Z PROGRAM ANALYTIC HIGHLIGHT

International Assessments Report

Lawrence Livermore National Laboratory

(U) Lawrence Livermore National Laboratory (LLNL), Global Security Principal Directorate, Z Program, prepared this report. The views expressed are those of the authors and not necessarily those of the sponsors.

(U) Comments are encouraged and feedback on this report and other Z Program products can be provided through our JWICS website, http://z.ic.gov/.

(U) Contacts

- Z Program Author
- Z Program Associate Program Leader
- Z Program Manager

Derivative declassifier review required prior to declassification

Classified By:	, Z Program Production Manager
Derived From:	
Declassify On:	

27 May 2020

China: Conditions Present for Laboratory Modification and Release of Human-Adapted Coronavirus in Wuhan in Late 2019

Z Program, Lawrence Livermore National Laboratory

We assess all of the necessary conditions for an accidental release of a laboratory-modified coronavirus—specifically a coronavirus adapted to recognize human cell receptors—were present at the Chinese Wuhan Institute of Virology (WIV) in mid-to-late 2019. As a result, we place equal weight on the hypothesis that the COVID-19 virus was a result of laboratory modification, along with that of a natural outbreak or the release from a laboratory of a naturally-occurring virus.

We judge that the following conditions need to be met to result in an accidental release of a laboratory-modified strain capable of producing the COVID-19 outbreak: (1) presence of precursor viruses with a high genetic similarity to the COVID-19 virus; (2) laboratory use of reverse genetic systems to modify coronaviruses; (3) laboratory testing to see if the virus can enter human cells and cause disease via ACE2 receptors;* and (4) accidents with coronavirus materials due to chance, negligence, or generally

* (U) Angiotensin-Converting Enzyme 2 (ACE2) is present on the surface of cells in the lungs, intestines, kidneys and other parts of the body. ACE2 plays a role in control of blood pressure but it also acts as a binding location for some viruses, including SARS-CoV-1 and SARS-CoV-2.

- [redacted] **Access to potential SARS-CoV-2 precursor** [redacted]
- [redacted] **Use of reverse genetic systems to modify** [redacted]
- [redacted] **Virus experiments with human ACE2 receptors.** The ACE2 receptor is the entry point for both SARS and COVID-19 viruses into mammalian cells. [redacted]
- [redacted] **Lax biosafety practices or accidents with coronavirus mouse** [redacted]

† (U) "Gain of function" is a term used for a class of experiments in which researchers introduce genetic changes—via reverse genetics, recombination, or spontaneous mutation—to a strain of interest. If the new strain exhibits increased transmissibility or virulence, generally via pathogenesis studies, then a "gain of function" was achieved.

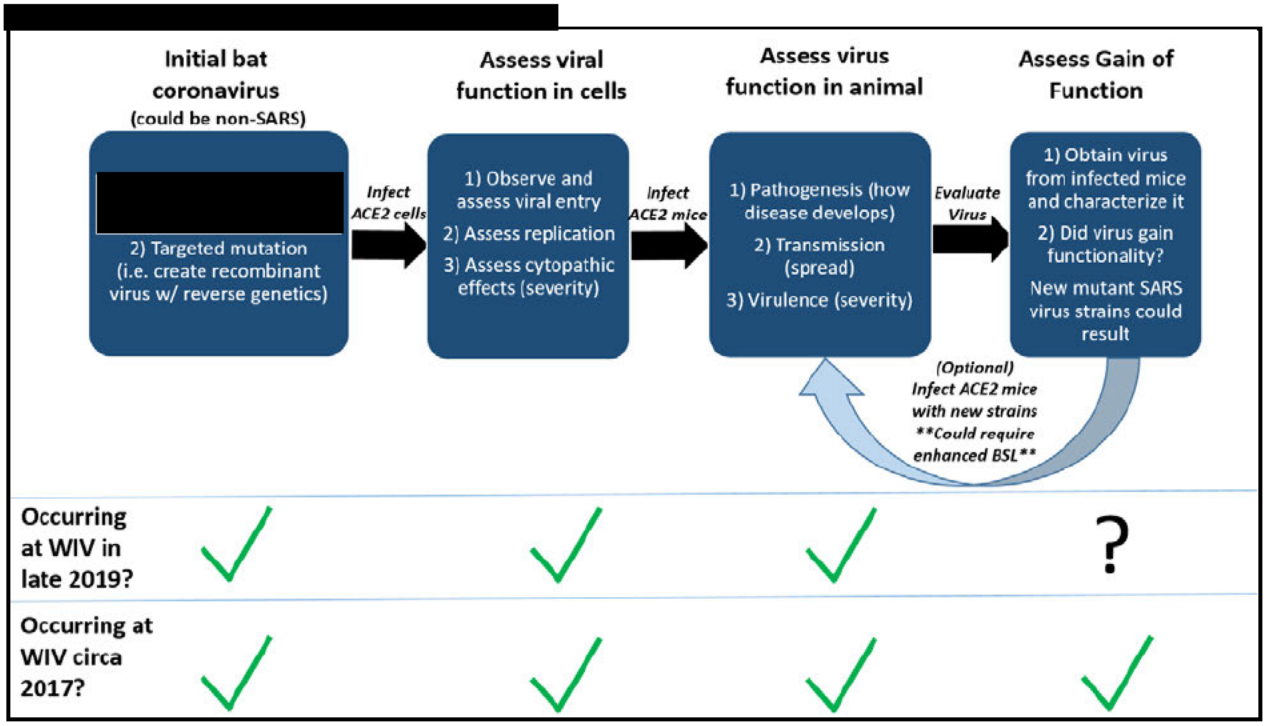


Figure 1. [redacted] Gain of function framework with bat coronaviruses

[redacted]

[redacted]

- [redacted]
- [redacted]

[redacted]

[redacted]

- [redacted]
- [redacted]
- [redacted]

(U) Scope Note

[redacted] This report evaluates the hypothesis that SARS-CoV-2 strain was the consequence of laboratory experiments and the outbreak began following an accident. We examine [redacted] conditions at the Wuhan Institute of Virology that would have needed to be in place to modify and accidentally release a bat-origin coronavirus like the COVID-19 virus. We identified these necessary conditions from scientific journal publications, [redacted] and Lawrence Livermore National Laboratory's subject matter expertise in virology.

[redacted] Our assessment about necessary conditions being present at the Wuhan Institute of Virology is based on scientific publications by the institute's researchers [redacted] providing additional details about [redacted] as well as ongoing and planned work. We deem these two categories of information to be of high quality based on their specificity and technical quality. We also used additional intelligence information from a CIA Field Analytic Conversation.

(U) Provide Feedback or Request a Document

(U) We invite your feedback. Use the JWICS website, http://z.ic.gov, or email to comment on this report. You can also comment on or request other Z Program products.

(U[redacted]) The information in this report is provided for intelligence purposes only, but may be used to develop potential investigative leads. No information contained in this report, nor any information derived therefrom may be used in any proceeding (whether criminal or civil), to include any trial, hearing, or other proceeding before any court, department agency, regulatory body, or other authority of the United States without the advance approval of the Attorney General and/or the agency or department that originated the information contained in this report. These restrictions apply to any information extracted from this document and used in derivative publications or briefings.

[redacted]

(U) Note: Document may not be used as the source for derivative classification nor can it be used as a source for preparers of classification guides.

(U) References

[redacted]

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

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

Agenda

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

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

Join from PC, Mac, Linux, iOS or Android: https://nasem.zoom.us/j/777284900
Telephone: +1 646 558 8656
Meeting ID: 777 284 900
International numbers available: https://nasem.zoom.us/u/aA3S9pYwW

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

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

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

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

KELVIN DROEGEMEIER
Director
Office of Science and Technology Policy

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

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

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

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

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

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

VIROLOGICA SINICA 2016, 31 (2): 160–167
DOI: 10.1007/s12250-016-3730-8

RESEARCH ARTICLE

Assembly of long DNA sequences using a new synthetic *Escherichia coli*-yeast shuttle vector

Zheng Hou#, Zheng Zhou#, Zonglin Wang, Gengfu Xiao✉

State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China

Synthetic biology is a newly developed field of research focused on designing and rebuilding novel biomolecular components, circuits, and networks. Synthetic biology can also help understand biological principles and engineer complex artificial metabolic systems. DNA manipulation on a large genome-wide scale is an inevitable challenge, but a necessary tool for synthetic biology. To improve the methods used for the synthesis of long DNA fragments, here we constructed a novel shuttle vector named *pGF* (plasmid Genome Fast) for DNA assembly *in vivo*. The BAC plasmid *pCC1BAC*, which can accommodate large DNA molecules, was chosen as the backbone. The sequence of the yeast artificial chromosome (YAC) regulatory element *CEN6-ARS4* was synthesized and inserted into the plasmid to enable it to replicate in yeast. The selection sequence *HIS3*, obtained by polymerase chain reaction (PCR) from the plasmid *pBS313*, was inserted for screening. This new synthetic shuttle vector can mediate the transformation-associated recombination (TAR) assembly of large DNA fragments in yeast, and the assembled products can be transformed into *Escherichia coli* for further amplification. We also conducted *in vivo* DNA assembly using *pGF* and yeast homologous recombination and constructed a 31-kb long DNA sequence from the *cyanophage PP* genome. Our findings show that this novel shuttle vector would be a useful tool for efficient genome-scale DNA reconstruction.

KEYWORDS synthetic biology; DNA fragment assembly; shuttle vector *pGF*; transformation-associated recombination (TAR)

INTRODUCTION

Synthetic biology aims to create small artificial biological circuits and networks, which will benefit the development of new biomedical therapeutics, metabolic engineering, and energy supply (Cameron et al., 2014; Khalil and Collins, 2010). Synthetic biology originates from and progresses with technological advancements in gene manipulation (Cameron et al., 2014). Thus, it is obvious that convenient and effective methods for assembling long DNA sequences are necessary tools for this innovative research field (Merryman and Gibson, 2012).

Received: 21 January 2016, Accepted: 17 March 2016,
Published online: 11 April 2016
# These authors contributed equally to this work.
✉Correspondence:
Phone: +86-27-87198685, Fax: +86-27-87198685,
Email: xiaogf@wh.iov.cn
ORCID: 0000-0001-9401-235X

Following the development of molecular cloning and PCR, the synthesis of DNA constructs less than 10 kb became easier. Nowadays, DNA fragments less than 20 kb can be constructed conveniently using SOEing PCR (splicing by overlap extension PCR) (Hou and Xiao, 2011; Shevchuk et al., 2004). However, a problem frequently encountered in PCR is the introduction of random errors during polymerization (Keohavong and Thilly, 1989), especially during the amplification of long and complex sequences. In the early 2000s, researchers built a circular DNA by assembling 500–800 bp segments using type IIS restriction enzymes (*Bsa* I and *Bbs* I) and DNA ligase (Kodumal et al., 2004). This ligation-based method had been improved to assemble as many as six DNA fragments at once. Later, another *in vitro* as-

sembly method was developed by Gibson and coworkers (Gibson et al., 2008a), which eliminated the need for restriction enzyme sites within the DNA fragments. Small DNA molecules were synthesized with 20–40 bp overlapping sequences for assembly. First, exonuclease was used to chew back the 5′ ends, and DNA polymerase was then used to fill gaps in the annealed products. Finally, DNA ligase was used to covalently seal the nicks in the assembly. Based on this method, Gibson further developed a one-step, isothermal assembly method and successfully synthesized an entire 16.3-kb long mouse mitochondrial genome (Gibson et al., 2010b). Another assembly method reported by Li and Elledge (2007) was based on *in vitro* homologous recombination using *RecA* recombinase.

The construction of long DNA through homologous recombination *in vivo* in yeast (Stemmer et al., 1995) is an alternative method. This method was first used to ligate DNA fragments with a plasmid vector and was referred to as transformation-associated recombination (TAR) by Larionov et al. (1996). Gibson *et al*. applied this method to assemble large DNA molecules. Several large DNA fragments were simultaneously assembled using a yeast artificial chromosome (YAC) and yielded the *Mycoplasma genitalium* genome (Gibson et al., 2008a; Gibson et al., 2008b). The 1.08-Mb long *Mycoplasmamycoides* genome was also chemically synthesized using this method (Gibson et al., 2010a). Unlike the *in vitro* assembly methods, TAR-based assembly requires no enzymes and takes advantage of the homologous recombination pathway in yeast to achieve a seamless ligation of the DNA fragments. This method especially facilitates the assembly of long DNA sequences.

To improve this method, we constructed an *E. coli*-yeast shuttle vector for the effective assembly of long DNA fragments. The YAC regulatory and selection sequences were introduced into the BAC plasmid to generate the novel plasmid named *pGF* (plasmid Genome Fast), which can mediate the homologous recombination reaction, plasmid replication in yeast, and plasmid amplification in *E. coli*. This novel shuttle vector derived from the BAC plasmid can accommodate large DNA molecules. The assembled plasmids containing the long DNA sequences can also be easily transformed into *E. coli* for large-scale amplification.

Cyanophage PP is widely distributed in freshwater and may play an important role in freshwater microbial loops (Zhou et al., 2013). Using our developed shuttle vector, we assembled 10 DNA fragments from the *cyanophage PP* genome and produced a ~31-kb long DNA sequence. Thus, the *pGF* plasmid was successfully applied for the synthesis of large DNA molecules. *pGF* and the associated TAR assembly method will promote development in the field of synthetic biology, including viral reverse genetics and bacterial metabolic engineering (Dueber et al., 2009; Lee et al., 2013).

MATERIALS AND METHODS

Strains and media

The yeast, *Saccharomyces cerevisiae* strain VL6–48 (ATCC), which is highly transformable and has HIS3 deletions, was used for transformation and *in vivo* homologous recombination. The yeast strain was cultured in standard rich medium containing yeast extract, peptone and dextrose (YEPD) or minimal medium CM with or without HIS. Medium supplemented with 1 mol/L D-sorbitol (Sigma Aldrich, St Louis, MO, USA) was used for spheroplast transformation. The BAC plasmid CopyControl™ *pCC1BAC*™ (Epicentre, Madison, WI, USA), which can accommodate large DNA fragments, was used as the vector backbone. YAC plasmid *pRS313* (ATCC) was used as the PCR template to obtain the *HIS3* sequence. Plasmids were electroporated into the electrocompetent cells of the *E. coli* strain EPI300 (Epicentre) and selected using chloramphenicol at a concentration of 25 μg/mL and ampicillin at a concentration of 50 μg/mL.

Isolation of plasmid DNA from yeast or *E. coli*

Small-scale isolation of supercoiled plasmids from yeast cells was performed using a TIANprep yeast plasmid DNA kit (Tiangen, Beijing, China). Briefly, the yeast cells were lysed by treatment with Lyticase. Proteins were then precipitated and eliminated, and the plasmids were further purified by affinity absorption columns. For large YACs, the circular plasmids from a large volume of yeast culture were isolated according to the protocol described by Noskov *et al*. (2011). Plasmid DNA from *E. coli* was isolated from a 5-mL overnight culture using a Plasmid Miniprep Kit (Omega Bio-tek, Doraville, GA, USA).

Co-transformation of the DNA fragments into yeast

To prepare the yeast spheroplast, the cells collected from 4 mL of yeast culture grown overnight were treated with zymolyase and β-mercaptoethanol to remove the cell wall. The DNA fragments and vector were then mixed with the prepared spheroplasts as described previously (Kouprina and Larionov, 2008). Positive yeast colonies were selected on histidine-deficient (−His) plates after incubation at 30 °C for 2–3 days.

Electroporation of *E. coli*

The purified plasmids were added into 100 μL of competent *E. coli* cells. After incubation on ice for 5 min, the cells were gently mixed and transferred into a 0.2 cm pre-chilled electroporation cuvette and pulsed with 2.5

kV, 25 μF, 200 Ω. The contents of the cuvette were then transferred into an Eppendorf tube, 1 mL SOB medium was added and incubated at 37 °C for 1 h while shaking at 225 rpm. All the recovered cells were then plated on LB-kanamycin plates.

Construction of the *E. coli*-yeast shuttle vector, *pGF*

To construct a shuttle plasmid that can replicate both in yeast and in *E. coli* cells, the yeast centromere sequence (*CEN*) and autonomously replicating sequence (*ARS*) were inserted into the BAC plasmid *pCC1BAC*, which formed the backbone. The yeast *HIS3* gene was also inserted to work as a selectable marker in yeast.

The *HIS3* selection marker was PCR amplified with specific primers using plasmid *pRS313* as the template. The *CEN6-ARS4* sequence was manually synthesized by Sangon Biotech Co. Ltd., based on the GenBank plasmid sequence with the accession number U03439. The *HIS3* and *CEN6-ARS4* sequences were then ligated and amplified by overlapping extension PCR. For the first step, 25 μL of PCR mixture containing 2.5 μL 10× KOD-Plus buffer, 2.5 μL 2 mmol/L dNTPs, 1.25 μL 25 mmol/L $MgSO_4$, 0.5 μL KOD-Plus polymerase, 1.5 μL *HIS3*, and 1.5 μL *CEN6-ARS4* templates was used without primers. The PCR conditions were as follows: 94 °C for 2 min, followed by 35 cycles of 94 °C for 15 s, 55 °C for 25 s, and 68 °C for 2 min, and a final incubation at 68 °C for 5 min. For the second round of PCR, the products obtained from the first round were used as the template and the primer pairs were designed to contain 5′ end overlapping sequences with ends of *Afe* I-linearized *pCC1BAC*. The PCR mixture (25 μL) contained 2.5 μL 10× KOD-Plus buffer, 2.5 μL 2 mmol/L dNTPs, 1.25 μL 25 mmol/L $MgSO_4$, 0.5 μL KOD-Plus polymerase, 1 μL template, and 1 μL of each primer. The PCR conditions were as follows: 94 °C for 2 min, followed by 28 cycles of 94 °C for 15 s, 58 °C for 25 s, and 68 °C for 2 min, and a final incubation at 68 °C for 5 min. The *pCC1BAC* plasmid was linearized with the restriction endonuclease *Afe* I, dephosphorylated using alkaline phosphatase *FastAP* (Thermofisher), purified, and then recovered using the E.Z.N.A. Gel Extraction Kit (Omega).

The *CEN6-ARS4-HIS3* sequence and the linearized *pCC1BAC* plasmid were co-transformed into yeast VL6–48 spheroplasts. The positive homologous recombinants were selected on −His plates after incubation at 30 °C for 2–3 days. After streaking in selective media, colonies were cultured in 5 mL −His medium and the plasmids were mini-prepared. The constructed novel shuttle plasmid was verified by sequencing and named as *pGF* (plasmid Genome Fast).

Preparation of the assembly vector and *cyanophage PP* fragments

The shuttle plasmid *pGF* was then used for the preparation of the assembly vector. This vector was PCR amplified using primers containing an approximate 20 bp overlap with ends of the *Bam*H I-linearized vector and a 40–60 bp overlap with the target DNA fragments. A rare-cutting restriction site *Not* I (5'-GCGGCCGC-3') was additionally added in the middle of the primers for the easy release of the assembled products from the circular plasmids.

The DNA fragments used for the assembly were amplified by PCR using the *cyanophage PP* genome as the template (Zhou et al., 2013). Each assembly unit of the DNA fragments (A1, A2, A3, A4, B1, B2, B3, B4 and C1 of ~3 kb each and C2 of ~4 kb) was amplified with specific primers containing 40–60 bp overlapping sequences with the adjacent fragments (as listed in Supplementary Table S1). The PCR products were then separated using 0.6% agarose gel electrophoresis and purified using the E.Z.N.A. Gel Extraction Kit (Omega).

The DNA fragments and *pGF* vector were co-transformed into yeast VL6–48 spheroplasts to achieve assembly of the long DNA sequence. The positive colonies were selected on −His plates after incubation at 30 °C for 2–3 days.

