

A Mathematical Method to Trace the Origin of COVID-19

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ABSTRACT

The novel coronavirus (COVID-19) has caused great harm to mankind. Tracing the origin of the COVID-19 virus is not an issue about politics nor public opinion, but about science. This paper adopts scientific and rigorous attitude without any presumed standpoints, uses mathematical methods to calculate about the origin of the virus based on the principles of molecular biology, and has obtained the probability of natural evolution, natural chimerism, and artificial chimerism, respectively. Furthermore, the paper has confirmed that currently there are no technical obstacles to the production of chimeric viruses through a review of existing artificial chimeric virus technologies, and has compared the technical differences between the Chinese virus research team and its American counterparts. On the basis of the World Health Organization report, the paper has clarified the probability that the virus originates in some U.S. laboratory with mathematical methods.

The paper has also analyzed the relationship between organizations and individuals related to the production of the virus through literature analysis, obtained a relationship diagram centered with American scientist Ralph S. Baric, and deduced the route of possible laboratory leaks. For the points denied by many parties for political reasons, the paper sorted out and summarized the news clues before the virus breakout in Wuhan, discovered the missed diagnosis process in the field of disease control in the United States, and inferred it is highly possible that during the 2019 U.S. "e-cigarette pneumonia" epidemic, a large number of SARS-Cov-2 (COVID-19) cases had already appeared.

Based on the actual process of the outbreak, this paper believes that the COVID-19 virus is most likely an artificial chimeric virus made by Baric's team and leaked through the laboratory. It firstly infected the people of Maryland and further spread to the people all around the world through frozen seafood. The author believes that scientific ethics and morals should be further promoted, because science is a double-edged sword. When scientists wield this sword, it must be clear in their minds that it may bring happiness to mankind, or disasters. Professor Ralph S. Baric is admired for his scientific achievements. He devoted his life to the research of virus science. His original intention is probably to provide solutions to diseases that humans may encounter in the future, but his anxiety for success or theft conducted by military forces has eventually led to the global disaster. This is a tragedy for the people of all races of mankind. The author hereby calls for the immediate cessation of the GOF (gain-of-function) research in American laboratories. At the same time, countries around the world should take this as a lesson and immediately stop research on biological and chemical weapons.

Keywords: COVID-19, SARS-Cov-2, novel coronavirus, virus traceability, epidemic analysis, virology basis

1. Introduction

Since 2019, the COVID-19 virus that has been circulating worldwide, it is the first pandemic in human society during the past 100 years. The pandemic has brought unprecedented severe challenges to our social economy, politics, and culture, and great harm to mankind as well. By the end of June 14, 2021, 175 million of the world population have been infected or are being infected by the virus, resulting in more than 3.79 million deaths [1].

Therefore, the use of scientific methods to determine the source of the virus will help countries in the world to coordinate for epidemic prevention, combat the virus, prevent the epidemic from rebounding, and prevent other types of virus pandemics that may occur in the future.

However, it is regrettable that during last two years, rumors about the origin of the virus flooded the Internet and international political remarks, some unfounded viewpoints have blinded the eyes of all sectors of society and have cast a thick layer of mist on the real virus origin. This situation has not only intensified the contradictions

between countries, but also largely misled the decision-making of some governments on epidemic prevention, causing unnecessary losses to human society. In fact, the question of where the virus comes from is a serious issue and can be solved with scientific principles. It must be treated seriously, objectively, and prudently in order to draw a cautious conclusion.

This paper will reasonably determine the source of the virus through mathematical calculations, probability statistics, literature analysis, and reconstruction of the timeline. The conclusions of the paper will objectively play a positive role in the development of human society and the protection of viruses.

