Post

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Some references for the article by @SharriMarkson

theaustralian.com.au
The Covid-19 conclusion we weren't allowed to know
Buried away inside one of the US intelligence agencies' secret laboratories, a group of eminent scientists examined the structure of Covid-19 in order to ...

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Defense Intelligence Agency's National Center for Medical Intelligence (NCMI) vs Office of the Director of National Intelligence (ODNI)

But the scientists at the Defence Intelligence Agency's National Centre for Medical Intelligence (NCMI) remain unknown and their endeavours to uncover the origins of Covid-19 have gone publicly unrecognised.

Worse, there have even been attempts, at the highest levels of the US government to censor them and keep their discoveries secret.

Today, for the first time, we hear their extraordinary story and reveal the lengths taken to hide from the public their categorical discovery and scientific conclusions. Sources familiar with the work that unfolded inside the intelligence agency and the scientists' interactions with the Office of the Director of National Intelligence spoke to The Australian for this investigation.

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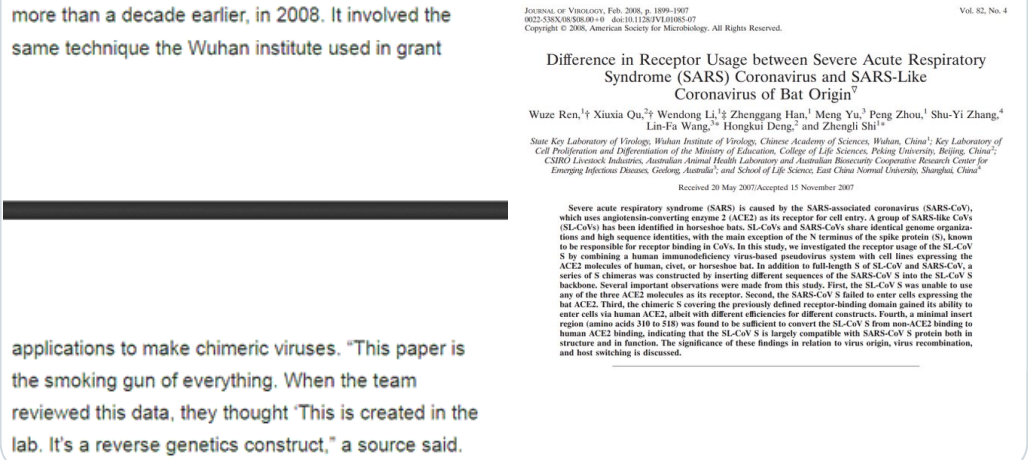
"a minimal insert region (amino acids 310 to 518) was found to be sufficient to convert the SL-CoV S from non-ACE2 binding to human ACE2 binding" (from 2008)

pubmed.ncbi.nlm.nih.gov/18077725/

One of the scientists discovered that the size and location of a fragment of Covid-19 resembled a fragment in Wuhan Institute of Virology research from more than a decade earlier, in 2008. It involved the same technique the Wuhan institute used in grant



JOURNAL OF VIROLOGY, Feb. 2008, p. 1899–1907 Vol. 82, No. 4
0022-538X/08/$08.00+0 doi:10.1128/JVI.01085-07
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Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin[▽]

Wuze Ren,[1]† Xiuxia Qu,[2]† Wendong Li,[1]‡ Zhenggang Han,[1] Meng Yu,[3] Peng Zhou,[1] Shu-Yi Zhang,[4] Lin-Fa Wang,[3]* Hongkui Deng,[2] and Zhengli Shi[1]*

State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China[1]; Key Laboratory of Cell Proliferation and Differentiation of the Ministry of Education, College of Life Sciences, Peking University, Beijing, China[2]; CSIRO Livestock Industries, Australian Animal Health Laboratory and Australian Biosecurity Cooperative Research Center for Emerging Infectious Diseases, Geelong, Australia[3]; and School of Life Science, East China Normal University, Shanghai, China[4]

Received 20 May 2007/Accepted 15 November 2007

Severe acute respiratory syndrome (SARS) is caused by the SARS-associated coronavirus (SARS-CoV), which uses angiotensin-converting enzyme 2 (ACE2) as its receptor for cell entry. A group of SARS-like CoVs (SL-CoVs) has been identified in horseshoe bats. SL-CoVs and SARS-CoVs share identical genome organizations and high sequence identities, with the main exception of the N terminus of the spike protein (S), known to be responsible for receptor binding in CoVs. In this study, we investigated the receptor usage of the SL-CoV S by combining a human immunodeficiency virus-based pseudovirus system with cell lines expressing the ACE2 molecules of human, civet, or horseshoe bat. In addition to full-length S of SL-CoV and SARS-CoV, a series of S chimeras was constructed by inserting different sequences of the SARS-CoV S into the SL-CoV S backbone. Several important observations were made from this study. First, the SL-CoV S was unable to use any of the three ACE2 molecules as its receptor. Second, the SARS-CoV S failed to enter cells expressing the bat ACE2. Third, the chimeric S covering the previously defined receptor-binding domain gained its ability to enter cells via human ACE2, albeit with different efficiencies for different constructs. Fourth, a minimal insert region (amino acids 310 to 518) was found to be sufficient to convert the SL-CoV S from non-ACE2 binding to human ACE2 binding, indicating that the SL-CoV S is largely compatible with SARS-CoV S protein both in structure and in function. The significance of these findings in relation to virus origin, virus recombination, and host switching is discussed.

applications to make chimeric viruses. "This paper is the smoking gun of everything. When the team reviewed this data, they thought 'This is created in the lab. It's a reverse genetics construct," a source said.