Restriction digestion and PCR analysis of the assembled long DNA sequences

Since the rare-cutting restriction site *Not* I was introduced in the linearized *pGF* shuttle plasmid, the assembled intermediates or the full 31-kb DNA sequence could be released by *Not* I digestion. *Eco*R I, which also exist as the unique restriction site in *pGF* and the assembly products, could be used to linearize the circular plasmid for determining the length of the synthetic DNA sequences.

The assembled plasmids were isolated from the yeasts or *E. coli* cells as described before. PCR analyses were performed using the 2× Taq PCR MasterMix kit with the specific pairs of primers (as listed in the Supplementary material) designed to amplify all the initial DNA fragments or the sequences across the neighboring DNA fragments. The PCR mixture (10 μL) contained 1 μL extracted DNA, 1 μL each of the forward and reverse primers, and 5 μL 2× Taq PCR mixture. The PCR conditions were as follows: 94 °C for 2 min, followed by 32 cycles of 98 °C for 15 s, 58 °C for 30 s, and 72 °C for 1 min, and a final incubation at 72 °C for 5 min. The PCR products were loaded on 1% agarose gels and the gels were run at 100 V for 30 min.

RESULTS

Construction of the shuttle plasmid *pGF*

As shown in Figure 1, the shuttle plasmid was constructed based on the BAC plasmid *pCC1BAC* and YAC plasmid *pRS313*. *pCC1BAC* normally replicates as a single copy under the regulation of the *F-factor*, and *SopA, B, and C* are all important for plasmid partitioning during cell division in *E. coli*. When an inducer is added, the number of plasmid copies could be increased to 10–20 in the EPI300 strain under the control of *oriV*. Besides, the phage *COS* sequence in the plasmid enables it to accommodate large-size DNA sequences. The YAC plasmid *pRS313* contains *CEN6* and the *ARS* associated with *HIS3* elements. The yeast centromere *CEN6* and the autonomous replicating sequence *ARS* enable the plasmid to replicate in yeast cells, while the *HIS3* is a selectable marker for positive colony screening. The yeast regulatory component *CEN6-ARS4* and the *HIS3* sequences were introduced into the appropriate sites of *pCC1BAC*. This novel synthetic plasmid can mediate the homologous recombination of DNA fragments and stably maintain the assembled plasmids in the yeast. Further, the assembled plasmids purified from the yeast cells could be transformed into *E. coli* for amplification.

To construct the shuttle plasmid *pGF* described above,

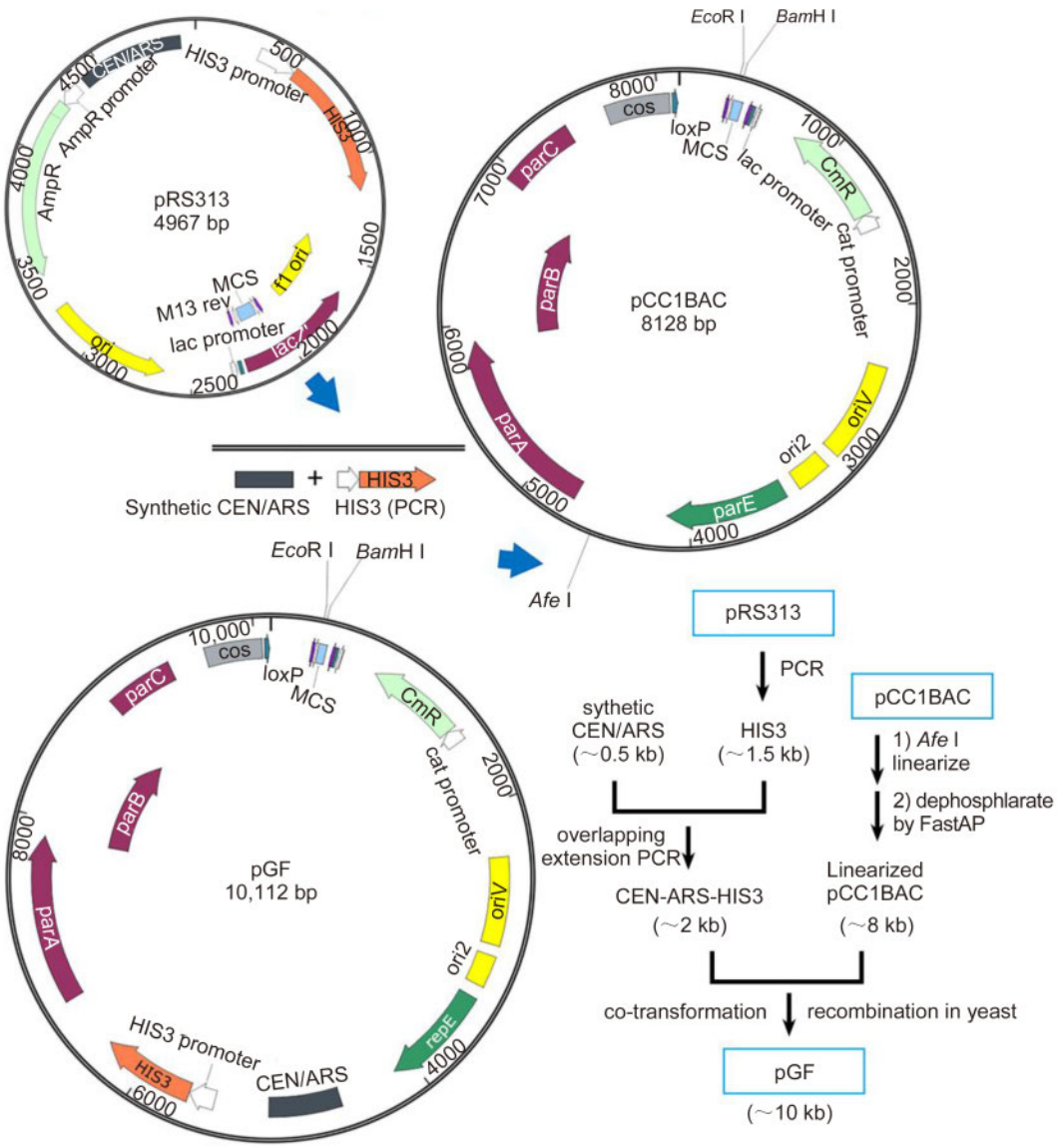


Figure 1. The construction of *pGF* shuttle plasmid used for *in vivo* TAR assembly of DNA fragments. The BAC plasmid *pCC1BAC* used as the backbone allows the replication of the assembled DNA in *E. coli* for amplification. *CEN6-ARS4* and *HIS3* sequences introduced at the *Afe* I sites of *pCC1BAC* allow the propagation of plasmids and positive colony selection in yeast.

the *CEN6-ARS4* and *HIS3* sequences were inserted into the *Afe* I site of the BAC plasmid *pCC1BAC*. Specifically, the *HIS3* sequence (~1.5 kb) was PCR amplified from the YAC plasmid *pRS313*, and the *CEN6-ARS4* sequence (~0.5 kb) was obtained by DNA synthesis based on the GenBank sequence with the accession number U03439. These two sequences were tandemly linked by overlapping extension PCR to generate the *CEN6-ARS4-HIS3* sequence (~2 kb). Then, the *CEN6-ARS4-HIS3* sequence was co-transformed with the *Afe* I-linearized *pCC1BAC* vector (~8 kb) into yeast and ligated by TAR homologous recombination. The positive colonies were selected and plasmids were isolated and sequenced. The successful assembly of the *pGF* vector (~10 kb) by TAR cloning indicated that this *in vivo* homologous recombination system in yeast could effectively ligate the DNA fragments into the vector with the 5′ end overlapping sequences.

Assembly of the 31-kb long DNA from the *cyanophage PP* genome

Figure 2 shows the flowchart for the assembly of 10 *cyanophage PP* DNA fragments into a ~31-kb DNA molecule. In the first step, the DNA fragments of Part A (A1, A2, A3 and A4, each of ~3 kb), Part B (B1, B2, B3 and B4, each of ~3 kb), or Part C (C1 of ~3 kb and C2 of ~4 kb) with the *pGF* vector were co-transformed into yeast. The neighboring fragments with overlapping ends could be ligated together by homologous recombination to generate *pGF*-Part A, Part B, or Part C, respectively. These plasmids were then digested by *Not* I so that the three intermediates Part A, Part B, and Part C could be released and recovered by agarose gel separation and extraction. Next, the assembled intermediates Part A (~12 kb), Part B (~12 kb) and Part C (~7 kb) with the vector *pGF* (~10 kb) were co-transformed into yeast cells and further assembled to form the 31-kb long DNA sequence.

According to the homologous recombination strategy, the *pGF* vector and the *cyanophage PP* DNA fragments should be prepared by PCR amplification to add the specific overlapping ends. The 5′ ends of the primers were designed to contain 20–40 bp extension sequences homologous to the neighboring fragments. A rare-cutting restriction site *Not* I (5'-GCGGCCGC-3') adjacent to the overlaps needed to be added to the primers for the amplification of the *pGF* vector for the convenient release of the assembly products. The products of PCR amplification of the *pGF* vector performed using high fidelity polymerase were exhibited as the main electrophoresis bands approximately 10 kb in size (Figure 3A). The Part A (A1, A2, A3 and A4, each of ~3 kb), Part B (B1, B2, B3 and B4 each of ~3 kb), and Part C (C1 of ~3 kb and C2 of ~4 kb) DNA fragments were also PCR amplified

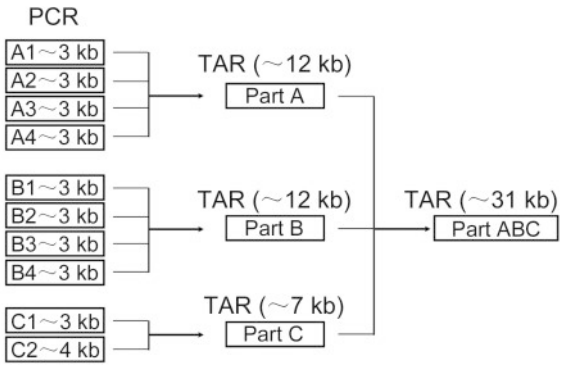


Figure 2. Scheme for the assembly of the ~31-kb DNA sequence. In the first stage of assembly, four DNA fragments of Part A and Part B and two DNA fragments of Part C were ligated together to generate the intermediates *pGF*-Part A, Part B, and Part C. In the next step, the assembled Part A, Part B, and Part C were released by digestion by the endonuclease *Not*I and recovered. The three intermediates together with *pGF* were then co-transformed into yeast cells to generate the complete ~31-kb PartABC integrated sequence in the *pGF* vector.

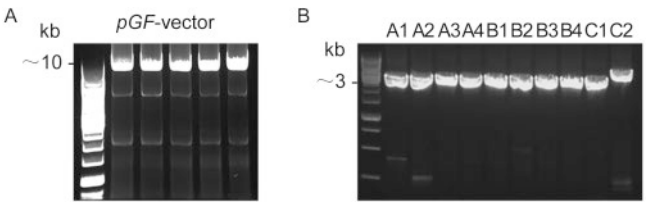


Figure 3. Preparation of the *pGF* vector and *cyanophage PP* DNA fragments. (A) The ~10-kb *pGF* vector was amplified using PCR and the homologous 5′ ends bracketing the inserted DNA fragments were inserted. (B) The DNA fragments A1-C2 were amplified using PCR from the *cyanophage PP* genome. Similarly, the 5′ end overlapping sequences were introduced using primer pairs.

and purified using the Gel Extraction Kit (Figure 3B). Alternatively, these ~3-kb long DNA fragments also could be obtained by chemical synthesis as described before (Hou and Xiao, 2011).

Next, the Part A, Part B, and Part C intermediates were assembled individually by transforming the PCR-amplified DNA fragments and *pGF* vectors into yeast protoplasts. The potential positive colonies were selected on His plates. As shown in Figure 4A, the assembled products of Part A, Part B, and Part C were isolated from the yeast cells and identified by restriction digestion. When the positive plasmids were digested with unique cut sites for *Eco*R I, the linearized *pGF*-Part A, -Part B, and -Part C separated on 0.6% agarose gels were exhib-

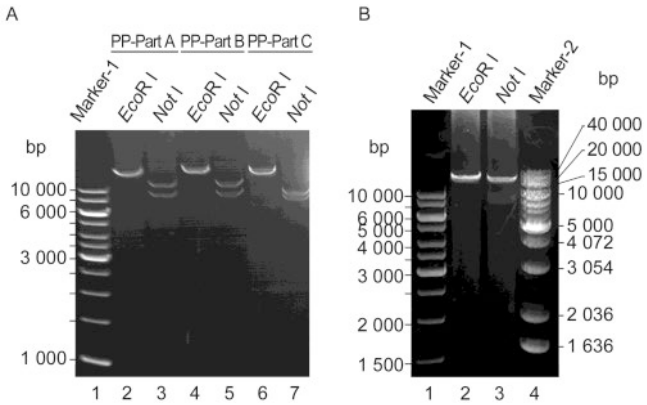


Figure 4. Restriction digestion analysis of the assembled DNA sequences. (A) Verification of the assembled intermediates of Part A, Part B, and Part C. Yeast colonies containing positive assemblies were verified by digestion with the endonucleases *Eco*R I (lanes 2, 4 and 6) and *Not* I (lanes 3, 5 and 7). A molecular weight marker was loaded in lane 1. (B) Analysis of the ~41-kb assembled *pGF*-PartABC by digestion with the endonucleases *Eco*R I (lane 2) and *Not* I (lane 3). Standard and high molecular weight markers were loaded in lane 1 and lane 4, respectively.

ited as single bands significantly larger than 10 kb in size (the maximum size of the Marker). *Not* I digestion was used to clearly resolve the inserted fragments in the assembly products. The electrophoresis of the assembled intermediates treated with *Not* I showed separated bands. The ~10 kb and ~12 kb bands in lane 3 corresponded to the free *pGF* vector and the assembled intermediate Part A, respectively. Similarly, the ~10 kb and ~12 kb bands in lane 5 corresponded to the free *pGF* vector and the assembled Part B intermediate, and the ~10 kb and ~7 kb bands in lane 7 corresponded to the free *pGF* vector and the assembled intermediate Part C, respectively. These results indicated that the *in vivo* recombination-based assembly method could effectively join 2–4 DNA fragments, each of ~3 kb. Moreover, the assembled products could be amplified using the shuttle vector *pGF* in *E. coli* and could be conveniently released from the vector by endonuclease digestion. The sequencing of the assembled intermediates by Sangon Biotech Co. Ltd. indicated that the sequences were accurate, which meant this *in vivo* recombination method using the shuttle vector *pGF* exhibited higher accuracy and greater convenience compared with conventional PCR-based methods.

The three assembled DNA intermediates together with the *pGF* vector were then co-transformed into yeast cells to generate *pGF*-Part ABC. As indicated in Figure. 4B, the *Eco*R I-linearized *pGF*-Part ABC was about 41 kb in size (lane 2), as determined using the high molecular weight marker, which was in accordance with the full length of the target product. As mentioned above, the plasmid *pGF*-Part ABC could release the inserted assembled long DNA sequence upon treatment with *Not* I. Lane 3 in Figure 4B shows that two bands of ~10 kb and ~31 kb were separated on a 0.6% agarose gel, which corresponded to the free *pGF* vector and the assembled Part ABC, respectively.

To further verify the positive colonies, the assembled plasmids were extracted and analyzed by PCR. As shown in Figure 5A, the PCR performed using the primer pairs of each DNA fragment all generated products with target sizes (A1, A2, A3, A4, B1, B2, B3, B4 and C1, each of ~3 kb and C2 of ~4 kb), which indicated that all the 10 *cyanophage PP* DNA fragments were present in *pGF*-Part ABC. Next, specific primer pairs (FV/RA1, FA1/RA2, FA2/RA3 and so on; Figure 5B) were designed to amplify the sequences across the two adjacent DNA fragments (as listed in Supplementary Table S2). The correct order of the assembly was verified by PCR amplification using these primers. The result showed that all the PCR products separated on the agarose gel exhibited molecular sizes consistent with those of the designed target products (indicated below the amplified fragments in Figure 5B). This result further confirmed the fact that the 10 *cyanophage PP* DNA fragments were assembled in the desired order and formed the 31-kb long DNA sequence.

One-step assembly of the 31-kb long DNA from the *cyanophage PP* genome

To investigate the assembling capability of the *in vivo* recombination system in yeast, we also tried to co-transform all the 10 *cyanophage PP* DNA fragments and the *pGF* vector into yeast protoplasts at once to achieve one-step assembly. The ~41-kb *pGF*-Part ABC, which contained the ~31-kb assembled Part ABC sequence and the 10-kb *pGF* vector, was successfully obtained by *in vivo* recombination. The assembled plasmids were isolated from the yeast cells and transformed into *E. coli* EPI300. The plasmids amplified in EPI300 were then extracted using a Plasmid Miniprep Kit and analyzed by endonuclease digestion and PCR as described above. As shown in Figure 6, after the plasmid was digested with *Not* I, the vector *pGF* and the released assembled DNA sequence were separated on a 0.6% agarose gel. The observed two bands corresponded to the ~10-kb free *pGF* vector and the ~31-kb assembled Part ABC. In addition, the PCR analyses further revealed the orderly assembly of all the fragments in *pGF*-Part ABC. These results were similar to those shown in Figure 5 and not shown anymore.

DISCUSSION

The assembly of long DNA molecules requires a more accurate and effective scheme rather than a routine ligation-based cloning method. Although PCR enzymes with high fidelity have been developed, the random errors introduced during the amplification process are an obvious limitation of long sequence PCR. The complexity of different DNA templates influences the accuracy of PCR, especially in the case of amplification of long DNA sequences (Kumar and Kaur, 2014; Varadaraj and Skinner, 1994). The *in vitro* Gibson assembly method can ligate several DNA fragments to produce large DNA sequences by using single-strand DNA 3′ overhangs. However, this method needs exonucleases to chew back from the DNA 5′ end, DNA polymerase to fill the gaps, and DNA ligase to remove nicks, which increases the cost of using this method. In addition, the concentrations of the DNA fragments and enzymes must be regulated accurately in order to achieve successful assembly. In addition, the yield of positive colonies may decrease when assembling more than 5 DNA fragments at once.

The shuttle plasmid *pGF* and *in vivo* TAR assembly method described here provides an alternative way to combine DNA fragments to form large DNA sequences.

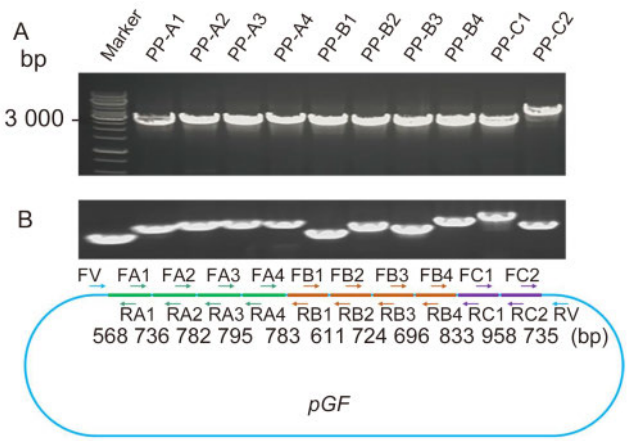


Figure 5. PCR analysis of the assembled ~41-kb long DNA sequence. (A) Amplicons of all the 10 *cyanophage PP* DNA fragments were present in the complete assembled product *pGF*-PartABC. (B) Amplification of the DNA sequences across the adjacent fragments. To ensure the correct order of the assembled DNA fragments, specific primers located on the inner side of each fragment were designed. The forward primers of the *pGF* vector (FV) and the reverse primer of A1 (RA1) were used in pairs to amplify the sequences across the vector and A1. Similarly, FA1/RA2, FA2/RA3, and so on were used in pairs to amplify the sequences across two adjacent fragments. The precise sizes of the target PCR products are marked.

