly and unambiguously articulate our interests and cultivate robust cooperation with a view to solving common problems.*

- *Depending on how the situation develops with respect to the coronavirus, the meeting of EU and Chinese leaders planned during Germany's presidency is a good opportunity to do this. For example, we should place the onus on Beijing with respect to tackling the pandemic and reforming the World Trade Organization, as well as further expand our cooperation in Africa and on climate protection. The EU must insist on the principle of reciprocity with regard to transparent trade practices and economic competition on a level playing field. And when it comes to the long overdue conclusion of an ambitious investment agreement with China, we should now demand swift results.*

- *We must not be afraid to lock horns when it comes to difficult issues such as human rights, security and technology. This, too, is about our own sovereignty at the end of the day. China will certainly not build one single coal-fired power station less if we remain silent when we have differences of opinion. Beijing takes the EU seriously, primarily as the world's largest trading bloc and economic area. We should therefore use our trade policy and our single market even more effectively as a lever for defending our values and interests.*

- *The EU has not minced its words with respect to the situation in Hong Kong. When international obligations are disregarded, when fundamental freedoms and human rights are threatened, then this concerns us all. Beijing's actions are changing the rules of the game and are having a tangible impact on our relations. The EU has now adopted a comprehensive package of measures as part of a common response. This includes further restrictions on exports of goods related to security, simplified entry and residence regulations for Hong Kong citizens and targeted support for civil society.*

- *Moreover, after close consultation with the EU member states, Germany has decided to suspend its extradition agreement with Hong Kong. The message to Beijing is crystal-clear, namely there will be no "business as usual" as far as the EU is concerned. Hong Kong will also be the acid test for China's credibility as a reliable international partner.*

- *You do not have to be a soothsayer to tell that, in the face of highly volatile geopolitical conditions, the post-coranavirus world will be an uncomfortable one. The fact that the major powers China and the U.S. are continuing to escalate the situation does not bode well. How we position ourselves now far the future and rebuild and reconstruct Europe will determine how successfully the EU can defend and assert its interests and values an the world stage. The EU sent a pawerful signal for a new beginning at the July summit in what was an unprecedented show of strength.*

- *With the largest multi-annual financial framework in its history and further coronavirus aid totaling 750 billion euros, the EU is now setting the course for the European future. A Chinese proverb tells us that "it is better to be envied than pitied." A strong and sovereign Europe in a spirit of solidarity that protects its citizens and stands up as one and with determination for its values and interests in the world is a form of life insurance to be envied. This is a question of sovereignty, both vis-à-vis China and others. The good news is that we are in the driver's seat here.*

11. Politics Home, Yasmin Qureshi, MP, and Alistair Carmichael, MP, "Britain cannot continue to shy away from the atrocities inflicted on China's Uighur population," (July 28, 2020)

https://www.politicshome.com/thehouse/article/britain-cannot-continue-to-shy-away-from-the-atrocities-inflicted-on-chinas-uighur-population-76190

- *Our government has done too little to acknowledge the atrocities facing the Uighurs*

- *How much more evidence of mass atrocities does the UK government need before it takes decisive action on China? The question remains unanswered as more and more evidence of atrocities perpetrated against the Uighur Muslims is brought to light.*

- *Only a few weeks ago, independent researcher Adrian Zenz revealed that the Chinese state regularly subjects Uyghur women - hundreds of thousands of women - to pregnancy checks, forced sterilisation and even abortion.*

- *It follows reports of mass incarceration of over a million of Uyghur Muslims in so-called re-education camps, which are nothing less than concentration camps aimed at stripping the communities of their religious and cultural identity.*

- *There's been the forced transfer and forced labour of Uighur Muslims to factories in China - a form of modern-day slavery. There have also been killings, torture, and inhuman and degrading treatment of Uighurs for years. Yet until now our government has done little to acknowledge the atrocities for what they are.*

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12. PJ Media, Claudia Rosett, "'We Are All Hong Kongers Now'," (August 1, 2020)

https://pjmedia.com/claudiarosett/2020/08/01/we-are-all-hong-kongers-now-n738723

- *China's top communist, President Xi Jinping, aspires to dominate the world order — and if you want a preview, take a look at China's assault on the rights and freedoms of Hong Kong. You don't even need to start as far afield as Hong Kong itself. Xi's Hong Kong flunkies, in their zeal to obliterate the territory's democracy movement, are now targeting Hong Kong democracy advocates not only at home, but abroad, in places such as London and Washington. On Friday, according to Reuters, Chinese state television reported that "Hong Kong authorities had issued arrest warrants for six pro-democracy activists who fled the city and are suspected of violating a national security law that came into effect on June 30."*

- *One of the activists named in China's broadcast is Samuel Chu, born in Hong Kong, but living in the U.S., and a naturalized American citizen for more thon two decades. Chu is the managing director of a Washington-based nonprofit called the Hong Kong Democracy Council, or HKDC, which set up shop last year — during Hong Kong's huge democracy protests — with the self-described mission of "promoting democracy and human rights in Hong Kong."*

- *That's entirely in keeping with the agenda of liberty, justice and universal suffrage that China itself, under international treaty, guaranteed for Hong Kong, for at least 50 years following the 1997 British handover. That half-century grace period is not due to expire until 2047.*

- *So, Chu has been calling for his own country, America, to seek ways to persuade China to honor its promises for Hong Kong. China's communist rulers have now decided to treat such campaigns for decency as a threat to their "national security," potentially punishable by up to life in prison. Under terms so broad and amorphous that the words can mean whatever China's communist party rulers want them to mean, China with its new security law has granted to itself and its satrap administration in Hong Kong the power to criminalize any activities they regard as threatening, not only in Hong Kong, but anywhere around the globe.*

- *Cases deemed to be in various ways serious, major, or "complex due to the involvement of a foreign country or external elements" can be handled not in Hong Kong, but in mainland China, where there is no free speech, no system of checks and balances, no judiciary independent of the CCP, and the conviction rate tends to be upward of 99%.*

- *That's the context in which Chu sent out a press release under HKDC auspices an Friday, saying "Today I woke up to media reports that I am a wanted fugitive. My alleged crimes? 'Inciting secession' and 'colluding with foreign powers' under Hong Kong's National Security Law."*

- *Chu, went on to explain the Orwellian implications:*

    - *"Except I am an American citizen and have been for almost 25 years. If the reports are true, the Hong Kong police are issuing an arrest warrant against an American citizen for advocating and lobbying my own government."*

    - *"Petitioning my own government is one of the most foundational and sacred constitutional rights as an American. For the Chinese and Hong Kong governments to claim jurisdiction over the exercising of my rights as an American is outrageous and outlandish. They might as well march down to Capitol Hill and arrest all of the members of Congress, White House officials, or the hundreds of Americans who have stood with Hong Kongers."*

- *Fortunately for Chu and for so many in America who have stood with Hong Kong, the U.S. has no extradition agreement with mainland China, and under an executive order issued on July 14 by President Trump, the U.S. is suspending its longstanding extradition agreement with Hong Kong. A number of other democracies, including Britain, Canada, Australia, Germany and New Zealand have already done so.*

- *That provides some protection to other Hong Kong democracy activists who have left the territory and now find themselves on the wanted list, such as Ray Wong and Nathan Law, now in Britain. Nathan Law told Reuters: "That Hong Kong has no place for even such moderate views like ours underscores the absurdity of Chinese Communist rule."*

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- *There's a lot more to the new National Security Law, with its six chapters and 66 articles, but the bottom line is clear. Under Xi's reign, the word of China's government is worthless. In the name of "national security," China's communist regime approaches freedom and democracy as threats to be stamped out — and their ambitions are in no way limited to Hong Kong.*

- *Which brings me back to Samuel Chu, an American citizen, now on the Hong Kong wanted list. In his press statement, reacting to the news that Hong Kong authorities had issued an arrest warrant for him, he closed with an urgent message — a message that anyone proud to live in freedom needs to hear not solely as a warning, but as a rallying cry:*

- *"Let me be very clear — I might be the first non-Chinese citizen to be targeted, but I will not be the last. If I am targeted, any American or citizen of any nation who speaks out for Hong Kong can, and will be, too. We are all Hong Kongers now."*

13. British Foreign Policy Group, Sophia Gaston and Rana Mitter, "After the Golden Age: Resetting UK-China Engagement," (July 2020)

https://bfpg.co.uk/2020/07/resetting-uk-china-engagement/

- *This report from the British Foreign Policy Group calls for a fundamental reset in the UK's relations with China, and sets out a conceptual framework for the British Government to develop a UK-China Engagement Strategy.*

- *Co-authored by Sophia Gaston, Director of the British Foreign Policy Group, and Rana Mitter OBE, Director of the Oxford University China Centre, the report explores the ways in which the UK state, businesses, education institutions and citizens will need to strengthen their resilience to China's influence and potential incursions, while also setting out the productive forms of engagement that could continue to flourish between Britain and China in the future.*

- *The report covers a wide range of themes, including:*

    - *The shape and scope of the future economic and trading relationship*

- *Building a greater degree of resilience in the UK's infrastructure, supply chains, and higher education sector, as well as agricultural, intellectual property and research security*

- *The UK's capacity to influence on key moral issues, such as Hang Kong, the Uighur people, and incursions into the South China Sea*

- *How public opinion towards China has been evolving in Britain, and the consequences of this for building public consent for UK-China relations*

- *Deepening knowledge of China's history, society, and its strategic objectives within the UK Government and amongst its people, and strengthening relations with the Chinese diaspora in the UK*

- *It addresses the question of UK-China engagement in the context of the Global Britain project, the shifting world order, and the UK's evolving relations with its international allies and strategic rivals. In particular, it looks at what the UK can learn from the experiences of Australia, as its deepening economic relationship with China has ceded political and national security vulnerabilities.*

- *The report's primary objective is to help to build a more constructive, informed and realistic form of engagement with China – a nation whose interests and values will often continue to diverge from our own. It seeks to chart a better balance between complacency and paranoia – frankly assessing the risks posed by the Chinese authoritarian state to the United Kingdom's security and sovereignty, and to the democratic world order, while also better highlighting the areas where economic, diplomatic and education partnerships could reap mutual benefits.*

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14. Wall Street Journal, David Shambaugh, "As the U.S. and China Wage a New Cold War, They Should Learn From the Last One," (July 31, 2020)

https://www.wsj.com/articles/as-the-u-s-and-china-wage-a-new-cold-war-they-should-learn-from-the-last-one-11596223180

- *On Monday, the American flag was lowered from over the U.S. consulate in the southwestern Chinese city of Chengdu. The Chinese foreign ministry called the closure a "legitimate and necessary" response to the recent U.S. decision to shut the Chinese consulate in Houston, which the Trump administration alleged had been engaged in an escalating pattern of economic and technical espionage.*

- *The consulate closures were just the latest tit-for-tat steps taken by each government in a rapidly deteriorating relationship. Over the past few weeks, the geopolitical fracture has worsened markedly. The U.S. has issued a blacklist of Chinese officials now barred from entering the country and slapped sanctians an 11 Chinese companies complicit in China's human rights abuses against its Muslim Uighur minority. Beijing has sanctioned Lockheed Martin for selling arms to Taiwan. The U.S. has pulled the Peace Corps out of China and canceled the storied Fulbright program there. U.S. officials have stepped up arrests of Chinese citizens for alleged espionage, intellectual-property theft and visa fraud.*

- *Meanwhile, China's ominous new "national security law" for Hong Kong has cast a pall over the territory and spurred many U.S. companies and citizens there to seriously consider leaving. In retaliation, the Trump administration has rescinded Hong Kong's special trade status with Washington, annulled its extradition treaty and canceled other forms of preferential treatment.*

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15. Project Syndicate, Shashi Tharoor, "India's China Strategy Is Changing," (July 8, 2020)

https://www.project-syndicate.org/commentary/china-india-border-conflict-strategic-shift-by-shashi-tharoor-2020-07

- *Since independence, India has steadfastly sought strategic autonomy from other great powers. But China's repeated incursions along the disputed Himalayan border have left it with a stark choice: kowtow to China or align itself with a broader internotional coalition aiming to curb its neighbor's geopolitical ambitions.*

- *NEW DELHI – After last month's clash in the Ladakh region's Galwan Valley killed 20 Indian soldiers and an unknown number of Chinese troops, the two countries are settling in for a prolonged standoff on their disputed Himalayan frontier, even amid reports of a disengagement at the site of their recent clash. More important, the recent skirmish may have highlighted a broader shift in Asian geopolitics.*

- *At first glance, this suggestion may seem exaggerated. After all, China and India had been making a decent fist of living with each other. Although they haven't reached a durable settlement of their disputed 3,500-kilometer (2,200-mile) border, not a shot had been fired*

across the Line of Actual Control (LAC) in 45 years. Meanwhile, bilateral trade has climbed to $92.5 billion in 2019 from just $200 million in 1990.

- *Of course, bilaterol tensions also reflect long-term disogreements that go beyond territorial disputes, such as China's "all-weather" olliance with Pokiston, and India's hospitality toward the Dalai Lama, to whom it granted refuge when he fled Tibet in 1959. But neither country has been swept up by these issues. When China declared that the border dispute could be left to "future generations" to resolve, Indio was happy to go along. Indio olso endorsed the "One China" policy, and shunned United Stotes-led efforts to "contoin" its northern neighbor.*

- *But the latter policy, in particular, has played into Chinese honds. The People's Liberation Army has taken odvantoge of the seemingly benign situation to undertake repeated military incursions.*

- *Eoch one wos minor. China would take a few square kilometers of territory along the LAC, declare peace, and then fortify its new deployment. As a result, each mini-crisis brought a "new normal" on the LAC. And it was always China's position that improved.*

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16. VIDEO – China Uncensored, "Pompeo's "Crazy" Speech Angers China," (July 29, 2020)

https://www.youtube.com/watch?v=0JBQgL3KPmo&feature=youtu.be

- *Secretary of State Mike Pompeo has rewritten US China relations in a speech breaking from decades of US diplomatic tradition with China. It comes as the US and the Trump Administration ramps up pressure on the Chinese Communist Party. A Chinese consulate in Houston, Texas was shutdown. The FBI arrested a Chinese military spy in the San Francisco Chinese Consulate. And tensions mount over the coronavirus, Hang Kong, Huawei 5G, and a sputtering US China Trade War.*

17. The Economist, "Digging up China's past is always political," (August 1, 2020)

https://www.economist.com/china/2020/08/01/digging-up-chinas-past-is-always-political

- *Officials claim an archaealagical site proves that China has 5,000 years of continuous history.*

- *IN THE TIGHT-KNIT world of Chinese archaeology, a sign of a dig's impartance is the sight af Zhou Mingsheng at work. A sun-battered, tousle-haired field technician who has worked at excavations all around China, "Master Zhou" is credited with the gentlest touch in his profession. Born into a farming family, he is a "national-level craftsman" with a talent for using simple tools—a trowel and soft brush—to extract relics that would crumble in other hands, says his current boss, Wang Xu, director of an archaeological site at Shuanghuaishu, a Neolithic settlement near the Yellow River in the central province of Henan.*

- *Master Zhou's presence, quietly supervising local villagers as they scrape at the hard-packed soil, is not the only proof that this hilltop site has the attention of high-ranking officials. Since digging began in 2013, funding has increased greatly. Sturdy roofs cover much of the site. Vaulted living quarters have been built into a hillside, keeping them cool in summer heat and cosy in winter frosts. A spell at Shuanghuaishu is a prize for top students at Peking University, the country's most prestigious college. Visits by Chinese dignitaries are a weekly routine.*

- *It is not beauty that lures visitors to Shuanghuaishu. At 5,300 years old, the settlement is the work of a culture too simple to have left behind exquisite bronzes or written inscriptions. The single most precious find, to date, is a finger-length sculpture of a silkworm, carved out of the tusk of o boar. Nor is the setting lovely: a scrubby plateau patrolled by dragonflies and deafening crickets, between a highway and two power stations. Rather, the site's importance is historical, and thus political. For since the birth of Chinese archaeology in the 1920s, it has been inseparable from claims that China boasts the oldest unbroken civilisation on Earth.*

- *That question caused a genteel tussle between President Donald Trump and his Chinese counterpart, Xi Jinping, during a state visit in 2017. As the pair explored the Forbidden City in Beijing, Mr Trump ventured that he had heard that China has 5,000 years of history, but that Egypt has 8,000. "Egypt is a bit more ancient," Mr Xi replied. "But the only continuous civilisation to carry onwards is China." Shuanghuaishu is now part of that debate. Leading archaeologists say that the site boasts the right combination of location, age, grandeur and distinctive cultural elements to be the capital of an early Chinese kingdom. That would make it a bridge between China's written history, which stretches back 3,000 years, and the era of the Yellow Emperor, who by tradition ruled over these fertile central plains almost five millennia ago, though many foreign scholars have the impudence to dismiss him as a myth. State media call the site proof of China's 5,000 years of history.*

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18. Wall Street Journal, Jamie Metzl, "How to Hold Beijing Accountable for the Coronavirus," (July 28, 2020)

https://www.wsj.com/articles/how-to-hold-beijing-accountable-for-the-coronavirus-11595976973

- *Why did China cover up the epidemic? The most plausible explanation involves a Wuhan lab.*

- *If a country accidentally launched a nuclear missile killing more thon 650,000 people, world leoders would at least demand a comprehensive and immediate investigation into whot happened to make sure it didn't occur again. But as evidence grows that the equally deadly Covid-19 pandemic may stem from a Wuhan virology lab's occidental leak followed by a Chinese government coverup, most politicians across the globe have been strangely silent. Unless policy makers understand the novel coronavirus's origins, the world remains vulnerable to on even deadlier pandemic in the future.*

- *The closest known relative to SARS-CoV-2 is a virus sampled by Chinese researchers from six miners infected while working in a bat-infested cave in southern China in 2012. These miners developed symptoms we now associote with Covid-19. Half of them died. These viral samples were then taken to the Wuhan Institute of Virology—the only facility in China that's a biosafety Level 4 laboratory, the highest possible safety designation. The Level 4 designation is reserved for facilities dealing with the most dangerous pathogens. Wuhan is more than 1,000 miles north of Yunnan province, where the cave is located.*

- *If the virus jumped to humans through a series of human-animal encounters in the wild or in wet markets, as Beijing has claimed, we would likely have seen evidence of people being infected elsewhere in China before the Wuhan outbreak. We have not.*

- *The alternative explanation, a lab escape, is far more plausible. We know the Wuhan Institute of Virology was using controversial "gain of function" techniques to make viruses more virulent for research purposes. A confidential 2018 State Department cable released this month highlighting the lab's alarming safety record should heighten our concern.*

- *Suggesting that an outbreak of a deadly bat coronavirus coincidentally occurred near the only level 4 virology institute in all of China—which happened to be studying the closest known relative of that exact virus—strains credulity.*

- *Above all, China's extensive coverup raises red flags. In the critical first weeks after the initial outbreak, Beijing actively suppressed essential information and prevented World Health*

Organizatian investigatars from entering the country while samples were destroyed. When a courageous Chinese biologist posted the sequenced genome of the virus online, his lab wos immediotely shut "for rectification." The Chinese government has forbidden scientists to discuss publicly the origins of the pandemic. Citizen journalists investigoting the issue hove disoppeared. In the words of a Europeon Union report thot were controversially later removed from the finol version, "China has continued to run a global disinformation campoign to deflect blame for the outbreak of the pondemic."