2 13 38 1,656

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Response to "Proximal Origin"

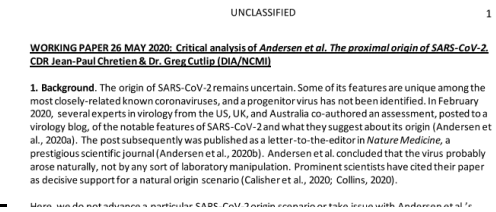
Available here: drasticresearch.files.wordpress.com/2023/05/an-arg...

When the Proximal Origins paper was published – claiming there was no evidence for a laboratory construct – Cutlip and his colleagues were stunned.

When Fauci and Francis Collins used it to insist the virus was natural, saying the matter had been settled, they were shocked.

These apolitical virologists could see beyond the inconclusive and biased commentary published by the esteemed medical journal.

They vehemently disagreed with the Proximal origin analysis.



UNCLASSIFIED 1

WORKING PAPER 26 MAY 2020: Critical analysis of *Andersen et al. The proximal origin of SARS-CoV-2.* CDR Jean-Paul Chretien & Dr. Greg Cutlip (DIA/NCMI)

1. Background. The origin of SARS-CoV-2 remains uncertain. Some of its features are unique among the most closely-related known coronaviruses, and a progenitor virus has not been identified. In February 2020, several experts in virology from the US, UK, and Australia co-authored an assessment, posted to a virology blog, of the notable features of SARS-CoV-2 and what they suggest about its origin (Andersen et al., 2020a). The post subsequently was published as a letter-to-the-editor in *Nature Medicine*, a prestigious scientific journal (Andersen et al., 2020b). Andersen et al. concluded that the virus probably arose naturally, not by any sort of laboratory manipulation. Prominent scientists have cited their paper as decisive support for a natural origin scenario (Calisher et al., 2020; Collins, 2020).

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Ingredients are (almost) there

> "In the context of this research, SARS-CoV-2 could have been synthesised by combining a backbone from a coronavirus similar to RaTG13 with the receptor binding domain of a coronavirus similar to the one recently isolated from pangolins. Such research might have aimed to investigate pangolins as possible intermediate hosts for bat coronaviruses potentially pathogenic for humans, and would have been consistent with the longstanding line of investigations described above."

2 3 27 715

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See this article from @Rossana38510044 and @ydeigin

onlinelibrary.wiley.com/doi/full/10.10...

The esteemed authors go on to say that “laboratories also have directly inserted furin cleavage sites into


CREATING CHIMERIC COVS WITH NOVEL RBDS HAS GONE ON FOR DECADES

Researchers have been generating chimeric CoVs for over two decades, long before the advent of modern sequencing or genetic engineering techniques. For example, in 1999, a group from Utrecht University used targeted RNA recombination to create a ‘cat-and-mouse’ CoV chimera: the RBDs of a feline and murine CoV were swapped, demonstrating that this exchange swapped also species tropism during in vitro experiments.[11]

In 2007, the Shi group at WIV created a series of ‘bat-man’ CoV chimeric spike proteins while trying to determine what exactly confers CoVs the ability to jump from one species to another. The researchers used different segments of the spike protein of the human SARS virus to replace corresponding segments in the spike protein of a bat viral backbone. It was concluded that a relatively short region (aa 310 to 518) of the spike protein ‘was necessary and sufficient to convert Rp3-S into a huACE2-binding molecule,’[12] that is to provide the bat CoV spike protein with a novel ability of binding to a human ACE2 receptor.

In 2008, the Baric group at the University of North Carolina (UNC) took the WIV research one step further. Instead of using human immunodeficiency viruses (HIV) pseudo-viruses with bat CoV spike proteins, a live chimeric CoV was created. Following the experiments of their 2007 WIV colleagues, the Baric group used a bat SARS-like CoV as a backbone and replaced its RBD with the RBD from human SARS.[13]

In 2015, the Shi and Baric groups joined forces and published probably the most famous gain-of-function virology paper, which described the creation of another synthetic chimeric virus.[11] This time the RBD of a mouse-adapted SARS backbone (SARS-MA15) was replaced by the RBD of RsSHC014, a bat strain previously isolated from human bats in 2011 by the Shi group. In 2016, the Baric group repeated their 2015 experiment using the same SARS-MA15 backbone and the RBD from Rs3367,[11] a close relative of RsSHC014 also previously found in Yunnan by WIV and renamed ‘WIV1’ after live culturing.[11]

Probably the largest reported number of novel chimeric viruses created was described in a 2017 paper from the Shi group at WIV,[12] in which the authors reported creating eight

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Between Proximal Origin and the 2021 Biden Intelligence request

After the group’s initial May 2020 paper, they continued to work on the virus, examining classified intelligence their agency and others collected, along with scientific papers in the public domain.

By June 2020, their genomic analysis of amino acids and nucleotides was producing fairly conclusive findings that Covid-19 was genetically engineered.

While their recommendations and working products are highly technical, there are four main reasons for why they found that SARS-CoV-2 was most likely genetically engineered.

They thought perhaps the backbone was related to the virus miners in Mojiang, China, caught in 2012 and had been modified.

Then came the discovery that was described internally as the smoking gun. The majority of the SARS-COV-2 virus genome is similar to bat coronaviruses. However, a small region of the spike gene, encoding the spike protein’s receptor binding

domain (RBD), is identical to that of the pangolin coronavirus MP789.

1 4 22 553

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Pangolin coronavirus isolate MP789, complete genome

ncbi.nlm.nih.gov/nuccore/MT1212...

1 1 19 427

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2008 minimal insert region = Pangolin MP789 = SARS2?

Hardham reported to NCMI that the size and location of the pangolin fragment in SARS-CoV-2 was similar to the same RBD fragment described in one of Wuhan institute’s previous research publications.