The shuttle plasmid *pGF* containing the YAC regulatory elements could be ligated with several DNA fragments with overlapping ends through homologous recombination in yeast. Moreover, the assembled products could be amplified in *E. coli*.

Using the yeast recombination system, the appropriate DNA fragments with 5′ end overlapping sequences could be assembled in the yeast cells. Notably, the 5′ overlapping sequences could be introduced into the DNA fragments by PCR using synthetic specific primers, thus eliminating the need for the chewing back step by exonuclease, which was required in the Gibson model. The homologous recombination-based TAR method is very helpful especially for the assembly of long DNA sequences. Using this method, the assembly and the modification of a viral genome from small DNA fragments could be conveniently achieved. The fidelity of the assembled large DNA molecule was only associated with the fidelity of the assembly units (relatively small DNA fragments). The sizes of the small DNA fragments used for the assembly were designed to be below 5 kb, so that the fidelity of the synthetic large DNA molecule could be guaranteed. Alternatively, DNA fragments less than 5 kb in size can also be easily obtained by using the DNA synthesizer.

Genomes of living organisms will always contain some gene regulatory elements such as long terminal repeat (LTR) sequences. It should be noted that these sequences always have a high G + C content and may form complex secondary structures, thus influencing effective assembly. To ensure the fidelity of such DNA fragments, a specific high-fidelity polymerases (such as Q5 High-Fidelity DNA polymerases from NEB) designed to amplify the high G + C template should be used, and DMSO and other reagents should be added at appropriate concentrations to lower the T_m value. In addition, the se-

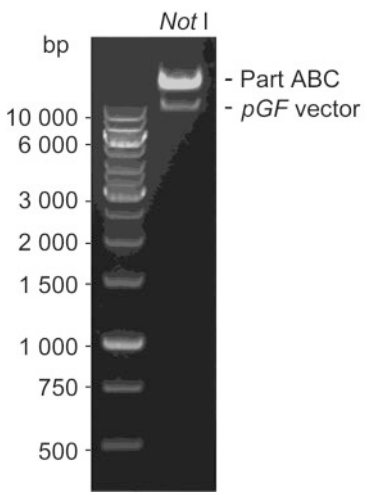


Figure 6. Verification of the one-step assembly of the plasmid *pGF*-Part ABC by digestion with the endonuclease *Not* I.

quences that readily form complex secondary structures should be arranged to be in the middle of the DNA fragments, and not at the 5′ or 3′ ends. Regulatory sequences may also sometimes be toxic for *E. coli*. The recombination-based assembly in yeast could circumvent the toxicity to *E. coli*, but the assembled products could be prepared only from large-scale culture of yeast cells in this case.

In conclusion, the present work provided a novel synthetic *E. coli*-yeast shuttle plasmid *pGF* and a TAR-based assembly method for the construction of large DNA sequences. Using this method, the reconstruction of a mini genome of various viruses from the relatively small torque teno virus (TTV) and adeno-associated virus (AAV) to the large baculovirus like autographa californica multicapsid nucleopolyhedrovirus (AcMNPV) could be achieved efficiently. The novel synthetic shuttle plasmid *pGF* and the associated DNA assembly method will not only aid in the design of artificial biological systems like in bacterial metabolic engineering, but will also accelerate the progress of synthetic virology including mini-genome construction and vaccine research and development against new recombination viruses.

ACKNOWLEDGMENTS

We thank Dr. Zhihong Hu, Dr. Zhengli Shi, and Dr. Fei Deng of the Wuhan Institute of Virology, Chinese Academy of Sciences, China, for their advice, encouragement, and support in conducting this work. This study was supported by the 973 program, Grant No. 2012CB 721102.

COMPLIANCE WITH ETHICS GUIDELINES

The authors declare that they have no conflict of interest. This article does not contain any studies with human or animal subjects performed by any of the authors.

AUTHOR CONTRIBUTIONS

ZH and ZLW carried out experiments for the construction of the *pGF* vector and *cyanophage PP* genome assembly; ZZ wrote the manuscript and participated in some of the experiments. GFX was the corresponding author who conceived and supervised the project.

Supplementary Tables are available on the website of *Virologica Sinica*: www.virosin.org; link.springer.com/journal/12250.

REFERENCES

Cameron DE, Bashor CJ, Collins JJ. 2014. A brief history of synthetic biology. Nat Rev Microbiol, 12: 381–390.

Dueber JE, Wu GC, Malmirchegini GR, Moon TS, Petzold CJ, Ullal AV, Prather KL, Keasling JD. 2009. Synthetic protein scaffolds provide modular control over metabolic flux. Nat Biotechnol, 27: 753–759.

Gibson DG, Benders GA, Andrews-Pfannkoch C, Denisova EA, Baden-Tillson H, Zaveri J, Stockwell TB, Brownley A, Thomas DW, Algire MA, Merryman C, Young L, Noskov VN, Glass JI, Venter JC, Hutchison CA, 3rd, Smith HO. 2008a. Complete chemical synthesis, assembly, and cloning of a Mycoplasma genitalium genome. Science, 319: 1215–1220.

Gibson DG, Benders GA, Axelrod KC, Zaveri J, Algire MA, Moodie M, Montague MG, Venter JC, Smith HO, Hutchison CA, 3rd. 2008b. One-step assembly in yeast of 25 overlapping DNA fragments to form a complete synthetic Mycoplasma genitalium genome. Proc Natl Acad Sci U S A, 105: 20404–20409.

Gibson DG, Glass JI, Lartigue C, Noskov VN, Chuang RY, Algire MA, Benders GA, Montague MG, Ma L, Moodie MM, Merryman C, Vashee S, Krishnakumar R, Assad-Garcia N, Andrews-Pfannkoch C, Denisova EA, Young L, Qi ZQ, Segall-Shapiro TH, Calvey CH, Parmar PP, Hutchison CA, 3rd, Smith HO, Venter JC. 2010a. Creation of a bacterial cell controlled by a chemically synthesized genome. Science, 329: 52–56.

Gibson DG, Smith HO, Hutchison CA, 3rd, Venter JC, Merryman C. 2010b. Chemical synthesis of the mouse mitochondrial genome. Nat Methods, 7: 901–903.

Hou Z, Xiao G. 2011. Total chemical synthesis, assembly of human torque teno virus genome. Virol Sin, 26: 181–189.

Keohavong P, Thilly WG. 1989. Fidelity of DNA polymerases in DNA amplification. Proc Natl Acad Sci U S A, 86: 9253–9257.

Khalil AS, Collins JJ. 2010. Synthetic biology: applications come of age. Nat Rev Genet, 11: 367–379.

Kodumal SJ, Patel KG, Reid R, Menzella HG, Welch M, Santi DV. 2004. Total synthesis of long DNA sequences: synthesis of a contiguous 32-kb polyketide synthase gene cluster. Proc Natl Acad Sci U S A, 101: 15573–15578.

Kouprina N, Larionov V. 2008. Selective isolation of genomic loci from complex genomes by transformation-associated recombination cloning in the yeast Saccharomyces cerevisiae. Nat Protoc, 3: 371–377.

Kumar A, Kaur J. 2014. Primer Based Approach for PCR Amplification of High GC Content Gene: Mycobacterium Gene as a Model. Mol Biol Int, 2014: 937308.

Larionov V, Kouprina N, Graves J, Chen XN, Korenberg JR, Resnick MA. 1996. Specific cloning of human DNA as yeast artificial chromosomes by transformation-associated recombination. Proc Natl Acad Sci U S A, 93: 491–496.

Lee BR, Cho S, Song Y, Kim SC, Cho BK. 2013. Emerging tools for synthetic genome design. Mol Cells, 35: 359–370.

Li MZ, Elledge SJ. 2007. Harnessing homologous recombination in vitro to generate recombinant DNA via SLIC. Nat Methods, 4: 251–256.

Merryman C, Gibson DG. 2012. Methods and applications for assembling large DNA constructs. Metab Eng, 14: 196–204.

Noskov VN, Chuang RY, Gibson DG, Leem SH, Larionov V, Kouprina N. 2011. Isolation of circular yeast artificial chromosomes for synthetic biology and functional genomics studies. Nat Protoc, 6: 89–96.

Shevchuk NA, Bryksin AV, Nusinovich YA, Cabello FC, Sutherland M, Ladisch S. 2004. Construction of long DNA molecules using long PCR-based fusion of several fragments simultaneously. Nucleic Acids Res, 32: e19.

Stemmer WP, Crameri A, Ha KD, Brennan TM, Heyneker HL. 1995. Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides. Gene, 164: 49–53.

Varadaraj K, Skinner DM. 1994. Denaturants or cosolvents improve the specificity of PCR amplification of a G + C-rich DNA using genetically engineered DNA polymerases. Gene, 140: 1–5.

Zhou Y, Lin J, Li N, Hu Z, Deng F. 2013. Characterization and genomic analysis of a plaque purified strain of cyanophage PP. Virol Sin, 28: 272–279.

(U) Robert F. Kennedy, Jr. and Children's Health Defense Call for Congressional Investigation of COVID origin

Identifiers:

Messaging System: [redacted]
Document Number: [redacted]
Ingestion ID: [redacted]
GUIDE: [redacted]

Dates:

Date Published: 21-Oct-2020 20:00:00
Date Received: 22-Oct-2020 10:33:24

Publisher:

[redacted]

(U) Full inquiry into circumstances leading to global loss of lives and economic devastation should be lawmakers' top priority

WASHINGTON, Oct. 22, 2020 /PRNewswire/ -- Robert F. Kennedy, Jr. and Children's Health Defense (CHD) are calling upon Congress to conduct a thorough investigation of the circumstances behind the global COVID-19 crisis that is taking an overwhelming toll on human lives and livelihoods. In a letter to lawmakers Mr. Kennedy, Chairman and Ms. Redwood, President of CHD, emphasized the urgent need to address the many unanswered questions regarding the origin of COVID-19.

"Consider this hypothetical scenario: an important gain-of-function experiment involving a virus with serious pandemic potential is performed in a well-regulated, world-class laboratory by experienced investigators, but the information from the experiment is then used by another scientist who does not have the same training and facilities and is not subject to the same regulations. In an unlikely but conceivable turn of events, what if that scientist becomes infected with the virus, which leads to an outbreak and ultimately triggers a pandemic?"

These are the words of Anthony Fauci, director of the NIAID, in a letter to the microbiology journal mBio advocating for gain-of-function experiments in 2012. But Dr. Fauci's scenario may not be purely hypothetical. Such concerns are supported by reports US science diplomats made to the State Department in 2018 after visiting the Wuhan Institute of Virology (WIV), a Chinese research laboratory conducting US funded gain-of-function research on bat coronaviruses. The reports warn about inadequate safety measures at the lab, which was conducting risky studies on coronaviruses from bats that could result in human transmission and a new SARS-like pandemic.

It would be unthinkable to not investigate the causes of the space shuttle Challenger disaster, the Chernobyl nuclear accident or the Exxon Valdez oil spill. Today we have a virus that has led to the deaths of thousands of people--mostly the elderly--caused severe global economic damage, and destroyed thousands of small businesses across America, and there is little serious consideration as to where this virus originated.

"It falls upon the leadership of the U.S. Congress to accept its moral duty and God-given and legally pre-ordained responsibility to launch complete and transparent investigations. If we do

nothing, history will hold us and our system of government accountable," stated Kennedy and Redwood.

Contact

Laura Bono

202.854.1310

View original content:http://www.prnewswire.com/news-releases/robert-f-kennedy-jr-and-childrens-health-defense-call-for-congressional-investigation-of-covid-origin-301158110.html

SOURCE Children's Health Defense

/Web site: http://www.childrenshealthdefense.org

(END)

Collection: OW

Creator:

[redacted]

#2
Compilation Title: PR NEWSWIRE

Description: (U) Full inquiry into circumstances leading to global loss of lives and economic devastation should be lawmakers' top priority

---

Language: eng

Source:

Publisher Type: open-source
Sourced Text: null
Language: eng
Source ID: prco20201022002592
Source Type: Wire Services
POC #1
Office Name: PR NEWSWIRE ASSOCIATION, INC.
POC #2
Office Name: [redacted]
Title: Robert F. Kennedy, Jr. and Children's Health Defense Call for Congressional Investigation of COVID origin
Compilation Title: PR NEWSWIRE
Information Date: 21-Oct-2020 20:00:00
Information Cutoff Date: 21-Oct-2020 20:00:00

Subject: PR NEWSWIRE

[redacted]

Weekly Accomplishments

8 Jul 2021 – 14 Jul 2021

In support of the POTUS's 90-day COVID ~~Surge~~review, recent accomplishments ~~by the NIC & NCPC~~ include:

[redacted]

[redacted] HPSCI CDA: Response to Foreign & Liaison Partner Collaboration on Determining the Origins of COVID-19 **Fri 7/09/21**

- NCPC, in collaboration with the NIC, is developing a response to be including in OLA CDA (ODNI-2021-00995) referring to which foreign and liaison partners have been the most helpful during the COVID-19 origins surge.

[redacted] Biological Science Expert Group (BSEG) Meeting on COVID-19 Origins **Mon 7/12/21**

- ~~NCPC solicited community questions, provided logistical support, and hosted an engagement between the Intelligence Community (IC) and members of the Biological Sciences Expert Group (BSEG).~~
- The BSEG was convened to review papers provided by [redacted] and DTIC regarding the correlation between Chinese Hazard Levels and Biosafety Levels. The experts discussed the protocols at WIV in the laboratory and during animal sample collection. BSEG was able to provide original Chinese biosafety protocols and standards that explain hazard standards and definition, as well as first-hand accounts of Chinese protocols and practices.
- This meeting was the second in a series of three IC engagements during the 90-day study with the BSEG and focused on technical issues or gaps related to IC reporting or academic literature on COVID-19 origins.

[redacted] IC Discussion with HHS/NIH on SARS-CoV-2 Origins. **Tue 7/13/21**

- NCPC organized a dual classified and unclassified engagement between the IC and HHS/National Institutes of Health (NIH) to provide an overview on how the IC is approaching the 90-day study to facilitate further conversations with technical SMEs at HHS to better inform IC analysts moving forward. ~~HHS reiterated a desire to support the IC and were receptive to the idea of an additional follow-up meeting.~~ Of note, NIH committed to providing the grant application and progress reports for WIV coronavirus research to the IC.
- NIH National Library of Medicine confirmed that, as described in the Bloom paper, rescinding sequence information is not usually done in that manner. NIH is conducting an internal review of this process. In the meantime, they committed to share historical server data.

[redacted] Re-Issue of CEM Releasable to include Finland/Sweden **Tue 7/13/21**

[redacted]

Commented [redacted] Recommend delete. They are expecting a published report tomorrow about NCMI's collaboration with Germans; No new information to move the needle. Chine may have potentially new of COVID challenge earlier to due to a published report date in summer 2019. This could also be a metadata error, in which DIA is still trying to verify.

[redacted]

Weekly Accomplishments

8 Jul 2021 – 14 Jul 2021

- In coordination with the IC, ODNI re-issued the CEM with expanded releasability to include Finland and Sweden in response to requests from Helsinki and Stockholm Stations.

Upcoming

[redacted] **Key Stakeholders Meeting** **Fri 7/23/21**

- The NIC is planning to have an in-person Key Stakeholder's meeting on 23 Jul to discuss Agency positions ahead of drafting the 90-day COVID Origins Tasking Assessment. The NIC will solicit each agency for their assessments on COVID origins.
- The meeting will be limited to one to two people from each agency and will include discussions on how to structure the final product.

[redacted]

[redacted]

From: [redacted]
Sent: Wednesday, July 14, 2021 3:12 PM
To: [redacted]
Cc: [redacted]
Subject: RE: Covid origins - Dr. Fauci recommendations

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Thanks for the feedback. In this particular case, given Dr Fauci's background we absolutely would like to follow-up on his outreach suggestions. In this case he's not a policymaker….he's a SME with a wealth of knowledge about current and historical research who probably knows better than most who the real Coronavirus experts are.

From: [redacted]
Sent: Wednesday, July 14, 2021 4:00 AM
To: [redacted]
Cc: [redacted]
Subject: RE: Covid origins - Dr. Fauci recommendations

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Hi [redacted]

Setting aside the process for contacting [redacted] individuals on any subject, I think the first question is whether the NIC wants to make the effort after it weighs whether to take a policymaker's recommendations on who we should consult as part of an IC study--particularly given the various strong views on the subject and statements regarding their own conclusions. If the NIC wants to proceed, we can then determine how we would facilitate such contact.

From: [redacted]
Sent: Tuesday, July 13, 2021 9:05 PM
To: [redacted]

Cc: [redacted]

Subject: FW: Covid origins - Dr. Fauci recommendations

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

All,

For those who don't know me, I'm the [redacted] and, as such, leading the IC's 90-day POTUS COVID origin study. Per below, Dr Fauci recommended that the IC reach out to the below individuals who were coauthors of the attached paper as part of the study. [redacted] is on the list of SMEs the IC has already consulted, [redacted], but [redacted] and [redacted], and, as far as I know, neither has been consulted. As of today, we have 43 days before our final paper is due to the President, so if we're going to reach out to them we need to do so ASAP. Is this doable? Please let me know if there's anything I can do to facilitate this from my end. Thanks! – [redacted]

[redacted]

From: Alan S. Macdougall-DNI- [redacted]
Sent: Monday, July 12, 2021 3:14 PM
To: [redacted]
Cc: [redacted]
Subject: FW: Covid origins - Dr. Fauci recommendations

Classification: UNCLASSIFIED[redacted]
==========
[redacted] and [redacted]

(U[redacted]) FYSA from last week's IC Weekly Update. We can discuss further based on my chat with [redacted]

VR,
Alan

From: [redacted]
Sent: Monday, July 12, 2021 2:50 PM

To: Alan S. Macdougall-DNI-
Cc: Morgan Muir-DNI-
Subject: Covid origins - Dr. Fauci recommendations

Classification: UNCLASSIFIED
==========

Alan – The article that Dr. Fauci highlighted last week is attached, and the authors whose views he thought were particularly important were:

-
-
-

As discussed, it might be worth considering the article and talking with these individuals in connection with the 90-day study. In addition, the COVID report rollout is scheduled to be discussed on Friday at the IC Weekly. Please provide any materials or information you want the DNI to convey NLT Thursday COB.

Thanks,

Chief of Staff, ODNI

==========
Classification: UNCLASSIFIED

==========
Classification: UNCLASSIFIED

==========
Classification:

==========
Classification:

==========
Classification:

On Friday 4 June, WCPMC met with the Director of the National Institute of Allergy and Infectious Diseases Dr. Anthony Fauci to present our analysis on the COVID origins topic as well as our approach to the intelligence question.

Dr. Fauci was particularly interested in the WIV's work on pangolins and asked for specifics on the type of experiments the Chinese were conducting on pangolin samples in the fall of 2019. He keyed in on specifics [redacted] He did not appear to be aware of [redacted]

He highlighted the importance of getting samples from the individuals at WIV who were ill in the fall of 2019. He encouraged the IC to examine [redacted] Dr. Fauci wondered aloud whether the USG had formally made this request to China in diplomatic or public health channels.

Dr. Fauci and CIA experts agreed on the importance of understanding whether SARS COV-2 originated from single or multiple viral lineages. He encouraged CIA to contact [redacted] a finding that we are currently evaluating with CIA SMEs and NCPC's Biological Sciences Expert Group. He also directed CIA to [redacted] Dr. Fauci also suggested the IC connect with [redacted] all three of whom have advocated for features of the virus that they judge to be consistent with a natural origin.