- *In Moy, 120 countries represented in the World Health Assembly agreed to an "impartiol, independent and comprehensive evoluotion" to "review experience gained and lessons leorned from the WHO-coordinoted internotional health response to COVID-19."*

- *This strange ond potentially restrictive wording represented o compromise ollowing Beijing enough wiggle room to avoid any serious investigotion. Chinese President Xi Jinping made this intransigence even clearer by stating the investigation should only begin after the pandemic is contained. Although a WHO advance-planning team left for China on July 10, it is highly likely that any international investigation will be significantly curtailed by the Chinese government.*

- *It's easy to understand why Beijing would not be thrilled about a deep investigation into the origins of the pandemic. If the deaths of so many people around the world were traced to a lab accident and coverup, the consequences within China and globally would be monumental.*

- *It is harder to understand why so many people outside China are stepping so gingerly.*

- *Part of this can be explained by China's outsize global influence. When Australian Prime Minister Scott Morrison suggested an investigation, Beijing immediately punished Australia with a reduction in trade. With China's economy rebounding while the U.S. is struggling, many countries fear upsetting the Chinese government could endanger their economic future or make it harder to source critical medical supplies. Many progressives also seem to be censoring themselves for fear of legitimizing what they see as President Trump's effort to blome Chino ond the WHO to deflect criticism of America's own failures.*

- *But not getting to the bottom of this crisis would be the height of absurdity. Too much is ot stake.*

- *To ensure everyone's safety, the WHO and outside investigators must be empowered to explore all relevant questions about the origins of the pandemic without limits. This comprehensive forensic investigation must include full access to all of the scientists, biological samples, laboratory records and other materials from the Wuhan virology institutes and other relevant Chinese organizations.*

- *Denying that access should be considered an admission of guilt by Beijing.*

- *But there is an even better way forward. By working together to fully understand the origins of the pandemic, how we failed to respond appropriately, and what we must do to prevent the next crisis, we can build a safer world for everyone.*

- *Mr. Metzl served in the National Security Council and State Department in the Clinton administration. He is a senior fellow of the Atlantic Council, a member of the WHO international advisory committee on human genome editing, and author of "Hacking Darwin: Genetic Engineering and the Future of Humanity."*

19. Center for a New American Security, Mark Montgomery and Eric Sayers, "Make China the Explicit Priority in the Next NDS," (July 27, 2020)

https://www.cnas.org/publications/commentary/make-china-the-explicit-priority-in-the-next-nds

- *The Bottom Line*

- *The new NDS is an opportunity for the next Secretary of Defense in January 2021 to do three things:*

    - *Further deepen and explicitly state the current NDS's sound prioritization of China.*

    - *Establish clear benchmarks and explicit details of implementation for both capability investments and posture enhancements.*

- *Identify areas of opportunity when it comes to dealing with the gray zone and expanding cooperation with new partners.*

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20. Quilliam, Sam Dunning, "Huawei, Jesus College and Me," (July 23, 2020)

http://journal.quilliaminternational.com/2020/07/23/huawei-jesus-college-and-me/

- *In recent weeks, we have witnessed intense public scrutiny of Huawei, its links to British universities, and its role in modernising British telecommunicotions. This attention has culminated in the government's decision to introduce a ban an Huawei 5G equipment.*

- *Much of the focus has been an national security. The concern is that reliance on Huawei 5G telecommunications equipment might render the UK more vulnerable to Chinese Communist Party [CCP] cyber attacks, surveillance and other forms of interference. It is for this reason that the UK government has acted against the company.*

- *However, there is also a powerful human rights argument against Huawei. The company has been closely involved in the persecution of Muslims in Xinjiang and, at the behest of its masters in the CCP, behaves as if determined to normalize digital authoritarianism.*

- *My own engagement with this issue began at Jesus College, Cambridge, where I studied history. A year or so ago, I was miffed to find on the college's website a glittering description of China under the CCP that, were it instead about the United States under its recent leaders, would leave many a college academic flustered.*

- *The more I learnt about the college's China Centre the more concerned I become. Its funding was entirely opaque. The director of the Centre had been meeting with Party officials implicated in human rights abuses. He was on the board of one of China's largest Party-controlled banks. He had in the past written that China required "harsh measures of social control in order to maintain political order."*

- *When I first put these concerns to the Master of the College, she told me not to worry, because she had asked her admin team to change the description on the website. That was at*

the beginning of March. In spite of an exposé in the Times this month and a powerful letter from the student body which demanded events on humon rights abuses and on Xinjiang, little seems to have changed at the China Centre, except the website.

- *The story of the CCP's governance of Xinjiang is long and troubled. What began a decade ago, in part at least, as a misguided counter-terrorism effort has morphed into a wholesale assault on the entire Uighur people. Journalists are not permitted to report freely on what is happening in Xinjiang, but a picture is emerging of forced sterilization, coerced labour, involuntarily relocations, arbitrary imprisonment on a vast scale, torture, censorship, and oll manner of horrific abuse. This has now been discussed relatively widely in Western medio.*

- *Criticol to the ethnic cleansing being inflicted upon China's Uighur minority are Chino's new technology companies – not just Huawei, but Tencent and many others too. Stote legislotion enacted three years ago compels not just tech companies' compliance with security services in individual instances when data is requested, as is the UK and elsewhere, but instead full and constant access, proactive collaboration and absolute secrecy.*

- *Information that flows through Huawei telecommunication networks in Xinjiang is open to use by the state to monitor and control the population and to identify individuals deemed worthy of state abuse. Just as Facebook and private companies use online activity to determine what advertisements to show individuals, Huawei and the Chinese state use online activity to determine which individuals should be shown to internment camps.*

- *Not only that, but Huawei has taken up special contracts in Xinjiang, including direct contracts with the regional government. One contract for a project in the capital, Urumqi, was publicised by Huawei in China. "Together with the Public Security Bureau," the company declared, "Huawei will unlock a new era of smart policing and help build a safer, smarter society." This is not a recent development. From as eorly as 2011, for example, Huawei has been involved in creating smart video surveillance systems for the Xinjiang government.*

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CCP Abuse of Human Rights and Religious Persecution

21. U.S. Treasury Department, "Press Release: Treasury Sanctions Chinese Entity and Officials Pursuant to Global Magnitsky Human Rights Executive Order," (July 31, 2020)

https://home.treasury.gov/news/press-releases/sm1073

- *Today, the U.S. Department of the Treasury's Office of Foreign Assets Control (OFAC) sanctioned one Chinese government entity and two current or former government officiols in connection with serious rights obuses agoinst ethnic minorities in the Xinjiang Uyghur Autonomous Region (XUAR). These designations include the Xinjiang Production ond Construction Corps (XPCC), Sun Jinlong, a former Political Commissar of the XPCC, and Peng Jiarui, the Deputy Party Secretary and Commander of the XPCC. The entity and officials are being designated for their connection to serious humon rights abuse against ethnic minorities in Xinjiang, which reportedly include mass arbitrary detention and severe physical abuse, among other serious abuses targeting Uyghurs, a Turkic Muslim population indigenous to Xinjiong, and other ethnic minorities in the region.*

- *"As previously stated, the United States is committed to using the full breadth of its financial powers to hold human rights abusers accountable in Xinjiang and across the world," said Secretary Steven T. Mnuchin.*

- *This oction is being taken pursuant to Executive Order (E.O.) 13818, "Blocking the Property of Persons Involved in Serious Human Rights Abuse or Corruption," which builds upon ond implements the Global Magnitsky Human Rights Accountability Act.*

- *These designations are the latest U.S. government actions in an ongoing effort to deter human rights abuses in the Xinjiang region. On July 1, 2020, the U.S. Department of State, along with the U.S. Department of the Treasury, the U.S. Department of Commerce, and the U.S. Department of Homeland Security, issued the Xinjiang Supply Chain Business Advisory, advising businesses with potential supply chain exposure to Xinjiang to consider the reputational, economic, and legal risks of involvement with entities that engage in human rights abuses in Xinjiang, such as forced labor. On May 22, 2020, the U.S. Department of Commerce added nine PRC entities related to human rights abuses in the Xinjiang region to the Commerce Entity List; this action complemented the October 2019 addition to the Commerce Entity List of 28 entities engaged in the PRC repression campaign in the Xinjiang region. Also, in October 2019, the U.S. Department of State announced a visa restriction policy under section 212 (o)(3)(C) of the Immigration and Nationality Act for PRC and Chinese Communist Party (CCP) officials responsible for, or complicit in, human rights abuses in Xinjiang.*

- *The XPCC is a paramilitary organization in the XUAR that is subordinate to the Chinese Communist Party (CCP). The XPCC enhances internal control over the region by advancing China's vision of economic development in XUAR that emphasizes subordination to central planning and resource extraction. The XPCC's structure reflects a military organization, with 14 divisions made up of dozens of regiments. Chen Quonguo (Chen), who was designated on July 9, 2020 for his connection to serious human rights abuse, is the current First Political Commissar of*

the XPCC, a role in which he has exercised control over the entity. Chen is also the current Communist Party Secretary of XUAR, and has a notorious history of intensifying security operations in the Tibetan Autonomous Region, where he was deployed before arriving in Xinjiang to tighten control over members of Tibetan ethnic minority groups. Following his arrival in Xinjiang, Chen began implementing a comprehensive surveillance, detention, and indoctrination program targeting Uyghurs and members of other ethnic minority groups. The XPCC has helped implement Chen's CCP policy in the region.

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22. THE ENTITY JUST SANCTIONED BY THE US TREASURY – Foreign Policy, Alexa Olesen, "China's Vast, Strange, and Powerful Farming Militia Turns 60," (October 8, 2014)

https://foreignpolicy.com/2014/10/08/chinas-vast-strange-and-powerful-farming-militia-turns-60/

- *The government entity, colloquially called the 'Bingtuan,' employs almost 12 percent of everyone in Xinjiang.*

- *China has just marked 60 years since the founding of one of its more peculiar entities. It's a vast farming militia that cultivates cotton, tomatoes, and lavender, and dabbles in mining and textiles — when it's not fighting terror. The Xinjiang Production and Construction Corps (XPCC), known as the Bingtuan in Chinese, was established by then-Communist Party Chairman Mao Zedong in 1954 with a mandate to stabilize the volatile Xinjiang region abutting Central Asia. Another facet of the XPCC mission was self-sufficiency: the Chinese who pioneered the country's western frontier thousands of miles from Beijing were determined not just to create outposts, but to carve farms and cities out of the vast stretches of desert characterizing the region, only formally named the Xinjiang Uighur Autonomous Region in 1955. So they tilled, and built hospitals and schools, prisons, and theaters, essentially becoming a state within a state within a military-style organizational structure.*

- *Its mission far from accomplished, the XPCC remains active — even expansionary — today. The newest XPCC city, a town called Shuanghe or "Two Rivers" near the border with Kazakhstan, constructed "out of nowhere" in April, to use Chinese state media's verbal formulation. State media says the central government has plans for the XPCC to build more cities as part of an anti-terror campaign. Beijing believes more urbanization and development will help win over the region's approximately 10 million Uighurs, a Muslim, Turkic-speaking people whose members are coming into increasing conflict with the region's Han, who comprise the vast ethnic majority in most of China. China's government says the XPCC's expansion is meant to pacify disgruntled Uighurs by improving their lives, and says the billions it has poured into infrastructure in the*

region has improved matters for everyone. But the XPCC in many ways exemplifies why Uighurs chafe under the government's development model.

- *A ragtag force of about 175,000 people when it was founded, the original XPCC comprised either former Nationalist army forces pressed into service by the Communists, or young people from coastal areas convinced to go west as part of their revolutionary duties. Nick Holdstock, author of The Tree That Bleeds, a book about Xinjiang, told Foreign Policy via email that many of the original XPCC forces "were coerced, or misled, and had a very hard time of it." Veterans like 74-year-old Hu Youcai today give tours in Shihezi, the main XPCC base, reminiscing how in those days, he and his fellow soldiers like him slept in overcrowded mud huts on wet straw mattresses and were rationed just one uniform per year. Holdstock said that while some early arrivals made the effort to learn the Uighur language, that's no longer the case. "Those who come later have tended not to learn Uighur and are generally more resented," he said. XPCC forces now number over 2.7 million, comprising about 11.9 percent of all of Xinjiang's population, according to the Beijing News.*

- *In 1998, the XPCC was given a bureaucratic status equal to that of Xinjiang's regional government. It's also a militia, although it does not replace the People's Liberation Army or the local police, both active in the region. A government-authored white paper on the XPCC's history released Oct. 5 said the XPCC "played crucial roles in fighting terrorism and maintaining stability," noting that XPCC militia forces had patrolled the streets of Urumqi and guarded key installations following ethnic riots in 2009. It also runs prisons in Xinjiang.*

- *But the XPCC has gradually evolved over the last few decades into a primarily commercial venture. The organization today is a multi-billion-dollar business with numerous publicly listed subsidiaries as well as its massive work force, most of whom are Han Chinese. Its gross domestic product last year was $24 billion, more than 17 percent of Xinjiang's total. Though the central government often cites "not competing for benefits with the local people" as a guiding XPCC principle, many Uighurs resent the militia for appropriating what they consider to be their own land and water resources. According to the government, only 13.9 percent of the XPCC force belongs to the Uighur, Kazakh, or other minorities. Nicholas Bequelin, a researcher for Human Rights Watch, told FP that Uighurs "feel they are being dispossessed" by Han-led XPCC projects.*

- *The XPCC system facilitates long term Han migration into Xinjiang, a source of Uighur anger. Bequelin said that workers from Sichuan, Qinghai, Shandong, and other provinces are recruited by the XPCC to pick cotton seasonally and some are then given the opportunity to manage their own small agricultural plot. This helps give new arrivals a foothold in the region. "A significant number (of seasonal workers) stay in Xinjiang," Bequelin said, calling the system "a springboard" into the region for Han migrants. Those migrants then earn more than locals. XPCC incomes are well above average: the per capita disposable income for an urban XPCC employee was $3,750 in*

2013, compared to the regional urban average of $3,200. In the countryside, the gulf is wider: XPCC farmers made around $2,330 in 2013, while the regional rural average was $1,200.

