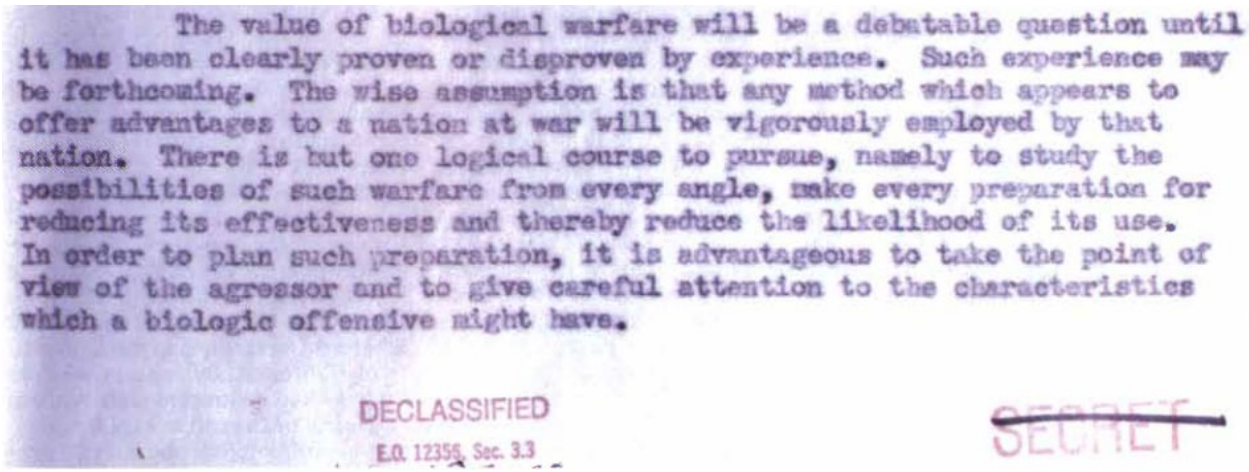
COVID-19’s Origin an Alternative Theory Summarized

3/11/20223

The United States Bioweapon Program

The U.S. Bioweapon program was *officially* born in Spring 1943 at Camp Detrick (Now known as Fort Detrick) in Maryland. the United States had signed but did not ratify the 1925 Geneva Protocol banning the use of biological as well as chemical weapons. In 1975 the U.S. ratified both the 1925 Geneva Protocol and the 1972 Biological Weapons Convention (BWC)—international treaties outlawing biological warfare. Democrat president Franklin Roosevelt ordered the creation of the program under the War Research Service (WRS), which was also headquartered at Fort Detrick, shortly after the National Academy of Sciences created a classified report encouraging President Roosevelt to create a bioweapon program.


The value of biological warfare will be a debatable question until it has been clearly proven or disproven by experience. Such experience may be forthcoming. The wise assumption is that any method which appears to offer advantages to a nation at war will be vigorously employed by that nation. There is but one logical course to pursue, namely to study the possibilities of such warfare from every angle, make every preparation for reducing its effectiveness and thereby reduce the likelihood of its use. In order to plan such preparation, it is advantageous to take the point of view of the agressor and to give careful attention to the characteristics which a biologic offensive might have.

DECLASSIFIED
E.O. 12356, Sec. 3.3

~~SECRET~~

The War Research Service (WRS) was created as a civilian agency initially tasked to supervise the military Chemical Warfare Service's (CWS) biological program. The agency was headed by George W. Merck, president of the Merck & Co. pharmaceutical firm which was founded in Germany prior to the first 2 world wars. The agency successfully developed offensive bioweapons such as Anthrax among others very quickly. The civilian agency was staffed by many U.S. academics like N. Paul Hudson of Ohio State University for example.

President Richard M. Nixon issued his "Statement on Chemical and Biological Defense Policies and Programs" on November 25, 1969 in a speech from Fort Detrick. The statement *officially* ended all U.S. offensive biological weapons programs. Nixon noted that biological weapons were “unreliable” despite the agency’s documented success and stated:

“The United States shall renounce the use of lethal biological agents and weapons, and all other methods of biological warfare. The United States will confine its biological research to defensive measures such as immunization and safety measures.”