Dr. Fauci expressed concern about Beijing's quick and thorough cleaning of the Huanan Seafood Market. He noted that Beijing may have made a serious epidemiological misstep that could have destroyed key clues as to how the pandemic began. He offered his opinion that the Chinese have shown they are better scientists than epidemiologists. In Dr. Fauci's view, it is not surprising that Chinese have not found evidence of a zoonotic transfer or an intermediate host of the virus, because the search for natural reservoir of the SARS virus took over a decade, and in the case of some strains of Ebolavirus, still has not been found. If the virus jumped to humans from an animal reservoir, he said it would be like "searching for a needle in a haystack."

[redacted]

From: [redacted]
Sent: Monday, July 26, 2021 1:26 PM
To: [redacted]
Subject: Wall Street Journal piece today on origins

Classification: UNCLASSIFIED
==========

FYI, Here's a WSJ piece today on Covid origins.

[redacted]

UNCLASSIFIED
(U) Anthony Fauci, Rand Paul and Wuhan
Identifiers:

Document Number:
[redacted]
Ingestion ID:
[redacted]
News ID:
[redacted]
GUIDE:
[redacted]

Dates:

Date of Version:
26-Jul-2021 06:03:26
Date Created:
26-Jul-2021 06:03:26

Coverage:

Geographic Area:
Wuhan, United States

Publisher:

Date:
20210726
Name:
Factiva, The Wall Street Journal

No one should expect the Chinese Communist Party to cooperate with a real inquiry into the origins of Covid-19. More disappointing is the lack of candor from American scientists and officials whose conflicts of interest deserve more scrutiny.

More than a year-and-a-half after Chinese researchers published a draft genome of Covid-19, the world still doesn't know where the virus came from. The leading theories are an accidental lab leak or zoonotic spillover from a bat or other intermediary species.

A World Health Organization team visited Wuhan this year but Chinese officials provided little useful information. Even WHO director-general Tedros Ghebreyesus, typically a Chinese ally, criticized Beijing for a lack of transparency. He called for an audit of laboratories in Wuhan as part of the origin investigation's next phase, but Beijing rejected the idea last week.

A senior Chinese public-health official said WHO's plan "did not respect common sense and violated science." The Chinese Foreign Ministry has called instead for an investigation into Fort Detrick, a U.S. military lab. A Wuhan Institute of Virology official said that his lab "did not contact, preserve or study the novel coronavirus, and it never designed, made or leaked the virus," according to Chinese state-media. He added that there have been zero pathogen leaks or human infections since the institute opened its high-level BSL-4 lab in 2018. A Chinese official must say this or risk disappearing.

The WIV has handled coronaviruses. U.S. experts visited the lab in 2017 and 2018 and warned about a dangerous mix of subpar safety standards and infectious bat coronaviruses. In January the State Department published a fact sheet warning that several WIV researchers had been sick with Covid-like symptoms in the fall of 2019. It also noted that the group had been conducting gain-of-function research that could possibly enable viruses to infect a new species -- all while collaborating with the People's Liberation Army. And the WIV's critical virus databases were taken offline, ostensibly for security purposes.

The U.S. knows something about the research conducted at the WIV, because American taxpayer dollars helped fund it. This was the crux of last week's dispute between Sen. Rand Paul and Anthony Fauci, who had cast doubt on the lab-leak hypothesis in the past. In their latest bout, the Kentucky Senator accused Dr. Fauci of lying to Congress, a federal crime, when he said this year that the National Institutes of Health had never funded gain-of-function research in Wuhan. The exchange descended into shouting.

The reality is complicated. The NIH gave almost $600,000 to the WIV through a nonprofit over several years to study bat coronaviruses. Mr. Paul cited a 2017 paper from WIV researchers that included experiments combining parts of viruses to study how to better infect human cells. But Dr. Fauci said the project was "judged by qualified staff up and down the chain as not being gain-of-function."

This might be technically true, as a 2014 federal government definition describes such research as that which "increase the ability of infectious agents to cause disease by enhancing its pathogenicity or by increasing its transmissibility." But some scientists think the government definition is too limited and can allow de facto gain-of-function research to bypass safety protocols. Rutgers molecular biologist Richard Ebright says the NIH-funded work "was -- unequivocally -- gain-of-function research."

In early 2020, Dr. Fauci emailed his deputy a paper co-written by gain-of-function pioneer Ralph Baric and a Wuhan scientist. The official responded that they would "try to determine if we have any distant ties to this work abroad." The next day Dr. Fauci organized a call with several nongovernment virologists, but the email chain after the meeting was redacted. Weeks later, a group of scientists published a letter in The Lancet

condemning "conspiracy theories suggesting that COVID-19 does not have a natural origin." Dr. Fauci and the public-health elite echoed the letter's views for months.

Mr. Paul, excitable as he may be, is a medical doctor who did his homework. The Senator clearly sees a political benefit in hammering Dr. Fauci and China, but the celebrity scientist and his allies have obvious conflicts of interest. The Lancet letter was organized by Peter Daszak, president of the EcoHealth Alliance, which had funneled the NIH money to the WIV.

Mr. Daszak, Dr. Fauci and all researchers involved in gain-of-function research would suffer significant reputational damage and perhaps lose funding if scientific research they supported caused a pandemic. On Sunday Dr. Fauci said the research cooperation was necessary because "SARS-CoV-1 originated in China." But exactly what did that cooperation yield?

Congress should thoroughly investigate the process that led to the approval of money for the WIV and possible gain-of-function research. It should also debate limits on this kind of research in the U.S. and push for international standards. While China is unlikely to budge, its opacity has aroused justifiable suspicion around the world, and the White House should keep the pressure on Beijing and the WHO.

Democrats and much of the media will avoid the topic because Mr. Paul and the populist right have taken up this cause. Such groupthink is what prevented the lab-leak theory from being treated seriously for more than a year. Making the same mistake twice is inexcusable.

Language:
en

Subject:
Anthony Fauci, Rand Paul and Wuhan

UNCLASSIFIED

[redacted]
Deputy NIO for WMD & Proliferation-Missiles
National Intelligence Council, [redacted]
[redacted]

==========
Classification: UNCLASSIFIED

[redacted]

From: [redacted]
Sent: Tuesday, December 3, 2024 8:35 AM
To: [redacted]
Subject: RE: HOT: Final Congressional COVID Report, Confirms Lab Leak

Classification: UNCLASSIFIED[redacted]
==========

ODNI was going to give them a heads up but not sure what happened to that… we probably need to engage OCA.

From: [redacted]
Sent: Tuesday, December 3, 2024 8:34 AM
To: [redacted]
Subject: RE: HOT: Final Congressional COVID Report, Confirms Lab Leak

Classification: UNCLASSIFIED[redacted]
==========

Does Congress have any idea about the Germans?

From: [redacted]
Sent: Tuesday, December 3, 2024 8:27 AM
To: [redacted]
Cc: [redacted]
Subject: RE: HOT: Final Congressional COVID Report, Confirms Lab Leak

Classification: UNCLASSIFIED[redacted]
==========

Hi [redacted]

Thanks for flagging—adding a bunch of people who should be tracking on this one.

Thanks again,

[redacted]
Worldwide BW Analyst
WCPMC/CBD/WMAAB
[redacted]

From: [redacted]
Sent: Tuesday, December 3, 2024 7:14 AM

To: [redacted]
Cc: [redacted]
[redacted]
Subject: HOT: Final Congressional COVID Report, Confirms Lab Leak

Classification: UNCLASSIFIED[redacted]
==========

Hi all,

The Select Subcommittee released a 520-page final report last night detailing the findings of its two-year investigation into the COVID-19 pandemic, which highlights lessons learned and a path forward for preparing for and responding to future pandemics.

The report concludes that COVID-19 most likely emerged from a laboratory in Wuhan, China, and criticizes the WHO's response to the pandemic, as well as the US government's handling of relief funds, mask mandates, and vaccine development. The report also identifies widespread corruption, misinformation, and obstruction of its investigation by government officials, researchers, and organizations, including Dr. Anthony Fauci, EcoHealth Alliance, and the Biden Administration's CDC.

<u>The leading theories that led the committee to their conclusions:</u>

1. The virus possesses a biological characteristic that is not found in nature.
2. Data shows that all COVID-19 cases stem from a single introduction into humans. This runs contrary to previous pandemics where there were multiple spillover events.
3. Wuhan is home to China's foremost SARS research lab, which has a history of conducting gain-of-function research at inadequate biosafety levels.
4. Wuhan Institute of Virology (WIV) researchers were sick with COVID-like virus in the fall of 2019, months before COVID-19 was discovered at the wet market.
5. By nearly all measures of science, if there was evidence of a natural origin it would have already surfaced.

I'll look into pulling over the entire assessment into HIVE for those interested. I'll continue to monitor the open source for any developments.

Thanks,
[redacted]

[redacted]
Open Source Specialist, WCPMC
Chemical & Biological Department (CBD)

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Tuesday, December 12, 2023 7:06 PM
To: [redacted]
Cc: [redacted]
Subject: Flagging: COVID origins questions today
Attachments: FW: in response to the DDCIA question related to the context of a Fauci e... (661 KB)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

OCA,

Just wanted to give you a heads up that an NSC director asked us for some talking points on CIA's engagement with Dr. Fauci ahead of a House Coronavirus subcommittee meeting tomorrow.

HHS, USAID, and DoS are attending a Coronavirus subcommittee hearing tomorrow on *Reforming the WHO: Ensuring Global Health Security and Accountability.* The NSC was concerned that questions about Fauci and CIA might come up after Rand Paul's interview promoting his new book on COVID origins, "*Deception: The Great COVID Cover-Up*.

We suggested that if questions in the hearing come up about CIA, then they need to be passed to CIA through official channels (ie OCA). **So there is no action for you or us right now: just flagging for your awareness.**

I've also attached for your reference the email we sent up to DDCIA a couple months ago on the background of our Fauci engagement.

The Rand Paul interview is transcribed below, but here's the key part:

So, there really was an orchestrated cover-up on this. We also now know that he [Fauci] was visiting the CIA in early 2020. We know that the CIA scientists, seven of them, voted six to one to say it came from the lab, and then they were reversed by superiors. We need to know whether Anthony Fauci influenced the superiors, or perhaps the opposite. Did the CIA influence Anthony Fauci?
But we also need to know how often he was visiting and what he was there for. Our understanding is that he wasn't recorded on visitor logs, but he was appearing frequently at the CIA. You have to realize that he was not a scientist in charge of a cure for cancer. He was also in charge of a lot of bioweapons money and in charge of a lot of things that had dual use.
And they won't reveal any of this to us. They had weekly meetings on dangerous dual-use research concerns and gain-of-function, and not one item of any of those meetings has been released to us, despite us asking for it for over three years.

[redacted]

[redacted]

From: [redacted]
Sent: Tuesday, December 12, 2023 12:26 PM
To: [redacted]
Subject: (U) COVID-19

Classification: UNCLASSIFIED
==========

MARIA **BARTIROMO**», FOX NEWS ANCHOR:
And that's South Dakota Governor Kristi Noem with me last week on this program with some disturbing commentary, communist China still controlling America's supply of medicine four years after the outbreak of COVID-19 from a lab in Wuhan that has killed more than 1.1 million Americans so far.
The CCP has yet to provide evidence on how that deadly virus originated and explain its cover-up that followed. Next month, Dr. Anthony Fauci is set to testify for two days before the House on the origins of COVID-19 and his handling of the pandemic, where Republicans are expected to grill him on overseeing funding of gain-of-function research at the Wuhan lab, as well as discrediting the theory the virus originated from a lab leak.
Joining me right now is Kentucky Senator Rand Paul. He is vowing to hold hearings on the origins of COVID in the Upper Chamber if Republicans retake control next year. Senator Paul is also the author of the new book "Deception: The Great COVID Cover-Up," available right now.
Senator, thanks very much for joining us this morning.

SEN. RAND PAUL (R-KY):
Thank you, Maria.

«**BARTIROMO**»:
Well, you have been an incredible truth-teller throughout all of this, and you have studied all of this now for several years.
What can you tell us about what you have learned, what you have taken away from the entire COVID experience?

PAUL:
Well, the problem is, is that the Chinese have destroyed any kind of reputation they had.
I mean, we can no longer believe any kind of pronouncements from them, which makes us suspicious. Right now, there's a host of disease affecting young people, respiratory disease and pneumonia, in China, and they tell us, well, there's nothing to see here.
And maybe that's true, but they have destroyed any kind of foundation we had in trusting them, and they still haven't come clean. In early 2020, when COVID came out, they said, oh, we're not having human-to-human transmission, and we don't seem to be having an extraordinary amount of flooding in the hospitals or deaths.
All of that was untrue, and they knew for at least three or four weeks. They also knew the sequence of the virus, and they kept that secret as well. I think they also knew that three of their workers got sick at the Wuhan Institute of Virology in November 2019. I think they knew all of this.
And I think they absolutely know it now, and the only way they can restore trust is to own up to it. Look, I don't blame them completely for this. I think it was an accident, but cover-up is not an accident. If they were to come clean and say, we're punishing the scientists who did what they weren't supposed to, I think then that we could restore some trust. But, right now, we have really no trust with the Chinese government.

«**BARTIROMO**»:
Well, what about the accountability here, and why the Biden administration does not push for it?

I mean, right now, as we speak, there are American investors continuing to underwrite the CCP by buying those companies that are tied to the Chinese military. It seems this administration is not willing to pull the economic lever, and that is shut off the capital markets to Chinese communist companies that may have been involved in that cover-up or tied to the military.

PAUL:
Well, we still continue to fight the Biden administration every day just for unclassified information, and they resist at every turn.
We have had to basically withhold nominees and withhold legislation to try to get anything from the Biden administration. And I'm not sure what it is. Either it's sympathy or believing that relations with China are so important that the truth can be obscured.
But there's also a certain amount of culpability in the Biden administration throughout several different departments, USAID, NIH, HHS. They're withholding documents because they funded the lab in Wuhan, not just once, not just twice, but for a decade they were funding.
And we have Anthony Fauci on record as saying that, even if a pandemic occurs, even if a gain-of-function research infects a scientist and a pandemic occurs, that the knowledge would be worth the risk. And I think most people who had a loved one die from COVID either here or around the world would disagree and think Anthony Fauci made a disastrous judgment call.
But he also took the research, and it didn't go before the normal scrutiny. There's a safety committee that was supposed to review this, and Anthony Fauci allowed this research to be done at his signature, at his conclusion, at his approval without the approval of the safety committee.
And this -- for this, he really should go down in history perhaps as one of the worst people in public office ever and responsible for probably more deaths than other -- any other individual in the medical world.

«**BARTIROMO**»:
Well, I mean, there was so much censorship of so much information that was vital for Americans to see and understand about COVID and about the vaccines, but they censored it.
Can we even trust health officials in this government?

PAUL:
Well, it was directed explicitly by him. We go over this in the book, because he commissioned scientists who were saying in private that they thought it was a manipulative virus, manipulated a lab and came from a lab.
He convinced them in public to say the opposite. He commissioned and edited a paper that said that absolutely this did not come from a lab, while, privately, all of these same scientists were saying, in all likelihood, it did come from a lab.
So, there really was an orchestrated cover-up on this. We also now know that he was visiting the CIA in early 2020. We know that the CIA scientists, seven of them, voted six to one to say it came from the lab, and then they were reversed by superiors. We need to know whether Anthony Fauci influenced the superiors, or perhaps the opposite. Did the CIA influence Anthony Fauci?
But we also need to know how often he was visiting and what he was there for. Our understanding is that he wasn't recorded on visitor logs, but he was appearing frequently at the CIA. You have to realize that he was not a scientist in charge of a cure for cancer. He was also in charge of a lot of bioweapons money and in charge of a lot of things that had dual use.
And they won't reveal any of this to us. They had weekly meetings on dangerous dual-use research concerns and gain-of-function, and not one item of any of those meetings has been released to us, despite us asking for it for over three years.

«**BARTIROMO**»:
Do you believe COVID was a bioweapon?

PAUL:

I think that it was probably developed for a vaccine. I think they developed a coronavirus. They inserted this cleavage site in to make it more infectious to humans, and then they had a vaccine very early on, because I think they were developing a vaccine against COVID, and then COVID got out.

«**BARTIROMO**»:
Yes.

PAUL:
But the interesting thing is the scientist, Dr. Zo Yusin [ph], who developed it, died mysteriously two months after the development of the virus. He fell from a tall building in Beijing. And there's a lot of questions as to the circumstances of his death.

«**BARTIROMO**»:
Wow. I did not realize that, that he died from a tall building in Beijing. That's incredible.
Let me switch gears, ask you about the supplemental package. You all are leaving for the holidays next week. But you're right now debating this $100 billion supplemental package that Joe Biden wants, money sent to Ukraine, if you're going to send money to Israel.
And the Republicans so far have dug in, saying, we want policy changes at the border. Where is this going?

PAUL:
We don't have the money.
And the biggest threat -- while I agree the border should be secured, an even bigger threat is to the dollar and to our currency. I follow Jim Grant. I think he's one of the smartest guys out there looking at the economy and the Fed. He predicted a lot of the things that happened in 2008, when we had the housing bubble burst.
He thinks we're due for interest rates, high interest rates, for a long period of time, but we're accumulating debt at a trillion dollars every three months now. This is an extraordinary thing. And interest rates are now becoming the highest or one of the largest items in our budget.
So, really, people can talk about wanting to help other countries. We don't have the money. It has to be printed up. It's destroying our currency. And it's why it costs more to go to the grocery store to buy your groceries. We can't allow this to happen.
There is a possibility we could go too far with this, and we could have a cataclysmic economic downturn, recession, depression, destruction of the currency.

«**BARTIROMO**»:
Wow.

PAUL:
I know that sounds over the top, but that's what I'm worried about, because we're accumulating debt so fast.

«**BARTIROMO**»:
Well, I agree with you about Jim Grant. Jim Grant is a regular of mine on "Mornings With Maria" over on the FOX Business Network. And he's been sounding the alarm about all of this debt for a long time.
But you have got a package at hand, and you have got a vote on this coming up. Where is this going? Is -- are you guys going to go to the holiday and not send any money to Ukraine? What do you expect this -- to happen? How does this play out, rather? Pardon me.

PAUL:
My hope is that Speaker Johnson will stick to his word.
He said Israel aid would be separate and paid for. He immediately voted for it, and the House passed it, and they paid for it by taking money away from the IRS. I hope he stands by his word. I think he has an enormous leverage, if he will use it.

Now, he's getting pushed by all the establishment Republicans, particularly on the Senate side. He's being pushed to put all the aid together with Ukraine. I think, if he keeps it separate and keeps it paid for, I think that he will win the day, ultimately. But he needs to realize he has all the power, if he will stay where he is and not capitulate.

«**BARTIROMO**»:
All right, Senator, we will be watching all of that.
Thank you again for being a truth-teller in all of these health issues.

PAUL:
Thank you.

«**BARTIROMO**»:
We appreciate your time this morning, sir.
Thank you, Senator Rand Paul, for joining us.

[redacted]
Director for Biodefense and Biotechnology Risk
National Security Council
[redacted]

==========
Classification: UNCLASSIFIED

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Wednesday, September 27, 2023 12:23 PM
To: [redacted]
Subject: FW: New York Post on Fauci influencing CIA on COVID origins and Congressional Letter to HHS
Attachments: Scan-20230927115303.pdf

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Chief, Weaponization, Modeling, and Agents Analysis Branch and Disease Threat Intelligence Cell
WCP/CBD
[redacted]

From: [redacted]
Sent: Wednesday, September 27, 2023 12:10 PM
To: [redacted]
Cc: [redacted]
Subject: New York Post on Fauci influencing CIA on COVID origins and Congressional Letter to HHS

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted].

All – found this NY Post article by chance just now on AIN. It is not in today's Media clips. The attachment also includes a letter from Congress to HHS.