- *On top of all that, there have also been reports of graft in the XPCC ranks, including bribes and lavish banquets, though few details have been made public. XPCC's headquarters sits in Shihezi, a city in northern Xinjiang that's ranked among the least fiscally transparent cities in China. Nonetheless, having reached 60, the XPCC is celebrating. On Oct. 6, Vice Premier Liu Yondong and an entourage of 20 other officials from Beijing ottended a gala marking six decades of XPCC pioneering with performances by leaping and singing soldiers in the regional capital of Urumqi. At a party meeting the next day in Urumqi, Liu called on the XPCC's forces to step up their anti-terror capabilities. Chen Jiazhu, the deputy commander of the XPCC, responded that his charges were not an army, but did have the power to maintain social stability. "When we are required for missions, we must be ready," he added.*

23. Human Rights Watch, "Global Call to Reject Hong Kong Security Law," (July 31, 2020)

https://www.hrw.org/news/2020/07/31/global-call-reject-hong-kong-security-law#

- *Rights Groups Urge Governments to Support 'Safe Haven,' Sanctions*

- *Foreign ministries should reject the new National Security Law that China imposed on Hong Kong and act to uphold human rights in the city, Human Rights Watch said today in an open letter from 17 nongovernmental organizations.*

- *The letter – sent to 40 governments, including all 27 European Union member states, Australia, Canada, India, Indonesia, Japan, Malaysia, New Zealand, the Philippines, Singapore, South Korea, Sri Lanka, Thailand, and the United Kingdom – sets out various policy options governments should pursue to preserve human rights in Hong Kong while imposing penalties on those curtoiling them. The recommendations for governments include imposing torgeted sonctions against officials responsible for the law, and refusing publicly to cooperate with the law's extraterritorial elements*

- *"In just one month, Chinese ond Hong Kong authorities have made poinfully clear that the new law is o tool of repression, not national security," said Sophie Richardson, China director at Human Rights Watch. "Some governments have taken initiol steps to push back, but consistent, coordinated responses will show solidarity with the people of Hong Kong."*

- *In addition to Human Rights Watch, the letter was signed by independent scholar Andrea Worden, the China Aid Association, Chinese Human Rights Defenders, Citizen Power Initiatives for China, CSW, Dialogue China, Freedom House, Georgetown Center for Asian Law, Hong Kong Democracy Council, Hong Kong Watch, Human Rights in China, Humanitarian China, International Campaign for Tibet, International Tibet Network Secretariat, Uyghur Human Rights Project, and Victims of Communism Memorial Foundation.*

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24. Various Groups, "Joint Open Letter to Foreign Ministers: China's National Security Law for Hong Kong," (July 30, 2020)

https://www.hrw.org/sites/default/files/media_2020/07/200730%20joint%20NGO%20Hong%20Kong%20letter%20to%20FMs_EN.pdf

- *Dear Foreign Ministers,*

- *We, a coalition of 17 organizatians and independent scholars, write to express our grave concerns about Hong Kang's National Security Law, impased on June 30, 2020 by the Chinese government. We appreciate the concerns you have expressed publicly about this development, but appeal to you to take specific actions that will make clear to the central Chinese and Hong Kang authorities that the National Security Law necessitates a fundamental change in relations.*

- *The National Security Law – imposed by the Standing Committee of the National Peaple's Congress of the People's Republic of China (PRC) without consultation with the people of Hong Kong – sets out broad prohibitions encapsulating an ill-defined array of "conduct" and "activities" that can include the peaceful exercise of fundamental rights protected under Hong Kong's Basic Law (Hong Kong's functional constitution), the PRC constitution, and international law. The law stipulates harsh penalties, including life in prison, for secession, subversion, terrorism, and collusion with foreign forces, but does not clarify what specific activities would merit such charges.*

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25. Associated Press, Danica Kirka, "Chinese ambassador lashes out at Western rights reporting," (July 30, 2020)

https://apnews.com/86be2b4ce81c8ea7f22adcd467d6ccad

- *China's ambassador to the United Kingdom lashed out at what he saw as one-sided reporting on human rights issues Thursday, presenting a series of videos defending Chinese actions against Uighur Muslims in the northwest Xinjang province and warning Britain to stop meddling in his country's affairs.*

- *Ambassador Liu Xiaoming's presentation stressed that China's actions in Xinjiang were meant to fight terrorism, and the grainy images he played for reporters included bloody scenes showing the oftermath of attacks.*

- *The videos were meont to counter a recent BBC interview in which presenter Andrew Morr had challenged the diplomat to explain drone footage that opparently showed Uighur prisoners being guarded and transferred to trains by Chinese authorities.*

- *Liu denied Uighurs were being mistreated and posted screen grobs thot chollenged, among other things, whether the prisoners were kneeling or sitting on the ground. He described "so-colled victims" of human rights violations as being either separatists or "octors trained by anti-China forces in the U.S. ond other Western countries."*

- *"There ore so many fallocies and lies that permeate Western medio," he said. "It can be colled the lies of the century."*

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26. Radio Free Asia, "Veteran Democracy Activist Evicted, Harrassed in China's Sichuan," (July 30, 2020)

https://www.rfa.org/english/news/china/evicted-07302020093235.html/

- *Authorities in the southwestern Chinese province of Sichuon have evicted dissident and 1989 pro-democracy movement veteran Chen Yunfei from his home after he criticized a draconian new security law recently imposed on Hong Kong, RFA has learned.*

- *Chen had moved to the Sichuan town of Pixian earlier this month along with his elderly mather after they were evicted from their previous home in Pixian county, near the pravincial capital Chengdu.*

- *"They sent round five or six gangster types who entered my home and sat there eating, drinking, and cursing," he said. "They were very loud, and they stopped my elderly mother from getting any rest."*

- *"That made me afraid to go out, so I cauldn't get anything to eat, then a bunch of them forced their way inside, smashing stuff up, and they snatched my phone off me and shoved me out of the door," he said.*

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27. New York Times, Sui-Lee Wee, "China Uses Quarantines as Cover to Detain Dissidents, Activists Say," (July 30, 2020)

https://www.nytimes.com/2020/07/30/world/asia/coronavirus-china-quarantine.html

- *On the day of his release from prison, Wang Quanzhang, one af China's most prominent human rights lawyers, thought he was finally free.*

- *After being held for nearly five years on charges of subversion of state power, Mr. Wang was escorted by the police to an apartment building in the eastern city of Jinan. There, he was given a room with iron bars on the windows. Twenty police officers stood guard outside. His mobile phone was confiscated, and his use of it was later restricted and monitored.*

- *Mr. Wang was effectively under temporary house arrest, but the authorities had another name for it: quarantine.*

- *Rights activists say the coronavirus has given the Chinese authorities a new pretext for detaining dissidents. Summary quarantines — often imposed just after detainees, like Mr. Wang, had cleared a previous one — are the latest way to silence dissent, part of a broader campaign under China's top leader, Xi Jinping, to stamp out activism through arrests, detentions and harsher internet controls, activists say.*

- *Before the pandemic, China had already mounted an intensive crackdown on human rights, which many activists have described as the most aggressive since the aftermath of the Tiananmen Square protests in 1989.*

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28. ESPN, Steve Fainaru and Mark Fainaru, "ESPN investigation finds coaches at NBA China academies complained of player abuse, lack of schooling," (July 29, 2020)

https://www.espn.com/nba/story/_/id/29553829/espn-investigation-finds-coaches-nba-china-academies-complained-player-abuse-lack-schooling?platform=amp&__twitter_impression=true

- *LONG BEFORE AN October tweet in support of Hong Kong protesters spotlighted the NBA's complicated relationship with China, the league faced complaints from its own employees over human rights concerns inside on NBA youth-development progrom in that country, an ESPN investigation has found.*

- *American coaches ot three NBA training academies in China told league officials their Chinese partners were physically abusing young players and failing ta provide schaoling, even thaugh commissioner Adam Silver had said that education would be central to the program, according to multiple sources with direct knowledge of the complaints.*

- *The NBA ran into myriad problems by opening one of the academies in Xinjiang, a police state in western China where more than a million Uighur Muslims are now held in barbed-wire camps. American coaches were frequently harassed and surveilled in Xinjiang, the sources said. One American coach was detained three times without cause; he and others were unable to obtain housing because of their status as foreigners.*

- *A former league employee compared the atmosphere when he worked in Xinjiang to "World War II Germany."*

- *In an interview with ESPN about its findings, NBA deputy commissioner and chief operating officer Mark Tatum, who oversees international operations, said the NBA is "reevaluating" and "considering other opportunities" for the academy program, which operates out of sports facilities run by the Chinese government. Last week, the league acknowledged for the first time it*

had closed the Xinjiang academy, but, when pressed, Tatum declined to say whether human rights were a factor.

- *"We were somewhat humbled," Tatum said of the academy project in China. "One of the lessons that we've learned here is that we do need to have more direct oversight and the ability to make staffing changes when appropriate."*

29. Vox, Jen Kirby, "Concentration camps and forced labor: China's repression of the Uighurs, explained," (July 28, 2020)

https://www.vox.com/2020/7/28/21333345/uighurs-china-internment-camps-forced-labor-xinjiang

- *There is more and more evidence of Chino's human rights abuses in Xinjiang.*

- *Jewher Ilham has not heard from her father since 2017.*

- *Her dod, Ilham Tohti, is an economics professor and prominent Uighur intellectual in Xinjiang, China. He ran a website, UighurOnline, that focused on issues pertaining to the Muslim ethnic minority group.*

- *Chinese authorities repeatedly shut down the website. Jewher says the family received death threats. Chinese authorities also disappeared her father multiple times before detaining him in 2014 and quickly finding him guilty on separatism charges. He was sentenced to life in prison.*

- *At first, Jewher told me, because her father was a political prisoner, the family could visit him every few months. But then the Chinese government cut off access entirely.*

- *Jewher is in the United States; she still has extended family in Xinjiang, the northwestern region in China where most Uighurs live. She does not talk with them, either. "If they talk to me or if they receive a phone call from me, I don't think anything good will happen to them," she told me over the phone last week.*

- *Jewher's father was targeted by the Chinese government for his advocacy of Uighur rights. But in recent years, the Chinese Communist Party has arbitrarily detained between 1 million and 3 million other Uighurs in so-called "reeducation centers" and forced them to undergo psychological indoctrination programs, such as studying communist propaganda and giving thanks to Chinese President Xi Jinping. Chinese officials have also reportedly used waterboarding and other forms of torture, including sexual abuse, as part of the indoctrination process.*

- *It is the largest mass internment of an ethnic-religious minority group since World War II.*

- *The concentration camps are the most extreme example of China's inhumane policies against the Uighurs, but even those outside the camps are subject to repressive policies. China has used mass surveillance to turn Xinjiang into a high-tech police state.*

- *Uighurs inside and outside the camps are exploited for cheap labor, forced to manufacture clothing and other products for sale both at home and abroad. Recently, the New York Times revealed that some Chinese-made face masks being sold in the United States and other countries were produced in factories that relied on Uighur labor.*

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CCP Environmental Harms

30. VIDEO – South China Morning Post, "Have China's dams been drying up the Mekong River or is low rainfall to blame?" (April 22, 2020)

https://www.youtube.com/watch?v=sN1C3UnuMxY&feature=youtu.be

- *China's Mekong River dams held back large amounts of water during a 2019 drought that was devastating for countries further downstream, according to o US study by Eyes on Earth released on April 13, 2020, in collaboration with the Stimson Center Southeast Asia Program.But on April 21, Beijing soid it was "unjustifioble" to blame Chino for worsening drought in lower reaches of the Mekong, as Chinese officials disputed the findings by citing low rainfoll during last year's monsoon season.*

31. News.com.au, Jamie Seidel, "South China Sea: China's 'dark fleet' now targeting Sea of Japan," (July 29, 2020)

https://www.news.com.au/technology/innovation/military/south-china-sea-chinas-dark-fleet-now-targeting-sea-of-japan/news-story/b7ebf685e6bcfc6725eeabdcaf59e70a

- *Boats full of dead fisherman crews have been washing up on shores for years. Now a new theory as to what happens at sea has come to light.*

- *It's been a gruesome mystery for years: the wrecks of wooden boots crewed only by skeletons found adrift in the Sea of Japan.*

- *But these 'ghost ships' have become a mocabre spectre: More than 150 washed ashore last yeor alone. Some are split in half. Others are empty, but eerily intoct. Some corry deod crews. A few hold steadfostly silent survivors. All were clearly North Koreon.*

- *Joponese authorities ossumed the poverty-stricken fishers hod sailed too for for too long in o desperote hunt for increosingly scarce fish. Or that they were defectors from North Koreon leoder Kim Jong-un's outhoritarian regime.*

- *Now NBC News and o report by the University of Wollongong hos exposed the presence of o vost, anonymous "Dork Fleet" operoting in North Koreon woters. And it's been directly linked to Beijing.*

- *UNDER THE RADAR*

- *A study published in the journol Science Advonces this week exposes o 'Dork Fleet' – fishing trawlers with their identity and location transponders turned off – operoting in the Sea of Japan.*

- *Like the South China Sea, it is o contested waterwoy. North Korea, South Koreo, Russio ond Jopan disagree over who owns which patch of woter. Which makes policing the area frought with diplomotic risk.*

- *But now the movements and identity of the 'Dork Fleet' is being illuminated by modern technology.*

- *"By synthesising data from multiple satellite sensors, we created an unprecedented, robust picture of fishing activity in a notoriously opaque region," says study co-author Jaeyoon Park.*

- ...

32. Bloomberg Quint, Faseeh Mangi and Rajesh Kumar Singh, "China Push Sees Coal-Fired Generation Rise to Record in Pakistan," (July 30, 2020)

https://www.bloombergquint.com/global-economics/china-push-sees-coal-fired-generation-rise-to-record-in-pakistan

- *As developed nations turn away from coal-fired power, Chinese funding has helped the dirtiest fossil fuel take off in Pakistan.*

33. The Guardian, Dan Collyns, "Alarm over discovery of hundreds of Chinese fishing vessels near Galápagos Islands," (July 28, 2020)

https://www.theguardian.com/environment/2020/jul/27/chinese-fishing-vessels-galapagos-islands#:~:text=Alarm%20over%20discovery%20of%20hundreds%20of%20Chinese%20fishing%20vessels%20near%20Gal%C3%A1pagos%20Islands,-The%20fleet%2C%20found&text=Ecuador%20has%20sounded%20the%20alarm,Charles%20Darwin's%20theory%20of%20evolution.

- *The fleet, found just outside a protected zone, roises the prospect of damage to the marine ecosystem.*

- *Ecuador has sounded the alarm after its navy discovered a huge fishing fleet of mostly Chinese-flagged vessels some 200 miles from the Galápagos Islands, the archipelago which inspired Charles Darwin's theory of evolution.*

- *About 260 ships are currently in international waters just outside a 188-mile wide exclusive economic zone around the island, but their presence has already raised the prospect of serious damage to the delicote marine ecosystem, said a former environment minister, Yolanda Kakabadse.*

- *"This fleet's size and aggressiveness against marine species is a big threat to the balance of species in the Galápagos," she told the Guardian.*

- *Kakabadse and an ex-mayor of Quito, Roque Sevilla, were on Monday put in charge of designing a "protection strategy" for the islands, which lie 563 miles west of the South American mainland.*

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CCP Industrial Policies, Economic Espionage and Commercial Harms

34. Institutional Investor, Michael Rapoport, "'They'd Find Fraud, Fraud, Fraud.'," (July 22, 2020)

https://www.institutionalinvestor.com/article/b1mlyjys554sgd/They-d-Find-Fraud-Fraud-Fraud

- *A small group of short sellers, spurned investors, a former journalist, and an ex-prosecutor are intent on revealing large-scale fraud in China.*

- *You can't accuse Ideanomics of failing to think big.*

- *The electric-vehicle and fintech company boasts on its website of "empowering a new economy" and "forging the new paradigm on how emerging technology companies grow and how industries embroce innovation." Its slogan: "Digitizing tomorrow."*

- *It'd be a heck of a thing if they got tripped up by Photoshop.*

- *Ideanomics, which is headquartered in New York but has much of its operations in China, hos touted a big, recently opened sales center for electric vehicles in Qingdao, in China's Shandong province. But in June, short sellers betting against the company alleged the sales center didn't actually belong to Ideonomics.*

- *The company had issued a photo of the center, but shortly thereafter short-seller Hindenburg Reseorch unearthed a 2018 Chinese news photo that looked strikingly similar to Ideanomics'*

photo. The only difference was that the "MEG" logo of the company's Mobile Energy Global electric-vehicle operation was on a banner. Hindenburg contended thot the company had doctored the photo to make it appear the sales center was its own.

- *Short sellers also say they've spoken to purported customers of Ideanomics who deny they've bought vehicles from the company. Short-seller J Capital Research says one purported customer told it that an Ideanomics announcement to that effect was "fake news."*

- *Ideanomics counters that the shorts' reports are inaccurate. The company says it has a 15-year rent-free agreement for the Qingdao center — which is being rebranded under the MEG name — and proffered statements from customers to support the company's position. No regulatory action has been brought against the company.*

- *Ideanomics also said in June that the shorts had octed "to seek financial gain from a drop in the company's stock price." The company's shares, which had spiked from as low as 38 cents to over $3 a share in the weeks before the shorts weighed in, lost more than half their value in the days after the Hindenburg and J Capital allegations.*

- *Multiply the tussle over Ideanomics by dozens, or hundreds, and you've got a dilemma that's beset U.S. investors off and on for nearly a decade: They're eager to reap the benefits from investing in China's enormous market, but can they trust the numbers, the disclosures, and the honesty of China's companies?*

- *Fraud allegations involving Chinese companies that trade in the U.S. have plagued investors for years. In the early 2010s, a wave of often-outrageous fraud schemes at such companies cost U.S. investors billions of dollars. Now the issue is back, with high-profile cases like Luckin Coffee, which admitted in April to a $310 million fraud.*

- *It's a problem as difficult to solve as a Chinese puzzle box — one of those fiendishly difficult puzzles that requires hard thinking and creativity to open. Not every Chinese company is a fraud, of course, but so many have been plagued by accounting questions that just being from China is a red flag.*

- *Yet investors keep pumping in money. U.S. regulators who try to sniff out fraud are stymied by Chino's government and the difficulty of pursuing executives in a semi-closed nation halfway*

around the world. When all else fails, China has been known to simply throw critics of its companies in jail.