In a 2008 paper by Shi Zhengli and Ren Wuze, the Wuhan researchers identified the minimal cassette that would be necessary to change the binding to different host ACE2 receptors – this refers to how the

virus crosses from species to species.

Once the Wuhan researchers identified the minimal RBD cassette, they proposed using this same technique in their future work – including in grant proposals sent to the National Institutes of Health and the Defence Advanced Research Projects Agency.

This same technique (minimal cassette) is found in SARS-CoV-2.

1 8 28 847

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Codon optimization, and a point mutation to add a restriction enzyme site.

Construction of expression plasmids. The construction of a codon-optimized spike (S) protein gene of SARS-CoV BJ01 (BJ01-S) in pcDNA3.1(+) was described previously (34, 46). The full-length S gene of a bat SL-CoV (Rp3) was cloned by PCR amplification from cDNA prepared using fecal samples from an *R. pearsonii* bat positive for SL-CoV (29). After codon optimization for the first 400 aa at the N terminus, the modified S gene was cloned into pcDNA3.1(+). For introduction of the RBM of SARS-CoV S into the SL-CoV S, the coding region from aa 424 to 494 of BJ01-S was used to replace the corresponding regions of Rp3-S, resulting in a chimeric S (CS) gene designated $CS_{424-494}$. Using the same strategy, a series of CS genes with BJ01-S sequences were constructed by stepwise replacement. To facilitate the construction of S chimeras, a point mutation (A to G) at nucleotide 1825 (the A residue of the ATG codon was designated nucleotide 1) was introduced to generate a unique EcoRI site in the S open reading frame. The chimera $CS_{424-494}$ was confirmed by full-length sequencing to ensure that no unexpected mutation was introduced during the PCR processes. For other chimeras constructed using $CS_{424-494}$ as a donor

2 4 30 675

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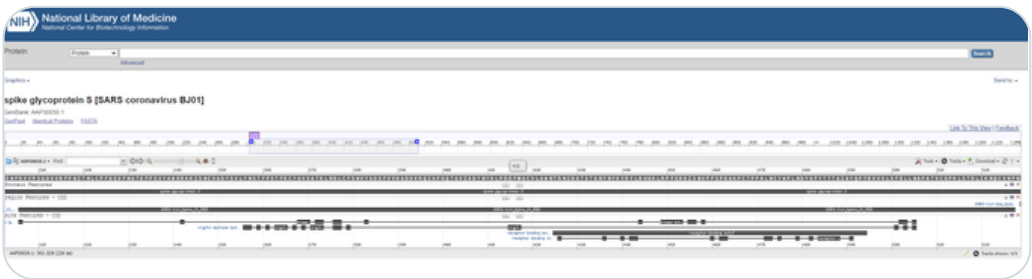
Minimal insertion?



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ncbi.nlm.nih.gov/protein/AAP300...

1 12 401

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Pangolin coronavirus isolate MP789
vs.
SARS coronavirus BJ01

1 12 414

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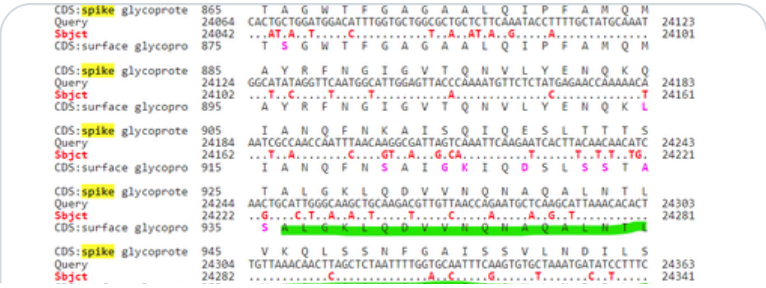
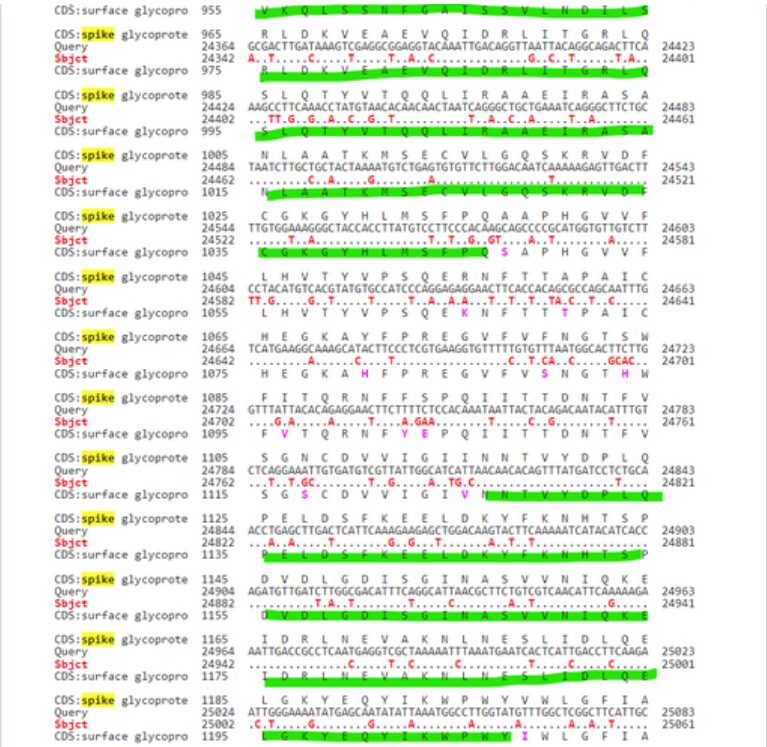
More fun with BLAST





2 1 14 499

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"This paper is a smoking gun of everything...this is created in the lab. It's a reverse genetics construct."