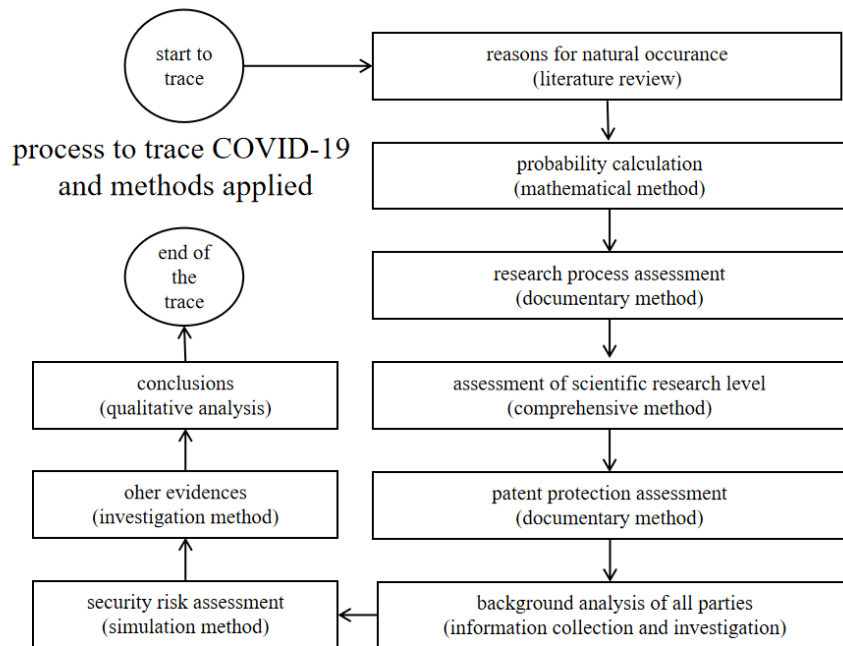


Figure 1. the process to trace COVID-19 and methods applied

2. Process and method

Life on the earth is diverse, including extremely tiny microorganisms in the soil, as well as common animals and plants, and human beings are just one of the many kinds. Although historically, biologists have used many ways to classify life, there are only two types from the perspective of modern molecular biology: DNA life and RNA life. Human beings are the former, and the novel coronavirus is the latter.

DNA is the abbreviation of deoxyribonucleic acid, it is composed of the ATGC bases (namely, adenine, thymine, guanine, cytosine), and RNA is the abbreviation of ribonucleic acid, it is composed of the AUGC bases (namely, adenine, uracil, guanine, cytosine). Both DNA and RNA are the genetic material of life. DNA life contains both DNA and RNA. RNA life only contains RNA. Compared with RNA life, DNA life contains more bases and relatively stable double-stranded DNA structure (dsDNA), it appears to be relatively complex and advanced. The genetic structure of single-stranded RNA (ssRNA) is

unstable and prone to various mutations. In addition to what was mentioned above, there are also single-stranded DNA (ssDNA) and double-stranded RNA (dsRNA) in life, but neither of them is within the scope of this paper.

The lengthy sequence of the four bases in RNA determines the properties of the protein produced by genetic material. The synthesized proteins are diverse, including protein enzymes with specific functions. This enzyme is a kind of macromolecule. It is generally a peptide chain composed of polypeptide bonds (dehydrated and condensed amino acid). The peptide chain possesses various catalytic and expression characteristics through its catalytic base group, binding base group and its structural characteristics in three-dimensional space.

Based on the principles of molecular biology discussed above, coronaviruses use their RNA as a genetic carrier and produce spike protein, envelope protein, membrane protein and so on in their transmission and replication processes. More specifically, the novel coronavirus, which is defined by the World Health Organization (WHO) as "COVID-19", is characterized by

first entering human cells and then intervening its own RNA through the "uncoating" process of membrane fusion into human cells, hijacking the translation process of human cells' genetic material, and using the material in the human body to synthesize large amounts of RNA (-) and RNA (+) which is identical to viral RNA, the newly synthesized RNA (-) will rely on the fragments of its entire chain to generate a variety of mRNA (+) which regenerates a new protein, so the new protein and the newly generated RNA (+) can jointly assemble a new virus, and the virus will be released to other human cells what are in the space surrounding the infected cell, thus the replication of virus genes and virus proliferation are completed.

2.1 Probability calculation of natural variation

The viral gene replication process described in this paper is a process that occurs in most cases, but it is generally believed that every RNA assembly process is affected by the physical and chemical environment in which the cell is located, incidents may occur. For example, a RNA (+) fragment which has the gene sequencing of UCUGGG, and its corresponding RNA (-) fragment AGACCC is likely to become UCACCC in an unstable replication process, in that case, when RNA (+) is regenerated, its gene sequencing will become AGUGGG. Such replication is virus mutation. Although the possibility of mutation is relatively low for a single virus, it is inevitable that mutation will occur with large number of viruses. Pradhan et al. sequenced the RNA fragment of the novel coronavirus and the original sequencing in the paper is TCTGGG [2]. As current sequencer cannot identify the U base in RNA, this article replaces T with U in order to avoid ambiguity and provide a more scientific description of RNA.