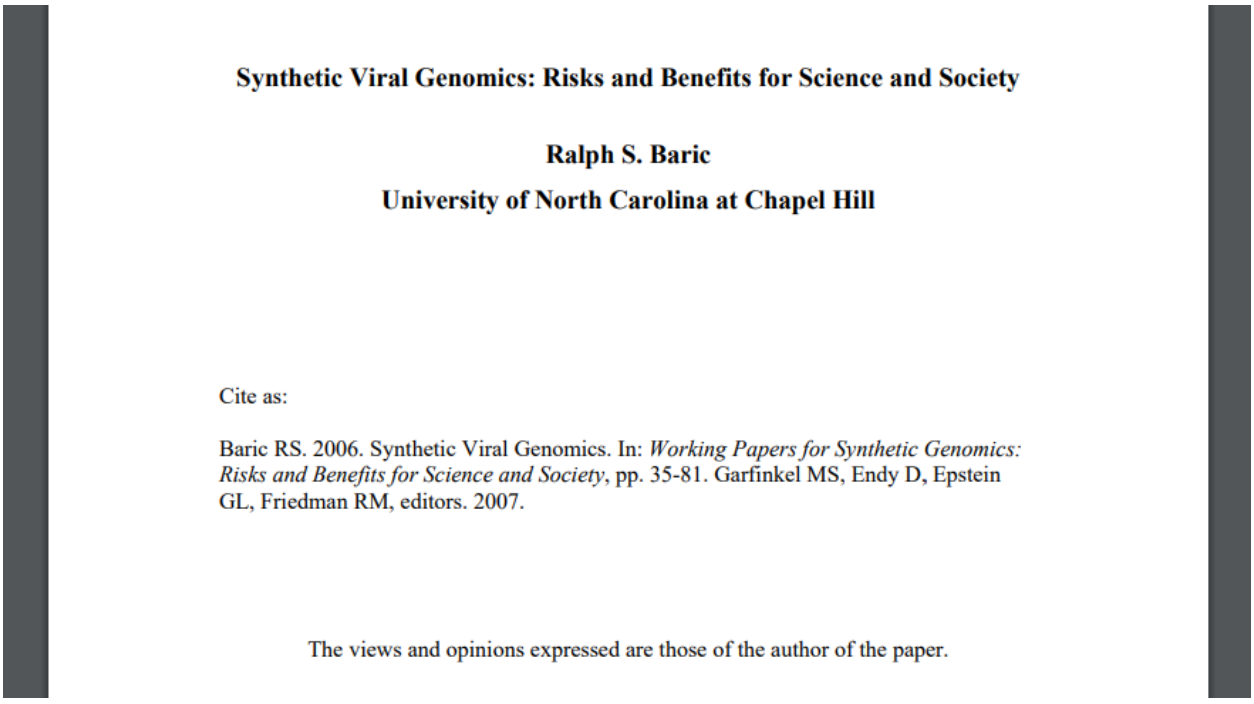
Just years later many new RNA viruses like Hepatitis C would become prevalent across the world and mass vaccinations programs would become a new normal. Biologic research and creation did not slow down, it was just being done for “defense” rather than offense *officially*.

Ralph Baric

Ralph S. Baric is a professor and scientist at the University of North Carolina at Chapel Hill, where he has worked on gain-of-function research related to coronaviruses for decades. According to UNC "he has spent the past three decades as a **world leader in the study of coronaviruses** and is responsible for UNC-Chapel Hill's world leadership in coronavirus research. **For these past three decades, Dr. Baric has warned that the emerging coronaviruses represent a significant and ongoing global health threat**, particularly because they can jump, without warning, from animals into the human population, and they tend to spread rapidly."

There had only been 2 previous outbreaks of coronaviruses prior to the 2019 SARS-CoV outbreak. The first SARS-CoV outbreak happened in 2002 and led to about 700 total deaths. The second outbreak, which was MERS-CoV happened in 2012 and led to about 800 total deaths. **Neither of these outbreaks represent "a significant and ongoing global health threat".** Baric had been wrong for 3 decades, **until the COVID-19 outbreak in 2019**. Many academics warned of the dangers of Baric's efforts to make coronaviruses more infectious and deadly through gain of function research, but that did not stop Baric from doing just that.

In 2006, Baric published a paper titled Synthetic Viral Genomics: Risks and Benefits for Science and Society in which he primarily discusses the risks and benefits of bioweapons. Obviously, any moral person knows there is no benefit to biological warfare, Baric clearly believes there are benefits to biological weapons.



Synthetic Viral Genomics: Risks and Benefits for Science and Society

Ralph S. Baric

University of North Carolina at Chapel Hill

Cite as:

Baric RS. 2006. Synthetic Viral Genomics. In: *Working Papers for Synthetic Genomics: Risks and Benefits for Science and Society*, pp. 35-81. Garfinkel MS, Endy D, Epstein GL, Friedman RM, editors. 2007.