Separately and below is the CLASSIFIED readout of one meeting with Dr. Fauci (thanks to [redacted] for pulling it). Not sure but appears this was a VTC rather than in person (see my highlight below):

[redacted]

From: [redacted]
Sent: Monday, June 7, 2021 7:18 AM
To: [redacted]
Subject: Quick Recap of 4 June Dr. Fauci Briefing

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========
Classification: [redacted]

Hi,

WPC/[redacted] WCP/[redacted] WCP/[redacted] and EAPMC/[redacted] attended the briefing. COO [redacted] also attended, and NSC Director Beth Cameron SAP & Senior Director for Global Health Security & Biodefense "mediated/facilitated" the briefing. [redacted] briefed the key points of the 4 May 2021 PDB/WIRe [redacted] Worldwide: Origin of COVID-19 Pandemic Remains Elusive. Briefing lasted about 40 minutes (with some audio technical difficulties).

Dr. Fauci offered the following thoughts/insights when asked about certain points Camille raised from the PDB/WIRe.

- On China's pangolin research, Dr. Fauci said it was important to obtain details of the experiments.
- On the 3 sick WIV researchers, Dr. Fauci said key gaps that need to be filled are 1) If they were sick, what does their medical records show; 2) Do we have blood culture of these sick researchers; and 3) Did we ask China about/for this information?
- On the single lineage issue, Dr. Fauci recommended that IC take a look at Tulane's [redacted] paper on two lineages from two separate markets (NFI). To Dr. Fauci, this paper's findings were a clear indication of natural origins of COVID-19. This research was republished with [redacted] recently.
    - Dr. Fauci reminded the group that even for SARS, it took 12 years to make the link to a bat even though it only took 4 months to identify the natural reservoir.
    - We still haven't identified source/origin of Ebola. We need to be careful of the links we make to these previous cases.
- Dr. Fauci noted that China has good scientists but made an epidemiological mistake when China "cleaned" the market… China inadvertently shot themselves in the foot. On single lineage, it's like looking for a needle in the haystack; it may not be a whole group of animals but a single animal, which is difficult to identify; and again, Dr. Fauci asked why China didn't look more carefully into the market before "cleaning" it out.
- Dr. Fauci recommended contacting a group of US scientists who closely follow this issue, especially to combine investigative/forensics/intel with scientific community's research, including [redacted], and [redacted] [WCP is already in contact/in the plans to contact some of these individuals.]

Thanks!
[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Wednesday, July 12, 2023 3:59 PM
To: [redacted]
Subject: FW: Readout of contentious HPSCI COVID Origins briefing

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

From: [redacted]
Sent: Thursday, September 23, 2021 3:50 PM
To: [redacted] Morgan Muir-DNI-[redacted]
Subject: Readout of contentious HPSCI COVID Origins briefing

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted] and I, along with three reps from NCPC and [redacted] from OLA, briefed the HPSCI this morning on the COVID Origins assessment. It did not go well. After Opening remarks from Reps Schiff and Nunes, I started off with prepared remarks that went about 10 minutes, going over the processes involved in the 90-day study and then highlighting the key takeaways. Rep Schiff asked a couple of easy questions and then turned it over to Rep Nunes, who yielded his time to Rep. Wenstrup. Then everything went downhill.

Rep Wenstrup spent the first big chunk of his time identifying a number of open source documents that he wanted read into the record (which was agreed to), in particular papers on the threat of SARS as a bioterror weapon (from 2005), statements Fauci made on the general idea of gain of function research back in 2012, Ralph Baric's work on chimeric viruses in 2015, and similar stuff. After quite a while of talking he finally started to ask questions. They mostly centered on the names of the experts the IC reached out to on COVID origins. I told him that I was unable to reveal the names of the experts we reach out to. Which is also exactly what I told the staffers during the pre-briefing we did on Tuesday. Rep Wenstrup even acknowledged before he asked the first time that he knew what my response would be but was going to ask anyway. He was, to put it mildly, not happy with my answer. In fact, he seemed pretty outraged. After that, it was more of the same. Every single minority member who asked questions spent the first two-three minutes of their allotted five minutes expressing outrage and disdain over my behavior. One, not sure who because this was all a blur, even said "shame on you." At one point, a member turned his time back to Rep Wenstrup who went through a long list of names of "experts" (air quotes because the expertise of some he named is iffy in my mind) and asked me if anyone in the IC had consulted with them…apparently because he wanted me to be on the record each time saying "I am not going to comment on that." I repeatedly tried to explain that IC policy was to not reveal the names of the experts we reached out

to for source protection reasons, which just seem to enrage then all even more. Several of the minority members claimed that they had been staunch defenders of the IC in the past but now "will not have your back." I heard a lot of "nobody has ever come in here and refused to answer our questions" and the comments/question got heated on their end and were pretty over the top. Several times I tried to answer a question only to be interrupted by whoever asked the question and a couple even said something along the lines of "I don't want to hear that 'it's against policy' crap."

Not to pick on the minority members, some of the majority members also were not pleased with the briefing. Rep. Speier seemed annoyed that our assessment focused too much on [redacted] and wanted us to agree to talk to one of her constituents who was in Wuhan in November of 2019 on a riverboat cruise (I kid you not). Her time ran out before she asked that and she didn't press the issue. Rep Krishnamoorthi also expressed surprise and disappointment over my refusal to identify the experts and said it made us (the IC) "look bad."

It seemed clear to me that few if any of the members actually read the Updated Assessment…or were paying attention to my prepared remarks. One of the minority members (I can't remember which) challenged me to identify anything new that I had mentioned up to that point that was not in open sources. That question frankly baffled me, but I pointed out that I had literally just talked about [redacted] WIV researchers who were reportedly sick in the Fall of 2019. Members from both parties seemed surprised and confused that FBI came to a different conclusion than other IC agencies. More than one asked me if FBI had access to information that they had not shared with the IC, and one member (I think it was Rep Carson) asked me and [redacted] if we thought FBI was an equal and honest partner in the processes (despite some of our issues with FBI, we both stated "yes"). Nobody seemed to understand what "low confidence" means; even after I explained multiple times that low confidence meant that we had [redacted] I got the same confused questions about confidence levels.

With regard to the minority members question on experts, I think this was a set-up. They were looking for a reason to distance themselves from the Updated Assessment and that was the issue they chose. Again, they knew we were not going to name the experts because this came up at the pre-brief Tuesday. And at no time during that call did any of the minority staffers indicate that this was going to be a problem [redacted] Maybe I could have explained the reason we weren't going to provide the names in a way that would have resulted in less vitriol…but I doubt it.

Anyway, I would expect the DNI to receive angry letters from the Hill calling my professionalism into question and demanding that the IC name names. And maybe that I be fired.

[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Thursday, July 13, 2023 8:46 AM
To: Michael L. Collins-DNI-
Cc: [redacted]
Subject: RE: Briefing to COVID Subcommittee on COVID Origins
Attachments: FW: Readout of contentious HPSCI COVID Origins briefing (18.4 KB)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

I talked to OLA yesterday afternoon. Apparently there is a push to do an open briefing in addition to the classified briefing for Wenstrup's committee, and because Morgan was (according to OLA) going to do the open briefing, they thought it made sense for him to do the classified briefing as well. I take it there's a meeting today between OLA and Morgan and maybe the DNI where they'll work this out.

What's a little concerning to me is that the person in OLA I spoke to also noted that they have been advised by "staffers" (presumably from the HPSCI) to not have me attend briefings involving Wenstrup. My impression is that this guidance originated back in late 2021 and was the result of the COVID-O briefing I gave the HPSCI after we published the 2021 NICA. That briefing admittedly didn't go well (readout of that meeting attached), but that's hardly a justification to not have me brief now, almost two years later. I am perfectly capable of briefing in front of a hostile audience.

From: [redacted]
Sent: Wednesday, July 12, 2023 1:15 PM
To: Michael L. Collins-DNI-[redacted]
Cc: [redacted]
Subject: RE: Briefing to COVID Subcommittee on COVID Origins

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

I reached back to OLA to see what the deal is. I'll let you know what I hear back.

From: Michael L. Collins-[redacted]
Sent: Wednesday, July 12, 2023 12:57 PM
To: [redacted]
Cc: [redacted]
Subject: FW: Briefing to COVID Subcommittee on COVID Origins

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Do you need me to call OLA on this? You should be the briefer. I'd like to talk in advance, however.

Mike

From: [redacted]
Sent: Wednesday, July 12, 2023 12:02 PM
To: Morgan Muir-DNI-[redacted]
Cc: Michael L. Collins-DNI-[redacted]
Subject: RE: Briefing to COVID Subcommittee on COVID Origins

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Ha…news to you that you were briefing? I don't think I ever said I didn't think I was the right choice…I just heard about it this morning. I have often joked about the last time I briefed Wenstrup on COVID-O, and how well that went…but I am more than happy to do so for this or any other briefing.

From: Morgan Muir-DNI-[redacted]
Sent: Wednesday, July 12, 2023 11:35 AM
To: [redacted]
Cc: Michael L. Collins-DNI-[redacted]
Subject: RE: Briefing to COVID Subcommittee on COVID Origins

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Hi,

Hmmm. News to me. I heard that you didn't think you were the right choice but I thought it was still up in the air.

I'll ask but she has never said that to me and it doesn't sound like her. We all know there is a division over there that can't be bridged but I have never heard percentages attached to either side.

M

From: [redacted]
Sent: Wednesday, July 12, 2023 10:41 AM

To: Morgan Muir-DNI-[redacted]
Cc: Michael L. Collins-DNI-[redacted]
Subject: Briefing to COVID Subcommittee on COVID Origins

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Hey Morgan,

I heard from CIA and OLA that you'll be leading the COVID origins briefing for Rep Wenstrup's COVID Subcommittee on the 27th. We're obviously ready to support this is any way you need. Just let us know. The briefing we did for the Subcommittee's staffers last month went pretty well. DOE and FBI didn't do a particularly good job explaining their assessments…but that's been the case for most of these briefings. CIA did get one strange question from the lead majority staffer about their position, though, that I wanted to flag as it may come up in your briefing. According to the staffer, the DNI told Rep Wenstrup that CIA was 2/3 in the "lab leak" camp but that they were being "held back" by 1/3 of the analysts. He asked the CIA briefer if that was true. She responded that she had never heard that…as did I. CBD management has pinged me a couple of times since to see if the DNI actually told Wenstrup this or if there was another explanation for the source of the claim. I imagine whoever CIA sends to the briefing with you will also want to know so they can answer accordingly. –[redacted]

[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Thursday, May 25, 2023 9:24 AM
To: [redacted]
Subject: FW: Here's the paper from May 2020
Attachments: Leaked Version.pdf

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Hi,

Update: Attached is the NCMI covid origins document that [redacted] provided by OCC; this is what was allegedly [redacted] the situation from their OCC colleagues who were notified by Legislative Affairs. Below are the links associated with the document.

You can see a flavor of the resulting coverage:

https://www.theblaze.com/news/leaked-pentagon-paper-indicates-the-us-government-suspected-all-along-that-fauci-s-covid-19-natural-origins-theory-was-rubbish

This account has screenshots

https://twitter.com/billybostickson/status/1658307176702828545
The individual is associated with drasticresearch.org, which has been tied to other leaked information.

Best,

[redacted]

[redacted]
National Counterproliferation and Biosecurity Center (NCBC)
Office of the Director of National Intelligence
[redacted]

From: [redacted]
Sent: Thursday, May 25, 2023 7:34 AM
To: [redacted]
Subject: RE: Here's the paper from May 2020

Classification: [redacted]

Classified By: [redacted]

Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted] – hopefully I didn't misspeak when we chatted. NCMI learned of this from our OCC colleagues who were notified by DARPA Legislative Affairs. They provided the links below for where the article was circulating on Monday. I've also attached a document that I was provided this morning that is allegedly what was posted on line. It does not contain your comments (thankfully) but is very similar to the V11 I shared with you yesterday.

You can see a flavor of the resulting coverage:

https://www.theblaze.com/news/leaked-pentagon-paper-indicates-the-us-government-suspected-all-along-that-fauci-s-covid-19-natural-origins-theory-was-rubbish

This account has screenshots

https://twitter.com/billybostickson/status/1658307176702828545
. The individual is associated with drasticresearch.org, which has been tied to other leaked information.

v/r

[redacted]

[redacted]

[redacted]

[redacted]

From: [redacted]
Sent: Wednesday, May 24, 2023 4:53 PM
To: [redacted]
Subject: RE: Here's the paper from May 2020

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========
Hi [redacted]

Thank you again for letting me know about the upcoming origins meeting. You mentioned NCMI found out via the news. Do you have a copy of the article(s)? If not, which news outlets did you see it in?

Thank you!

[redacted]

From: [redacted]
Sent: Wednesday, May 24, 2023 2:05 PM
To: [redacted]
Subject: Here's the paper from May 2020

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Here you go

[redacted]

[redacted]

[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Wednesday, March 16, 2022 8:04 AM
To: [redacted]
Subject: FW: ACTION REQUIRED: [redacted] (U[redacted]) FOIA Litigation Search Request | DF-2021-00235 (21-cv-01619)

Classification: UNCLASSIFIED[redacted]
==========

Stand down on this for now. Maybe we'll get clarification that will lower the burden of this ridiculous request. Also note, however, that this is one of six requests this person filed on COVID origin stuff…so more probably on the way to us.

From: [redacted]
Sent: Wednesday, March 16, 2022 7:51 AM
To: DNI_MI_NIC_TASKERS Mailbox[redacted]
Subject: RE: ACTION REQUIRED: [redacted] (U[redacted]) FOIA Litigation Search Request | DF-2021-00235 (21-cv-01619)

Classification: UNCLASSIFIED[redacted]
==========

What are we supposed to do with this? Shouldn't this be sent to the "senior" DOS, NIH, or ODNI officials for them to search their records? And what is a "senior" official for these agencies? –[redacted]

From: [redacted] **On Behalf Of** DNI_MI_NIC_TASKERS Mailbox
Sent: Tuesday, March 15, 2022 9:58 PM
To: DNI_MI_NIC[redacted] DNI_MI_NIC[redacted]
Cc: DNI_MI_NIC_TASKERS Mailbox[redacted]
Subject: ACTION REQUIRED: [redacted] (U[redacted]) FOIA Litigation Search Request | DF-2021-00235 (21-cv-01619)
Importance: High

Classification: UNCLASSIFIED[redacted]
==========

NIC[redacted], D/[redacted]

Suspense: COB Tuesday, 15 MAR 2022

This FOIA specifically asks for all records, communications, or briefings created, generated, forwarded, transmitted, sent, shared, saved, received, or reviewed by any senior level DOS, NIH, or ODNI official referencing, connected to, or regarding in any way Anthony Fauci, the Wuhan Institute of Virology, and COVID-19 (including any shorthand, pseudonyms, or synonyms used for those terms).

Timeline: May 1, 2020, to the date this request is processed

Keyword Search: Fauci AND Wuhan
: Fauci AND COVID-19 AND Wuhan
: Fauci AND COVID AND Origins
: Biden AND COVID-19 AND Wuhan
: Biden AND COVID AND Origins

Thanks,
[redacted]

[redacted]
Analytic Program Manager
National Intelligence Council
Office of the Director of National Intelligence
ODNI | DDMI | NIC FO
[redacted]
Booz Allen Hamilton Contractor Support

From: [redacted] **On Behalf Of** DNI_MI_Taskers Mailbox
Sent: Monday, March 07, 2022 1:01 PM
To: DNI-MI-NIMC-Taskers Mailbox [redacted] DNI_MI_NIC_TASKERS Mailbox [redacted]
Subject: FW: [Direct][Action] [redacted] (U[redacted]) FOIA Litigation Search Request | DF-2021-00235 (21-cv-01619)
Importance: High

Classification: UNCLASSIFIED[redacted]
==========

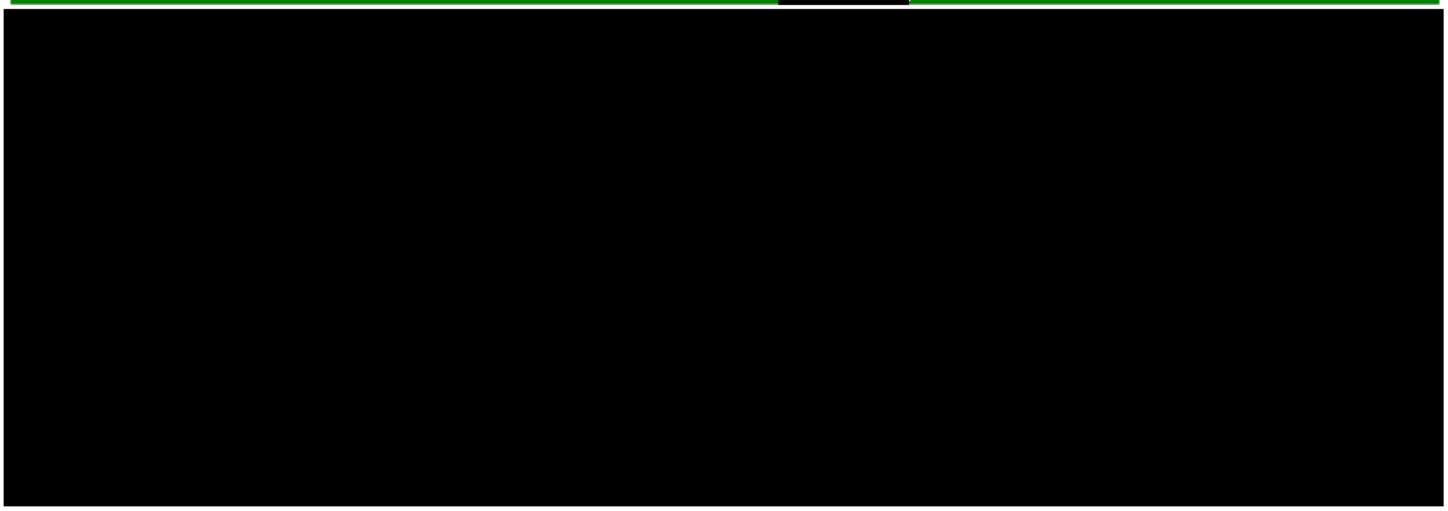
Attn: NIMC, NIC
Action: Please provide any responsive materials for the subject FOIA.
Suspense to MI FO: COB 15 MAR 2022

From: [redacted]
Sent: Friday, March 4, 2022 5:05 PM
To: DNI_MI_Taskers Mailbox [redacted]
Cc: [redacted]
Subject: [Direct][Action] [redacted] (U[redacted]) FOIA Litigation Search Request | DF-2021-00235 (21-cv-01619)
Importance: High

Classification: UNCLASSIFIED[redacted]

==========

UNCLASSIFIED[redacted]



UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Monday, September 27, 2021 12:24 PM
To: [redacted]
Subject: RE: Wash Examiner

Classification: UNCLASSIFIED[redacted]
==========

Do we have the actual letter?

From: [redacted]
Sent: Monday, September 27, 2021 12:00 PM
To: [redacted]
Subject: FW: Wash Examiner

Classification: UNCLASSIFIED[redacted]
==========

FYI Only

[redacted]
Legislative Liaison Officer (NIM-EA, NIM-SA, JHTS)
Management Advisory Group Rep
ODNI Legislative Affairs
[redacted]

ODNI OFFICE OF LEGISLATIVE AFFAIRS

From: [redacted]
Sent: Monday, September 27, 2021 9:20 AM
To: Matthew Rhoades ; [redacted] ;
[redacted]
Subject: Wash Examiner

House Intel GOP demand Biden instruct top spy office to reveal scientists who helped with COVID-19 origins report

by Jerry Dunleavy, Justice Department Reporter
|

| September 26, 2021 07:20 PM

House Intelligence Committee Republicans accused the Biden administration's top intelligence office of "stonewalling" congressional overseers from learning about outside doctors and scientists whom U.S. spy agencies relied upon to put together a report assessing the origins of COVID-19.