When a viral RNA mutates during its replication, a single base may mutate to other base or a group of bases, for example, the base of AGA may mutate to AAA, ACA, AUA or AxA, where $x=\{AGA, AA, \dots\}$, that is, x represents a string of bases. Therefore, assuming that m is the length of the base sequencing of RNA, the probability of a single base mutating to a certain fixed pattern is:

$$P_c(m)=1/(4^m)$$

Taking the RNA sequencing result of one of the COVID-19 virus samples as an example, its genome sequence is a single-stranded RNA with 29903bp, and the probability of obtaining a fixed single-base mutation result in natural mutation is $1/(2.5114277 \times 10^{18003})$, this

number has a value that is too large to be described by text, so it means that it is almost impossible to find this natural mutation virus in a fixed direction among so many mutated versions.

Fortunately for humans, most of the mutations produced by the virus during the replication process are invalid or meaningless, because in most cases the change of a single base won't change its protein synthesis, so viruses with variant RNA base follow the principle of natural selection, and their outcomes include: (1) natural extinction; (2) maintaining similar characteristics for transmission with the mutation; (3) carrying the mutation and producing new characteristics for transmission and gradually disappearing; (4) carrying the mutation and generating new characteristics and spread in a wide range, etc. The four kinds of situations are named as disabled viruses, weakly mutated viruses, degraded viruses, and evolved viruses. Among them, only the rarest case 4 will pose great threat to humans. In addition, scientists often use the principle of virus mutation to establish viral RNA genealogy, and determine the path and sequence of virus transmission according to different base mutation points.

2.2 Probability calculation of natural chimerism

In nature, chimerism between organisms is also an accidental phenomenon. This is a general term for one biological cell carrying the characteristics of another biological cell. For example, letting the offspring of a horse contain the characteristics of a donkey is the process of biological chimerism. The chimerism herein refers specifically to genetic chimerism between viral RNAs.

SARS-Cov virus and HIV-1 virus are both RNA viruses. When the two viruses simultaneously infect the same human cell, as in the virus replication and multiplication process described above, assembly errors may occur during RNA replication. This assembly error is a kind of natural variation, that is, the special case of AGA becoming AxA referred to in the example in section 2.1.

At the beginning of 2020, Indian scholar Prashant Pradhan (Kusuma School of biological sciences, Indian institute of technology) and others wrote an article called *Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag* [3] and claims that four embedding sites were found in the spike protein (S) of the COVID-19 virus, these embedding fragments are not found in other coronaviruses. What is important is that the amino acid residues in all the four embedding sites are

identical or similar to those in HIV1gp120 or HIV-1Gag. The authors of the article implicitly stated that someone used gene editing technology to edit the RNA of SARS-CoV, inserting four fragments of the HIV virus, creating the SARS-CoV-2 virus. The combined effect of these four fragments equipped the SARS-CoV-2 virus with stronger transmission capacity than SARS-CoV.

Subsequently, Chuan Xiao (Department of Chemistry and Biochemistry, The University of Texas at El Paso, El Paso, TX, USA), an overseas Chinese living in the United States and others wrote *HIV-1 did not contribute to the 2019-nCoV genome* [4]. In this article, it is believed that these four RNA fragments are not only exclusive to the HIV-1 virus, and researchers also discovered that these fragments are present in bat-infected coronaviruses in 2013. This proves that the conclusion presented by Indian scholars are inaccurate, so Prashant Pradhan retracted the paper.

This paper does not intend to take a stand in the dispute between the two parties, but the research process showed by the papers and the data can support the fact that compared with SARS-CoV, COVID-19 (also known as SARS-CoV-2) virus has four foreign embedded RNA fragments, although it is still uncertain whether the four fragments are directly derived from HIV-1 RNA virus, the probability of its natural occurrence can be calculated.