In that very same paper Baric goes on to describe a powerful technique that provides the bioterrorist with a **"scapegoat" option; leaving a sequence signature that misdirects efforts at tracking the true originators of the crime.**

Synthetic DNAs and systematic assembly approaches also provide unparalleled power for building genomes of any given sequence, simultaneously providing novel capabilities for nefarious use. For example, genome sequences represent fingerprints that allow geographic mapping of the likely origin of a given virus. Recombinant viruses generated from classic recombinant DNA techniques will carry the signature of the parental virus used in the process as well as novel restriction sites that were engineered into the genome during the cloning process. In contrast, synthetic viral genomes can be designed to be

identical with exact virus strains circulating in any given location from any year. This powerful technique provides the bioterrorist with a "scapegoat" option; leaving a sequence signature that misdirects efforts at tracking the true originators of the crime. Even better, the approach could be used to build mistrust and/or precipitate open warfare between nations. A simple example might involve the use of the picornavirus foot and mouth disease virus, which is not present on the North American continent, yet is endemic in Africa, Asia, the Middle East and South America. North American herds are not vaccinated against this pathogen, the virus is highly contagious, and the disease is subject to international quarantine. Geographically distinct FMDV strains contain unique sequence signatures allowing ready determination of origin. A North American outbreak of an infectious "synthetic" FMDV virus containing signature sequences reminiscent of strains found in select Middle East or Asian nations that are viewed as terrorist states by the US government would inflame worsening tensions and could provide a ready excuse for military retaliation. Project costs would likely be less than $50K, including synthesis,

Baric literally describes how the **U.S. Government could create a synthetic virus** that appears to be created from somewhere else and **then use that to inflame worsening tensions and justify U.S. military retaliation**.

In 2021, Baric was elected member of the U.S. National Academy of Sciences (The same one that originally encouraged the development of a U.S. bioweapon program).

What is COVID-19?

Before going any further it will be important to understand a few facts about COVID-19 and what makes it so much more infectious and deadly than previous coronaviruses. COVID-19 has an insertion of **a furin cleavage site (FCS)** in its spike protein. This Furin Cleavage site has **NEVER** been recorded in any previous coronavirus. Many studies demonstrate a critical role for the furin cleavage site insertion in COVID-19 replication and pathogenesis. **Without the Furin Cleavage Site, the coronavirus would have remained a non-issue**. The **insertion of a Furin Cleavage Site allows the coronavirus to bind to the Human ACE2 receptor and replicate** (remember this it is very important).

The genome sequence that you can see for the amino acid sequence of the Furin Cleavage Site is: CAGACTAATTCTCCTCGGCGGGCACGTAGT which is 30 nucleotides coding for 10 amino acids. The chances of this sequence to naturally arise are extremely small (you are over 60,000 times more likely to be stuck by lightning). That is without accounting for the 3 gp120 HIV inserts also found in COVID-19 but not found in any other coronavirus. So that leaves synthetic (lab) insertion or recombination from another virus naturally, the problem is this sequence has **NEVER** been found in any known virus so that can't be it either.

Surprisingly, **this exact sequence can be found** in the US patent 9,587,003 filed on Feb. 4, 2016, which is a patent from none other than the **Pharmaceutical company Moderna** (who created 1 of the currently 2 FDA approved COVID-19 vaccines for the U.S. Government and made millions of dollars).

For 2 years **despite this clear evidence** of COVID-19 being lab created academics, the U.S. Government, the media, the pharmaceutical industry, and others **have denied the so called "lab leak theory"** and staunchly **claimed COVID-19 mutated in Chinese bats (remember the scapegoat)**.

Now in 2023 academics, the U.S. Government, the media, the pharmaceutical industry, and others have flipped and decided a "lab leak" is the most likely origin of COVID-19 while pointing the finger at China's Wuhan institute of Virology labs.

China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety and Global Health Security

The primary purpose of this section is to demonstrate how closely the U.S. group and Chinese group of scientists were. The photo below is from China January 2019, this was the last time the workshop was held before the COVID-19 pandemic began.

According to the National Academies of Sciences: Since 2015, the National Academies of Sciences has organized a series of meetings on the challenges of **emerging infections, laboratory safety, and global health security** with the Chinese Academy of Sciences (CAS), Chinese Center for Disease Control and Prevention (CCDC), and other Chinese life science and public health organizations. Academy members and other top-flight American researchers in human and animal virology and immunology participated, including current and former directors of BSL-4 laboratories, former CDC, and former uniform military biodefense experts. They have met with China's BSL-4 laboratory directors and researchers from top universities and research centers across China. The topics discussed included basic and applied research on infectious diseases; the challenges of combating emerging infections; life-science collaboration and **research-data sharing**; high-containment biological laboratory management, safety and security; and responsible conduct in the use of gene editing in infectious disease research.