They also found scientific papers in which Shi Zhengli, who had worked at Utrecht University in The Netherlands, described working with furin cleavage sites in the precise location where they appeared in SARS-CoV-2. "Shi helped research furin cleavage sites in The Netherlands laboratory that are very similar to SARS-CoV-2," sources close to the inquiry told The Australian.

[redacted]

"This paper is the smoking gun of everything. Figure 7 is literally the description of the pangolin RBD insert. When the team reviewed this data, they thought 'This is created in the lab. It's a reverse genetics construct.' They identified the minimal cassette required to change the host range."

10 7 29 1,265

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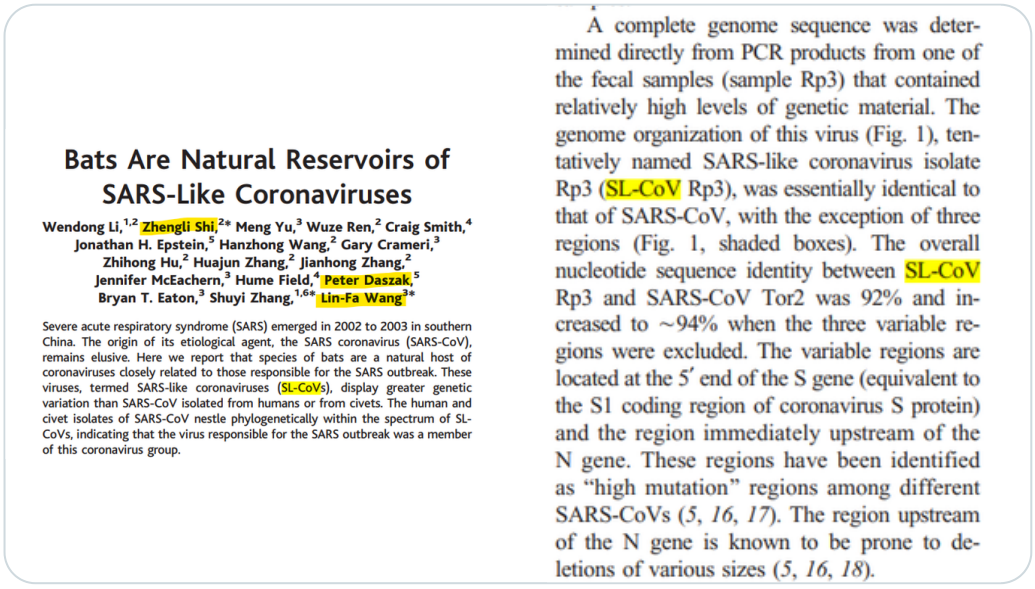
The paper that discovered SL-CoV Rp3, that they used as the "not human ACE2 using" baseline virus from 2005.

ecohealthalliance.org/wp-content/upl...



Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,[1,2] Zhengli Shi,[2]* Meng Yu,[3] Wuze Ren,[2] Craig Smith,[4] Jonathan H. Epstein,[5] Hanzhong Wang,[2] Gary Crameri,[3] Zhihong Hu,[2] Huajun Zhang,[2] Jianhong Zhang,[2] Jennifer McEachern,[3] Hume Field,[4] Peter Daszak,[5] Bryan T. Eaton,[3] Shuyi Zhang,[1,6]* Lin-Fa Wang[3]*

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoVs), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

A complete genome sequence was determined directly from PCR products from one of the fecal samples (sample Rp3) that contained relatively high levels of genetic material. The genome organization of this virus (Fig. 1), tentatively named SARS-like coronavirus isolate Rp3 (SL-CoV Rp3), was essentially identical to that of SARS-CoV, with the exception of three regions (Fig. 1, shaded boxes). The overall nucleotide sequence identity between SL-CoV Rp3 and SARS-CoV Tor2 was 92% and increased to ~94% when the three variable regions were excluded. The variable regions are located at the 5′ end of the S gene (equivalent to the S1 coding region of coronavirus S protein) and the region immediately upstream of the N gene. These regions have been identified as "high mutation" regions among different SARS-CoVs (*5*, *16*, *17*). The region upstream of the N gene is known to be prone to deletions of various sizes (*5*, *16*, *18*).

1 7 219

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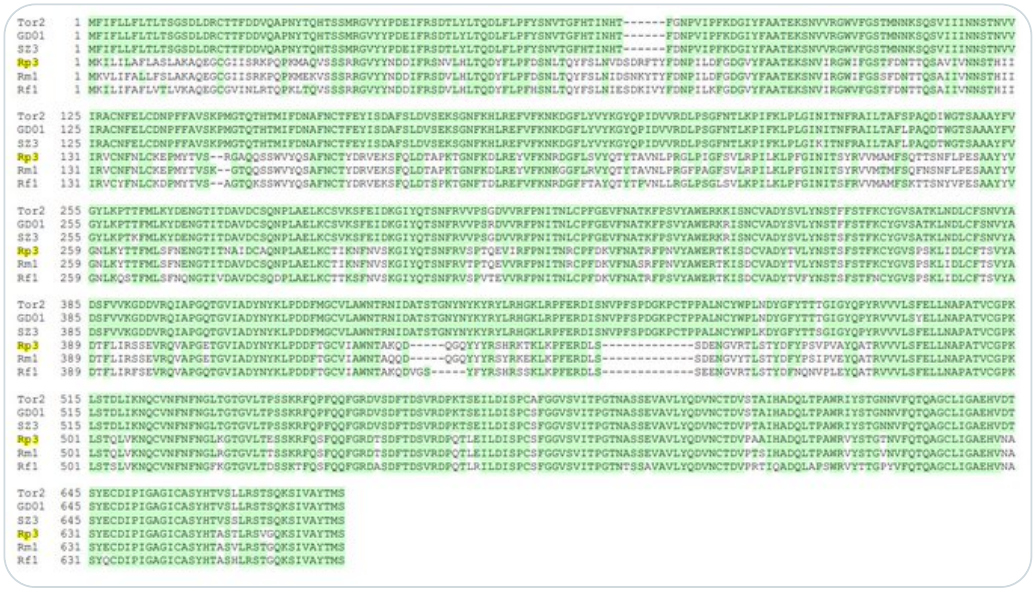
From the supplementary material

science.org/doi/10.1126/sc...