Suppose the event of embedding 4 RNA fragments is Q, the introduced RNA comes from an organism called OTH, and the probability of bats, humans, or camels suffering from SARS-CoV is $P(\text{SARS-CoV})$, and the probability of two viruses appear in the same cell is $P(\text{Cell})$, then:

$$P(Q) = P(\text{OTH}) * P(\text{SARS-CoV}) * P(\text{Cell}) * P_c(m)^4$$

In order to make the formula more visual, this paper uses data verification as in the method of thought experiment.

Thought experiment: Set the organism OTH as in the bat, that is, set $P(\text{OTH})=1$, use the method of limits to expand the data and assume that all bats carry this gene, expand the data and set $P(\text{SARS-CoV.bat})=1$ with the method of limits and assume that all bats carry the SARS-CoV virus, and it is also necessary to set two genes to exist in the same bat cell, that is, $P(\text{Cell})=1$, then $P(Q)=P_c(m)^4$. Based on the description in section 2.1, the value of the probability of natural mutation of the virus $P_c(m)$ is infinitely close to 0, so the value of $P_c(m)^4$ is also infinitely close to 0. Therefore, it is almost impossible

for a virus to complete its natural chimeric evolution to possess certain characteristic from the perspective of natural evolution.

2.3 Logical operations resulting from the nature

Logical operation is an important part of mathematical calculations. This paper introduces logical operations to analyze problems related to virus evolution.

Assuming that SARS-CoV evolved into COVID-19 is Event, then:

$$PB(\text{Event}) = PB(A) \wedge PB(B) \wedge PB(\text{Manmade})$$

A is a non-chimeric natural mutation, B is a natural chimera, and C is an artificial chimera, which means $(PB(A) \wedge PB(B))$ and $PB(\text{Manmade})$ are mutually exclusive events, $P(Q) \in P_c(m)$, then:

$$PB(\text{Event}) = P_c(m) + PB(\text{Manmade})$$

As the World Health Organization has confirmed the evolution of SARS-CoV to COVID-19, so $PB(\text{Event})=1$. In order to minimize the disputes, this paper enlarges the value of $PB(A)$ to 0.1%, as in the thought experiment described in section 2.2, $P(Q) = 0.000000000001$.

It can be learned that $PB(\text{Manmade}) = 0.998999999999$. This value shows that the probability of artificial chimeric virus is greater than 99.9%. This paper analyzes from the perspective of an impartial third party, and does not presume any conclusions. On this basis of objective analysis and various scientific research methods, conclusive and credible conclusions will be made. It is this kind of thinking that prompted the author of this article to further study and research in the field of genetic engineering and virology, and thus discuss this issue in the following sections from different aspects.

It can be seen that $PB(\text{Manmade}) = 0.998999999999$. This value shows that the probability of artificial chimeric virus is greater than 99.9%. This paper is delivered from the perspective of an impartial third party, and does not presuppose a conclusion. Reasonable and objective analysis based on various scientific research methods is applied, so as to make our conclusions conclusive and credible. On this issue, there is a paradox. From the perspective of biological evolution, the possibility of creating a genetically intelligent life is almost zero, but how to explain the natural existence of human beings? In fact, this is caused by the population base. Without the hard-to-calculate evolution of many types of microorganisms and primates in history, there would be no humans. Evolution here includes the population base at

different historical time nodes, and genetic variation on a time scale of hundreds of millions of years. So when only bats and a few animals in the world carry the coronavirus, the probability of its natural occurrence we calculated has scientific significance. However, when hundreds of millions of humans in the world have been infected by this virus, then the population size of the virus will be calculated according to the method of "number of patients * number of viruses per person * probability of mutation". Through this method, we can obviously conclude that the possibility of new variants of the virus is extremely high. It explains why there are so many COVID-19 mutant strains in various countries, the probability is still valid. According to the current epidemic prevention situation of all countries in the world, we feel that this virus and its various variants may accompany humans for a long period of time in the future. It is based on this kind of thinking that the author of this article further studies and researches in the field of genetic engineering and virology, and thus expands the discussion to the following sections.