The meetings enabled scientists from the United States and China to **discuss research findings on diseases of mutual concern to China and the United States**, to share best practices and lessons learned for managing and operating high containment biological laboratories, and to establish new collaborative research and institutional partnerships.

These meetings would also allow the U.S. group to gather valuable information that could later be used to turn China into Ralph Baric's "scapegoat". At this workshop the U.S. group could easily receive sequences of the Wuhan Institute of Virology's latest strains of coronaviruses, which could then be

taken and used to create COVID-19 for approximately $6,000 according to Ralph Baric. (More on this later) Below is a summary of what Baric said at this very workshop:

> **Dr. Ralph Baric,** a professor at the University of North Carolina Chapel Hill and an expert in coronaviruses, provided an overview of the selection and design of pathogen properties, along with information gaps and barriers. He noted the rapid pace of advance and decreasing cost of nucleic acid synthesis; the first coronavirus to be synthesized cost roughly $42,000, a price that would now be $6,000. The largest genome currently synthesized is a 520kb mycobacterium, indicating that it is now possible to synthesize the genomes of most RNA and DNA viruses. In addition, high fidelity sequences are available for many viruses, rendering it possible to synthesize viral genomes and recover viable virus for many strains.

The low cost of synthesizing viruses will be very relevant to the later mentioned DARPA DEFUSE proposal. Below is a list of all participants of the workshop and their current affiliations at the time:

American Participants

Ralph Baric, Professor
Department of Epidemiology, University of North Carolina, Chapel Hill

David Franz, Professor
USAMRIID (retired)

Douglas Gladue, Scientist
U.S. Department of Agriculture

Diane Griffin, Professor
Department of Molecular Microbiology and Immunology of Johns Hopkins Bloomberg School of Public Health

Stephen Higgs, Professor
Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University

Joseph Kanabrocki, Professor
Microbiology in the Biological Sciences Division of the University of Chicago

James Le Duc, Professor
Galveston National Laboratory, Department of Microbiology and Immunology, University of Texas Medical Branch, Galveston

David Relman, Professor

Department of Microbiology and Immunology, Stanford University School of Medicine

Linda Saif, Professor
Department of Veterinary Preventive Medicine, Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University

Pei-Yong Shi, Professor
Department of Biochemistry and Molecular Biology, University of Texas Medical Branch

David Swayne, Center Director
Agricultural Research Service, United States Department of Agriculture

Katherine Bowman, Senior Program Officer
National Academy of Sciences

Benjamin Rusek, Senior Program Officer
National Academy of Sciences

Chinese Participants

George F. Gao, Academician,
Director-General Chinese Center for Disease Control and Prevention

Zhigao Bu, Professor
Harbin Veterinary Research Institute, CAAS

Wen Dang, Doctor
Lanzhou Veterinary Research Institute, CAAS

Wuxiang Guan, Professor Wuhan Institute of Virology, CAS
Yunzhang Hu, Professor
Institute of Medical Biology, Chinese Academy of Medical Sciences

Mifang Liang, Professor
National Institute for Viral Disease Control and Prevention, China CDC
Chunbo Lou, Professor Institute of Microbiology, CAS

Hongsheng Ouyang, Professor
Jilin University
Chengfeng Qin, Professor
Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences

Hualan Chen, Academician
Harbin Veterinary Research Institute, CAAS

Gong Cheng, Professor
Tsinghua University

Rui Gong, Professor
Wuhan Institute of Virology, CAS

Qian Han, Professor
Hainan University

Chengjun Li, Professor
Harbin Veterinary Research Institute, CAAS

Longding Liu, Professor
Institute of Medical Biology, Chinese Academy of Medical Sciences

Jiahai Lu, Professor
Sun Yat-sen University

Jiancheng Qi, Professor
National Biological Protection Engineering Center

Zhengli Shi, Professor
Wuhan Institute of Virology, CAS

Dayan Wang, Professor
Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College

Jianwei Wang, Professor

National Institute for Viral Disease Control and Prevention, China CDC

Changjiang Weng, Professor
Harbin Veterinary Research Institute, CAAS

Kongming Wu, Vice President
Chinese Academy of Agricultural Sciences

Xiaodong Wu, Professor
China Animal Health and Epidemiology Center

Xaoli Xue, Professor
Laboratory of Synthetic Biology, Shanghai Institute of Plant Physiology, CAS