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Tor2    1 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHT------FGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVV
GD01    1 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHT------FDNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVV
SZ3     1 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHT------FDNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVV
Rp3     1 MKILILAFLASLAKAQEGCGIISRKPQPKMAQVSSSRRGVYYNDDIFRSNVLHLTQDYFLPFDSNLTQYFSLNVDSDRFTYFDNPILDFGDGVYFAATEKSNVIRGWIFGSTFDNTTQSAVIVNNSTHII
Rm1     1 MKVLIFALLFSLAKAQEGCGIISRKPQPKMEKVSSSRRGVYYNDDIFRSDVLHLTQDYFLPFDSNLTQYFSLNIDSNKYTYFDNPILDFGDGVYFAATEKSNVIRGWIFGSSFDNTTQSAIIVNNSTHII
Rf1     1 MKILIFAFLVTLVKAQEGCGVINLRTQPKLTQVSSSRRGVYYNDDIFRSDVLHLTQDYFLPFHSNLTQYFSLNIESDKIVYFDNPILKFGDGVYFAATEKSNVIRGWVFGSTFDNTTQSAIIVNNSTHII

Tor2  125 IRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAAYFV
GD01  125 IRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFLPAQDTWGTSAAAYFV
SZ3   125 IRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGIKITNFRAILTAFLPAQDTWGTSAAAYFV
Rp3   131 IRVCNFNLCKEPMYTVS--RGAQQSSWVYQSAFNCTYDRVEKSFQLDTAPKTGNFKDLREYVFKNRDGFLSVYQTYTAVNLPRGLPIGFSVLRPILKLPFGINITSYRVVMAMFSQTTSNFLPESAAYYV
Rm1   131 IRVCNFNLCKEPMYTVSK--GTQQSSWVYQSAFNCTYDRVEKSFQLDTAPKTGNFKDLREYVFKNKGGFLRVYQTYTAVNLPRGFPAGFSVLRPILKLPFGINITSYRVVMTMFSQFNSNFLPESAAYYV
Rf1   131 IRVCYFNLCKDPMYTVS--AGTQKSSWVYQSAFNCTYDRVEKSFQLDTSPKTGNFTDLREFVFKNRDGFFTAYQTYTPVNLLAGLPSGLSVLKPILKLPFGINITSFRVVMAMFSKTTSNYVPESAAYYV

Tor2  255 GYLKPTTFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYA
GD01  255 GYLKPTTFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSRDVVRFPNITNLCPFGEVFNATKFPSVYAWERKRISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYA
SZ3   255 GYLKPTKFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKRISNCVADYSVLYNSTSFSTFKCYGVSATKLNDLCFSNVYA
Rp3   259 GNLKYTTFMLSFNENGTITNAIDCAQNPLAELKCTIKNFNVSKGIYQTSNFRVSPTQEVIRFPNITNRCPFDKVFNATRFPNVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYA
Rm1   259 GNLKYTTFMLSFNENGTITDAVDCSQNPLAELKCTIKNFNVSKGIYQTSNFRVTPTQEVVRFPNITNRCPFDKVFNASRFPNVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYA
Rf1   259 GNLKQSTFMLSFNQNGTIVDAVDCSQDPLAELKCTTKSFNVSKGIYQTSNFRVSPVTEVVRFPNITNLCPFDKVFNATRFPSVYAWERTKISDCVADYTVFYNSTSFSTFNCYGVSPSKLIDLCFTSVYA

Tor2  385 DSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK
GD01  385 DSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSYELLNAPATVCGPK
SZ3   385 DSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLKDYGFYTTSGIGYQPYRVVVLSFELLNAPATVCGPK
Rp3   389 DTFLIRSSEVRQVAPGETGVIADYNYKLPDDFTGCVIAWNTAKQD-----QGQYYYRSHRKTKLKPFERDLS----------SDENGVRTLSTYDFYPSVPVAYQATRVVVLSFELLNAPATVCGPK
Rm1   389 DTFLIRSSEVRQVAPGETGVIADYNYKLPDDFTGCVIAWNTAQQD-----QGQYYYRSYRKEKLKPFERDLS----------SDENGVYTLSTYDFYPSIPVEYQATRVVVLSFELLNAPATVCGPK
Rf1   389 DTFLIRFSEVRQVAPGQTGVIADYNYKLPDDFTGCVIAWNTAKQDVGS-----YFYRSHRSSKLKPFERDLS----------SEENGVRTLSTYDFNQNVPLEYQATRVVVLSFELLNAPATVCGPK

Tor2  515 LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDT
GD01  515 LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDT
SZ3   515 LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVPTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDT
Rp3   501 LSTQLVKNQCVNFNFNGLKGTGVLTESSKRFQSFQQFGRDTSDFTDSVRDPQTLEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVPAAIHADQLTPAWRVYSTGTNVFQTQAGCLIGAEHVNA
Rm1   501 LSTQLVKNQCVNFNFNGLRGTGVLTTSSKRFQSFQQFGRDTSDFTDSVRDPQTLEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVPTSIHADQLTPAWRVYSTGVNVFQTQAGCLIGAEHVNA
Rf1   501 LSTSLVKNQCVNFNFNGFKGTGVLTDSSKTFQSFQQFGRDASDFTDSVRDPQTLRILDISPCSFGGVSVITPGTNTSSAVAVLYQDVNCTDVPRTIQADQLAPSWRVYTTGPYVFQTQAGCLIGAEHVNA