2.4 Ralph S. Baric's research of artificial chimeric virus

As scientists continue to deepen their understanding of biological genetic genes, the replication and translation mechanisms of coronaviruses have gradually become clear. The cloning, transformation and chimerism of coronavirus genes through existing artificial technologies are already mature practice. But as this technology is exclusive to a few scientists and their research groups in the United States, it is rarely known to the world. After the outbreak of the novel coronavirus epidemic, the relevant research results of Professor Ralph S. Baric, who is called the "Father of Coronavirus", have been carefully studies. Professor Ralph S. Baric, born in the United States in 1954, is a microbiology expert and chief scientific researcher that studies coronavirus all around the world. He graduated from North Carolina State University in 1977, graduated from North Carolina State University in 1983 with master and doctoral degrees, and worked in the Microbiology and Neurology Laboratory of the Medical School in the University of Southern California from 1982 to 1986 as his postdoctoral research work. From March 1986 to June 1990, he was an assistant professor in the Department and Laboratory of Parasitology in the University of North Carolina at Chapel Hill, and an associate professor in the Department of Epidemiology in the University of North Carolina at Chapel Hill from July 1990 to June 1993. From

1993 to July 2001, he was an associate professor in the Department of Epidemiology in the University of North Carolina at Chapel Hill. From July 1993 to 2001, he was an associate professor in the Department of Microbiology and Immunology in the University of North Carolina at Chapel Hill. Since July 2002 until now, he has been a professor in the Department of Microbiology and Immunology in the University of North Carolina at Chapel Hill.

Professor Baric's achievements include, but are not limited to, being awarded the title of Outstanding Young Man of the United States in 1987, Established Investigator of the American Heart Association from 1989 to 1994, a member of the editorial board of the Journal of Virology in 2004, World Technology Finalist and Member in 2004, permanent member of Virology B Study Section, member of Biological Sciences Expert Group (BSEG), member of the internal advisory board of the Pacific Northwest Regional Center for Excellence since 2009, providing the National Academy of Sciences with the gene sequence methods for classification of select agents, and becoming a fellow of the National Academy of Microbiology in 2010, after the outbreak of COVID-19 in 2019, Baric was awarded the title of member of the National Academy of Sciences in 2021.

Professor Baric has devoted himself to the research, cloning, and genetic modification of coronaviruses for many years. At the same time, he pays attention to the cultivation of talents and teams. He has trained more than 45 senior researchers in the field of virus research, including: Allison Totura from the Molecular and Translational Science Division of the Medicine Institute of Infectious Diseases (focusing on the SARS virus) in Fort Detrick of US Army; Sheila Peel, senior researcher of the Retroviral Division of the U.S. Army Research Institute; Damon Deming of the U.S. Food and Drug Administration; Professor Matthew Friedman of the United States Department of Veterans Affairs; Patrick Harrington of the U.S. Food and Drug Administration; Lisa Hensley, senior scientist of the U.S. Army Medical Research Institute for Infectious Diseases; Dr. Eric Donaldson of the U.S. Food and Drug Administration and so on.

Professor Baric has published more than 400 papers in his own name or as an instructor since 1983. In June 1983, he published his first research about coronavirus, studying the structure and synthesis mechanism of the mRNA of mouse hepatitis virus [5]. In the following years, Professor Baric devoted himself to the molecular biology research of

coronavirus, including its RNA transcription, translation, protein synthesis, etc., and published dozens of high-quality papers as first authors. In December 1989, Baric disclosed for the first time the specific situation of viral gene recombination research in his laboratory, and described the impact of gene recombination on the virus. Since then, he started to do more in-depth research in the field of coronavirus RNA [6].