Yang Xue, Associate Professor
Tianjin University

Ruifu Yang, Professor
Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences

Zhiming Yuan, Professor
Wuhan Institute of Virology, CAS

Peijun Zhai, Professor
China National Accreditation Service for Conformity Assessment (CNAS)

Pingping Zhang, Doctor
Institute of Microbiology and Epidemiology
Academy of Military Medical Sciences

Tietao Zhang, Professor
International bureau, CAAS

Weiwen Zhang, Professor
Tianjin University

Chihong Zhao, Professor
National Institute for Viral Disease Control and Prevention, China CDC

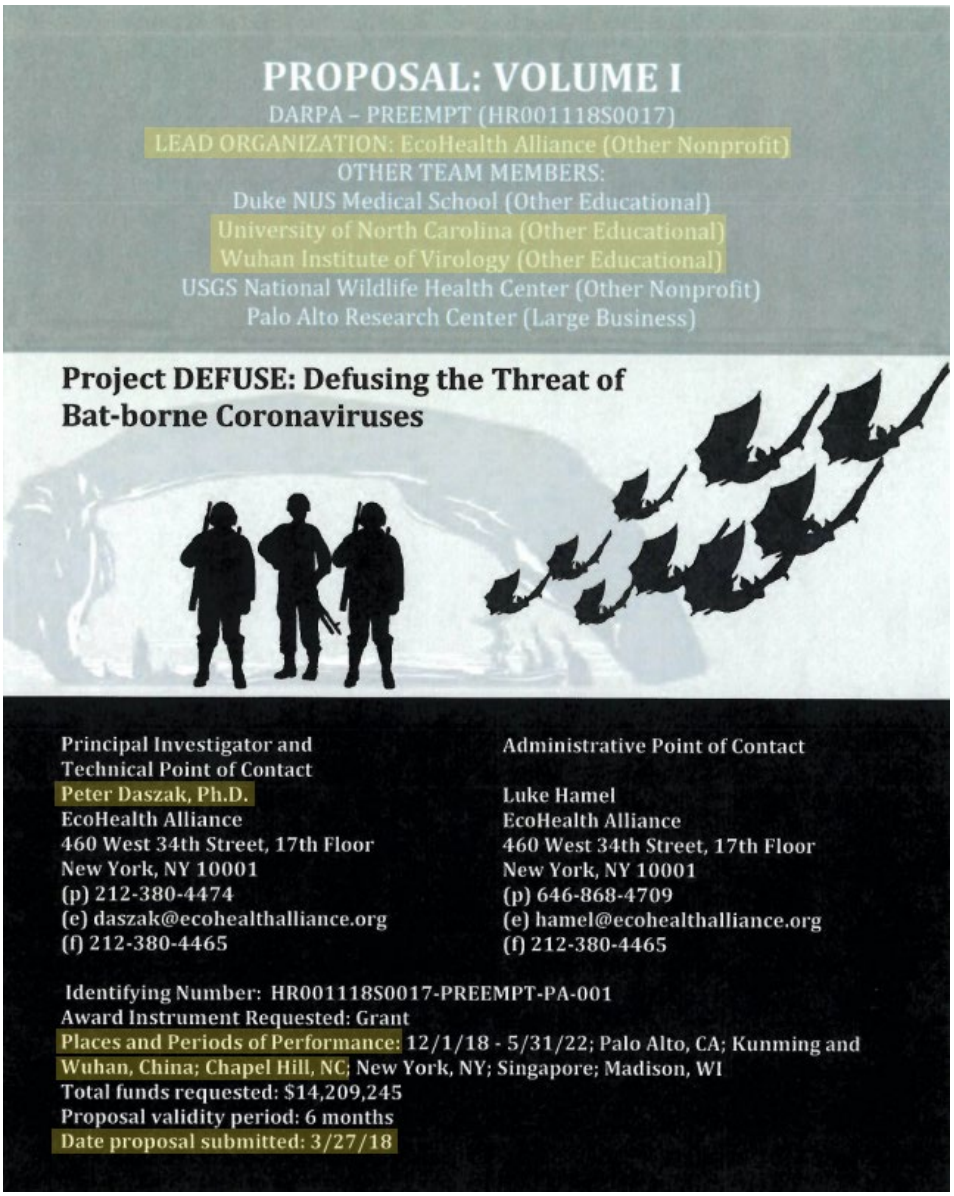
Tongyan Zhao, Professor
Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences

Yong Zhao, Doctor
Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences

Haixue Zheng, Professor
Lanzhou Veterinary Research Institute, CAAS

The DEFUSE Proposal

In 2018 The EcoHealth Alliance in collaboration with Ralph Baric's Lab at UNC submitted a proposal to DARPA to receive funding for "**Project DEFUSE: Defusing the threat of bat-borne coronaviruses**"