Rep. Devin Nunes, the ranking member on the panel, was joined by nine fellow GOP members who said they had no confidence in the origins assessment because the Office of the Director of National Intelligence personnel who briefed them had declined to identify which scientists were consulted during the investigation, which did not provide a definitive conclusion on whether the virus was transmitted to humans naturally or through a lab leak in China.

"This is fundamental oversight of the IC?s work. We need this information to determine whether there was any selection bias in choosing the outside scientists to consult. We also need it to determine whether any of the scientists had conflicts of interest that should affect the weight given their analyses," the Republicans wrote in a letter to Biden dated Friday.

Nunes, a California Republican, revealed the letter during an appearance on Sunday Morning Futures on Fox News.

?It looks like there needs to be an entire new report that needs to be written, because Republican members on the committee have basically had enough of this. It just looks like this is another attempt to obfuscate and protect China

once again by the Biden administration," he told

host Maria Bartiromo.

The interview took place shortly after the

Wall Street Journal

reported

that a panel of scientists investigating the origins of the COVID-19 virus had disbanded, citing concerns about its links to EcoHealth Alliance, a New York-based nonprofit group that had used U.S. funds for research on bat coronaviruses with the Wuhan Institute of Virology. EcoHealth Alliance President Peter Daszak, who dismissed

the lab leak hypothesis in March, recused himself from the investigation over the summer.

A letter

signed by 27 scientists, including Daszak, was published in Lancet in February 2020, dismissing the lab leak hypothesis as a conspiracy theory. Numerous outlets pointed to the letter and to Daszak, who had recruited scientists to sign the letter, to shut down the debate over COVID-19?s origins.

Dr. Anthony Fauci quietly worked behind the scenes to cast doubt on the lab leak hypothesis in 2020, and he and Daszak were in communication at the time, emails

show.

Daszak was also a key member of the World Health Organization-China

joint study team earlier this year. The WHO-China

report was widely considered a failure, partly due to the lack of access to key data and Chinese influence over the investigation.

The WHO-China study deemed the lab leak theory ?extremely unlikely,? and meeting minutes with the Wuhan lab dismissed it as a ?conspiracy theory.?

In July, WHO Director-General Tedros Adhanom Ghebreyesus said

there was a "premature push" to dismiss the lab theory, but the Chinese government shot down

the suggestion of a second investigation.

In their new letter, the House Intelligence Republicans claimed ODNI staff did not respect the oversight role the panel has over the U.S. intelligence community.

?Shockingly, ODNI has repeatedly refused to tell the Committee which scientists the IC consulted. When pressed on the basis for this refusal during our hearing, ODNI staff acknowledged there is no law or regulation prohibiting them from revealing these names to us. Instead, they simply refused again in a hostile manner, claiming it is their ?policy? to do so,? the GOP group said.

After Biden called on

the intelligence community to ?redouble? its origins investigation in May and gave it a 90-day clock, an unclassified report was released by ODNI last month.

The assessment stated

that one U.S. intelligence agency assesses with ?moderate confidence? that COVID-19 most likely emerged from a Chinese government lab

in Wuhan, while four U.S. spy agencies and the National Intelligence Council believe with ?low confidence? COVID-19 most likely has a natural origin. Other parts of the U.S. intelligence community remain on the fence.

The one unnamed spy agency leaning toward the Wuhan lab theory with "moderate confidence" assessed that "the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling" by the Wuhan Institute of Virology. The four unnamed spy agencies, along with the NIC, with "low confidence" in the natural origin hypothesis assessed "the initial SARS-CoV-2 infection was most likely caused by natural exposure to an animal infected with it or a close progenitor virus.?

The Republicans argued in their letter that the intelligence community failed to live up to Biden's own words when he said on May 26, ?I have asked the Intelligence Community to keep Congress fully apprised of its work," and urged him to crack down.

?Outside doctors and scientists who were consulted for their technical analyses of COVID?s potential origins are not clandestine sources or spies. They are consultants and there is no basis for stonewalling the Committee about their identities ? I respectfully ask that you rectify this situation by instructing the ODNI to cease stonewalling Congressional oversight and to immediately disclose to the Committee the full list of all outside doctors and

scientists consulted in the investigation of COVID?s origins," Nunes and his fellow Republicans wrote.

Nunes also stressed that what ODNI presented in the summer did not match what he demanded in the spring.

?In May, I wrote to you requesting that you initiate a whole-of-government effort to identify the origins of the virus. However, you opted for a much narrower review solely by the Intelligence Community,? Nunes and his fellow Republicans told Biden. ?The Committee has reviewed the resulting IC report and received a briefing from Office of the Director of National Intelligence personnel. Based on the IC?s appalling lack of transparency and the ODNI staff?s hostile response to simple questions, we have little confidence in the DNI?s report.?

The Washington Examiner reached out to ODNI for comment.

https://www.washingtonexaminer.com/news/house-intelligence-gop-demand-biden-instruct-top-spy-office-reveal-scientists-helped-covid-19-origins-report

[redacted]

Public Affairs Officer

Office of the Director of National Intelligence (ODNI)

[redacted]

[redacted]

[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Friday, September 24, 2021 10:50 AM
To: [redacted]
Subject: FW: Readout of contentious HPSCI COVID Origins briefing

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

FYI…fun stuff. Morgan says he won't fire me.

From: [redacted]
Sent: Thursday, September 23, 2021 3:50 PM
To: [redacted] Morgan Muir-DNI-[redacted]
Subject: Readout of contentious HPSCI COVID Origins briefing

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted] and I, along with three reps from NCPC and [redacted] from OLA, briefed the HPSCI this morning on the COVID Origins assessment. It did not go well. After Opening remarks from Reps Schiff and Nunes, I started off with prepared remarks that went about 10 minutes, going over the processes involved in the 90-day study and then highlighting the key takeaways. Rep Schiff asked a couple of easy questions and then turned it over to Rep Nunes, who yielded his time to Rep. Wenstrup. Then everything went downhill.

Rep Wenstrup spent the first big chunk of his time identifying a number of open source documents that he wanted read into the record (which was agreed to), in particular papers on the threat of SARS as a bioterror weapon (from 2005), statements Fauci made on the general idea of gain of function research back in 2012, Ralph Baric's work on chimeric viruses in 2015, and similar stuff. After quite a while of talking he finally started to ask questions. They mostly centered on the names of the experts the IC reached out to on COVID origins. I told him that I was unable to reveal the names of the experts we reach out to. Which is also exactly what I told the staffers during the pre-briefing we did on Tuesday. Rep Wenstrup even acknowledged before he asked the first time that he knew what my response would be but was going to ask anyway. He was, to put it mildly, not happy with my answer. In fact, he seemed pretty outraged. After that, it was more of the same. Every single minority member who asked questions spent the first two-three minutes of their allotted five minutes expressing outrage and disdain over my behavior. One, not sure who because this was all a blur, even said "shame on you." At one point, a member turned his time back to Rep Wenstrup who went through a long list of names of "experts" (air quotes because the expertise of some he named is iffy in my mind) and asked me if anyone in the IC had consulted with them…apparently because he wanted me to be on the record each time saying "I am not going to comment on that." I repeatedly tried to explain that IC policy was to not reveal the names of the experts we reached out

to for source protection reasons, which just seem to enrage then all even more. Several of the minority members claimed that they had been staunch defenders of the IC in the past but now "will not have your back." I heard a lot of "nobody has ever come in here and refused to answer our questions" and the comments/question got heated on their end and were pretty over the top. Several times I tried to answer a question only to be interrupted by whoever asked the question and a couple even said something along the lines of "I don't want to hear that 'it's against policy' crap."

Not to pick on the minority members, some of the majority members also were not pleased with the briefing. Rep. Speier seemed annoyed that our assessment focused too much on [redacted] and wanted us to agree to talk to one of her constituents who was in Wuhan in November of 2019 on a riverboat cruise (I kid you not). Her time ran out before she asked that and she didn't press the issue. Rep Krishnamoorthi also expressed surprise and disappointment over my refusal to identify the experts and said it made us (the IC) "look bad."

It seemed clear to me that few if any of the members actually read the Updated Assessment…or were paying attention to my prepared remarks. One of the minority members (I can't remember which) challenged me to identify anything new that I had mentioned up to that point that was not in open sources. That question frankly baffled me, but I pointed out that I had literally just talked about [redacted] WIV researchers who were reportedly sick in the Fall of 2019. Members from both parties seemed surprised and confused that FBI came to a different conclusion than other IC agencies. More than one asked me if FBI had access to information that they had not shared with the IC, and one member (I think it was Rep Carson) asked me and [redacted] if we thought FBI was an equal and honest partner in the processes (despite some of our issues with FBI, we both stated "yes"). Nobody seemed to understand what "low confidence" means; even after I explained multiple times that low confidence meant that [redacted] I got the same confused questions about confidence levels.

With regard to the minority members question on experts, I think this was a set-up. They were looking for a reason to distance themselves from the Updated Assessment and that was the issue they chose. Again, they knew we were not going to name the experts because this came up at the pre-brief Tuesday. And at no time during that call did any of the minority staffers indicate that this was going to be a problem. Maybe I could have explained the reason we weren't going to provide the names in a way that would have resulted in less vitriol…but I doubt it.

Anyway, I would expect the DNI to receive angry letters from the Hill calling my professionalism into question and demanding that the IC name names. And maybe that I be fired.

[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]-
Sent: Tuesday, June 15, 2021 11:52 AM
To: [redacted]
Subject: FW: [AIN] FW:

Classification: UNCLASSIFIED[redacted]
==========

From: [redacted]
Sent: Tuesday, June 15, 2021 11:43 AM
To: [redacted]
Subject: FW: [AIN] FW:

Classification: UNCLASSIFIED[redacted]
==========

fyi

First on CNN: HHS watchdog announces review of NIH grants that likely includes money connected to Wuhan lab

By Kristen Holmes and
Priscilla Alvarez , CNN

Updated 10:30 AM ET, Tue June 15, 2021

US intelligence working on report about Covid-19 origins 04:04

(CNN)Federal government investigators said Tuesday that they are launching a review into how the National Institutes of Health manages and monitors its grant program, which likely includes money connected to a Wuhan lab that GOP lawmakers have been scrutinizing.

Republicans have zeroed in on NIH's relationship with EcoHealth Alliance, the global nonprofit that helped fund some research at China's Wuhan Institute of Virology, to attack Dr. Anthony Fauci
and
score political points.

The comprehensive review also coincides with renewed questions

over the origin of the Covid-19 virus and the potential role that China's Wuhan Institute of Virology may have played.

"We share stakeholders' concerns regarding compliance and oversight of NIH grant funds. We have been monitoring this issue for some time and consider it a high-priority matter that can pose a threat to the integrity of the NIH grant program," Tesia Williams, the director of communications for the Department of Health and Human Services Office of Inspector General, told CNN.

"Based on our preliminary research and analysis, HHS-OIG has decided to conduct an extensive audit reviewing how NIH monitored selected grants and how the grantees and subgrantees used and managed federal funds between years 2014 through 2021," Williams said.

Roughly 80% of NIH funding goes to supporting research grants, including grants to foreign organizations. According to the work plan on the review, it will look at how these grants are monitored and making sure the recipient's use and management of NIH grant funds is in accordance with federal requirements.

One NIH official, who spoke under the condition of anonymity in order to discuss the review openly, called it "political" in nature but believed that ultimately it would be a good thing and would clear NIH of any wrongdoing.

"It's an opportunity to educate the public," the official said.

Questions about the relationship between NIH and EcoHealth Alliance have grown louder after Fauci, the director of the National Institute of Allergy and Infectious Diseases within NIH, confirmed to lawmakers earlier this year that hundreds of thousands of dollars that NIH had given to the New York-based global nonprofit went to the Wuhan Institute of Virology to study coronaviruses in bats.

"About $600,000 was spent over a five-year period," Fauci said during a congressional budget hearing. "That comes to anywhere between $125 (thousand) and $150,000 per year that went to collaboration with Wuhan."

A recent US intelligence report found that several researchers at China's Wuhan Institute of Virology fell ill in November 2019

 and had to be hospitalized, a new detail about the severity of their symptoms. It's not clear what might have affected the researchers, there is no indication they caught Covid-19 and the lab strongly denied the report, calling it a lie to push the so-called lab-leak theory for the disease origin.

There are competing theories about how the pandemic got started. One is that it developed naturally in the wild and transferred from animal to human, as many other viruses have in the past. Another is that such a naturally originating virus was studied in a lab and accidentally infected someone. A third theory, most widely discounted by scientists, is that it was engineered in a lab and somehow leaked to humans.

For much of 2020, pursuing the lab leak theory was treated publicly as xenophobic, and, thanks in part to an open letter signed by 27 scientists and published in an influential medical journal in February 2020, scientifically unsound.

But in recent months

, the classified intelligence emerged that three researchers at the Wuhan Institute of Virology who were conducting the kind of controversial research that some scientists now believe may have led to the pandemic had gotten sick in the autumn of 2019, before the outbreak was known to have begun, although there's no evidence they were infected with Covid-19.

Conservative attacks on Fauci have also intensified after media organizations released a trove of the doctor's emails.

In one email sent to Fauci in April 2020, an executive at EcoHealth Alliance thanked him for publicly stating that scientific evidence supports a natural origin for the coronavirus and not a lab release
.

Fauci recently told CNN's John Berman the email was being misconstrued and called claims he had a cozy relationship with the people behind the Wuhan lab research "nonsense."

"I have always said, and will say today to you, John, that I still believe the most likely origin is from an animal species to a human, but I keep an absolutely open mind that if there may be other origins of that, there may be another reason, it could have been a lab leak," Fauci told Berman. "I believe if you look historically, what happens in the animal-human interface, that in fact the more likelihood is that you're dealing with a jump of species. But I keep an open mind all the time. And that's the reason why I have been public that we should continue to look for the origin.

"You can misconstrue it however you want -- that email was from a person to me saying 'thank you' for whatever it is he thought I said, and I said that I think the most likely origin is a jumping of species. I still do think it is, at the same time as I'm keeping an open mind that it might be a lab leak."

Nonetheless, Republicans are using the emails -- and controversy about how the pandemic began and whether US government grant money can be connected to it -- to fundraise and campaign against the Biden administration.

GOP Sen. Rand Paul of Kentucky

has lashed out at Fauci, calling for his ouster.

"He's continuously and deliberately misleading the public at every turn. It's time to FIRE FAUCI," a Paul fundraising email read. "There are 2,000 emails proving Fauci chose his own ego over the facts."

Florida Sen. Marco Rubio recently penned a Fox News op-ed

titled "If Biden Believes in Science, He Must Fire Fauci."

President Joe Biden was asked earlier this month if he still had confidence in Fauci.

"Yes, I am very confident in Dr. Fauci," Biden said.

CNN's Maggie Fox contributed to this report.

.

.

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Monday, June 14, 2021 12:49 PM
To: [redacted]
Cc: [redacted]
Subject: RE: [redacted] Update for NCPC - Tuesday, 8 June

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

FYI: there's likely going to be a follow-on to that Fauci briefing adding the NIC and we may get pulled into it.

[redacted]

[redacted]

From: [redacted]
Sent: Monday, June 14, 2021 12:36 PM
To: [redacted]
Subject: FW: [redacted] Update for NCPC - Tuesday, 8 June

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted]

FYI.

[redacted] briefed Dr. Fauci on the COVID origins on 4 June.

- *4 June:* [redacted] ***Briefing for Dr. Anthony Fauci on COVID Origins:*** [redacted] *officers met with the Chief Medical Advisor to the President and Director of the National Institute of Allergy and Infectious Diseases, Dr. Anthony Fauci, to present our analysis on the COVID origins topic as well as our approach to the intelligence question. Dr. Fauci expressed concern about Beijing's quick and thorough cleaning of the Wuhan wet market, which may have destroyed clues related to the pandemic's origin. He did not find it alerting that China had not yet found any evidence of a zoonotic transmission or intermediate animal host. He was particularly interested in the specific details* [redacted] *provided on the research WIV was doing and on their work with pangolins.*

V/r

[redacted]

Office of the National Intelligence Management for Counterproliferation (NIM-CP)

[redacted]

From: [redacted]
Sent: Monday, June 14, 2021 12:25 PM
To: [redacted]
Subject: [redacted] Update for NCPC - Tuesday, 8 June

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Colleagues,

Here is the latest from [redacted] in terms of their engagements.

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Wednesday, February 17, 2021 9:12 PM
To: [redacted]
Subject: Came across this gem...

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

SO MANY CONSPIRACIES.

[redacted]

(U) New Zealand: The superspreaders behind top Covid-19 conspiracy theories - NZ Herald
Identifiers:

Document Number:
[redacted]
DIN:
[redacted]
Document Version:
1
Ingestion ID:
[redacted]
GUIDE:
[redacted]

Source:

Publisher Type:
open-source
Sourced Text:
null
Language:
eng
Source ID:
[redacted]
Country Code:

NZL
Source Type:
Internet
City:
Auckland
Country Code:
NZL
Compilation Title:
The New Zealand Herald Online
Description:
Auckland The New Zealand Herald Online in English Website of a daily newspaper distributed mainly in the greater Auckland area, but with the highest readership in New Zealand. Audited circulation of 108,790 as of 2018. Owned New Zealand Media and Entertainment; URL: http://www.nzherald.co.nz/ (source last reviewed 15 Mar 19)
Information Date:
15-Feb-2021 19:00:00
Information Cutoff Date:
15-Feb-2021 19:00:01
Originating System:
OSE

Dates:

Date Posted:
16-Feb-2021 04:57:06
Date Published:
16-Feb-2021 04:57:13
Date Received:
16-Feb-2021 12:28:29

Description:
(U) As the coronavirus spread across the globe, so too did speculation about its origins. Perhaps the virus escaped from a lab. Maybe it was engineered as a bioweapon.Legitimate questions about the virus created perfect conditions for conspiracy theories....

(U) **PRODUCT DESCRIPTION**

(U) The body of this product is a transcription of original English-language material.

(U) **CAVEATS**

(U) Computer selected and disseminated without OSE editorial intervention.

(U) **BODY**

(U) As the coronavirus spread across the globe, so too did speculation about its origins. Perhaps the virus escaped from a lab. Maybe it was engineered as a bioweapon.

(U) Legitimate questions about the virus created perfect conditions for conspiracy theories. In the absence of knowledge, guesswork and propaganda flourished.

(U) College professors with no evidence or training in virology were touted as experts. Anonymous social media users posed as high-level intelligence officials. And from China to Iran to Russia to the United States, governments amplified claims for their own motives.

(U) The Associated Press collaborated with the Atlantic Council's Digital Forensic Research Lab on a nine-month investigation to identify the people and organisations behind some of the most viral misinformation about the origins of the coronavirus.

(U) Their claims were explosive. Their evidence was weak. These are the superspreaders.

(U) FRANCIS BOYLE

(U) WHO HE IS: A Harvard-trained law professor at the University of Illinois, Boyle drafted a 1989 law banning biological weapons and has advised the nation of Bosnia and Herzegovina and the Palestinian Authority.

(U) Francis Boyle, a law professor at the University of Illinois. Photo / APBoyle has no academic degree in virology or biology but is a longstanding critic of research on pathogens. He has claimed Israeli intelligence was involved in the 1993 World Trade Centre bombing; that SARS, the swine flu and Ebola have been genetically modified; and that West Nile virus and Lyme disease escaped from a US biowarfare lab. He has also claimed that Microsoft founder Bill Gates "was involved" in the spread of Zika.

(U) COVID CLAIM: Boyle says the coronavirus is a genetically engineered bioweapon that escaped from a high-level lab in Wuhan, China. He maintains it shows signs of nanotechnological tinkering and the insertion of proteins from HIV, the human immunodeficiency virus. He alleges that US researchers helped create it, and that thousands of doctors, scientists, and elected leaders are conspiring to hide the truth.