In his early research, after a breakthrough in genetic engineering in May 2000, his team developed a systematic method for assembling functional full-length genomes of large-scale RNA and DNA virus. This method makes it clear that the coronavirus is a virus containing the largest single-stranded positive-polarity RNA genome in nature, with a length of about 30,000 bp. The genome has an unstable region, which hinders the development of a full-length infectious cDNA structure. On this basis, his team cloned and recombined the coronavirus found in gastrointestinal tract of pigs, and realized the artificial modification of the coronavirus through the TGEV method [7]. This is the first time that Baric has proposed this method that can modify virus genes. On May 21, 2001, the team applied for a patent after further optimizing the method of virus cloning. The patent relates to the targeted assembly of large viral genomes, which can reconstruct viral RNA in vitro and re-introduce it into different hosts for continuous proliferation of the new virus, it is a huge breakthrough in human recombinant viruses. The entire experiment was conducted with coronavirus as the research object. The patent was granted in July 2003. In the following years, Baric has been committed to the genetic recombination and chimerism of various coronavirus RNAs [8]. On October 31, 2002, the team realized the synthesis technology based on heterologous RNA virus, so that the recombinant virus has the protein characteristics of different viruses. This technology was applied for a patent. So far, scientists have basically solved the problem of virus modification and gene reassembly, and can produce coronaviruses with different functions, transmission capabilities and new characteristics when needed [9].

In December 2002, the first SARS (SARS-Cov-1) patient was found in Guangdong Province, and the SARS epidemic broke out. A few months after that, the virus disappeared inexplicably. Most Chinese scientists believed that the outbreak of the SARS virus might be related to the Guangdong people's habit of eating paguma larvata, and some Chinese scientists believed that this virus was the

product of American laboratories [10].

In terms of RNA virus chimeric experiment, in August 2006, Baric's team used genetic recombination method to cultivate many progeny SARS viruses, and discovered a mutation that "successfully caused rapid death of mice" in the 15th generation. This new type can infect human and cause pneumonia with comparatively high mortality. This is also the earliest source of the "MA15" chimeric gene, which was in a bitter dispute in the society in 2020 [11]. In December 2006, his team discovered that nsp10 is a key regulator of coronavirus RNA synthesis and may play an important role in multiple protein processing, and zinc ions may inhibit virus replication [12], this is also the earliest source of the Trump administration's emphasis on zinc ion therapy after the COVID-19 epidemic.

In terms of virus modification of bats, in August 2008, in order to prove that "a coronavirus carried by bats can spread to humans across species", the team carried out genetic recombination of the original virus, combining the RNA fragments of SARS-Cov virus with SCoV virus RNA, and a new type of coronavirus RNA modification project was completed, allowing the virus to spread through the human ACE2 protein, and proved that "virus with edited gene can achieve cross-species transmission." In addition, the experimenters also reconstructed the influenza virus that prevailed in 1918 [13]. In June 2009, his team modified a new SARS-CoV strain (v2163), determined the relationship between the expression of special proteins in the organism and the lethality of the virus, and made it clear that the high expression of IL-6 is related to the high mortality [14]. In April 2012, his team genetically modified the coronavirus isolated from Chinese horseshoe bats in 2005 and proved that while SARS-CoV, mouse-adapted SARS-CoV (MA15), and chimeric SARS-CoVs bearing the spike genes of early human strains replicated inefficiently, HCoV-NL63 replicated for multiple passages in the immortalized lung cells from this bat species [15], which also shows that the human coronavirus can establish a reverse zoonotic transmission cycle of zoonotic diseases, the transmission cycle allows certain coronaviruses to easily circulate and exchange genetic material between bats and other mammalian strains, including humans. This conclusion is made on the basis of artificial modification conducted by the Baric team. This kind of large-scale gene collection and modification around the world is likely to cause the leak of new artificial coronaviruses and spread them to laboratory personnel and the people around the

laboratory.

The chimeric virus was initially successful. In December 2012, his team confirmed that the change of synonymous codons brought by genetic modification and targeted breeding technology affects the structure and efficiency of the frameshift signal. The slight difference in frameshift efficiency leads to significant differences in RNA production and TCID₅₀, which further indicates that the frameshift frequency must be maintained above a certain threshold to obtain the best virus production. At this time, Baric team has been able to change the production efficiency and viability of the virus through genetic technology [16]. In June 2014, they further studied the transmission mechanism of the novel coronavirus through chimeric viruses, and conducted experiments using SARS-CoV-MA15 and MERS-CoV [17]. Conditions must be created to justify the concerns about the new chimeric viruses. In June 2015, Baric's team used the SARS-CoV reverse genetics system to generate and characterize a chimeric virus that expresses the spike of bat coronavirus SHC014 in the backbone of mouse-adapted SARS-CoV. The results show that the 2b virus encoding the SHC014 spike in the wild-type backbone can effectively use multiple homologues of human angiotensin converting enzyme II (ACE2) which is a SARS receptor, effectively replicate in primary human airway cells, and titer equivalent to the SARS-CoV epidemic strain was obtained in vitro. Baric also produced an infectious full-length SHC014 recombinant virus in the laboratory at the University of North Carolina, and it has demonstrated robust virus replication in vitro and in vivo. This is a research led by Baric team. The authors include 13 American scientists and 2 Chinese scientists. The main contribution of Chinese scientists is the preparation of experimental specimens [18].