PROPOSAL: VOLUME I

DARPA – PREEMPT (HR001118S0017)

LEAD ORGANIZATION: EcoHealth Alliance (Other Nonprofit)

OTHER TEAM MEMBERS:

Duke NUS Medical School (Other Educational)

University of North Carolina (Other Educational)

Wuhan Institute of Virology (Other Educational)

USGS National Wildlife Health Center (Other Nonprofit)

Palo Alto Research Center (Large Business)

Project DEFUSE: Defusing the Threat of Bat-borne Coronaviruses

Principal Investigator and Technical Point of Contact
Peter Daszak, Ph.D.
EcoHealth Alliance
460 West 34th Street, 17th Floor
New York, NY 10001
(p) 212-380-4474
(e) daszak@ecohealthalliance.org
(f) 212-380-4465

Administrative Point of Contact
Luke Hamel
EcoHealth Alliance
460 West 34th Street, 17th Floor
New York, NY 10001
(p) 646-868-4709
(e) hamel@ecohealthalliance.org
(f) 212-380-4465

Identifying Number: HR001118S0017-PREEMPT-PA-001
Award Instrument Requested: Grant
Places and Periods of Performance: 12/1/18 - 5/31/22; Palo Alto, CA; Kunming and Wuhan, China; Chapel Hill, NC; New York, NY; Singapore; Madison, WI
Total funds requested: $14,209,245
Proposal validity period: 6 months
Date proposal submitted: 3/27/18

The proposal details the group's plan to synthesize novel coronaviruses. They would **evaluate how coronaviruses could use the human ACE2 (like COVID-19 does) to grow in human cells**. **They would also insert human specific furin cleavage sites** to evaluate growth potential in monkey and Human airway epithelial cells, which is suspiciously **the exact same way COVID-19 would infect humans less than 2 years later**…

Testing Synthetic Modifications: We will synthesize QS with novel combinations of mutations to determine the effects of specific genetic traits and the jump potential of future and unknown recombinants. *RBD deletions:* Small deletions at specific sites in the SARSr-CoV RBD alter risk of human infection. We will analyze the functional consequences of these RBD deletions on SARSr-CoV hACE2 receptor usage, growth in HAE cultures and *in vivo* pathogenesis. First, we will delete these regions, sequentially and in combination, in SHC014 and SARS-CoV Urbani, anticipating that the introduction of deletions will prevent virus growth in Vero cells and HAE[58]. In parallel, we will evaluate whether RBD deletion repair restores the ability of low risk strains to use human ACE2 and grow in human cells. *S2 Proteolytic Cleavage and Glycosylation Sites:* After receptor binding, a variety of cell surface or endosomal proteases[68-71] cleave the SARS-CoV S glycoprotein causing massive changes in S structure [72] and activating fusion-mediated entry[64,73]. We will analyze all SARSr-CoV S gene sequences for appropriately conserved proteolytic cleavage sites in S2 and for the presence of potential furin cleavage sites[74,75]. SARSr-CoV S with mismatches in proteolytic cleavage sites can be activated by exogenous trypsin or cathepsin L. Where clear mismatches occur, we will introduce appropriate human-specific cleavage sites and evaluate growth potential in Vero cells and HAE cultures. In SARS-CoV, we will ablate several of these sites based on pseudotyped particle studies and evaluate the impact of select SARSr-CoV S changes on virus replication and pathogenesis. We will also review deep sequence data for low abundant high risk SARSr-CoV that encode functional proteolytic cleavage sites, and if so, introduce these changes into the appropriate high abundant, low risk parental strain. *N-linked glycosylation:* Some glycosylation events regulate SARS-CoV particle binding DC-SIGN/L-SIGN, alternative receptors for SARS-CoV entry into macrophages or monocytes[76,77]. Mutations that introduced two new N-linked glycosylation sites may have been involved in the emergence of human SARS-CoV from civet and raccoon dogs[77]. While the sites are absent from civet and raccoon dog strains and clade 2 SARSr-CoV, they are present in WIV1, WIV16 and SHC014, supporting a potential role for these sites in host jumping. To evaluate this, we will sequentially introduce clade 2 disrupting residues of SARS-CoV and SHC014 and evaluate virus growth in Vero cells, nonpermissive cells ectopically expressing DC-SIGN, and in human monocytes and macrophages anticipating reduced virus growth efficiency. We will introduce the clade I mutations that result in N-linked glycosylation in rs4237 RBD deletion repaired strains, evaluating virus growth efficiency in HAE, Vero cells, or nonpermissive cells ± ectopic DC-SIGN expression[77]. *In vivo*, we will evaluate pathogenesis in transgenic hACE2 mice.