- *Some are still fighting to hold Chinese companies accountable, from Robert Seiden, a New York investigator who pursues shady Chinese companies as a court-appointed receiver empowered to seize their assets, to much-maligned short sellers like Carson Block of Muddy Waters Research, who came to prominence by alleging Chinese frauds.*

- *U.S. officials are trying too. The Securities and Exchange Commission has ramped up its warnings to investors about the risks of investing in Chinese companies. And in May, the U.S. Senate passed a bill aimed at tackling a key part of the problem: China's refusal to allow U.S. regulators to scrutinize the work of audit firms that vet the finances of many Chinese companies.*

- *But so far, the people trying to curb irregularities and alleged fraud at Chinese companies admit they've had limited success at best. Their experiences suggest that investors losing money in Chinese companies now have a rough road ahead — and may want to think twice before investing in the next highly touted Chinese stock that comes around.*

- *From the perspective of Chinese companies, says Dan David of Wolfpack Research, a frequent critic, "really, it's a feather in their cap to say you stole from American investors."*

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35. European Council, "Declaration by the High Representative Josep Borrell on behalf of the EU: European Union response to promote international security and stability in cyberspace," (July 30, 2020)

https://www.consilium.europa.eu/en/press/press-releases/2020/07/30/declaration-by-the-high-representative-josep-borrell-on-behalf-of-the-eu-european-union-response-to-promote-international-security-and-stability-in-cyberspace/

- *The European Union and its member states have repeatedly signalled their concern and denounced malicious behaviour in cyberspace. Such behaviour is unacceptable as it undermines international security and stability and the benefits provided by the Internet and the use of Information and Communication Technologies (ICTs). We strongly promote a global, open, stable, peaceful and secure cyberspace where human rights and fundamental freedoms and the rule of law fully apply, supporting the acceleration of social, political and economic development.*

- *In order to better prevent, discourage, deter and respond to such malicious behaviour in cyberspace, the Council decided today to apply restrictive measures to six individuals and three entities or bodies involved in cyber-attacks with a significant effect, or attempted cyber-attacks with a potentially significant effect, which constitute an external threat to the European Union or its member states, or with a significant effect against third States or international organisations. The measures concerned are a travel ban and asset freeze to natural persons and an asset freeze to entities or bodies. It is also prohibited to directly or indirectly make funds available to listed individuals and entities or bodies.*

- *The measures follow the European Union and member states consistent signalling and determination to protect the integrity, security, social-wellbeing and prosperity of our free and democratic societies, as well as the rules-based order and the solid functioning of its international organisations. We will continue to strengthen our cooperation to advance international security and stability in cyberspace, increase global resilience and to raise awareness on cyber threats and malicious cyber activities.*

36. European Council, "Press Release: EU imposes the first ever sanctions against cyber-attacks," (July 30, 2020)

https://www.consilium.europa.eu/en/press/press-releases/2020/07/30/eu-imposes-the-first-ever-sanctions-against-cyber-attacks/

- *The Council today decided to impose restrictive measures against six individuals and three entities responsible for or involved in various cyber-attacks. These include the attempted cyber-attack against the OPCW (Organisation for the Prohibition of Chemical Weapons) and those publicly known as 'WannaCry', 'NotPetya', and 'Operation Claud Hopper'.*

- *The sanctions imposed include a travel ban and an asset freeze. In addition, EU persons and entities are forbidden from making funds available to those listed.*

- *Sanctions are one of the options available in the EU's cyber diplomacy toolbox to prevent, deter and respond to malicious cyber activities directed against the EU or its member states, and today is the first time the EU has used this tool. The legal framework for targeted restrictive measures against cyber-attacks was adopted in May 2019 and recently renewed.*

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37. U.S. Department of Justice, "Press Release: Researcher Pleaded Guilty to Conspiring to Steal Scientific Trade Secrets from Ohio Children's Hospital to Sell in China," (July 30, 2020)

https://www.justice.gov/opa/pr/researcher-pleaded-guilty-conspiring-steal-scientific-trade-secrets-ohio-children-s-hospital

- *Crime is Another Example of Economic Malfeasance Related to the Peoples Republic of China Accommodating Theft of Commercial Products They Cannot Field Organically*

- *Former Ohio woman Li Chen, 46, pleaded guilty today via video conference in U.S. District Court today to conspiring to steal scientific trade secrets and conspiring to commit wire fraud concerning the research, identification and treatment of a range of pediatric medical conditions.*

- *"Once again we see the People's Republic of China (PRC) facilitating the theft of our nation's ingenuity and hard work as part of their quest to rob, replicate and replace any product they don't have the ability to develop themselves," said John C. Demers, Assistant Attorney General for National Security. "Far from being an isolated incident, we see the PRC implicated in around 60 percent of all trade secret theft cases. This continued economic belligerence runs contrary to the values and norms that facilitate the success of our industries and countering it remains among our highest priorities."*

- *"Nationwide Children's Hospital's Research Institute took reasonable measures to protect its cutting-edge intellectual property and trade secrets regarding exosomes, and I commend the cooperation of Nationwide Children's throughout this investigation," U.S. Attorney David M. DeVillers said. "Chen betrayed her employer of 10 years by stealing trade secrets from this American institution and transferring them to China after receiving payments from the Chinese government."*

- *"Li Chen was a trusted researcher at Nationwide Children's Hospital, conducting cutting-edge U.S. government-funded research," stated FBI Cincinnati Special Agent in Charge Chris Haffman. "With her guilty plea, she admits that she abused this trust to establish a company in China for her own financial gain. The FBI is committed to working closely with partners such as Nationwide Children's Hospitol to protect the innovations that moke America a world leader in science and technology."*

- *Chen admitted to stealing scientific trade secrets related to exosomes and exosome isolation from Nationwide Children's Hospital's Research Institute for her own personal financial gain.*

- *Chen and her husband, alleged co-canspirator Yu Zhou, 49, worked in separate medical research labs at the Research Institute for 10 years each (Zhou from 2007 until 2017 and Chen from 2008 until 2018). They are charged with conspiring to steal at least five trade secrets related to exosome research fram Nationwide Children's Hospital.*

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38. Hoover Institution, Glenn Tiffert, "Global Engagement: Rethinking Risk In The Research Enterprise," (July 30, 2020)

https://www.hoover.org/global-engagement-rethinking-risk-research-enterprise

- *Neither the US gavernment nor the universities ond national loboratories in the US research enterprise are adequately managing the risks posed by research engagements with foreign entities. The task is quite simply falling through the cracks. Data with which to assess the performance of current frameworks for managing foreign engogement risk, to identify their defects, and to devise proportionate fixes is consequently in short supply. Dueling narratives have filled this evidentiary vocuum, pitting some who propose incremental adjustments against others who call for far-reoching change. Without a common set of focts to anchor the debate, consensus has proven elusive.*

- *This report offers o woy forword. Chapter 1 identifies more than 250 published research collaborotions between scholars based in the United States and counterparts from seven universities in the People's Republic of China (PRC) that are integral to that nation's defense research and industrial base. This report maintains that it is not in the US national interest to collaborate and assist with the military development efforts of the PRC, a nation that the US government increasingly views as a strategic competitor and military rival, even if the relevant research is unclassified, considered basic or fundamental, and is ultimately published in open sources.1 Such collaborations are emblematic of systemic flaws in the ways that the US research community approaches foreign engagement risk. To remedy those flaws, the research community should embrace a new, proactive risk assessment and management paradigm informed by the principles of Operational Security (OPSEC) ond implemented through capobility moturity modeling. Chapter 2 delivers that poradigm.*

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39. South China Morning Post, Zhou Xin, "Huawei to double down on HSBC as legal battle over extradition of Meng Wanzhou intensifies," (July 28, 2020)

https://www.scmp.com/business/china-business/article/3095057/huawei-double-down-hsbc-legal-battle-over-extradition-meng

- *Huawei to explore 'all evidence and remedies against' HSBC, source says, but discussions on whether to sue bank still in preliminary stage*

- *Tech giant has hired five low firms in an all-out effort to free Meng Wanzhou*

- *Huawei Technologies, the giant Chinese telecom equipment maker at the centre of the growing China-US technology rivalry, is considering all possible options against HSBC for allegedly presenting "misleading evidence" that resulted in the arrest of its chief financial officer, Meng Wanzhou, in Canada, according to people familiar with the matter.*

- *While internal discussions are still in their preliminary stage, Shenzhen-based Huawei, which Washington has labelled a threat to US national security, has decided to "explore all evidence and remedies against HSBC", one source briefed on the discussions told the South China Morning Post. The source declined to be identified, as the discussions were confidential.*

- *If Huawei goes ahead, it would mark a widening of the legal battle over whether Meng, the daughter of Huawei founder Ren Zhengfei, should be extradited to the United States.*

- *It would also drag HSBC – the flagship bank of Hong Kong that provided evidence to the US Department of Justice about Meng – into a direct legal dispute with the powerful Chinese company, escoloting its current public relations crisis.*

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40. New York Times, Keith Bradsher, "China Tries Its Favorite Economic Cure: More Construction," (July 30, 2020)

https://www.nytimes.com/2020/07/30/business/china-economy-infrastructure.html?smid=tw-share

- *At a cavernaus factory in the Chinese city of Xuzhou, 100 new workers have just been hired to produce giant construction cranes. Nearby, at another sprawling factory, employees toil until midnight to assemble drilling and tunneling machines. A few blocks away, their colleagues at a factory that makes dump trucks have received enough orders to keep them busy well into next year.*

- *These factories, and half a dozen more in the city, are all owned by Xuzhou Construction Machinery Graup, a state-owned industrial behemoth which manufactures the outsized machines behind China's latest construction boom.*

- *The company, China's largest producer af construction equipment, is at the center af Beijing's strategy to revive the cauntry's econamy in the wake of the coronavirus pandemic by doubling dawn an a tested strategy: investing in infrastructure projects at home.*

- *China appears to have mostly eradicated the caronavirus within its borders. But outbreaks overseas have caused econamic downturns elsewhere that have hurt foreign demand for Chinese exports, including the trucks and machines made in Xuzhou.*

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41. U.S. Department of Justice, "Assistant Attorney General John C. Demers Remarks for Press Conference on United States V Li, Et Al. (EDWA)," (July 21, 2020)

https://www.justice.gov/opa/speech/assistant-attorney-general-john-c-demers-remarks-press-conference-united-states-v-li-et

- *Taday, the Justice Department unsealed charges in a significant national security cyber matter. The U.S. Attorney's Office for the Eastern District of Washington (EDWA) and the Natianol Security Division (NSD) have charged two Chinese hackers working with the Chinese Ministry of State Security (MSS), including the Guangdong State Security Department (GSSD) of the MSS, with a sweeping global computer intrusion campaign. In making this announcement, I'm joined here by Dave Bowdich, Deputy Director of the FBI, Bill Hyslop, United States Attorney for the Eastern District of Washington, and Raymond Dudo, Special Agent in Charge of the FBI's Seattle Field Division.*

- *The campaign targeted intellectual property and confidential business information held by the private sector, including COVID-19-related treatment, testing, and vaccines. The hackers also targeted the online accounts of non-governmental organizations and individual dissidents, clergy, and democratic and human rights activists in the United States, China, Hong Kong, and abroad. Targeted industries included high tech manufacturing; medical device, civil, and industrial engineering; business, educational, and gaming software; solar energy; pharmaceuticals; and defense. According to the indictment, these malicious cyber activities began more than ten years ago and were ongoing as of the date of the indictment. During that time, the hackers stole terabytes of data from hundreds of targets, establishing themselves as a prolific threat to U.S. and foreign networks.*

- *The activities outlined in the indictment are concrete examples of two concerning trends: first, and one we've seen for some time, China is using cyber-enabled theft as part of a global campaign to "rob, replicate, and replace" non-Chinese companies in the global marketplace, and second, and one that is perhaps less appreciated by the public and international partners, China is providing a safe haven for criminals who, as in this case, are hacking in part for their own personal profit but willing to help the state.*

- *As the indictment shows, the hackers targeted technology companies in countries with high technology industries, including in Australia, Belgium, Germany, Japan, Lithuania, the Netherlands, Spain, South Korea, Sweden, the United Kingdom, and the United States. These intrusions are yet another example of China's brazen willingness to engage in theft through computer intrusions contrary to their international commitments – such as their 2015 understanding with the United States, and similar understandings with other countries, not to "conduct or knowingly support cyber-enabled theft of intellectual property, including trade secrets or other confidential business information,"[1] with the intent of providing competitive advantages to companies or commercial sectors.*

- *Unsurprisingly, the intrusions targeted industries outlined in "Made in China 2025" – China's ten-year plan for targeting strategic advanced technology manufacturing industries for development. While the plan calls for an innovation-driven approach, cases like this one[2] show it is as much a roadmap to theft as it is guidance to innovate. The intrusions in this case targeted 8 of the 10 technology sectors identified in the plan: next generation information technology, robotics and automated machine tools, aircraft and aircraft components, maritime vessels and marine engineering equipment, clean energy vehicles, new materials, biotechnology, and advanced rail.*

- *The indictment specifically outlines how stealing intellectual property from companies in these high-tech industries could help Chinese companies replicate the targeted technology and eventually edge out their non-Chinese competitors.*

- *For example, from one target, a Maryland technology and manufacturing firm, the defendants obtained competitive business intelligence, in the form of testing mechanisms and results, product composition, manufacturing processes, and supply chain data that would have revealed to competitors what products the firm was intending to bring to the market. The same stolen information would have allowed competitors to save on research and development costs and time, thereby providing them a competitive edge in the global marketplace. Similar concrete examples of stolen research and development data include a Massachusetts pharmaceutical company, which suffered the theft of the chemical structure of, and engineering processes for, anti-infective agents, and a California pharmaceutical company, which suffered the theft of the chemical structure of, and testing data for, the treatment far a common chronic disease.*

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42. CNN, Sherisse Pham and Swati Gupta, "India is blocking more apps in the wake of the TikTok ban," (July 28, 2020)

https://www.cnn.com/2020/07/28/tech/india-china-apps-ban-hnk-intl/index.html

- *India is banning dozens more apps and reportedly reviewing hundreds of others from well-known Chinese companies, as tensions between the world's most populous countries continue to rise.*

- *The Indian government banned an additional 47 apps, all clones or variations of 59 other apps India blocked last month on national security grounds, an official at India's Ministry of Electronics and Information Technology told CNN Business on Tuesday.*

- *Caught up in the initial ban were several prominent Chinese apps, including the wildly popular video sharing app TikTok. App clones or variants would likely include lighter versions designed for entry-level smortphones with limited memory.*

- *"Although the decision is based on the fact the new apps are the clones of the previously banned apps, we believe that this signals a strong intent from the Indian government's point of*

view on their stand about data security and privacy," said Tarun Pathak, associate director at Counterpoint Research. "This will surely open up a lot of discussion about other apps as well."

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43. OilPrice.com, "Why The Iran-China Oil Alliance Is So Important," (July 30, 2020)

https://oilprice.com/Geopolitics/Asia/Why-The-Iran-China-Oil-Alliance-Is-So-Important.html

- *The steady rise in U.S. strategic competition with the People's Republic of China (PRC) over trade and the South China Sea already has so many dimensions that it is sometimes easy to ignore shifts in the PRC's behavior in other areas. On July 6, 2020, Iranian Foreign Minister Javad Zarif announced that Iran was negotiating an agreement with the PRC - with which it long has had trade and strategic links - which would now make the two countries the equivalent of strategic partners.*

- *This expanded U.S.-PRC competition to new parts of the world. Perhaps more importantly, the move is a substantive and significant response to India's success in militarily outmaneuvering the PRC in Kashmir during June 2020.*

- *The PRC-Iran accord means the end of Indian use of the Iranian port of Chah Bahar and the construction of a rail link from that port city northward to link with a new rail spur into Afghanistan. India's moves into Kashmir in 2019-2020 are widely perceived in Beijing to presage a new move by India to cut off the PRC-Pakistan landbridge through Pakistani controlled Azad (Free) Kashmir, giving India its own landbridge to Central Asia.*

- *Thus, after the confrontation between the Indian Army and People's Liberation Army (PLA) troops in the Ladakh region of Kashmir on June 15-16, 2020, Beijing determined it would respond by cutting Indian access to Central Asia through Iran. The first signs came as the Iran-PRC deal was announced and the Iranian government canceled the Chah Bahar to Zahedan rail link which was to be built by India, citing Indian delays on the 628 km project. The Iranian government said that it would complete the line on its own, with a $400 million investment from the Iranian National Development Fund to the Iranian Railways.*

- *Indian Prime Minister Narendra Modi had gone to Tehran in May 2016 to sign the Chah Bahar deal, but work was indeed delayed as India fretted that the project might invoke U.S. sanctions against India.*

44. New York Times, "Exclusive: Portugal Telcos Won't Use Huawei for Core 5G Networks Though No Government Ban," (July 30, 2020)

https://www.nytimes.com/reuters/2020/07/30/business/30reuters-huawei-5g-portugal-exclusive.html

- *The three companies who dominate Portugal's mobile phone market said they would not use Huawei [HWT.UL] technology in their core 5G networks despite the government not banning the Chinese group from supplying critical infrastructure.*

- *NOS, Vodafone and Altice - which together serve nearly 100% of Portugal's mobile customers - all said they had decided not to use Huawei kit in the core systems of their 5G networks, which covers servers, gateways and routers that forward traffic to the antennas.*

- *The question of whether or not to use Huawei for next-generation mobile networks has become a major issue in Europe amid intense diplomatic pressure from the United States to ban the Chinese group.*

- *The Portuguese government has so far not taken a stance, but Infrastructure Minister Pedro Nuno Santos told Reuters it has "no 'a priori' issues with any manufacturer."*

- *Nuno Santos revealed that a group created by the Portuguese government to assess risks and cybersecurity issues relating to 5G had completed its work and had not drawn any conclusions directed against any particular supplier.*

- *Huawei did not immediately reply to a request for comment.*

- *Core mobile networks carry higher surveillance risks because they incorporate more sophisticated software that processes sensitive information such as customers' personal data.*

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45. Reuters, Joyce Lee, "Samsung Electronics to halt production at its last computer factory in China," (August 1, 2020)

https://www.reuters.com/article/us-samsung-elec-china-pc/samsung-electronics-to-halt-production-at-its-last-computer-factory-in-china-idUSKBN24X3K4