In terms about infection experiment and drug development, in September 2015, his team conducted a chimeric experiment on the spike protein of WIV1 and wild SARS-Cov, according to the RNA sequence study, the WIV1 coronavirus (CoV) cluster has limited ability to infect humans directly, additional adaptation is required if the virus is kept active in human body and continue its spreading [19]. The RNA sequence of the artificial chimeric virus in this experiment has not been found by the author of this paper, so there is a possibility that the team created the existing COVID-19 virus in this experiment. In November 2016, based on the long-time development of

molecular biology and the completion of the human genome map, the team believed that a human model infected by the virus can be established, so as to know the specific process and principle about why and how human DNA produces antibodies to a virus [20], which helps to further understand the relationship between virus proteins and human genes, and observe the procedure of RNA viruses replication in the human body and how immunity and anti-virus protection procedures are stimulated, the induction process can even be used as a basis to evaluate the immune response of different races to the virus. In June 2017, his team believed that the coronavirus (cov) has a tendency to spread rapidly to new hosts and can cause serious diseases. Based on the successive emergence of SARS-CoV and MERS-CoV, the experimenters conducted in vivo experiments on three strains of SARS-CoV- (HKU3, WIV1, SHC014), which proved the preventive property and early administration of GS-5734 significantly reduced the pulmonary viral load and improved the clinical symptoms and respiratory function of the disease [21]. It is worth noting that the drug coded GS-5734 is Remdesivir produced by Gilead.

As for the future-oriented research, on October 13, 2017 and September 28, 2018, his team applied for a patent for artificial modification of dengue virus, which can be used to introduce protein production genes of different viruses into dengue virus [22], this method can give dengue virus transmission characteristics of other viruses, such as COVID-19-like infection and transmission mechanism. In December 2018, his team used animal samples from the Catoctin Wildlife Sanctuary and Zoo in Thurmont, Maryland to conduct an artificial infection study of the severe acute respiratory syndrome (SARS)-like WIV1-coronavirus (CoV), which uses human blood vessels angiotensin converting enzyme 2 (ACE2) as the receptor and proves that this virus has a limited ability to infect animals [23]. In October 2019, his team published research results and claimed that the coronavirus carried by bats can infect humans without additional adaptation, but there are some additional barriers that limit the emergence of zoonotic coronaviruses. Through molecular biology research, the team successfully broke through the infection limit, proving that the zoonotic coronavirus can spread rapidly in human community after transformation [24]. The team artificially bred chimeric viruses and BATCoV (WIV1-CoV, WIV16-CoV, SHC014-CoV) viruses in the experiment. The paper was submitted on October 16, 2019.

According to the review speed of the journal, the research is supposed to have started around April 2019. Since the complete RNA of the artificial chimeric virus was not published in the paper, we cannot be sure whether this experiment leaked the COVID-19 virus. In addition, the content of the Baric team's paper is almost always from the standpoint of the virus, which makes readers feel a little uncomfortable. It seems that the virus is the relatives of the team, and it is their mission to help the virus invade the human body. Thereafter, at the end of the following 2019, Chinese scientists formally detected the outbreak of a new type of coronavirus (COVID-19 or SARS-Cov-2).

Professor Baric and his team have been committed to the research of coronaviruses for nearly 40 years, and have a large number of research results and intellectual property rights. The multiple virus chimeric transformation methods invented can be used for virus research and development, as well as producing viruses for experiments. Take the patents numbered US007618802B2 and WO 2005/035712 A2 as examples, in the lists of co-inventors, personnel of Fort Detrick, Maryland can be seen on both of them. This approach is more conducive to the covert sharing of patents and makes staff of Fort Detrick Laboratory free from patent royalties in future virus preparations.