Tor2  645 SYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMS
GD01  645 SYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMS
SZ3   645 SYECDIPIGAGICASYHTVSSLRSTSQKSIVAYTMS
Rp3   631 SYECDIPIGAGICASYHTASTLRSVGQKSIVAYTMS
Rm1   631 SYECDIPIGAGICASYHTASVLRSTGQKSIVAYTMS
Rf1   631 SYQCDIPIGAGICASYHTASHLRSTGQKSIVAYTMS
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1 6 235

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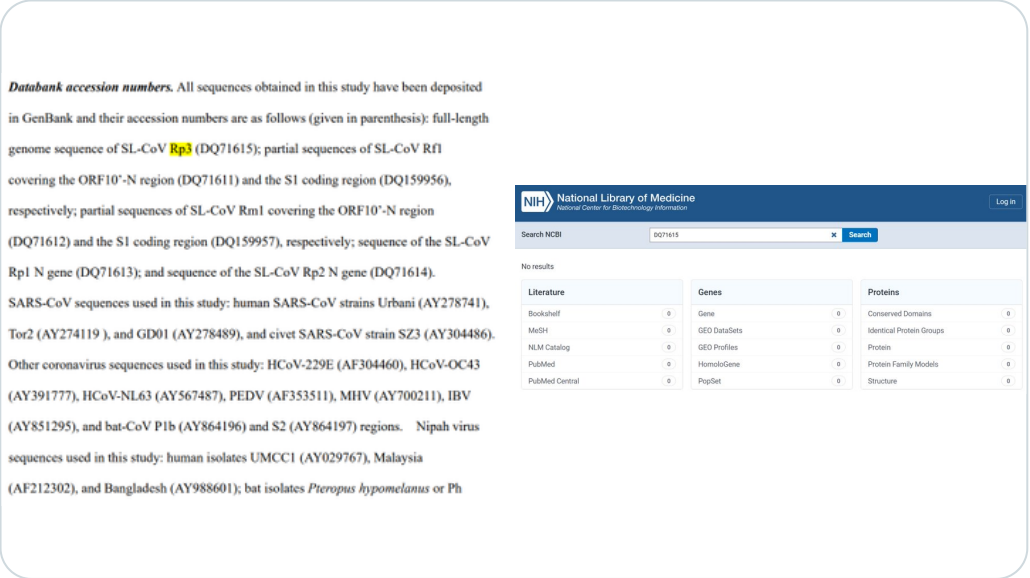
Seems weird...The sequence for SL-CoV Rp3 (DQ71615) is not there



Databank accession numbers. All sequences obtained in this study have been deposited in GenBank and their accession numbers are as follows (given in parenthesis): full-length genome sequence of SL-CoV Rp3 (DQ71615); partial sequences of SL-CoV Rf1 covering the ORF10'-N region (DQ71611) and the S1 coding region (DQ159956), respectively; partial sequences of SL-CoV Rm1 covering the ORF10'-N region (DQ71612) and the S1 coding region (DQ159957), respectively; sequence of the SL-CoV Rp1 N gene (DQ71613); and sequence of the SL-CoV Rp2 N gene (DQ71614). SARS-CoV sequences used in this study: human SARS-CoV strains Urbani (AY278741), Tor2 (AY274119), and GD01 (AY278489), and civet SARS-CoV strain SZ3 (AY304486). Other coronavirus sequences used in this study: HCoV-229E (AF304460), HCoV-OC43 (AY391777), HCoV-NL63 (AY567487), PEDV (AF353511), MHV (AY700211), IBV (AY851295), and bat-CoV P1b (AY864196) and S2 (AY864197) regions. Nipah virus sequences used in this study: human isolates UMCC1 (AY029767), Malaysia (AF212302), and Bangladesh (AY988601); bat isolates *Pteropus hypomelanus* or Ph

1 6 227

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From a later paper
ncbi.nlm.nih.gov/nuccore/DQ0716...

2 5 313

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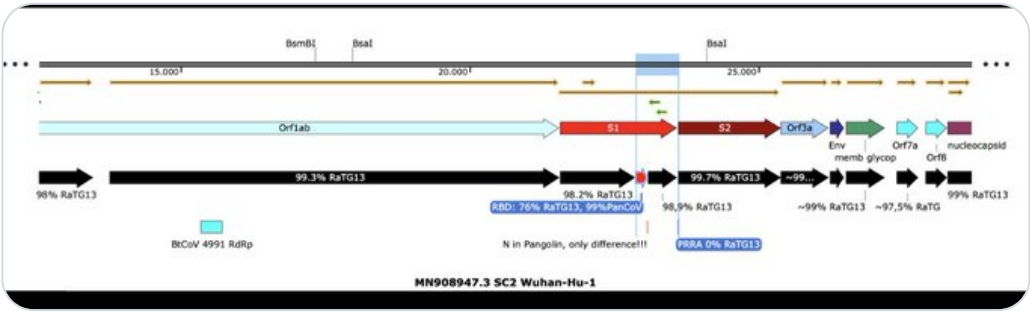
Guess it was missing the leading zero

2 6 355

Louis R Nemzer @BiophysicsFL · Aug 25

OK, Short version. Although the "perfect insertion" of the FCS got alot of attention, there is another swap that the Intel people noticed. The receptor binding motif of one virus inside the backbone of another, just like the WIV did in 2008
h/t @VBruttel



Dr. rer. nat. Valentin Bruttel @VBruttel · Aug 25

Replying to @jbkinney

so basically what @BiophysicsFL is describing here?
twitter.com/BiophysicsFL/s...
makes sense.
WIV wasn't making their own complete reverse genetic systems in 2008 IIRC....