The document lists Ralph Baric's labs tasks as assessing **pathogenesis in the Human ACE2**, synthetically modifying **the spike protein with cleavage sites and glycosylation sites**, and even **testing effects of high-consequence micro-variants** on human crossover potential. **Which is exactly what this same group of researchers told us happened naturally less than 2 years later**.

PI-TA-01 Task 4: Experimental assays of SARSr-CoV QS jump potential (UNC)
Sub-Task 4.1 Conduct pre-screening via structural protein modeling, mutation identification, pseudovirus assays. (UNC). ***Subtask 4.2*** Conduct *in vitro* testing of chimeric viruses against host cell lines (UNC). ***Subtask 4.3*** Assess *in vivo* pathogenesis in hACE2 transgenic mice (UNC). ***Subtask 4.4*** Validate results from chimeric viruses with full-genome QS (UNC). ***Subtask 4.5*** Test synthetic modifications to viral spike proteins including RBD deletions, S2 Proteolytic Cleavage and Glycosylation Sites, N-linked glycosylation (UNC). ***Subtask 4.6*** Test effects of low-abundance, high-consequence micro-variations on jump potential. (UNC)
Milestone(s): Initiation and completion of each experimental sub-task.
Deliverables: Laboratory confirmed list of higher risk SARSr-CoV QS with zoonotic capability. Candidate SARSr-CoV for animal experiments. Data made available.

DARPA refused the proposal with 2 out of 3 reviewers saying the proposal was "selectable but not recommended" because of the risks of Gain of Function research. This does not mean this research was not done by the group, it just means DARPA didn't fund it at that time. It doesn't even mean that DARPA didn't later fund it. Remember Baric said himself a novel coronavirus could be synthesized for $6,000 which is nothing for these organizations. Baric even admits he is close with DARPA in his own emails:

Message

From: Baric, Ralph S [/O=UNC EXCHANGE/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=RBARIC]
Sent: 3/17/2016 9:23:15 PM
To: Olshan, Andrew F [/O=UNC EXCHANGE/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=Uepafo]
Subject: RE: Visit with DARPA Defense Science Office Director

I have some DARPA funding so its always nice to talk with them. Also got close a couple of times, funny organization, personal interactions are key. Then they fund the same group over and over. I'm around april 6th. ralph

---

From: Olshan, Andrew F
Sent: Thursday, March 17, 2016 4:45 PM
To: Meshnick, Steven R; Baric, Ralph S
Subject: FW: Visit with DARPA Defense Science Office Director

Is DARPA of relevance to you and/or our faculty?

Andy

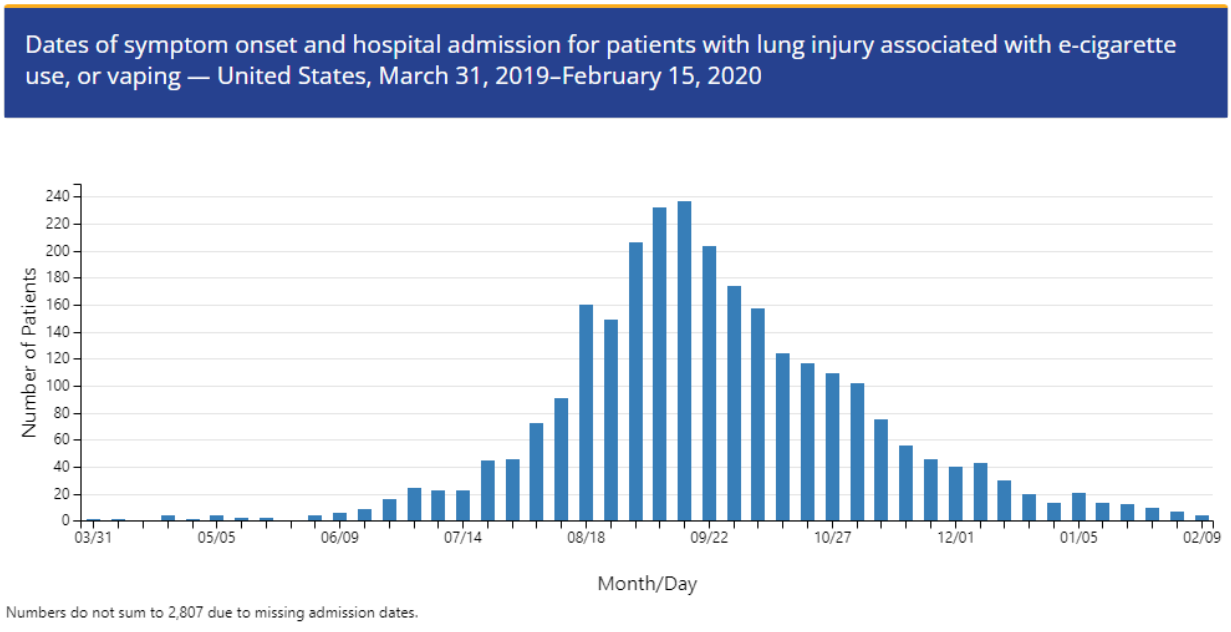
--
Andrew F. Olshan, Ph.D.
Barbara S. Hulka Distinguished Professor and Chair
Department of Epidemiology
2101B McGavran-Greenberg Hall
Gillings School of Global Public Health, CB#7435,
University of North Carolina
Chapel Hill, NC 27599
Email: andy_olshan@unc.edu
Ph:
FAX:

How many coincidences are too many?

We are expected to believe that Ralph Baric and EcoHealth Alliance proposed ways to frame other countries for bioweapon creation, requested funding to insert Furin Cleavage Sites, and glycoprotein's into coronavirus and when exactly that happened just months later it was either natural or the Wuhan institute of Virology doing what Ralph Baric was planning on doing? The evidence clearly points to COVID-19 being created in America, and it even points to COVID-19 spreading in America before China.

EVALI

In the summer of 2019, a mysterious respiratory disease was detected spreading across the United States. It was originally blamed on E-cigarette, or vaping, product use-associated lung injury or EVALI. Oddly enough EVALI symptoms essentially perfectly mirrored COVID-19 symptoms with the exception of the loss of taste which the virus could have easily mutated to cause by 2020 when COVID-19 was *officially* detected in the United States. EVALI is no longer a thing, so we are also expected to believe vaping was only getting people sick right up until COVID-19 was *officially* detected in the U.S. then all the sudden vapes magically decided to stop making people sick… The CDC's own data shows EVALI spreading across the states months before anyone got sick in China, and as soon as COVID-19 *officially* reaches the United States, no more EVALI.



How did COVID-19 get to Wuhan?

If COVID-19 was created in a U.S. lab and not at the Wuhan Institute of Virology how did it get to Wuhan in late 2019? Well that's actually very simple, the U.S. military took it to Wuhan when they visited for the World Military Games held from October 18–27, 2019 hosted in Wuhan, China. 59 U.S. Military members actually played in the games, but many more U.S. government employees were in Wuhan along with them. Multiple studies have even found the 2019 Military games to be the very first COVID-19 super spreader event in the world.

Why did the Wuhan Institute of Virology take their database offline?

It could be because China quickly realized what was happening to them, the U.S. government and researchers would have already known that database could be used to frame China. More likely it's because A memorandum of understanding between the Wuhan lab and the Galveston National Laboratory at the University of Texas Medical Branch states that each lab **can ask the other to return or "destroy" any so-called "secret files"** — any communications, documents, data or equipment resulting from their collaboration — and ask that they wipe any copies.

"The party is entitled to ask the other to destroy and/or return the secret files, materials and equipment without any backups," it states.

This right is retained even after the agreement's five-year term ends in October 2022. All documents are eligible for destruction under the agreement's broad language.

"All cooperation … shall be treated as confidential information by the parties," the agreement states.

Why would the U.S. government do this?

It's no secret that tensions between China and the United States have been rising especially since America began funding Ukraine in its war against Russia. Like Ralph Baric said in 2006, a scenario exactly like the one described in this paper could be used by the United States to escalate tensions further and justify military intervention which is clearly what the U.S. government has been considering for a long time. Not only that, the COVID-19 pandemic expanded the wealth gap even more in the United States. The rich elite and big industries like the pharmaceutical industry in the United States made massive profits as a result of the Pandemic, and coincidently they are also some of the biggest donors and lobbyist for the U.S. government.

Recommendation

Thus far the U.S. Government and congress has essentially ignored the possibility that COVID-19 was created and released right here in the United States. The COVID committee should immediately question the American participants listed above as well as employees of other U.S. NGOs like EcoHealth Alliance under oath. Finding the true origin is extremely important to ensure lab made viruses are not released for any reason in the future and it could help those injured by COVID-19 and the COVID vaccines recover. Millions are dead, millions were hurt by the pandemic and the mandates, and the U.S. citizens deserve answers, not a war with China.