(U) Boyle promoted his claim in an email to a list of news organizations and personal contacts on January 24, 2020. That same day, he was interviewed on a podcast called "Geopolitics and Empire." That podcast was cited by a little-known Indian website, GreatGameIndia, and went viral, with Boyle's comments picked up and featured in Iranian-state TV, Russian state media, and fringe websites in the US and around the world. He's since repeated his claims on Alex Jones' show Infowars.

(U) EVIDENCE? Boyle bases his argument on circumstantial evidence: the presence of a Biosafety Level 4 lab in Wuhan, the fact that other viruses have escaped from other labs in the past, and his belief that governments around the world are engaged in a secret arms race over biological weapons.

(U) Biosafety Level 4 labs - or BSL4 labs - have the highest level of biosafety precautions.

(U) "It seemed to me that obviously, this came out of the Wuhan BSL 4," Boyle told The Associated Press.

(U) A World Heath Organisation team concluded it was extremely unlikely the virus escaped from the Wuhan lab, and other experts have said the virus shows no signs of genetic manipulation.

(U) GREATGAMEINDIA

(U) WHAT IT IS: A website that was an early promoter of the theory that the coronavirus was engineered.

(U) Its January 26, 2020, story on "Coronavirus bioweapon-How China Stole the Coronavirus From Canada and Weaponised It" was picked up by far-right financial blog Zero Hedge and shared to thousands of social media users before it was promoted by conservative website RedStateWatcher and received more than 6 million engagements.

(U) COVID CLAIM: GreatGameIndia claims that the virus, which has now killed more than 2 million people worldwide, was first found in the lungs of a Saudi man and then sent to labs in the Netherlands and then Canada, where it was stolen by Chinese scientists. The article relies in part on speculation from Dany Shoham, a virologist and former lieutenant colonel in Israeli military intelligence.

(U) Shoham was quoted discussing the possibility that Covid is linked to bioweapon research in a January 26, 2020, article in the conservative US newspaper The Washington Times. In that article, Shoham was quoted saying there was no evidence to support the idea that the virus has escaped from a lab, but GreatGameIndia did not include that context in its piece.

(U) "We do stand by our report," said website co-founder Shelley Kasli wrote in an email. "In fact, recently Canadians released documents which corroborated our findings with Chinese scientists... A lot of information is still classified."

(U) EVIDENCE? The coronavirus most likely first appeared in humans after jumping from an animal, a World Health Organisation panel announced this month, saying an alternate theory that the virus leaked from a Chinese lab was unlikely.

(U) America's top scientists have likewise concluded the virus is of natural origin, citing clues in its genome and its similarity to SARS, or severe acute respiratory syndrome. Vincent Racaniello, a professor of microbiology and immunology at Columbia University, who has been studying the virus since its genome was first recorded, has said it is clear that the virus was not engineered or accidentally released.

(U) "It is something that is clearly selected in nature," Racaniello said. "There are two examples where the sequence tells us that humans had no hand in making this virus because they would not have known to do these things."

(U) THE CENTRE FOR RESEARCH ON GLOBALISATION

(U) WHAT IT IS: The Montreal-based centre publishes articles on global politics and policy, including a healthy dose of conspiracy theories on vaccines and the September 11, 2001, terrorist attacks. It's led by Michel Chossudovsky, a professor emeritus of economics at the University of Ottawa and a conspiracy theorist who has argued the US military can control the weather.

(U) The centre publishes authors from around the world - many of whom have advanced baseless claims about the origins of the outbreak. In February, for instance, the centre published an interview with Igor Nikulin suggesting the coronavirus was a US bioweapon created to target Chinese people.

(U) The centre's website, globalresearch.ca., "has become deeply enmeshed in Russia's broader disinformation and propaganda ecosystem" by peddling anti-US conspiracy theories, according to a 2020 US State Department report which found that seven of its supposed writers do not even exist but were created by Russian military intelligence.

(U) COVID CLAIM: While the centre has published several articles about the virus, one suggesting it originated in the US caught the attention of top Chinese officials.

(U) On March 12, Chinese Foreign Ministry spokesperson Zhao Lijian retweeted an article published by the centre titled: "China's Coronavirus: A Shocking Update. Did The Virus Originate in the US?"

(U) "This article is very much important to each and every one of us," he posted in English on Twitter. "Please read and retweet it. Covid-19: Further Evidence that the Virus Originated in the US."

(U) He also tweeted: "It might be US army who brought the epidemic to Wuhan. Be transparent! Make public your data! US owe us an explanation."

(U) The story by Larry Romanoff, a regular author at the centre, cites several debunked theories, including one that members of the US military brought the virus to China during the Military World Games in fall 2019. Romanoff concludes that it has now "been proven" that the virus originated from outside of China, despite scientific consensus that it did.

(U) EVIDENCE? The World Health Organisation has concluded that the coronavirus emerged in China, where the first cases and deaths were reported. No evidence has surfaced to suggest the virus was imported into China by the US.

(U) Chossudovsky and Romanoff did not respond to repeated messages seeking comment. Romanoff's biography lists him as a visiting professor at Fudan University in Shanghai, but he is not listed among the university's faculty. The university did not respond to an email asking about Romanoff's employment.

(U) Romanoff's original article was taken down in the spring, but Zhao's tweet remains up.

(U) IGOR NIKULIN

(U) WHO IS HE? A four-time failed political candidate, Nikulin is prominently quoted in Russian state media and fringe publications in the west as a biologist and former weapons inspector in Iraq who served on a UN commission on biological and chemical weapons in the 1990s.

(U) COVID CLAIM: Nikulin argues the US created the virus and used it to attack China. He first voiced the belief in a January 20, 2020, story by Zvezda, a state media outlet tied to the Russian military. He appeared on Russian state TV at least 18 times between January 27, 2020, and late April of that year.

(U) Russian national Igor Nikulin last year. Photo / APOnce the virus reached the US, Nikulin changed his theory, saying "globalists" were using the virus to depopulate the earth.

(U) Nikulin has expressed support for weaponising misinformation to hurt the US in the past. On his website, he suggests claiming the US created HIV as a way to weaken America from within. Russian intelligence mounted a similar 1980s disinformation campaign dubbed "Operation INFEKTION."

(U) "If you prove and declare... that the virus was bred in American laboratories, the American economy will collapse under the onslaught of billions of lawsuits by millions of AIDS carriers around the world," Nikulin wrote on his website.

(U) EVIDENCE? Nikulin offered no evidence to support his assertions, and there are reasons to doubt his veracity.

(U) Former UN weapons inspector Richard Butler, for whom Nikulin claims to have worked, said he had no memory of Nikulin, and that his story sounded "sloppily fabricated, and not credible."

(U) No UN records could be found to confirm his employment.

(U) In an exchange with the AP over Facebook, Nikulin insisted his claims and background are accurate, though he said some records from UN work were destroyed in an American bombing during the Iraq invasion.

(U) When told that Butler didn't know him, Nikulin responded "This is his opinion."

(U) GREG RUBINI

(U) WHO HE IS: Greg Rubini is the name of an internet conspiracy theorist who claims to have high-level contacts in intelligence and listed his location on Twitter as "classified," until he was kicked off the platform. His posts have been retweeted thousands of times by supporters of QAnon, a conspiracy theory centered on the baseless belief that Trump is waging a secret campaign against enemies in the "deep state" and a secret sect of satanic paedophiles and cannibals.

(U) COVID CLAIM: Rubini has tweeted that Dr Anthony Fauci created the coronavirus and that it was used as a bioweapon to reduce the world's population and undermine Trump.

(U) EVIDENCE? Rubini's doesn't appear to be the intelligence insider that he pretends to be.

(U) Greg Rubini's permanently suspended Twitter account. Photo / APBuzzfeed attempted to track down Rubini last year and determined it is the alias of a 61-year-old Italian man who has worked in marketing and music promotions. A previous version of his Twitter bio indicates he is a fan of classic rock and the films of Stanley Kubrick.

(U) Attempts to reach Rubini online and through business contacts were unsuccessful.

(U) Rubini has bristled at efforts to verify his claims. When a social media user asked: "My question to you @GregRubini is, 'Where and what is your proof?' Rubini responded curtly: "And my question is: why should I give it to you?"

(U) Twitter suspended Rubini's account in November 2020 for repeated violations of its policies.

(U) KEVIN BARRETT

(U) WHO HE IS: A former lecturer on Islam at the University of Wisconsin-Madison, Barrett left the university amid criticism for his claims that the September 11, 2001, terrorist attacks were orchestrated by people linked to the US and Israeli governments.

(U) Barrett calls himself "a professional conspiracy theorist, for want of a better term" and has argued government conspiracies were behind the 2004 Madrid bombing, the 2005 London bombing, the 2013 Boston Marathon bombing and the 2016 Orlando nightclub shooting.

(U) COVID CLAIM: Barrett said he is "80%" sure coronavirus was created by elements within the US government as a bioweapon and used to attack China.

(U) University of Wisconsin-Madison lecturer Kevin Barrett in 2006. Photo / APIran was a secondary target, he has argued. Writing for Iran's PressTV, he said the early outbreak in that country "suggests that the Americans and/or their partners the Israelis... may have deliberately attacked Iran."

(U) Barrett further detailed his views during an interview with the AP.

(U) "It seemed fairly obvious to me that the first hypothesis one would look at when something as extraordinary as this Covid pandemic hits, is that it would be a US bio-war strike," he said.

(U) EVIDENCE? Barrett cited reports that the US warned its allies in November 2019 about a dangerous virus emerging from China. Barrett said that's long before authorities in China knew about the severity of the outbreak.

(U) Official sources have denied issuing any warning. If the US did know about the virus that soon, it was likely thanks to intelligence sources within China, which may have known about the virus as early as November 2019, according to former Secretary of State Mike Pompeo.

(U) LUC MONTAGNIER

(U) WHO HE IS: Montagnier is a world-renowned virologist who won the Nobel prize in 2008 for discovering HIV.

(U) COVID CLAIM: During an April interview with the French news channel CNews, Montagnier claimed that the coronavirus did not originate in nature and was manipulated. Montagnier said that in the process of making the vaccine for AIDS, someone took the genetic material and added it to the coronavirus.

(U) Scientist Luc Montagnier in Paris in 2006. Photo / APMontagnier cites a retracted paper published in January from Indian scientists who had said they had found sequences of HIV in the coronavirus. AP made multiple unsuccessful attempts to contact Montagnier.

(U) EVIDENCE: Experts who have looked at the genome sequence of the virus have said it has no HIV-1 sequences. In January, Indian scientists published a paper on bioRXIV, a repository for scientific papers that have not yet been peer-reviewed or published in a traditional scientific journal. The paper said that the scientists had found "uncanny similarity of unique inserts" in Covid-19 and HIV. Social media users picked up the paper as proof that the virus was engineered. As soon as it was published, the scientific community widely debunked the paper on social media. It was later withdrawn.

(U) SUPREME LEADER ALI KHAMENEI and HOSSEIN SALAMI

(U) WHO THEY ARE: Khamenei is the second and current Supreme Leader of the Islamic Republic of Iran. He has the final say on all matters of state, including the economy, military and health divisions.

(U) Since being elected to office in 1981, Khamenei has maintained his skeptical view of the US as Iran's foremost enemy. The tensions between the two countries boiled over in 2018 when Trump pulled the US out of the Iran nuclear deal and reimposed crippling sanctions. At the time, Khamenei remarked, "I said from the first day: Don't trust America."

(U) Hossein Salami was appointed by Khamenei as commander of Iran's Revolutionary Guard in April 2019. He leads the country's paramilitary force that oversees Iran's ballistic missile programme and responds to threats from both inside and outside the country.

(U) COVID CLAIM: Salami declared on March 5, 2020, that Iran was engaged in a fight against a virus that might be the product of an American biological attack. On those grounds, Salami ordered a Ground Force Biological Defence Manoeuvre to test the country's ability to combat a biological attack. Beginning March 16, the Ground Force, in close collaboration with the Health Ministry, began holding nationwide biodefense drills.

(U) Iranian supreme leader Ayatollah Ali Khamenei. Photo / APKhamenei was among the first and most powerful world leaders to suggest the coronavirus could be a biological weapon created by the US. During his annual address on March 22 to millions of Iranians for the Persian New Year, Khamenei questioned why the US would offer aid to countries like Iran if they themselves were suffering and accused of making the virus.

(U) Khamenei went on to refuse US assistance, saying "possibly (US) medicine is a way to spread the virus more." Last month, he refused to accept coronavirus vaccines manufactured in Britain and the US, calling them "forbidden." The Iranian Mission to the United Nations in New York did not respond to multiple requests for comment.

(U) EVIDENCE: There is no evidence that the US created the virus or used it as a weapon to attack Iran.

(U) **SOURCE DESCRIPTOR**

(U) Auckland The New Zealand Herald Online in English -- Auckland The New Zealand Herald Online in English Website of a daily newspaper distributed mainly in the greater Auckland area, but with the highest readership in New Zealand. Audited circulation of 108,790 as of 2018. Owned New Zealand Media and Entertainment; URL: http://www.nzherald.co.nz/ (source last reviewed 15 Mar 19)

Attachments:
e2bc6a76-0b63-4c...

Publisher:

#1
Agency Acronym:
CIA
Office Name:
OSE
Phone Numbers:
[redacted]
Email Addresses:
[redacted]

#2
LNI Producer:
OSE

Creator:

#1
Agency Acronym:

CIA
Office Name:
OSE
Phone Numbers:
[redacted]
Email Addresses:
[redacted]

#2
Compilation Title:
The New Zealand Herald Online

==========
Classification: [redacted]

[redacted]

From: [redacted]
Sent: Thursday, September 17, 2020 2:04 PM
To: [redacted]
Subject: RE: Readout: Friday 10am: COVID-19 Weekly Analytic Synch VTC (Conference ID: [redacted]

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Sure thing, I've added you to this list. There is a VTC tomorrow (10-1130, conf ID [redacted] if you are available. Also flagging the wider CIA COVID email slug ([redacted]) if you want to get added to that group for broader SA.

[redacted]

[redacted]
Office of the Director of National Intelligence
[redacted]

In the event I am out of the office, please contact the following alternate POCs at the NIC:

- NIC COVID alias: [redacted]
- NIO WMD & Proliferation: [redacted]

As of early July, the NIO-WMD team will be on an alternating BLUE/GOLD schedule as follows:

- BLUE: [redacted] ([redacted]) and [redacted] (COVID – [redacted])
- GOLD: [redacted] (COVID – [redacted]), [redacted] ([redacted])and [redacted] ([redacted])

From: [redacted]
Sent: Thursday, September 17, 2020 1:57 PM
To: [redacted]
Subject: FW: Readout: Friday 10am: COVID-19 Weekly Analytic Synch VTC (Conference ID: 149422246)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Hello,

I was wondering if I could be added for distro for these VTCs? I'm the [redacted] and am currently helping out with one related effort – [redacted]

Thanks,
[redacted]

From: [redacted]
Sent: Friday, September 11, 2020 11:01 AM
To: [redacted]

[redacted]

Cc: [redacted]
Subject: Readout: Friday 10am: COVID-19 Weekly Analytic Synch VTC (Conference ID: [redacted]

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Good morning,

Today's COVID VTC discussed IC efforts to understand vaccine progress as most agencies reported a steady-state workload for the week. Highlights include:

- (U[redacted]) As NIC/WMD works to balance our WMD and COVID workloads, we welcome your feedback on the frequency of these VTCs. Does your department or agency rely on the weekly nature of these meetups to help with workforce turnover? Do you prefer that the VTCs continue but are open to whatever schedule suits the

NIC's COVID coordinators? Would you prefer something less frequent, like every other week or not at all, to free up a few hours in your schedule? Let [redacted] (cc'ed) and me know!

- [redacted] Frequent questions regarding vaccines continue to revolve around cyber/CI concerns, foreign capabilities, "who's in the lead," and prospects for challenge trials.
- [redacted] CIA's [redacted] reported that [redacted] is progressing through review [redacted]. [redacted] flagged an upcoming graphic for the WIRe regarding COVID-19 vaccines at or near phase III clinical trials.
- [redacted]

[redacted] will be the NIC's COVID coordinator next week!

[redacted]

In the event I am out of the office, please contact the following alternate POCs at the NIC:

- NIC COVID alias: [redacted]
- NIO WMD & Proliferation: [redacted]

As of early September, WMD's team schedule is the following:

- 9/8-11: [redacted] (COVID – [redacted]), [redacted] ([redacted]), and [redacted] ([redacted])
- 9/14-18: [redacted] (Acting NIO for WMD & Proliferation – [redacted]) and [redacted] (COVID – [redacted])

From: [redacted]
Sent: Friday, September 11, 2020 8:50 AM
Subject: FW: Friday 10am: COVID-19 Weekly Analytic Synch VTC (Conference ID: [redacted]

Classification: UNCLASSIFIED[redacted]
==========

See you at 10!

From: [redacted]
Sent: Wednesday, September 09, 2020 9:31 AM
Subject: Friday 10am: COVID-19 Weekly Analytic Synch VTC (Conference ID: [redacted]

Classification: UNCLASSIFIED[redacted]
==========

Good morning,

The NIC will host the weekly COVID-19 analytic synch VTC this Friday, 11 September, from 1000-1130 AM EDT. Topics of discussion will include introductions and a summary of key questions, policy engagements, and recent or upcoming production.

For those interested, new to COVID-19, or in touch with colleagues at home, I thought I'd flag this free course by MIT on COVID-19, which involves one one-hour lecture each week. Details, including a syllabus, are available at https://biology.mit.edu/undergraduate/current-students/subject-offerings/covid-19-sars-cov-2-and-the-pandemic/. Upcoming topics include vaccines, immunology, and epidemiology related to COVID-19. Please follow your agency's guidance for outside training. About 2000 people watched the first lecture, which did not have an ASL interpreter but did have captions in English. Lectures are available a few days later on YouTube.

> ***COVID-19, SARS-CoV-2 and the Pandemic***
> *In Fall 2020, all MIT students and the general public are welcome to join Professors Richard Young and Facundo Batista as they discuss the science of the pandemic during this new class. Special guest speakers include: Anthony Fauci, David Baltimore, Britt Glaunsinger, Bruce Walker, Eric Lander, Michel Nussenzweig, Akiko Iwasaki, Arlene Sharpe, Kizzmekia Corbett, and others. The class will run from September 1, 2020 through December 8, 2020 and begin each Tuesday at 11:30 a.m. ET. The live stream will be available to the public, but only registered students may ask questions during the Q&A. Miss a class? You'll be able to view a video of the lecture on this page.*

If you have any VTC questions or would like to be added to Friday's conference, please do not hesitate to contact the Video Operations Center (VOC) at [redacted] (I cannot add gateways and such myself). If you are dialing in, you can call the VOC from a secure phone up to 10 minutes before the meeting. Have the conference ID ready, the VOC will then transfer your secure phone into the meeting.