- *Samsung Electronics Co will halt operations of its last computer factory in China, the South Korean tech giant said on Saturday, the latest manufacturer to shift production from the world's second-biggest economy.*

- *Companies are rethinking their production and supply chains amid rising Chinese labour costs, a U.S.-China trade war and the blow from the COVID-19 pandemic.*

- *Around half the 1,700 employees on contract at Samsung Electronics Suzhou Computer will be affected, excluding those involved in research and development, the South China Morning Post reported on Friday, citing a notice to Samsung staff.*

- *The factory shipped $4.3 billion worth of goods out of China in 2012, a figure that had sunk to $1 billion by 2018, the Hong Kong newspaper said.*

- *A Samsung spokeswoman declined to comment on the factory's revenue and shipments, or details regarding employees.*

- *"China remains an important market for Samsung and we will continue to provide superior products and services for Chinese consumers," the company said in a statement.*

- *Samsung shut its last smartphone factory in China last year. Its remaining facilities include two semiconductor manufacturing sites in Suzhou and Xi'an.*

46. U.S. Department of Justice, "Press Release: Harvard University Professor Charged with Tax Offenses," (July 28, 2020)

https://www.justice.gov/opa/pr/harvard-university-professor-charged-tax-offenses

- *Dr. Charles Lieber was previously indicted on charges of making false statements to federal authorities regarding his participation in China's Thousand Talents Program*

- *The former Chair of Harvard University's Chemistry and Chemical Biology Department was charged today in a superseding indictment with tax offenses for failing to report income he received from Wuhan University of Technology (WUT) in Wuhan, China.*

- *Dr. Charles Lieber, 61, was indicted by a federal grand jury in Boston on two caunts af making and subscribing a false income tax return and two counts of failing to file reports of foreign bank and financial accounts (FBAR) with the Internal Revenue Service (IRS). In June 2020, Lieber was indicted on two counts of making false statements to federal authorities. Lieber was arrested an Jan. 28, 2020.*

- *The superseding indictment alleges that Lieber served as the Principal Investigator of the Lieber Research Group at Harvard University, which received more than $15 million in federal research grants between 2008 and 2019. Unbeknownst to his employer, Harvard University, Lieber allegedly became a "Strategic Scientist" at WUT and, later, a contractual participant in China's Thousand Talents Plan from at least 2012 through 2015. China's Thousand Talents Plan is one of the most prominent Chinese talent recruitment plans designed to attract, recruit and cultivate high-level scientific talent in furtherance of China's scientific development, economic prosperity and national security.*

- *Under the terms of Lieber's three-year Thousand Talents contract, WUT allegedly paid Lieber a salary of up to $50,000 per month, living expenses of up to $150,000 and awarded him more than $1.5 million to establish a research lab at WUT. It is alleged that in 2018 and 2019, Lieber lied to federal authorities about his involvement in the Thousand Talents Plan and his affiliation with WUT.*

- *According to the superseding indictment, in tax years 2013 and 2014, Lieber earned income from WUT in the form of salary and other payments made to him pursuant to the Strategic Scientist and Thousand Talents Contracts, which he did not disclose to the IRS an his federal income tax returns. The superseding indictment also alleges that Lieber, together with WUT officials, opened a bank account at a Chinese bank during a trip to Wuhan in 2012. Thereafter, between at least 2013 and 2015, WUT periodically deposited portions of Lieber's salary into that account. U.S. taxpayers are required to report the existence of any foreign bank account that holds more than $10,000 at any time during a given year by the filing an FBAR with the IRS. Lieber allegedly failed to file FBARs for the years 2014 and 2015.*

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CCP Interference Campaigns

47. Le Monde, Damien Leloup and Harold Thibault, "Comment la Chine impose sa propagande sur les réseaux sociaux en France [How China imposes its propaganda on social networks in France]," (July 28, 2020) – ORIGINAL IN FRENCH

https://www.lemonde.fr/pixels/article/2020/07/28/la-propagande-chinoise-s-invite-sur-les-reseaux-sociaux-en-france_6047454_4408996.html

- [GOOGLE TRANSLATE] *The Facebook page of the state-run CGTN has more likes than all other French-speaking media, a probable manipulation which illustrates Beijing's desire to promote its vision.*

- *What is the most popular French-language media on Facebook? It is neither Le Monde (4.6 million "likes"), nor Le Figaro (3.2 million), not more than France Inter (1.4 million), nor even France 24 and its international audience (9 ,8000000). This is French CGTN, which, with more than 20 million "likes", largely crushes all other media, to the point of being the fourth most "liked" French page in the world, according to figures from specialized site Socialbakers .*

- *Does the name mean anything to you? It's normal. CGTN, which was called CCTV until 2016, is a very little watched television channel in France - its audience is not even measured in the Médiamétrie rankings. However, it has colossal means, since it is the international state channel of China, which broadcasts both reports on its culture and press releases denouncing Western interference in Chinese politics.*

- *Analysis of the content published on its Facebook page shows that the videos are very little seen there - a thousand views on average - and that its messages accumulate very few comments, signs that its real audience is small.*

- *Inconsistent figure*

- *The channel, which did not follow up on Le Monde's requests , has it resorted to manipulations to artificially increase its number of "likes"? The possible manipulation illustrates Beijing's desire to promote its vision around the world. On YouTube, she only has a little over 100,000 subscribers, a figure not very consistent with her number of subscribers on Facebook. By*

way of comparison, the French-speaking version of the Russian channel RT (ex-Russia Today), which skilfully plays with the codes of social networks and whose broadcasts are enjoying a certain popularity among supporters of "yellow vests"os in a part of the French extreme right, only gathers 1.1 million "likes" on Facebook, but regularly collects several hundred comments on its publications.

- *Most of the messages published by CGTN on Facebook lend themselves, it is true, little to comments: apart from some animal photographs, sure values of social networks, the channel publishes mainly posts presenting artificial intelligence as the "new impetus of economic development. Chinese " or paraphrasing the latest press release from the Embassy of the Ministry of Foreign Affairs in Beijing.*

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48. Associated Press, "Vatican allegedly hacked by China ahead of key talks," (July 29, 2020)

https://apnews.com/86d667d57bca41ddbc6f289d48f2dfe0

- *The Vatican and the Catholic Diocese of Hong Kong have been the targets of alleged Chinese state-backed hackers ahead of talks on renewal of a landmark 2018 deal that helped thaw diplomatic relations between the Vatican and China, according to a monitoring group.*

- *The alleged attacks by a group called RedDelta began in May with an eye on September talks to renew a provisional agreement on bishop appointments, according to a report Tuesday by the U.S.-based Recorded Future, which tracks state-backed cyber attacks. The attacks were first reported by the New York Times.*

- *The Vatican had no immediate comment. The Chinese foreign ministry denied any involvement, calling the report ''groundless speculation."*

- *Recorded Future said that the Hong Kong Study Mission to China — a key link between the Vatican and China — and the Pontifical Institute for Foreign Missions alsa were targeted.*

- *''The suspected intrusion into the Vatican would offer RedDelta insight into the negatiating positian of the Holy See ahead of the deal's September 2020 renewal," the report said. It alsa*

could provide "valuable intelligence" about Hong Kong-based Catholic entities' position on the pro-democracy movement.

- *The attacks continued at least thraugh July 21. They included an apparent phishing attempt with a document on Vatican Secretariat of State letterhead directed to the head of the Hong Kong Study Mission to China.*

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49. VIDEO – PBS News Hour, "Why the U.S. ordered a Chinese consulate closed — and what it means for foreign policy," (July 22, 2020)

https://www.pbs.org/newshour/show/why-the-u-s-ordered-a-chinese-consulate-closed-and-what-it-means-for-u-s-foreign-policy

- *The Trump administration has ordered China to close its Houston consulate -- the latest action in an escalating fight between the two countries. The State Department cited concerns about espionage and intellectual property theft as justification for the move. Nick Schifrin reports and talks to Yale Law School's Susan Thornton, former acting assistant secretary of state, and author Gordon Chang.*

50. U.S. Department of Justice, "Press Release: Singaporean National Pleads Guilty to Acting in the United States as an Illegal Agent of Chinese Intelligence," (July 24, 2020)

https://www.justice.gov/opa/pr/singaporean-national-pleads-guilty-acting-united-states-illegal-agent-chinese-intelligence

- *Jun Wei Yeo, also known as Dickson Yeo, entered a plea of guilty today to one count of acting within the United Stotes as an illegal ogent of o foreign power without first notifying the Attorney Generol, in violation of 18 U.S.C. § 951. Yeo's plea was entered via videoconference before the Honorable Tanya S. Chutkan in the U.S. District Court for the District of Columbia.*

- *The announcement was made by John G. Demers, Assistant Attorney General; Michael R. Sherwin, Acting U.S. Attorney for the District of Columbia; Timothy R. Slater, Assistant Director in Charge of the Federal Bureau of Investigation's (FBI) Washington Field Office; and Alan E. Kohler, Jr., Assistant Director of the FBI's Counterintelligence Division.*

- *"The Chinese Government uses an array of duplicity to obtain sensitive information from unsuspecting Americans," said Assistant Attorney General for the Justice Department's National Security Divisian John C. Demers. "Yeo was central to one such scheme, using coreer networking sites and a false consulting firm to lure Americans who might be af interest to the Chinese gavernment. This is yet another exomple of the Chinese government's exploitatian of the openness of American society."*

- *"Tadoy's guilty plea underscores the ways thot the Chinese government cantinues to torget Americans with access to sensitive government information, including using the Internet and nan-Chinese natianols to target Americans wha never leave the United States," said Michael R. Sherwin, Acting U.S. Attorney for the District af Columbia. "We will continue to prosecute those who use deceptive practices an the Internet and elsewhere to undermine our national security."*

- *"At the direction of Chinese intelligence operatives, the defendant targeted U.S. government employees and an Army officer to obtain informotion for the government of China. Mr. Yeo admits he set up a fake consulting compony to further his scheme, looked for susceptible individuols who were vulnerable to recruitment, and tried to ovoid detection by U.S. authorities," said Alan E. Kohler Jr., Assistant Director of the FBI's Counterintelligence Division. "But this isn't just about this particular defendant. This case is yet onother reminder thot China is relentless in its pursuit of U.S. technology and policy information in order to advance its own interests. The FBI and our partners will be just os aggressive in uncovering these hidden efforts and charging individuols who break our laws."*

- *"Mr. Yeo admitted that he not only provided valuable information to Chinese intelligence, but also that he knowingly recruited others in the U.S. to do the same," said FBI Woshington Field Office Assistant Director in Chorge Timothy R. Sloter. "The tactics Mr. Yeo used to torget cleared individuals on professionol networking social media sites are just one facet of the full court press Chino employs on a daily bosis to obtoin non-public U.S. government information. The FBI urges citizens, especially those holding security clearances, to be cautious when being approached by individuals on social media sites with implousible career opportunities. We are committed to holding those occountable who attempt to work for Chinese intelligence and other odversaries to the detriment of our national security."*

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51. Axios, Alayna Treene, "FBI director Wray warns of China election interference," (July 30, 2020)

https://www.axios.com/fbi-counterintelligence-china-election-interference-87aa1353-dd92-4010-baf7-cbb521179aa2.html?stream=top

- *FBI Director Christopher Wray and other intelligence community officials warned about China's increased capability to interfere in U.S. elections in separate classified hearings with the Senate Intelligence Committee this week, two sources familiar with the hearings tell Axios.*

- *What we're hearing: Wray and other officials cited concerns that China is developing the ability to interfere with lacal election systems and target members of Cangress to influence China policy, the sources said.*

    - *Wray appeared before committee members on Tuesday afternoon, and the other intel officials, including William Evanina, the director of the National Counterintelligence and Security Center (NCSC), testified on Wednesday.*

    - *An official with the Office of the Director of National Intelligence, which includes the NCSC, said it has been praviding "rabust intelligence-based briefings on electian security to the presidential campaigns, palitical committees, and Congressional audiences" but declined to comment on the details.*

    - *A spokesman for Senator Marco Rubio (R-Fla.), acting Chairman of the Senate Select Cammittee an Intelligence, tald Axios that Rubio is "increasingly concerned about how China is expanding its influence and interference efforts in America. They have a proven capability to carry out cyber attacks and spread disinformation and the clear intent to influence our government policies and pressure policy makers, including members of Congress."*

    - *"They have resources which are far greater than those of Russia," his spokesman added.*

    - *The FBI declined to comment.*

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52. Financial Times, Katrina Manson, Kadhim Shubber and Hannah Murphy, "LinkedIn spy scandal shines spotlight on China's online espionage," (July 31, 2020)

https://www.ft.com/content/0a0e62a9-65ba-494c-a7bb-86f5f66d627f

- *Dickson Yeo, a visiting scholar at George Washington University, liked to tout his US-Asia connections. "Bridging North America with Beijing, Tokyo and south-east Asia," the Singaporean doctoral candidate wrote on his LinkedIn profile, where he advertised his credentials as a political risk analyst with connections to hundreds of policymakers in the US capital.*

- *But last week Mr Yeo admitted in court that he had been working for the Chinese intelligence service. He used the LinkedIn social media network to target Americans in the military and government and harvest information from them.*

- *The case underscores growing fears among intelligence agencies around the world that they are unable to parry China's increasingly astute online espionage efforts aimed at officials with high-level security clearances.*

- *"Foreign spies continue to aggressively use fake profiles on professional networking sites to target Americans who have access to government or commercial secrets," said Bill Evanina, director of the National Counterintelligence and Security Center, the federal government body that leads US counter-intelligence efforts.*

- *Spies are known to pose as headhunters or people with enticing career opportunities in order to connect with individuals viewed as potential sources who could be tapped for information, he explained, noting that thousands of people were targeted on networking websites traditionally used to brandish professional credentials or secure a new job.*

- *Ryan Kalember at Proofpoint, a cyber security group, said recent events had created a "perfect storm" for China's cyber espionage campaign. The coronavirus lockdown meant many more people were spending large amounts of time at home and online while rising US-China tensions created an incentive to step up espionage efforts, he said.*

- ...

53. Politics Home, Alain Tolhurst, "Senior Tory says Chinese hackers ran email impersonation campaign to discredit him after criticism of Beijing," (July 28, 2020)

https://www.politicshome.com/news/article/senior-tory-says-chinese-hackers-ran-email-impersonation-campaign-to-discredit-him-after-criticism-of-beijing

- *A senior Conservative MP has accused Chinese hackers of impersonating him online to try and discredit him after he criticised Beijing.*

- *Tom Tugendhat, chair of the foreign affairs select committee, said professional contacts received bizarre fake press releases, while friends and family were sent untrue claims about his private life.*

- *He told Times Radio many of the emails were "pretty pathetic really", but were designed to be "problematic" and only began after he started speaking out against China.*

- *The National Cyber Security Centre (NCSC) were called in to examine the attacks on his communications, along with Google's security team.*

- *They found the spoof emails originated in China, and Mr Tugendhat said it was "extremely unlikely that it was not state-led".*

- ...

54. The News, Ademola Adegbamigbe, "Controversy: Nigerian Rail Projects and the China Debt Trap," (August 1, 2020)

https://www.thenewsnigeria.com.ng/2020/08/01/controversy-nigerian-rail-projects-and-the-china-debt-trap/

- *China's loan to Nigeria to finance heavy projects like the railways is currently generating acrimonious debates. On one side are people who believe that there is nothing wrong with obtaining such facility. On the other are critics who are ready to swear by their grandfathers' coffins that a foreign loan like this could erode a debtar country's sovereignty.*

- *This controversy started when Mr Rotimi Amaechi, Transport Minister, granted an interview about the terms of the loan agreement. In his words: "I have told the House of Representatives that first I just got to know that there is a clause in the agreement (with China). It is simple; for example, the loan to construct Ibadan to Kano rail is $5.3bn. The implication is that if by the end of the day, you don't pay back our money, whatever we need to take from you, we will take from you. But what the Chinese normally do is that they go after the same asset to recover their money. So whot is wrong with that? It is part of their responsibility, but for now they will jeopardise the obility of government to roise money if we continue to ask questions thot will moke Chino to raise eyebrow and start wondering whot is wrong."*

- *He warned that the country might lose such facilities for the Port Harcourt-Aba, Umuahio-Enugu, Markurdi, Gombe, Jos, Damoturu ond Maiduguri projects. The Minister added thot Nigeria could olso lose the money it seeks for the Ibadan to Kano roil project, which include Ilorin, Minna and Kano. He added, "And then the loan for Lagos to Calabar being pursued with the Russians may also be lost, ond the oreas covered include Ore, Bennin to Asoba, Onitsha, Warri, Uyo, Calabor." He told journolists further that Federal Government had "mapped out plans to repay the loans, as an escrow occount had been opened to pay in the money."*

- *One of the critics, Igbonekwu Ogazimora, warned: "Did you hear Amaechi? If the Chinese gives you money, they ask you to woive your sovereignty and this meons they will go after the very asset they built to recover their money. And how do they take over assets without some measure of force? They bring in their police and army to do so. That is what they are doing in Zambia and some other countries. Before you know it, Nigerio is a Chinese Colony. It is in the interest of Nigeria that the federoting units, States, make it clear they ore not port of this or we find ourselves as slaves in a few decades from now."*

- *China has become the Shylock (in Shokkespeare's Mechant of Venice), of contemporary times. It is also like the situation in the Bible (2 Kings 4:1) when the wife of a man from the compony of the prophets cried out to Elisha, "Your servont my husband is deod, and you know that he revered the LORD. But now his creditor is coming to take my two boys as his slaves." According to o publication by New York Times, Chino's drive to become the developing world's biggest banker is bockfiring. "Over the last two decodes, it unleashed a global lending spree, showering countries with hundreds of billions of dollars, in an effort to expand its influence and become a political and economic superpower. Borrowers put up ports, mines and other crown jewels as collateral. Now, as the world economy reels, countries are increasingly telling Beijing they can't pay the money back."*

- ...