1 3 20 551

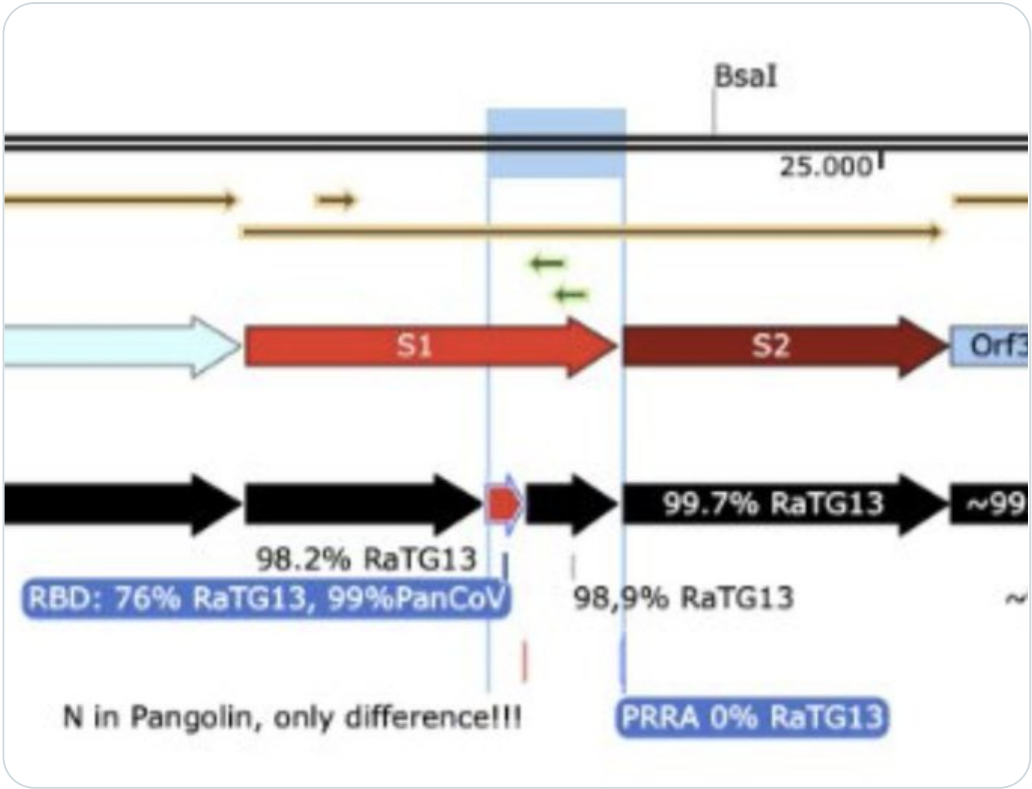
Louis R Nemzer @BiophysicsFL · Aug 25

So you end up with TWO 'immaculate insertions' into a RaTG13/BANAL - like backbone.

🟣The FCS that appears in no other known Sarbecovirus

🟣The Receptor Binding Motif from the 'pangolin' viruses of sketchy origin

Very hard to rationalize as a natural 'recombinant' or 'mosaic'



3 10 29 904

JeanTargetter🍣🧬 @Kingkiko61 · Aug 24

The “non-ACE2 binding to human ACE2 binding” statement demonstrates how appallingly irresponsible the “Proximal Origin” team was. They should’ve warned, early on, of the potential for an airborne-transmissible virus when China and WHO said it wasn’t.

3 14 200

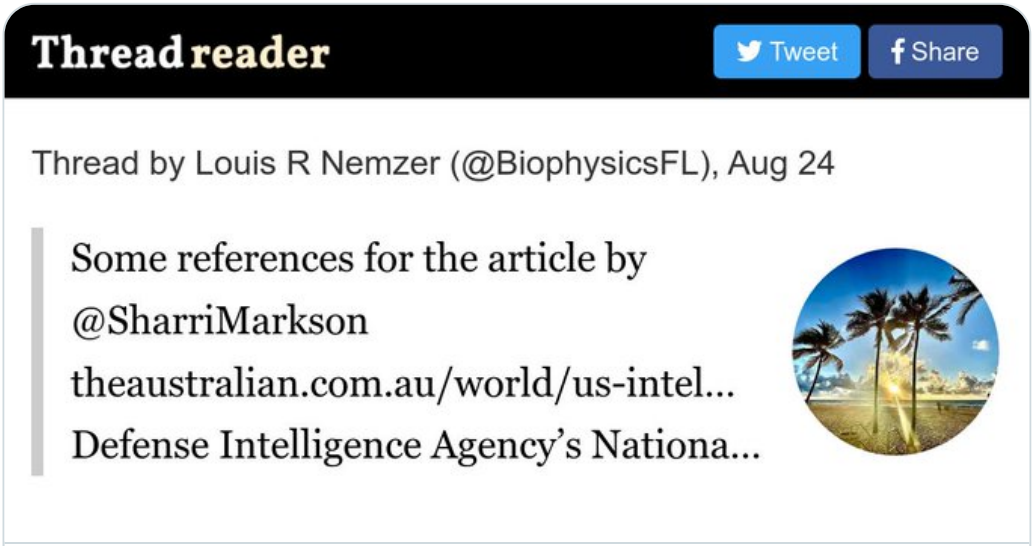
Dr. Patapúfete @clauss_martin · Aug 26

great job thank you @threadreaderapp unroll please

1 1 16

Thread Reader App @threadreaderapp · Aug 26

@clauss_martin Hello, please find the unroll here: threadreaderapp.com/thread/1694739... Talk to you soon.



threadreaderapp.com
Thread by @BiophysicsFL on Thread Reader App
@BiophysicsFL: Some references for the article by @SharriMarkson theaustralian.com.au/world/us-intel... Defense Intelligence Agency's ...