Conference ID: [redacted]	Conference Name: **COVID COI Synch**
Subject: **POC-** [redacted]	
Notes: **CIA3-** [redacted]	
Start Setup Time: **11 SEP 2020 09:50** EST/DST	End Conference Time: **11 SEP 2020 11:30** EST/DST
Start Conference Time: **11 SEP 2020 10:00** EST/DST	Requestor: **CIA 3**
Conference Status: **Resolved**	
NCMI 1	**Resolved**
CIA [redacted]	**Resolved**
NGA NCE [redacted]	**Resolved**
FBI CLK [redacted]	**Resolved**
CDC ATLANTA	**Resolved**
DHS HQ GW 3	**Resolved**
NSAW GATEWAY 03	**Resolved**
ONI [redacted]	**Resolved**
ROWE VTC [redacted]	**Resolved**

LLNL-NAI 2 **Resolved**

A2 BLDG [redacted] **Resolved**

[redacted]

In the event I am out of the office, please contact the following alternate POCs at the NIC:

- NIC COVID alias: [redacted]
- NIO WMD & Proliferation: [redacted]

As of early September, WMD's team schedule is the following:

- 9/8-11: [redacted] (COVID – [redacted]), [redacted] ([redacted]), and [redacted] ([redacted])
- 9/14-18: [redacted] (Acting NIO for WMD & Proliferation – [redacted]) and [redacted] (COVID – [redacted])

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: UNCLASSIFIED[redacted]

==========

Classification: [redacted]

==========

Classification: [redacted]

==========

Classification: [redacted]

==========

Classification: [redacted]

[redacted]

From: [redacted]
Sent: Tuesday, September 15, 2020 6:12 PM
To: [redacted]
Subject: RE: PubMed Legacy Search CoV (UNCLASSIFIED[redacted])

Classification: UNCLASSIFIED[redacted]
==========

Here's what Daily Beast wrote. My remarks, which you'd probably already expect me to say

- Coming from a lab (we think this is possible) =/= manmade (we think this is unlikely based on available evidence)
- Coming from a lab =/= intentionally released from a lab (we def think this is unlikely)
- New virus =/= suspicious virus
- I do think that some journals/media organizations are slamming down any lab-related theories as conspiracies, so, sure, I'd be frustrated if I wanted attention, too.

https://www.thedailybeast.com/steve-bannon-linked-groups-push-study-claiming-china-manufactured-covid/

Steve Bannon Is Behind Bogus Study That China Created COVID

The study goes against basically all scientific evidence and expert opinion.
But it fits with the former Trump adviser?s anti-China posture.

Adam Rawnsley

Lachlan Markay

Updated Sep. 15, 2020 4:18PM ET / Published Sep. 15, 2020 3:16PM ET

A new study purporting to show that the novel coronavirus was manufactured in a Chinese lab was published by a pair of nonprofit groups linked to Steve Bannon, the former top Trump strategist now facing felony fraud charges.

The study, co-authored by a Chinese virologist who fled Hong Kong this year, claims that ?laboratory manipulation is part of the history of SARS-CoV-2.? Its findings were quickly picked up by a handful of prominent news organizations such as theNew York Post, which hyped the ?explosive? allegations that run counter to virtually all existing scientific literature on the source of the virus.

The study is the work of the Rule of Law Society and the Rule of Law Foundation, sister nonprofit organizations that Bannon was instrumental in creating. According to documents posted on the Society?s website last year, he served as that group?s chair. The Bannon connection was first spotted by Carl

Bergstrom, a biology professor at the University of Washington, whocalled the study ?bizarre and unfounded.?

A search of Google Scholar and the Rule of Law Society and Rule of Law Foundation websites indicates that the organizations have not previously published scientific or medical research, and it?s unclear whether the paper received any peer review. It was posted on Monday on the website Zenodo, a publicly available repository of scientific and academic research to which anyone can upload their work.

Both of the nonprofits behind the study were formed in conjunction with exiled Chinese billionaire Guo Wengui, with whom Bannon has collaborated on a number of advocacy efforts targeting the Chinese government and business endeavors that have drawn the scrutiny of federal law enforcement officials.

In addition to their work on the Rule of Law nonprofits, Bannon and Guo have also collaborated on a news website, G News, that has published stories suggesting that the coronavirus was manufactured by the Chinese military.

In July, Bannon appeared to tease forthcoming scientific studies supporting his contention that the coronavirus originated in a lab in Wuhan, China. He told theDaily Mail that scientists from the lab had ?defected? to the U.S. and were collaborating
with American intelligence agencies. On the ?War Room: Pandemic? podcast, Bannon has hosted others who have speculated that the virus may have been a Chinese ?bioweapon,? but he has said that he believes the most plausible explanation is that it ?came out of experiments that were going on? at that Wuhan lab.

That?s a line that has been echoed by some prominent U.S. officials. President Donald Trump and Secretary of State Mike Pompeo have both alluded to intelligence reports supporting that theory. ?This evidence is circumstantial, to be sure,? wrote Sen. Tom Cotton (R-AR) in an April column

for theWall Street Journal, ?but it all points toward the Wuhan labs.?

While an accidental leak from the virology lab in Wuhan remains a theoretical possible source of the initial outbreak in the city, the vast majority of the scientific literature on the virus has determined that its origins were natural, and that it was not laboratory manufactured. Dr. Anthony Fauci, the Trump administration?s coronavirus point-person, has stressed repeatedly that all evidence indicates the virus was not man-made.

The study published by Bannon?s group on Monday is therefore particularly incendiary. ?This virus is not from nature,? declared Dr. Li-Meng Yan, one of the scientists who conducted the study, during a Monday appearance on a British talk show. She called reports that the virus originated in a Wuhan meat market ?a smoke screen? designed to obscure its true origins.

But other virologists don?t agree and say the paper makes false claims about a number of basic facts. ?Basically, it's all circumstantial and some of it is entirely fictional,? Dr. Angela Rasmussen, a virologist at Columbia University, told The Daily Beast of the study.

The paper leads with a claim that the coronavirus' genes are "suspiciously similar to that of a bat coronavirus discovered by military laboratories" in China?an assertion Rasmussen says, that shouldn?t be surprising because they are related SARS-like coronaviruses.

The study?s authors made a similar claim about a portion of the SARS-CoV-2 spike protein?which viruses use to breach and infect cells?and wrote that it?s similar to the original SARS virus in a ?suspicious manner? and suggests

genetic manipulation. ?SARS-CoV also used ACE2 as a cellular receptor, as do other SARS-like bat coronaviruses,? Rasmussen says. ?It is not suspicious and is in fact expected that the receptor binding domains that bind the same protein would be similar.?

Rasmussen also said that the paper misrepresented basic facts about another part of coronavirus spike proteins known as furin cleavage sites. The authors claim that SARS-CoV-2?s cleavage site is ?unique? and unseen elsewhere in nature. But according to Rasmussen, ?Furin cleavage sites occur naturally in many other beta-CoVs, including MERS-CoV and other SARS-like bat coronaviruses.?

Yan has said that she fled China to avoid reprisals from the government there over her allegations that it was not being forthcoming about the origin and nature of the virus. She said she warned officials in December that the virus was highly transmissible between humans but that her allegations were ignored.

The University of Hong Kong?s school of public health, where Yan was employed, has disputed her allegations that the university failed to heed her warnings prior to the
outbreak in China.

In August, Yan appeared on Bannon?s podcast. During that show, Bannon said that he was ?still not in the camp that believes they purposely let it out but I?ve been strongly in the camp from the beginning that it came out of the Wuhan P4 lab.?

Unrelated to his work with the Rule of Law groups, Bannon is also facing felony charges over what federal prosecutors say was an effort to extract millions of dollars from a nonprofit seeking to privately finance the construction of a wall on the southern U.S. border. Bannon has pleaded not guilty to the charges.

From: [redacted]
Sent: Tuesday, September 15, 2020 12:19 PM
To: [redacted]
Subject: FW: PubMed Legacy Search CoV (UNCLASSIFIED[redacted])

Classification: UNCLASSIFIED[redacted]
==========

[redacted] –

I know you've got a lot going on…. But if you have 5 minutes, I'd love to hear your take on this.

[redacted]

[redacted]

NIO/WMD Alias: [redacted] -- please use if you don't hear from me
[redacted]

[redacted]

From: [redacted]
Sent: Tuesday, September 15, 2020 12:04 PM
To: [redacted]
Subject: FW: PubMed Legacy Search CoV (UNCLASSIFIED [redacted])

Classification: UNCLASSIFIED[redacted]
==========

FYI

[redacted]
National Intelligence Council / Office of the Director of National Intelligence
[redacted]

From: [redacted]
Sent: Tuesday, September 15, 2020 11:34 AM
To: [redacted]
Cc: [redacted]
Subject: RE: PubMed Legacy Search CoV (UNCLASSIFIED [redacted])

Classification: UNCLASSIFIED[redacted]
==========

(U) Check out attached….plausible?

[redacted]

From: [redacted]
Sent: Monday, September 14, 2020 2:07 PM
To: [redacted]
Cc: [redacted]
Subject: PubMed Legacy Search CoV

Classification: UNCLASSIFIED[redacted]
==========

[redacted]

I wanted to get this to you despite it still being in a very, very, rough format. If you feel that you'd like to share it, please do so with the caveat that this is simply a data catch at this point. In that light, with respect to the attachments:

1. **Word file.** This is simply a cut/paste of a retrieval from a PubMed Legacy Search Engine (not the new one) using the search parameters in the Advanced Search box as (coronavirus) AND (wuhan institute of virology) on 28-Aug-20. The format chosen was Abstract (Text) with 200 articles. There were 130 references retrieved. Please note that the new search engine introduced on the site ~February 2020 does not seem to allow retrieval of the institutional affiliations.

2. **Excel Spread Sheet**. The Reference numbers on the sheet are the ones assigned to the references in the word file. The retrieval is reverse chronology. Whenever possible duplicate institutions WERE NOT included in the collaboration list. Sub-departments were sometimes delineated but NOT within WIV.. e.g. collaborations were recorded by Institution not individual researcher, duplicate institutions generally entered once from 2015 onward. The collaborations go roughly 10 institutions deep, if there were additional institutions they might have been included in the "additional collaborations column" OR just noted as more collaborations (e.g. 22 institutions listed). I tried to provide a general sense of what technologies were used out to, if needed, five major categories. Here are two examples:

Article 26:

- Nucleotide analog inhibitors, antivirals (remdesivir and favipiravir)
- in vitro pharmaceutical assays
- structural and kinetic analyses

Article 40:

- Protein design and synthesis (Mpro - mediates viral replication and transcription)
- anti-viral development Protein structure and function analysis (x-ray crystallography)
- pharmacokinetic and toxicity analysis in vivo

3. **PowerPoint.** This is simply my trying to visual some of the items on the spread sheet. It's in the rough stages. Your comments, concerns and questions are more than welcome. I think it's probably fairly self-explanatory. The boxes which are filled in white are Asian institutions, those which are filled with color are non-Asian. The colored borders show affiliations by article, there isn't a rhyme or reason for the color selection. The black lines are simply my trying to follow author affiliations (by institution) which occur more than once on the page. It's an unfinished visual representation.

Anyway, I'll still be working on it to try to get a sense of the science and technology behind the articles. I haven't reached out yet to the individual you've e-introduced me to. My apologies, I need to get in touch with them. Once again, questions and comments are more than welcome.

V/r,
[redacted]

[redacted]
Senior Science and Technology Advisor (Microbiologist/Geneticist)
Perspecta
Contractor Support:
ODNI/PC/STG (Science & Technology Group)
[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Tuesday, February 4, 2020 3:36 PM
To: [redacted]
Cc: [redacted]
Subject: FW: Readout from NAS Meeting on Coronavirus

Classification: UNCLASSIFIED[redacted]
==========

DIA Friends,

FYI: [redacted] notes from the meeting yesterday for those interested. [redacted] is out today at the FELIX TEM, so if you have any questions for [redacted] it'll have to wait till tomorrow.

P.s. In [redacted] absence, I confirmed with [redacted] it was ok forward…just in case you're wondering about me forwarding others' emails in case that would make you think twice about ever sending me stuff! ☺

-[redacted]

[redacted]

From: [redacted]
Sent: Monday, February 03, 2020 5:34 PM
To: [redacted]
Cc: [redacted]
Subject: Readout from NAS Meeting on Coronavirus

Classification: UNCLASSIFIED[redacted]
==========

Good afternoon, ETB Bio folks!

This afternoon a meeting on coronavirus was held at the National Academy of Science (NAS, or NASEM). We (IC) were asked to just listen. This was not a technical meeting, but rather a meeting on what the academic community of experts in this virus would like to see in terms of additional data. A readout follows:

Short version:

- Consensus: Not BW. If someone was trying to optimize this for BW, we know too much about SARS that wasn't implemented
- Consensus: Natural or laboratory accident
- Additional sequences with temporal and geographic diversity would be helpful, particularly from early December. Value was placed on temporal over geographic diversity, but the academics want it all if they can get it.
- 1-2 products from the National Academy will go out soon. First is a "Based on science…" article on their website that will discuss the findings from the meeting and provide a public-facing vehicle for the findings. Second may be a letter from the Presidents of the Academies. [redacted]
- [redacted] and others will be making a request that all sequences and data related to 2019-nCoV be made open source.

Attendees (gov):

NAS: [redacted] (chair), [redacted]

HHS: [redacted] (chair), [redacted] (phone)

ODNI: [redacted] (chair)

NIAID: Anthony Fauci (phone)

OSTP: [redacted] (phone)

Several intel folks. Will share the list later.

Attendees (academic, via phone):

[redacted] (NYU) (academic chair)

[redacted] (Scripps)

[redacted] (the Hutch)

Peter Gaszak (EcoHealth Alliance) – collaboration with Wuhan Institute of Virology (WIV)

Ralph Baric (UNC) – collaboration with WIV

[redacted] (Johns Hopkins)

[redacted] (Iowa)

Charge of the committee: "OSTP and HHS requested that the NASEM examine and identify data requirements that would help determine the origins of the 2019-nCoV, specifically from an evolutionary/structural biology standpoint. NASEM will also consider whether this should include more temporally and geographically diverse clinical isolates, etc. This review will help prepare for future events by establishing a process for quickly assembling subject matter experts for evaluation of other potentially threatening organisms."

Backstory (Why was this work request made?): Head of [redacted] along with [redacted] and the [redacted] called Fauci (NIAID) on Friday night. Callers have background in bat coronavirus and were concerned by inserts they were seeing at Furin cleavage sites that don't follow the expert's expectations ("improbable mutations"). They likened it to a ten step process (as an example for explanation and not to be taken as a literal 10 step process) where we have sequences from step 1-6 and from step 10, but are missing steps 7-9. Was the step 10 sequence derived via modification, serial passage, or have we just not found sequences that show steps 7-9? A call with more experts was held on Saturday where it was noted that WIV had been working on gain of function of hACE2 receptor binding. On Sunday, another call was held with [redacted], and other experts. On that call, two experts said that the sequences were natural, the rest (number not given) said they were unsure. It was determined that a panel of experts should be convened, probably operating under WHO to not cause problems with China and limit access, to investigate further. [redacted] also suggested a US-based look into the issue. Today's meeting was to discuss data requirements.

Key Points:

Baric:

- He is not aware of WIV introducing mutations into the hACE2 receptor. He is aware of some chimera work, which was published.
- Insertion of furin cleaved site not unprecedented. He gave some examples where this was done as part of mouse adaptation during passage. However, that work was not done in this group of coronaviruses.
- In terms of Baric's involvement on the panel, he did mention that he has been linked to chimera work in 2016 that social media claims is linked to nCoV and he suggested that could make his membership a political problem. The academics and the academy disagreed. I think he was bringing it up as more of a "no surprises" thing rather than trying to be excused from the committee.

[redacted]

- Mutations in hACE2 do NOT look like perfect engineering (i.e. the sequences were not modified to give textbook perfect binding). If the sequence were engineered, one would expect that it would be engineered as perfectly as possible. Hence, evidence for natural evolution.
- Wet markets as vehicles for passage
- Binding was optimized to humans based on modelling (Baric dissented). 3 papers are currently on biorXiv. Questions: Was this the case early in the outbreak or was this affinity acquired through other host, etc?
- Biochemical data for hACE2 receptor modification would be useful
- With furin site introduction, it could open new classes of drugs to try
- Rules out BW ("nothing there"); consistent with natural evolution
- Several hundred sequences that the Chinese currently have are not being made available
- Can't rule out lab accident
- Will never be able to distinguish between natural vs. lab accident with current data
- Can rule out BW

[redacted]

- Earliest available samples are from Dec 24. Need samples before this time point (both market and non-market) from Wuhan more than we need geographically-diverse samples
- Europe, Australia, and Singapore are sharing genomes. Not a hindrance. CDC is the central point for sequencing efforts for US samples.
- Phylogenetics are clear, but tying modifications to function is not clear. Need sequences from animal reservoir and human from earlier in the outbreak.
- Quite possible there were other mutations/strains that sputtered out in early December before dying off and 2019-nCoV took over. Need sequences from that time period to check.
- Agreed with [redacted] that lab accident can't be ruled out, but also that there is no way to distinguish from natural at this time.

[redacted]

- Needs obth temporally and geographically diverse samples
- We are assuming that there is only a single lineage/introduction, when there may be multiple. Need more sequences from earlier than Dec 24 to try to find out ([redacted] comment: Finally!).
- Request should prioritize sequences over isolates. Isolates can be made synthetically if needed. Other members wanted isolates.

Daszak:

- 96% homology across the genome to strains that infect bats.
- Possible that other animal viruses have the same inserts and they could have been acquired in the host
- The range of the bat is southeast Asia. Might be worth getting samples from neighboring countries.
- Communication in China has dried up (scientists who normally talk are not doing so). Daszak stated that the folks at WIV are normally more open that typical Chinese, state-sponsored scientists based on prior interactions

Others had a random comment here or there, but the principals are all listed above.

I'm happy to go into further detail or answer any questions when I am back in the office.

-[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

==========
Classification: UNCLASSIFIED[redacted]

[redacted]

From: [redacted]
Sent: Sunday, February 9, 2020 10:25 PM
To: [redacted]
Cc: [redacted]
Subject: RE: Assessment on coronavirus (updated)
Attachments: [redacted]

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted]

[redacted]

From: [redacted]
Sent: Monday, February 10, 2020 10:28 AM
To: [redacted]
Cc: [redacted]

Subject: RE: [redacted] Assessment on coronavirus (updated)
Importance: High

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

[redacted] – Absolutely will keep you abreast of updates from [redacted]

[redacted] – To your question, other than comments by at least one [redacted], I am not aware of any part of the [redacted] leaning towards a different explanation for the cause of the virus. I am tracking the situation here and will alert this distro to any updates.

Best Regards,
[redacted]

[redacted]

From: [redacted]
Sent: Saturday, February 08, 2020 1:48 AM
To: [redacted]
Cc: [redacted]
Subject: RE: [redacted] Assessment on coronavirus (updated)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Yes, thanks for keeping me in the loop. I am going to be the ODNI lead coordinator on coronavirus going forward, so appreciate folks keeping me copied in.

[redacted]

[redacted])

From: [redacted]
Sent: Friday, February 07, 2020 9:12 AM
To: [redacted]
Cc: [redacted]
Subject: RE: [redacted] Assessment on coronavirus (updated)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

Thanks [redacted] Please include [redacted] on any coronavirus-related notes as he is the NIC POC on this: [redacted]

Have you heard any [redacted] SMEs/"experts" outside the [redacted] that are leaning towards a different explanation (ie genetically engineered and/or lab accident)? [redacted] piece is consistent with [redacted] (also attached) so [redacted]

[redacted]

From: [redacted]
Sent: Thursday, February 06, 2020 6:13 PM
To: [redacted]

[redacted]

Subject: [redacted] Assessment on coronavirus (updated)

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

All –

Correctly classified version of [redacted] assessment attached.

Cheers,
[redacted]

[redacted]

From: [redacted]
Sent: Friday, February 07, 2020 9:55 AM
To: [redacted]

Subject: RE: [redacted] Assessment on coronavirus

Classification: [redacted]

Classified By: [redacted]
Derived From: [redacted]
Declassify On: [redacted]
==========

All –

I was just informed that the [redacted] assessment I sent earlier is going to be reissued (I've attempted to recall the original). The language will not change, but Text Box 2 was missing a [redacted] which will be added. I'll send the corrected version as soon as I receive it.

[redacted]

[redacted]

From: [redacted]
Sent: Friday, February 07, 2020 9:21 AM
To: [redacted]
Subject: [redacted] Assessment on coronavirus

All,

Please find attached [redacted] assessment on 2019-nCoV that published this morning.

It is in-line with the standing NCMI assessment.

Best Regards,
[redacted]

[redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]

==========
Classification: [redacted]