55. Pew Research Center, "Americans Fault China for Its Role in the Spread of COVID-19," (July 30, 2020)

https://www.pewresearch.org/global/2020/07/30/americans-fault-china-for-its-role-in-the-spread-of-covid-19/

- *Unfavorable views of China reach new historic high, and a majority supports taking a tougher stand on human rights*

- *Americans' views of China have continued to sour, according to o new Pew Research Center survey. Today, 73% of U.S. adults say they have an unfavorable view of the country, up 26 percentage points since 2018. Since Morch alone, negotive views of China have increosed 7 points, and there is a widespread sense that China mishandled the initial outbreak ond subsequent spread of COVID-19.*

- *Around two-thirds of Americans (64%) say China has done a bad job dealing with the coronavirus outbreak. Around three-quarters (78%) place a great deal or fair amount of the blame for the global spread of the coronavirus on the Chinese government's initial handling of the COVID-19 outbreak in Wuhan.*

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56. New Zealand Herald, Audrey Young, "China accuses NZ of 'gross interference' in its internal affairs over Hong Kong move," (July 28, 2020)

https://www.nzherald.co.nz/nz/news/article.cfm?c_id=1&objectid=12351738

- *China has accused New Zealand of "gross interference in China's internal affairs" after NZ's decision to suspend its extradition treaty with Hong Kong.*

- *Ambassador Wu Xi said China had lodged its grave concerns about the move, announced today by Foreign Minister Winston Peters.*

- *Peters said that since China had passed new national security legislation for Hong Kong, New Zealand could no longer trust that Hong Kong's criminal justice system was independent from China.*

- *"The New Zealand Government's decision is a serious violation of international law and basic norms governing international relations," she said.*

- ...

57. National Endowment for Democracy, Nicholas Wright, "Artificial Intelligence and Democratic Norms," (August 1, 2020)

https://www.ned.org/sharp-power-and-democratic-resilience-series-artificial-intelligence-and-democratic-norms/

- *This report discusses how to establish democratically accountable rules and norms that harness the benefits of artificial intelligence-related technologies, without infringing on fundamental rights and creating technological affordances that could facilitate authoritarian concentration of power. Absent these purposeful efforts, societies risk spiraling into new authoritarian forms of surveillance-based governance. Civil society around the world has o crucial role to play in helping democracies resist authoritarian pressure an the global surveillance environment. Organizations focused on diverse issues including privacy, human rights, free expression, technological standards, public health, and consumer protection can help identify, explain, and collaboratively address the complex challenges that arise from AI-related technologies.*

    - *"Digital authoritarian competitors stand ready to exploit a lack of foresight in democracies and monipulate the development of global surveillance to serve their own interests."*

- *KEY IDEAS*

    - *Building ond maintaining data silos. Authoritarian regimes can turbocharge AI by training it on two types of data that liberal democracies should not similarly exploit or combine: "broad data" generated at volume on digital devices, and high quality "ground truth data," such as tax returns and medical records. While conventional wisdom says that data must be integrated rather than isolated, siloing data limits authoritarian offordances and enhances security. Civil society must consider whot silos ore necessory to prevent misuse of dato.*

- *Affarding new madels of "digital savereignty" for use by liberal democracies. Authoritarian states advocate for digital sovereignty as a state-based model of control over the internet. There is a critical need to develop alternatives. Civil society can help think through new models that balance sovereignty with the protection of individual freedoms.*

- *Support tech–civil society collaborations and develop resilience. Civil saciety, in cooperation with government and big tech corporations where passible, can aim to correct market failures—like privileging advertising and marketing taals over individual privacy—by giving citizens the means to safeguard democratic integrity against malign information operotions, while preserving essential openness of the information environment.*

- *Resist sharp power in international fora. Norm-setting and technical standardization of AI-related technologies happen at a global scale. Civil saciety should promote transparent, multistakeholder AI governance and develop AI standards that encourage demacratic practices and individual privacy.*

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58. Phayul, Choekyi Lhamo, "German university to close Confucius Institutes by the end of 2020," (July 30, 2020)

https://www.phayul.com/2020/07/30/44103/

- *The University of Hamburg in Germany is reportedly cutting ties with the Confucius Institute (CI) by the end of this year. A German daily newspaper Die Welt cited risks involving "political influence and information leak" for the move.*

- *Another university in Germany, Heinrich Heine University Dusseldorf also ended its ties with Hanban or Confucius Institute Headquarters in 2016 over concerns over CCP's political influence. German universities have joined the US and other European universities in criticizing the role of China's CI which allegedly function as a propaganda arms for the Chinese Communist Party (CCP).*

- *The Free Democratic Party (FDP) has proposed a bill to control these Beijing sponsored language centres to safeguard academic freedom in Germany. The report also suggests that*

University in Bonn is also assessing its cooperation and continued operations with the school's CI. However, Germany's Goethe University Frankfurt has dismissed such allegations that such CI facilities propagate CCP's agenda.

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59. Washington Free Beacon, Yuichiro Kakutani, "Harvard Taps Former CCP Official to Conduct Polling in China," (July 31, 2020)

https://freebeacon.com/coronavirus/harvard-hires-ex-regime-official-to-poll-china/

- *A recent Harvard University poll found that the Chinese government enjoys near-universal support from its citizens, findings that Beijing has quickly exploited.*

- *That poll, however, was conducted by a company led by a former Chinese government official, a fact that raises questions about its reliability—and one that the university did not disclose.*

- *The poll, conducted by the Horizon Research Consultancy Group, found that 93 percent of Chinese citizens approve of the country's Communist regime. Horizon Research is a Chinese polling company with extensive business and institutional ties to the Chinese government.*

- *The university, which has received at least $76 million from Chinese entities since 2014, downplayed the relationship. A university spokesman, Daniel Harsha, told the Washington Free Beacon that Horizon is a "reputable domestic Chinese polling firm." Withholding the name of the firm, Harsha said, was necessary to protect the company from "political reprisals."*

- *Foreign policy experts, however, question the reliability of surveys conducted by Chinese firms within the country.*

- *"I think it's impossible to get reliable data, given that people in China are necessarily going to feel concerned that their answers are going to have wider implications," said Zack Cooper, a research fellow at the American Enterprise Institute. "One possibility is that people feel much more watched now.... They are responding less honestly to polling."*

- *Harvard acknowledged that those living under authoritarian regimes are less likely to give candid opinions, but said the university stands by the results of the poll because researchers "odhered to the highest scholarly standards."*

- *"[Intimidation] is alwoys o possibility in authoritarion or semi-authoritarian country, but it does not make attempts by social scientists to measure public opinion illegitimate," Harsha said.*

- *The Harvard study, conducted by scholars affiliated with the school's Ash Center for Democratic Governance tracked public approval for the Chinese central government—as well as lower levels of government—between 2003 and 2016. It found that public approval for all levels of government has increased during the 13-year period. The researchers published their findings in an academic journal in late 2019 and once again as a "policy brief" in July 2020.*

- *While Harvard declined to identify the polling company in both reports, professor Anthony Saich, one of three researchers behind the study, told both the Economist and the New York Times in 2015 that he worked with Horizon Research to conduct the survey. Harvard did not respond to additional questions about why it is withholding information it readily provided five years ago.*

- *Horizon Research was founded by Yuan Yue, a former official at the Chinese Ministry of Justice who now serves as Horizon's chairman. The company, now known as Dataway, has extensive business ties with the Chinese government, working with more than 20 state governments, according to a 2019 case study on the company. Horizon Research has also directly worked with Chinese government officials, hosting workshops for party officials and collaborating with an appendage of the State Council, the chief administrative organ of the Chinese state.*

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60. The Australian, Matthew Denholm, "Beijing 'agents of influence' operating in Tasmania," (July 28, 2020)

https://www.theaustralian.com.au/nation/politics/beijing-agents-of-influence-operating-in-tasmania/news-story/39b5307b430a41b5903d8d890f4af0c4

- *A network of members of the Chinese Communist Party-linked United Front is operating in Tasmania, taking its cue from Beijing in spreading CCP propaganda and influence, say several China experts.*

- *Mark Harrison, adjunct director of the Australian National University's Australian Centre on China in the World, said the Tasmanian network was small but "disproportionately visible".*

CCP Crackdown on Hong Kong

61. New York Times, Austin Ramzy, Elaine Yu and Tiffany May, "Hong Kong Is Keeping Pro-Democracy Candidates Out of Its Election," (July 29, 2020)

https://www.nytimes.com/2020/07/29/world/asia/hong-kong-arrests-security-law.html

- *Twelve candidates, including several prominent democracy advocates, were barred from an upcoming legislative election, and four activists were arrested over online posts.*

- *Weeks after the Chinese government imposed a new natianal security law on Hong Kong, raising fears of a broader crackdawn an the semiautanomous territory, the city's authorities have taken aggressive steps against the pro-democracy opposition.*

- *Officials an Thursday barred 12 candidates, including well-known pro-democracy figures, from the September legislative electian. The disqualifications came a day after the police made what appeared ta be the first targeted arrests of faur activists accused of posting pro-independence messages online.*

- *Local news outlets also reported that the government was considering postponing the election by as much as a year because of the coronavirus pandemic, though pro-democracy lawmakers argued it would be a naked attempt to avoid a loss at the polls.*

- *Opposition candidates soid they had hoped to ride a wave of protests and public discontent to electorol success on Sept. 6. But they hod also acknowledged the fear that the government would disqualify candidotes on the nebulous grounds that they would not uphold the Basic Low, the Hong Kong Constitution.*

- ...

62. Hong Kong Democracy Council, "Pro-democracy candidates disqualified from LegCo elections," (July 30, 2020)

https://hkdc.us/wp-content/uploads/2020/07/Pro-Democracy-Candidates-Disqualified-from-LegCo-Elections-July-30-2020-2.pdf

- *In response to the outrogeous decision by Hong Kong government ond election officials to disqualify ot least 12 pro-democracy candidotes from stonding in the upcoming Legislotive Council elections scheduled for September 6, 2020.*

- *HKDC's Manoging Director, Samuel, Chu, releoses the following statement:*

- *"The politicol purge continues in Hong Kong today. We stond with the 12 brave pro-democracy condidates who got disquolified and banned from LegCo elections. They are the true leoders for the real Hong Kong.*

- *We are outraged but not surprised. In the face of the determination demonstrated in the "Democrats 35+" primaries earlier this month in which more than 600,000 Hong Kongers cost their votes despite long lines, intimidation ond horossment, the Lam administration disqualified the pro-democracy condidates in an ottempt to prevent them from winning the majority in the LegCo, following the pro-Democracy camp's landslide victory in the District Council Elections last November.*

- *This is what dictators do - disqualify opposition and delay democratic elections, os Carrie Lam has hinted she might do, when they know they have lost the people.*

- ...

63. The Spectator, Johnny Patterson, "Welcome to Authoritarian Hong Kong," (July 31, 2020)

https://www.spectator.co.uk/article/welcome-to-authoritarian-hong-kong

- *The natianal security law in Hang Kang has been passed for just over a month, but the scape af Beijing's plans are now clear. This is a constitutional coup. The safeguards which have historically defended human rights in Hong Kong have been shattered. Rule of law has been replaced with rule by law – and the Communist Party's word is law.*

- *Thursday 30 July brought home the reality of the new status quo. Hong Kongers woke up to the news that four young people aged between 16 and 21 years old – representing a small group of students who campaigned for Hong Kong independence last year – heard a midnight knock on the door and were arrested. Their crime? Posting on social media, or 'organising and inciting secession' in the new dystopian Hong Kang. This carries up to ten years in jail. It's akin to Boris Johnson choosing ta lock up members of the youth branch of the SNP.*

- ...

64. New York Times, Austin Ramzy and Tiffany May, "Hong Kong University to Fire Law Professor Who Inspired Protests," (July 28, 2020)

https://www.nytimes.com/2020/07/28/world/asia/benny-tai-hong-kong-university.html

- *Benny Tai was convicted af public nuisance charges related to his leading role in the 2014 pro-democracy Umbrella Movement.*

- *The University af Hang Kang's governing body vated an Tuesday ta fire an assaciate law professar wha was convicted last year af charges related ta his leading role in the 2014 Umbrella Movement protests and has remained a key figure in the city's pro-democracy movement.*

- *The legal scholar, Benny Tai, was convicted of public nuisance charges last year [nytimes.com] and sentenced to 16 months in prisan [nytimes.com], but he was released and remains an bail while his case is under appeal.*

- *The university had faced widespread calls from members of the pro-Beijing establishment to dismiss Mr. Tai. But his supporters argued that dismissing him would undermine academic freedom that has already been imperiled by a new national security law imposed by Beijing.*

- *The decision "marks the end of academic freedam in Hong Kang," Mr. Tai said in a Facebook post [focebook.com]. "Academic staff in education institutions in Hong Kong are na langer free ta make contraversial statements to the general public about politically or sacially contraversial matters."*

- *Last year the university began an investigation into Mr. Tai thot led to Tuesdoy's decision by the school's council, o body dominated by members from outside the university. Arthur Li, its choir, is also on odviser to Carrie Lom, Hong Kong's chief executive.*

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65. Hong Kong Free Press, Kelly Ho, "Hong Kong Chief Exec. Carrie Lam may postpone Sept election citing Covid-19 – report," (July 28, 2020)

https://hongkongfp.com/2020/07/28/just-in-hong-kong-chief-exec-carrie-lam-may-postpone-sept-election-citing-covid-19-report/

- *The Hong Kong government may postpone the 2020 Legislotive Council election omid the current wave of coronavirus infections, according to local medio citing sources.*

- *The Hong Kong Economic Times and Citizen News reported thot Chief Executive Carrie Lam is set to hold a special meeting with the Executive Council on Tuesday and may announce that the race will be postponed.*

- *On Saturdoy, former Legislative Council president Jasper Tsong suggested that the election could be deloyed for at least o year. He said that, during the coronavirus outbreak, it would be difficult to fully implement onti-epidemic measures and maintain social distancing.*

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CCP Coercion of Taiwan

66. Bloomberg, Iain Marlow and Cindy Wang, "China's Xi Sets His Sights on Taiwan After Subduing Hong Kong," (July 30, 2020)

https://www.bloomberg.com/news/articles/2020-07-30/china-set-its-sights-on-taiwan-after-hong-kong-crackdown

- *The leader wants to continue on the path of Mao and Deng by bringing more territory under Beijing's control.*

- *Ever since Mao Zedong triumphed in 1949, prompting his Nationalist enemies to flee to Taiwan, Communist Party leaders have bolstered their legitimacy to rule by taming rebellious corners of China's vast periphery.*

- *The quest to capture lost territory prompted Mao's army to subdue Tibet, where cadres co-opted Buddhist monasteries and eventually built a railway that ensured well-supplied garrisons of troops across the Himalayan plateau. He also reclaimed Xinjiang in the far west, a Muslim desert region the size of Iran where Silk Road traders once crossed paths with Uighurs—who have now been reduced to about 30% of the population of their own homeland after millions of China's dominant Han ethnicity moved in. After Moo's deoth, Deng Xiooping further helped restore China's glory following the so-called century of humiliotion when he negotiated the return of two cities lost to coloniol powers. The U.K. honded over Hong Kong in 1997, ond Portugal followed two years later with Macao.*

- *Xi Jinping has consolidated control in all of these places since taking power in 2012 and bolstered Beijing's hold on disputed reefs in the South China Sea. Most notably, he set up a vast police state in Xinjiang that sent Muslims en masse to reeducation camps, and just in July he imposed a sweeping national security law in Hong Kong aimed at stamping out dissent in a city that many in the West once hoped would spur China to embrace democracy.*

- ...

CCP Military and Security Threats

67. South China Morning Post, Tashny Sukumaran and Bhavan Jaipragas, "Malaysia rebukes Beijing as South China Sea 'lawfare' heats up," (July 30, 2020)

https://www.scmp.com/week-asia/politics/article/3095406/malaysia-rebukes-beijing-south-china-sea-lawfare-heats

- *Unusually strong statement by Malaysia takes issue with Beijing for claiming it had no right to seek establishment of continental shelf in northern waters*

- *Move reflects Malaysia's rejection of China's 'nine-dash line'*

- *A battle of diplomatic notes to the United Nations between claimants in the South China Sea dispute has taken a fresh turn, with Malaysia rebuking China for claiming Kuala Lumpur had no right to seek the establishment of its continental shelf in the northern part of the waters.*

- *Instead, Prime Minister Muhyiddin Yassin's government, in a note verbale to the world body dated July 29, stressed that its application was fully within its rights under the UN Convention for the Law of the Sea (Unclos).*

- *The unusually strong statement, seen by This Week in Asia on Thursday, said Malaysia rejected "in its entirety the contents" of an earlier note by Beijing on December 12.*

- *The Chinese note had itself been a response to a Malaysian submission to on Unclos body stating that there were areas of potential overlapping claims in the areas where it was seeking to delimit its territory. China at the time had said the Malaysian submission "seriously infringed China's sovereignty, sovereign rights and jurisdiction in the South China Sea".*

- *In its latest response, Malaysia said it rejected "China's claims to historic rights, or other sovereign rights or jurisdiction, with respect to the maritime areas of the South China Seo encompassed by the relevant part of the 'nine-dash line'."*

- ...