14

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Sourced from across Twitter

Ema Nymton @EmaNymton90 · 3h

1\ People are saying that the natural origin scenario of Worobey and co. is the most parsimonius explanation, but that is only true if you ignore the facts, when you look at the details, it gets quite whacky

3 12 35 1,484

Raccoon Dog's Breakfast @breakfast_dogs · 2h

Really? How was it acquired illegally Eddie? Certainly wasn't me, I've no idea how to hack Sydney Uni. China probably does though, maybe it was them?

Eddie Holmes @edwardcholmes · 1h
This email was acquired illegally. I will be following up on this.

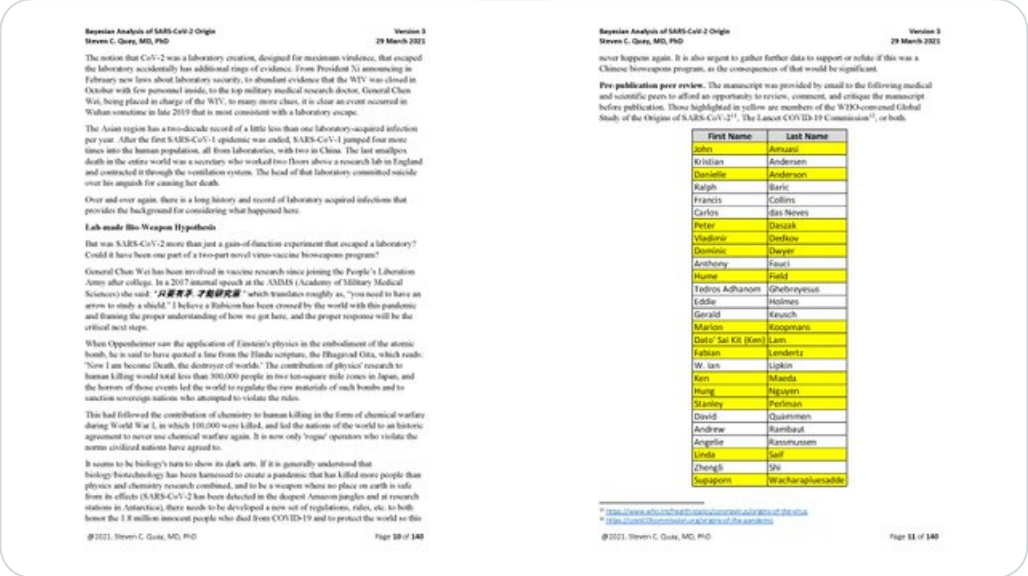
> **Raccoon Dog's Breakfast** ✓
> @breakfast_dogs
>
> Many LL people have seen this email and discussed it privately and publicly, but no-one has posted it. Supposedly this is to protect a source, but I doubt. Perhaps they received legal threats?
>
> Idk, I haven't, sue me. It should have been released immediately imo.
>
> Background...

11 17 44 1,454

Dr Steven Quay ✓ @quay_dr · 11h
In this Mar 21 version of my Dec 20 analysis at the request of US State Dept, I compared the role chemists, physicists, & now biologists played in the last 110 y in killing other humans

'Oppenheimer' dramatized this well.

But biologists win the contest for 'deadliest' science.


Bayesian Analysis of SARS-CoV-2 Origin — Version 3
Steven C. Quay, MD, PhD — 29 March 2021

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 with few personnel inside, to the top military medical research doctor, General Chen Wei, being placed in charge of the WIV, to many more clues, it is clear an event occurred in Wuhan sometime in late 2019 that is most consistent with a laboratory escape.

The Asian region has a two-decade record of a little less than one laboratory-acquired infection per year. After the first SARS-CoV-1 epidemic was ended, SARS-CoV-1 jumped four more times into the human population, all from laboratories, with two in China. The last smallpox death in the entire world was a secretary who worked two floors above a research lab in England and contracted it through the ventilation system. The head of that laboratory committed suicide over his anguish for causing her death.

Over and over again, there is a long history and record of laboratory acquired infections that provides the background for considering what happened here.

Lab-made Bio-Weapon Hypothesis

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 Chan Wei has been involved in vaccine research since joining the People's Liberation Army 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." 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, and the horrors of those events led the world to regulate the raw materials of such bombs and to sanction sovereign nations who attempted to violate the rules.

This had followed the contribution of chemistry to human killing in the form of chemical warfare during World War I, in which 100,000 were killed, and 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 physics and 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

@2021, Steven C. Quay, MD, PhD — Page 10 of 140

Bayesian Analysis of SARS-CoV-2 Origin — Version 3
Steven C. Quay, MD, PhD — 29 March 2021

never happen 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.

Pre-publication peer review. The manuscript was provided by email to the following medical and scientific peers to afford an opportunity to review, comment, and critique the manuscript before publication. Those highlighted in yellow are members of the WHO-convened Global Study of the Origins of SARS-CoV-2[14], The Lancet COVID-19 Commission[15], or both.

First Name	Last Name
John	Amuasi
Kristian	Andersen
Danielle	Anderson
Ralph	Baric
Francis	Collins
Carlos	das Neves
Peter	Daszak
Vladimir	Dedkov
Dominic	Dwyer
Anthony	Fauci
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@2021, Steven C. Quay, MD, PhD — Page 11 of 140

4 7 26 839

Francesco Esposito @FrancescoEsp33 · 23h
1/ After watching the Oppenheimer movie I'm thinking that what was done at the time with the Manhattan project, making the world of physics lose its innocence for the first time, could represent what is happening today with the field of biology.

4 6 33 1,189