68. VIDEO – South China Morning Post, "Washington's hardened position on Beijing's claims in South China Sea heightens US-China tensions," (July 14, 2020)

https://www.youtube.com/watch?time_continue=4&v=IbmpAk0zrbM&feature=emb_logo

- *US Secretary of State Mike Pompeo made an online statement on July 13, 2020, in which he shared Washington's hardened position on the South China Sea. He rejected most of Beijing's claims within the so-called nine-dash line that encompasses 90 per cent of the strategic area. China's foreign ministry hit back on July 14, calling the US challenge "groundless" and an effort to sow discord. Tension between the two superpowers had already been on the rise over trade, Covid-19 and human rights issues.*

69. South China Morning Post, Kristin Huang, "South China Sea: Beijing reclassifies navigation area to increase control, experts say," (July 31, 2020)

https://www.scmp.com/news/china/diplomacy/article/3095550/south-china-sea-beijing-reclassifies-navigation-area-increase

- *Change to regulation drawn up in 1974 indicative of Beijing's drive to bring as much of the disputed waterway under its control as possible*

- *Country is facing growing criticism on the world stage over its claims to almost all of the South China Sea*

- *China has changed the wording of a shipping regulation to identify a stretch of water between Hainan province and the Paracels Islands in the South China Sea as a "coastal" rather than "offshore" navigation area.*

- *Observers said the move was indicative of Beijing's drive to bring as much of the disputed waterway under its control as possible.*

- *The word change appeared in an amended version of a regulation – drawn up in 1974 – regarding technical rules for the statutory testing of seagoing vessels. It will take effect on Saturday.*

- *The regulation, titled "Technical Rules for the Statutory Testing of Seagoing Vessels on Domestic Voyages" establishes the "Hainan-Xisha Navigation Area", which is bound by two points on Hainan island – China's most southerly province – and three in the Paracels, or Xisha as they are known in Mandarin.*

- ...

70. New York Times, James Anderson, "China's Arms Buildup Threatens the Nuclear Balance," (July 29, 2020)

https://www.nytimes.com/2020/07/29/opinion/russia-china-nuclear-weapons.html?referringSource=articleShare

- *Nuclear arms cantrol is at a crassroads — not because we are approaching the deadline on an extensian of the 2010 New Strategic Arms Reductian Treaty, but because China's nuclear expansian threatens ta upend decades af relative nuclear stability between the United States and Russia.*

- *The United States and Russia have been reducing their strategic nuclear arsenals since the end of the Cold War. The 1991 Start Treaty allawed each side 6,000 deployable strategic nuclear warheads; the 2010 treaty, known as New Start, lowered that limit ta 1,550 operationally deployed strategic nuclear warheads.*

- *But stability at these lower force levels will be challenged by China's nuclear ambitions. China is clearly moving away from the small, limited nuclear force of its past. It is fielding modern land- and sea-based strategic systems and plans to introduce an air-launched ballistic missile delivered by heavy bombers in the near future, achieving its own strategic nuclear triad.*

- *The Defense Intelligence Agency estimates that China will at least double the size of its nuclear arsenal aver the next decade and is building the production capacity to expand it further. Given China's secrecy abaut its nuclear forces, and its manifestly aggressive strategic intentians, this nuclear expansion may go even further, well beyond Beijing's old "minimum deterrence" doctrine.*

- *Still, it is in China's interest to reverse its dangerous nuclear buildup, lest it set off a nuclear arms race involving the United Stotes and Russia, and perhaps encourage other nuclear pawers to increase their forces to keep pace.*

- *Meonwhile, the United States is replacing its aging nuclear weapons systems. Our intention is to remain within the New Start limits of 700 strategic missiles and bombers ond 1,550 deployed strategic warheads.*

- *But as Chinese nuclear forces grow in size and sophistication, the United States will have no choice but to reassess and adjust its own nuclear force requirements. In the past, the United States classified China's small nuclear arsenal as a subset of U.S. nuclear force requirements, which have been largely driven by the Soviet and then Russian threat.*

- *But this will not remain the case if U.S. nuclear forces remain at historically low levels and China's continue to expand with no discernible constraint. And the less we know about what China is doing and why, the more the United States must rely on worst case scenarios to size its nuclear forces accordingly.*

- *China's nuclear expansion and its refusal to engage in meaningful dialogue will affect stability on multiple levels. Increased U.S. nuclear force requirements to ensure credible deterrence against China would affect the United States-Russia strategic nuclear balance and threaten to undermine the prospects for further negotiated reductions. We should assume that Russia will also assess the implications of China's expansion.*

- ...

Sender: "Feith, David" <(b)(6) @state.gov>
Recipient: Stilwell, David R (b)(6) @state.gov>

From: (b)(6) @state.gov>
To: Gibbs, Jeffrey J <(b)(6) @state.gov>
Subject: FW: A chronological account of GOF R&D with WIV/Shih efforts referenced
Date: Tue, 15 Dec 2020 17:08:00 +0000

Per Asher's point, see item 10 below.

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Sent: Tuesday, December 15, 2020 10:43 AM
To: Asher, David (b)(6) @state.gov>; (b)(6) @state.gov>; Gross, Laura J (b)(6) @state.gov>; Paulopol, Andreea I (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) G@state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: (b)(6) @state.gov>
Subject: A chronological account of GOF R&D with WIV/Shih efforts referenced

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In the process of exploring virus functions, various accidents often occur. The unfinished version of biological and chemical weapons is often more dangerous than the completed version. Such weapons have not yet been controlled. Once leaked, the consequences would be disastrous. Complete biological and chemical weapons are not so dangerous because they have been controlled. However, the research and development process of biochemical weapons will definitely go through the process of natural pathogens → (uncontrolled) acquisition of functional modified pathogens → (uncontrolled) weapon-level pathogens → controlled biochemical weapons. Such semi-finished products are always the most dangerous.
(探索病毒功能的改造过程中，经常会出现各种意外。未完成版的生化武器往往比完成版的生化武器更加危险。这样的武器尚未被控制，一旦泄漏，后果不堪设想。完整的生化武器因为已经受控，反而没有这么危险。
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Sender: (b)(6) @state.gov>
Recipient: Gibbs, Jeffrey J <(b)(6) @state.gov>

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From: "Asher, David" (b)(6) @state.gov>

To: Gibbs, Jeffrey J <(b)(6) @state.gov>;
DiNanno, Thomas G <(b)(6) @state.gov>

CC: (b)(6) (b)(6) @state.gov>;
(b)(6) @state.gov>;
(b)(6) @state.gov>

Subject: DRAFT: Hello from the US Department of State — interes ted in getting your take on potential COV19 origins and implications

Date: Wed, 23 Dec 2020 23:29:19 +0000

What do you think about reaching out to Ebright at Rutgers in light of Mike's research?

————————-

Dear Professor Ebright,

(b)(5) Deliberative Process

Best regards,

David Asher

Sender: "Asher, David" (b)(6) @state.gov>

Recipient: Gibbs, Jeffrey J (b)(6) @state.gov>;
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To stop the next pandemic, we need to unravel the origins of COVID-19

David A. Relman[a,b,c,d,1]

We find ourselves ten months into one of the most catastrophic global health events of our lifetime and, disturbingly, we still do not know how it began. What's even more troubling is that despite the critical importance of this question, efforts to investigate the origins of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus and of the associated disease, coronavirus disease 2019 (COVID-19), have become mired in politics, poorly supported assumptions and assertions, and incomplete information.

SARS-CoV-2 is a betacoronavirus whose apparent closest relatives, RaTG13 and RmYN02, are reported to have been collected from bats in 2013 and 2019, respectively, in Yunnan Province, China (1). COVID-19 was first reported in December 2019 more than 1,000 miles away in Wuhan City, Hubei Province, China. Beyond these facts, the "origin story" is missing many key details, including a plausible and suitably detailed recent evolutionary history of the virus, the identity and provenance of its most recent ancestors, and surprisingly, the place, time, and mechanism of transmission of the first human infection. Even though a definitive answer may not be forthcoming, and even though an objective analysis requires addressing

To avoid or mitigate the dire consequences of this and future pandemics (here, people in PPE bury a victim in Delhi, India in June), unraveling the origins of SARS-CoV-2 and COVID-19 will be essential—even though a definitive answer may be elusive, and an objective analysis means broaching some uncomfortable possibilities. Image credit: Shutterstock/PradeepGaurs.

[a]Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305; [b]Department of Microbiology & Immunology, Stanford University School of Medicine, Stanford, CA 94305; [c]Center for International Security and Cooperation, Stanford University, Stanford, CA 94305; and [d]Infectious Diseases Section, Veterans Affairs Palo Alto Health Care System, Palo Alto, CA 94304

The author declares no competing interest.

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First published November 3, 2020.

some level of possibility that we pursue this question. Preventing the next pandemic depends on understanding the origins of this one.

There are several potential origin scenarios. First, SARS-CoV-2 may have evolved in bats, which are known reservoirs of immense coronavirus diversity (2), and then spread directly, or indirectly via an intermediate host, to humans through natural mechanisms. The degree of anticipated but undiscovered natural diversity clearly lends support to this scenario, as well as support to other scenarios. Second, SARS-CoV-2 or a recent ancestor virus may have been collected by humans from a bat or other animal and then brought to a laboratory where it was stored knowingly or unknowingly, propagated and perhaps manipulated genetically to understand its biological properties, and then released accidentally.

Some have argued that a deliberate engineering scenario is unlikely because one would not have had the insight *a priori* to design the current pandemic virus (3). This argument fails to acknowledge the possibility that two or more as yet undisclosed ancestors (i.e., more proximal ancestors than RaTG13 and RmYN02) had already been discovered and were being studied in a laboratory—for example, one with the SARS-CoV-2 backbone and spike protein receptor-binding domain, and the other with the SARS-CoV-2 polybasic furin cleavage site. It would have been a logical next step to wonder about the properties of a recombinant virus and then create it in the laboratory. Alternatively, the complete SARS-CoV-2 sequence could have been recovered from a bat sample and viable virus resurrected from a synthetic genome to study it, before that virus accidentally escaped from the laboratory. The third scenario, seemingly much less likely, involves laboratory manipulation or release, with the clear intention of causing harm.

Even though strong opinions abound, none of these scenarios can be confidently ruled in or ruled out with currently available facts. Just because there are no public reports of more immediate, proximal ancestors in natural hosts, doesn't mean that these ancestors don't exist in natural hosts or that COVID-19 didn't began as a spillover event. Nor does it mean that they have not been recovered and studied, or deliberately recombined in a laboratory.

Why do these distinctions matter? If we find more concrete evidence of a "spill-over" event with SARS-CoV-2 passing directly from bat to human, then efforts to understand and manage the bat–human interface need to be significantly strengthened. But if SARS-CoV-2 escaped from a lab to cause the pandemic, it will become critical to understand the chain of events and prevent this from happening again. Rather than resorting to hunches or finger-pointing, each scenario must be systematically and objectively analyzed using the best available science-based approaches. There is a path to greater clarity. It requires scientific rigor, forensic approaches, deliberate methods, transparency, and cooperation.

In an effort to reveal the origins of the pandemic, researchers so far have focused on the SARS-CoV-2 genome sequences. However, the study of the pandemic virus tells us only so much. First, the closest known relatives, RaTG13 and RmYN02, are not that close (4). Second, there is probably more than one recent ancestral lineage that contributes to SARS-CoV-2 because its genome shows evidence of recombination between different parental viruses. In nature, recombination is common among coronaviruses. But it's also common in some research laboratories where recombinant engineering is used to study those viruses. The bottom line is simple: We need to identify the immediate parent(s) of SARS-CoV-2, and they're missing.

To find its parents and understand its recent history, we need 1) additional genome sequences of coronaviruses from relevant bats and other suspect hosts—some of these likely exist already in laboratories, given the efforts so far undertaken to survey bats in particular (2, 5); 2) measurements of SARS-CoV-2 evolution under a variety of defined conditions so that differences between viral genomes can be understood better as differences in time on an evolutionary clock; and 3) data from antibody surveys of humans at high risk of coronavirus exposure and from past cases of similar disease, so that previously unrecognized encounters can be revealed. In addition, we need to address whether there is information about host or environmental samples that contain recent ancestors of SARS-CoV-2, data perhaps not yet publicly available. More generally, are there relevant scientific data, including from coronavirus engineering work in laboratories, that have not been shared widely? Who knew what about relevant viruses and cases of disease before December 2019, and when? This information will go a long way toward clarifying the origins of this pandemic, even if certainty continues to elude us.

A deliberative process for investigating the origins of this pandemic must be representative of all relevant disciplines, expertise, and stakeholders; must achieve political neutrality, scientific balance, and access to all relevant information and samples; and must operate with transparency and independent oversight. Without these features, it will not be credible, trustworthy, or effective.

The means are just as important as the goals. An investigative process should be transparent, collaborative, international, and, to the extent possible, devoid of political interest. Recent, productive scientific collaborations between the United States and China, for example, provide hope that such a process can be achieved. But the kind of effort required will need to expand far beyond what's taken place so far, and nations other than the United States and China will need to be involved. Conflicts of interest by researchers, administrators, and policymakers on all sides must be revealed and addressed, and all relevant global

constituted, be included." Both the WHO and *The Lancet* COVID-19 Commission (6) have hinted that they have taken some first steps, but their efforts so far have been cloaked in secrecy (7, 8). A deliberative process for investigating the origins of this pandemic must be representative of all relevant disciplines, expertise, and stakeholders; must achieve political neutrality, scientific balance, and access to all relevant information and samples; and must operate with transparency and independent oversight. Without these features, it will not be credible, trustworthy, or effective.

A more complete understanding of the origins of COVID-19 clearly serves the interests of every person in every country on this planet. It will limit further recriminations and diminish the likelihood of conflict; it will lead to more effective responses to this pandemic, as well as efforts to anticipate and prevent the next one. It will also advance our discussions about risky science. And it will do something else: Delineating COVID-19's origin story will help elucidate the nature of our very precarious coexistence within the biosphere.

1 Y.-Z. Zhang, E. C. Holmes, A genomic perspective on the origin and emergence of SARS-CoV-2. *Cell* **181**, 223–227 (2020).

2 A. Latinne *et al.*, Origin and cross-species transmission of bat coronaviruses in China. *Nat. Commun.* **11**, 4235 (2020).

3 K. G. Andersen, A. Rambaut, W. I. Lipkin, E. C. Holmes, R. F. Garry, The proximal origin of SARS-CoV-2. *Nat. Med.* **26**, 450–452 (2020).

4 M. F. Boni *et al.*, Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. *Nat. Microbiol.* (2020).

5 Z. Wu *et al.*, Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. *ISME J.* **10**, 609–620 (2016).

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8 P. Nuki, S. Newey, Scientists to examine possibility Covid leaked from lab as part of investigation into virus origins. *The Telegraph*, 15 September 2020. https://www.telegraph.co.uk/global-health/science-and-disease/scientists-examine-possibility-covid-leaked-lab-part-investigation/. Accessed 27 September 2020.

From: (b)(6) Beijing)
Sent: Mon, 6 Apr 2020 19:59:28 +0000
To: CGRCU Internal Site
Subject: ~~(SBU)~~ Coronavirus Global Response Coordination Unit SitRep No. 99 - 04.06.2020 1600ET

U.S. DEPARTMENT *of* STATE
Coronavirus Global Response Coordination Unit/Repatriations Task Force

SITREP No. 99
April 6, 2020 - 1600 ET

(U) Latest Update

- (U) There are 1,309,439 confirmed cases worldwide, 72,638 deaths, and 273,546 recovered patients. ***(Johns Hopkins CSSE)***

~~(SBU)~~ Repatriation Efforts

- ~~(SBU)~~ The majority of U.S. citizens in Peru that requested repatriation assistance have been successfully returned (more than 5,000) with roughly 2,300 still awaiting assistance. ***(Repatriation Task Force)***
- ~~(SBU)~~ Mission India repatriated roughly 1,000 American citizens this past weekend; approximately 5,000 American citizens are still awaiting assistance, more flights are scheduled for this week. ***(Repatriation Task Force)***
- ~~(SBU)~~ 275 U.S. citizens and residents were repatriated from Bangladesh on April 5. ***(SCA)***

~~(SBU)~~ Global Coronavirus Developments

- (U) UK PM Boris Johnson was admitted to the ICU for COVID-19. ***(WaPo)***
- (U) Queen Elizabeth II delivered a rallying message to the UK; it is the fourth time since her reign began that she has given such an address. ***(BBC)***
- ~~(SBU)~~ Iran's Health Ministry Spokesman claimed China provided false information about Wuhan's death toll, and argued that China had misled other countries in its fight against the outbreak. ***(20 RPO DUBAI 182)***
- (U) The UN expressed alarm at a "horrifying global surge in domestic violence" linked to lockdowns imposed in response to the pandemic. ***(Al Jazeera)***
- ~~(SBU)~~ Qatar's public health statistics show the majority of cases come from the young male migrant population. ***(20 DOHA 278)***

- (U) Poland will hold its presidential election in May even if the nationwide lockdown remains in place. ***(NYT)***
- (U) A partially built COVID-19 testing center was destroyed by local residents in Abidjan who feared facility patients would spread the epidemic. ***(France24)***

~~(SBU)~~ International Assistance

- ~~(SBU)~~ Russia has to date dispatched/pledged over 4,000 test kits, 80 tons of medical equipment, 200 personnel, and specialized military vehicles to over 20 countries. ***(20 MOSCOW 394)***
- ~~(SBU)~~ The President of the European Commission called for a "Marshall Plan" for Europe in the next EU budget. ***(20 USEU BRUSSELS 278)***
- ~~(SBU)~~ On April 7, the Eurogroup will resume discussions on a financial instrument to address the crisis; up to $259 billion could be made available from the European Stability Mechanism. ***(20 USEU BRUSSELS 278)***
- (U) Australian aid groups called for increased Australian assistance to vulnerable neighbors in the Pacific. ***(The Guardian)***
- (U) 14 Latin American countries requested assistance totaling $4.48 billion from the IMF amid the COVID-19 outbreak. ***(FT)***
- ~~(SBU)~~ Romania accessed a World Bank $432 million line of credit to combat the pandemic. ***(20 BUCHAREST 408)***

~~(SBU)~~ Third Country Response Efforts and International Travel

- (U) Japan will declare a month long state of emergency in Tokyo and six other prefectures. ***(Japan Times)***
- (U) Turkey will minimize troop movement in Syria to contain the pandemic. ***(Al Jazeera)***
- ~~(SBU)~~ Saudi Arabia issued directives to allow Saudi citizens to return home, despite its international flight ban. ***(20 RIYADH 490)***
- (U) More than 20,000 Pakistani workers in the UAE are seeking to return home. ***(NYT)***

~~(SBU)~~ Economic and Supply Chain Impact

- ~~(SBU)~~ Nearly 500,000 Croatians have filed for unemployment benefits. ***(20 ZAGREB 340)***
- ~~(SBU)~~ Azerbaijan approved a $588 million economic stimulus plan. ***(20 BAKU 286)***
- ~~(SBU)~~ Pakistan's pilot union called for an end to flights. ***(20 ISLAMABAD 704)***

- ~~(SBU)~~ Rwanda anticipates a need for $300 to 500 million for economic losses from now until June. ***(20 KIGALI 284)***

~~(SBU)~~ Post Operations

- ~~(SBU)~~ The Department extended AD/OD for Embassy Ashgabat for an additional thirty days. ***(State 35792)***
- ~~(SBU)~~ The Department extended AD for Consulate General Milan for an additional thirty days. ***(State 35790)***

Approved (b)(6)
For additional information, please visit https://usdos.sharepoint.com/sites/S_CGRCU/Public/. The Coronavirus Global Response Coordination Unit may be reached at 202-647-1255 or S_CGRCU@groups.state.gov. The Repatriations Task Force may be reached at 202-647-4888 or TF_7A01@groups.state.gov.

U.S. DEPARTMENT *of* STATE
Coronavirus Global Response Coordination Unit/Repatriations Task Force

SITREP No. 98
April 6, 2020 - 00630 ET

(U) Latest Update

- (U) There are 1,277,962 confirmed cases worldwide, 69,555 deaths, and 264,439 recovered patients. ***(Johns Hopkins CSSE)***

~~(SBU)~~ Repatriation Efforts

- ~~(SBU)~~ Over 44,000 U.S. citizens and residents have repatriated via 446 flights from 73 countries. ***(Repatriation Task Force)***
- ~~(SBU)~~ There are 80 upcoming repatriation flights currently scheduled worldwide for a total of 9,219 passengers. ***(Repatriation Task Force)***
- ~~(SBU)~~ 450 U.S. citizens and residents were repatriated from Peru on April 5, making 5,600 to date. ***(Repatriation Task Force)***
- ~~(SBU)~~ Two charter flights with 350 U.S. citizens and residents departed India on April 5. ***(Repatriation Task Force)***
- ~~(SBU)~~ An April 5 flight brought 224 U.S. citizens out of Egypt, as well as 89 permanent residents and others, including foreign medical personnel. ***(Repatriation Task Force)***
- ~~(SBU)~~ 3 U.S. citizens were successfully repatriated from Burundi via Belgium on April 5. ***(Embassy Brussels)***
- ~~(SBU)~~ 267 passengers departed Rangoon on an April 6 repatriation flight, including 252 U.S. citizens and 9 LPRs. ***(Embassy Rangoon)***
- ~~(SBU)~~ 303 passengers departed Nepal on April 5, including 226 U.S. citizens and 62 LPRs. ***(Embassy Kathmandu)***

~~(SBU)~~ Global Coronavirus Developments

- ~~(SBU)~~ On April 5, South Sudan confirmed its first COVID-19 case. ***(20 JUBA 966)***
- (U) British Prime Minister Boris Johnson was admitted to hospital for tests on April 5 ten days after testing positive for the virus. ***(Reuters)***
- (U) On April 5, Barbados and Haiti reported their first deaths linked to the coronavirus outbreak. ***(Reuters)***

(U) Medical Supply Chain Efforts

- ~~(SBU)~~ A FEMA distribution center received on April 5 Taiwan's donation of 100,000 N95 masks and 300,000 standard surgical masks. ***(FEMA Liaison)***

(U) International Assistance

- ~~(SBU)~~ Following a Philippine government request for "epidemic prevention" assistance, a 12-person team of Western and traditional medicine-trained PRC doctors arrived in Manila on April 5. ***(20 MANILA 568)***

(U) Third Country Response Efforts and International Travel

- ~~(SBU)~~ On April 3, an imam at the Grand Mosque in Mecca stressed prayer as the best means to combat COVID-19 ***(20 JEDDAH 144)***.
- (U) Malta placed 1,000 African migrants under mandatory quarantine on April 5 at the camp in Hal Far after an outbreak of COVID-19. ***(Reuters)***
- (U) Guatemala asked the United States to limit the deportations to 25 persons per plane due to concerns about the spread of the coronavirus. ***(Reuters)***

(U) Economic and Supply Chain Impact

- ~~(SBU)~~ The Costa Rican government announced plans to charter a plane to pick up $350,000 of PPE purchased from China; additional flights possible in the future. ***(Embassy San Jose)***

~~(SBU)~~ Support for U.S. Citizens

- ~~(SBU)~~ Asymptomatic U.S. citizens disembarked the Coral Princess April 5. Eleven passengers, including three U.S. citizens, were medevacked to local hospitals. Cruise line charter flights returned passengers to Australia, the UK, and Europe; more flights scheduled for April 6. ***(OFM)***

Approved: (b)(6)

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U.S. DEPARTMENT *of* STATE

Coronavirus Global Response Coordination Unit/Repatriations Task Force

SITREP No. 75
March 23, 2020 - 1600 ET

(U) Latest Update

- (U) There are 372,563 confirmed cases worldwide, 16,381 deaths, and 100,885 recovered patients. ***(Johns Hopkins CSSE)***

~~(SBU)~~ Repatriation Efforts

- ~~(SBU)~~ CA chartered two American Airlines flights per day to Guatemala for three consecutive days starting March 23. Each aircraft has the capacity for 160 passengers. ***(Embassy Guatemala City)***
- ~~(SBU)~~ An American Airlines flight carrying 209 passengers has already departed Lima and is set to arrive in Miami. On March 23, a United Airlines flight carrying 264 passengers is scheduled to depart Lima. On March 24, American Airlines will repeat these flights with same capacity. 20 large flights are anticipated in addition to the four listed above to evacuate U.S. citizens from Peru. ***(Repatriation Task Force).***

~~(SBU)~~ Global Coronavirus Developments

- (U) UN Secretary-General Guterres on March 23 called for a global ceasefire so the world can focus on fighting the coronavirus pandemic. ***(Reuters)***
- (U) The IMF predicts that the coronavirus will cause a global recession in 2020 that could be worse than that seen during the global financial crisis of 2008-2009, but that the world's economic output should recover in 2021. ***(Reuters)***
- (U) Julian Assange's lawyers will apply for his release on bail because of the risk of contracting coronavirus while in prison. ***(Bloomberg)***
- (U) The EU urged its 27 members on Monday to unblock their borders and allow freight vehicles to cross from one country to another within 15 minutes to ensure the flow of basic supplies and medical equipment. ***(Reuters)***
- (U) President Trump wrote a letter to Kim Jung-Un offering assistance in fighting COVID-19; North Korea expressed "sincere gratitude" for the letter. North Korea has not reported any cases, though experts fear Pyongyang is hiding an outbreak. ***(Council on Foreign Relations)***
- (U) The WHO launched global megatrial of the four most promising coronavirus treatments. ***(Science Magazine)***

(U) International Assistance

- (U) Iranian Supreme Leader rejected U.S. offers of aid during a televised address and suggested the U.S. may have created the virus. ***(ConGen Dubai)***
- (U) The United States informed the International Atomic Energy Agency (IAEA) that an additional $5 million of U.S. voluntary contributions to the IAEA will be allocated to supporting the agency's efforts to combat the COVID-19 outbreak. ***(UNVIE)***
- (U) The World Bank could deploy as much as $150 billion in resources for COVID-19 assistance and recovery over the next 15 months. ***(Reuters)***
- (U) Facebook's Mark Zuckerberg and Apple's Tim Cook have pledged to donate masks to medical professionals in the U.S. and Europe amid the COVID-19 outbreak. ***(CNBC)***

(U) Third Country Response Efforts and International Travel

- (U) Canada announced $5,000 loans for citizens stuck abroad. ***(WHA)***
- (U) Germany repatriated some 120,000 of 200,000 tourists overseas. ***(Reuters)***
- (U) The British army will deliver PPE to healthcare workers. (***CNBC)***
- (U) Canada and Australia will not compete in the Olympics. ***(Kyodo, Reuters)***
- (U) Nepal closed all international border for traveler movement for a week; the flow of goods and imports will continue. ***(20 KATHMANDU 332)***

(U) Economic and Supply Chain Impact

- (U) Most factories in mainland China are staffed at 60 to 80 percent; there remain challenges to getting key personnel and parts to where they are needed. ***(20 HONG KONG 568)***
- ~~(SBU)~~ Lithuania established a $5.8 billion legislative package to stimulate the economy. ***(20 VILNIUS 178)***
- (U) Turkish Airlines will ground all its international flights as of March 27, except those to Hong Kong, Moscow, Addis Ababa, New York and D.C. Aegean Airlines will suspend all its international flights. ***(20 ANKARA 384, Reuters)***

~~(SBU)~~ Support for U.S. Citizens

- ~~(SBU)~~ All but two passengers of the Silverseas Silver Cloud, and all but 87 of the Norwegian Spirit's passengers have flown out of South Africa. Those remaining are awaiting their regularly scheduled commercial flights. ***(Embassy Pretaria)***
- ~~(SBU)~~ 2,038 Norwegian Jewel passengers docked and are disembarking in Honolulu on March 23. ***(Embassy Canberra)***
- ~~(SBU)~~ 20 U.S. citizens on the Carnival Seaboune docked in Perth and have onward air travel to the United States on March 24. ***(Embassy Canberra)***

Approved: (b)(6)

For additional information, please visit https://usdos.sharepoint.com/sites/S_CGRCU/Public/. The Coronavirus Global Response Coordination Unit may be reached at 202-647-1255 or S_CGRCU@groups.state.gov. The Repatriations Task Force may be reached at 202-647-4888 or TF_7A01@groups.state.gov.

~~SENSITIVE BUT UNCLASSIFIED~~

From: (b)(6)
Sent: Wed, 2 Dec 2020 13:19:54 +0000
To: Gibbs, Jeffrey J; Yu, Miles; Asher, David; DiNanno, Thomas G; Feith, David; (b)(6)
Cc: (b)(6)
Subject: RE: your input

Jeff & Dave – Enjoyed both drafts. Time permits only two quick observations/inputs from Jeff's piece:

(b)(5) Deliberative Process

(b)(5) Deliberative Process

(b)(5) Deliberative Process

-----Original Message-----
From: Gibbs, Jeffrey J (b)(6) @state.gov>
Sent: Tuesday, December 1, 2020 5:38 PM
To: Yu, Miles (b)(6) @state.gov>; Asher, David (b)(6) @state.gov>; (b)(6)
(b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>;
(b)(6) @state.gov>; (b)(6) @state.gov>
Subject: RE: your input

Here are my thoughts on the matter. Dave & (b)(6 please feel free to embellish and confirm my draft of the first answer.

(b)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

Jeff Gibbs
Senior Advisor
AVC Bureau
Department of State
(b)(6) office
cell

~~SBU~~ - DELIBERATIVE PROCESS

-----Original Message-----
From: Yu, Miles (b)(6) @state.gov>
Sent: Tuesday, December 1, 2020 3:01 PM
To: Asher, David (b)(6) @state.gov>; Gibbs, Jeffrey J (b)(6) @state.gov>; (b)(6)
(b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>;
(b)(6) @state.gov>; (b)(6) @state.gov>
Subject: your input

Colleagues,
The Secretary will be interviewed by a news organization later this week and he needs some talking points for the following potential questions. While working on my own TPs sheet, I realized that it's better to post the list of potential questions to you all for your sage input.

I think this group is well positioned to answer the first question, which is very crucial and it has to be precise, safe and backlash-free.

Please give me your best shot on these TPs for all questions, which do not have to be perfect and comprehensive, 2-3 bullets (except for the first one, which could be as long as it needs be) for each will suffice. And send them back to me tomorrow, COB. All info for the TPs should be unclass material.

You are welcome to provide additional potential questions with TPs attached.

Thanks for your help.

Miles

--Where the virus came from

(b)(5) Deliberative Process

Dr. M. Miles Yu

Policy Planning Staff
Office of the Secretary of State
Washington, DC
(b)(6) office)
mobile)

~~SBU - DELIBERATIVE PROCESS~~

From: Feith, David
Sent: Fri, 4 Dec 2020 18:53:04 +0000
To: (b)(6) Stilwell, David R
Cc: Fritz, Jonathan D; Buangan, Richard L; EAP-Press; (b)(6) ; Keshap, Atul
Subject: RE: Urgent HHS statement for review
Attachments: HHS draft statement on COVID origins with State EAP.docx

Many thanks. Please see edits in track-changes attached. Also clean copied here for the traveling party:

State/EAP edits to draft HHS statement
December 4, 2020

(b)(5) Deliberative Process

(b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:28 PM
To: Feith, David (b)(6) @state.gov>; Stilwell, David R (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: Re: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Standing by and waiting for your edits/comments.

(b)(6

From: Feith, David (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:26 PM
To: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; Keshap, Atul (b)(6) @state.gov>
Subject: RE: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Hi all – please confirm we are not/not sending EAP clearance on this yet. Thanks.

From: Feith, David
Sent: Friday, December 4, 2020 1:11 PM
To: Stilwell, David R (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: Fritz, Jonathan D (b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: RE: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Seeing this now, will send suggestions in a minute --

From: Stilwell, David R (b)(6) @state.gov>
Sent: Friday, December 4, 2020 1:06 PM
To: (b)(6) @state.gov>

Cc: Fritz, Jonathan D <(b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: Re: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Good. There's some great reporting out of Taiwan on this topic. Can we point them to TACRO?

Get Outlook for iOS

From: (b)(6) <(b)(6) @state.gov>
Sent: Friday, December 4, 2020 11:30:57 AM
To: Stilwell, David R (b)(6) @state.gov>
Cc: Fritz, Jonathan D <(b)(6) @state.gov>; Buangan, Richard L (b)(6) @state.gov>; Feith, David (b)(6) @state.gov>; EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>
Subject: FOR A/S STILWELL CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

A/S Stilwell,
Please see the statement below in response to the WSJ article that PRC is using to claim COVID did not start in Wuhan. CM has made edits below in yellow.

Apologies for the short fuse. Would appreciate your earliest clearance so that we can get our edits in.

Thank you,

(b)(6)

(b)(5) Deliberative Process

(b)(5) Deliberative Process

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 12:13 PM
To: (b)(6) @state.gov>; (b)(6) @state.gov>
Cc: EAP-Press <EAP-Press@state.gov>
Subject: RE: FOR SARAH/BROOKE CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Clear for CM. FO should see this one – recommend including Feith when you send it up to Buangan and Fritz.

(b)(6)
Director, Office of Chinese and Mongolian Affairs
Bureau of East Asian and Pacific Affairs
(b)(6) @@state.gov
(b)(6) desk)
mobile)

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 12:04 PM
To: (b)(6) @state.gov>; EAP-CM-Global-DL <EAP-CM-Global-DL@state.gov>; EAP-CM-Bilat Unit-DL <EAPCMBilatUnit@state.gov>; EAP-CM-ECON-DL <EAP-CM-ECON-DL@state.gov>

Cc: EAP-Press <EAP-Press@state.gov>
Subject: Re: CLEARANCE ASAP: 11:30 AM: Urgent HHS statement for review

Hi (b)(6)

Some edits for CM/Econ below in yellow highlights. Since the CDC study was about cases before the President stopped travel from China, it does not show how that helped as implied in the third paragraph.

(b)(6)

Environment, Science, Technology, and Health Officer

Office of Chinese and Mongolian Affairs

U.S. Department of State

(b)(6) (work)

(telework)

From: (b)(6) @state.gov>
Sent: Friday, December 4, 2020 10:16 AM
To: EAP-Press <EAP-Press@state.gov>; (b)(6) @state.gov>; IO-Press-DL <IO-Press-DL@state.gov>
Cc: OES-PA-DG <OES-PA-DG@state.gov>
Subject: 11:30 AM: Urgent HHS statement for review

Hello, please see HHS reactive statement below in response to the WSJ article that China is using to claim COVID did not start in Wuhan. I would appreciate your comments/clearance by 11:30.

Thank you,
(b)(6)
OES/PPO

****

The draft reactive statement below is in response to the WSJ article that China is using to claim COVID did not start in Wuhan. Once HHS comments have been received, it will go to State Dept for review.

https://www.wsj.com/articles/covid-19-likely-in-u-s-in-mid-december-2019-cdc-scientists-report-11606782449

(b)(5) Deliberative Process

Withheld pursuant to exemption

)(5) Deliberative Process

(b)(5) Deliberative Process