In October 2014, the Obama administration believed that Baric Laboratory's use of SARS, MERS, and influenza viruses for gain of function transformation research posed a potential threat to public health. Through the White House Office of Science and Technology Policy and the US Health and Public Service Ministry, a ban was issued, announcing the suspension of funding to similar researches, and requiring researchers in related fields to immediately stop related research until the risks and benefits are approved by the National Science Advisory Board for Biosecurity (NSABB) and the National Research Council (NRC). Afterwards, Professor Baric's team was obviously more cautious when publish their papers, but the team just stopped accepting support, the research project and virus chimeric work were not stopped because of the order.

In summary, the chimeric virus method was invented by Professor Baric, his team has the most authoritative interpretation power and the strongest chimeric virus ability among all the scientists. As some of the patents are world patents, if scientists from other countries need to use the patent in their research, they have to apply for the right to use and pay patent royalty. But no matter from the perspective of scientific research safety or scientific

research ethics, the development of chimeric viruses and viral infection research on this basis should be opposed and resisted.

2.5 Shi Zhengli's virus research

If you search the internet and social media for COVID-19 virus, you will find that beneath Trump's nonsense, there are now many voices questioning Shi Zhengli. In fact, according to the investigation conducted by the author, China's scientific research capability in the field of molecular biology is still very rudimentary compared with the mature scientific research system in the United States, and virus chimerism is a relatively complex process, and the professional technology and professional software used in the process are exclusive to Baric's team. In addition, the auxiliary software, gene comparison equipment, and big data platform that are helpful to the chimeric technology are also exclusive to the United States. Anyone who uses it requires authorization and leaves traces of use. Therefore, if there are virus products of chimera that are not authorized by the United States in the world, the chimeric process must take place in the United States, including Professor Baric's laboratory and Fort Detrick Laboratory, the latter has the same patent use rights and has former students of Professor Baric.

In a widely circulated paper published by Shi Zhengli and her colleagues, Shi Zhengli is only the second corresponding author of this paper. In fact, this is a study led by the Baric team. There are 13 American scientists and 2 Chinese scientists among the authors, and it is clearly stated at the end of the paper that the main contribution of Chinese scientists is the preparation of experimental specimens [25]. In this study, the specimen collection work in China was mainly done by Shi Zhengli's student Xing-Yi Ge. He used Shi Zhengli's research funding and later resigned to teach at Hunan University in 2016. He is now a doctoral supervisor in the School of Bioengineering.

In fact, according to Chinese law, no one can take biological samples of unclear safety out of the country. It is even more impossible for a foreign scientist to go deep into the forests of southern China to collect and investigate biological samples. If Professor Baric's team hope to obtain the SHC014CoV virus from bats and conduct gain-of-function chimeric gene virus research in the North Carolina laboratory, they must rely on the collection work of Xing-Yi Ge and Shi Zhengli, and both of them are undoubtedly unaware of the subsequent experiments, all

they can get is some humble research funding. Things like this are very common in Middle East, Central Asia, Africa, South America and other regions. Baric and others can rely on the outpost laboratories of biological weapons of the US military bases or be advertised as a reason for international scientific cooperation to carry out large-scale natural virus collection and transformation.

2.6 WHO investigation results

The World Health Organization conducted an investigation on the origin of the virus in Wuhan, China from January 14, 2021 to February 10, 2021, and released a complete investigation report on March 30, 2021. Through extensive and rigorous investigations, the report has reached three conclusions on the source of the virus. It is very likely that the novel coronavirus that has been circulating in Wuhan comes from zoonotic diseases, it is possible that the virus comes from frozen seafood, and it highly unlikely that the virus comes from laboratories [26].

According to the results of this investigation, we can determine that in Wuhan, China, frozen seafood in the seafood market, including frozen fish and shrimp imported from other countries, have the same virus carrying potential as mink, pangolin, bat and other animals. It is not yet certain that through which channel that the virus was introduced to Wuhan, and several transmissions by the outer packaging of frozen seafood products occurred in 2020 are similar to the case of South China Seafood Market in Wuhan, for example, the imported seafood in Dalian of Liaoning Province, Yantai of Shandong Province, Pingxiang of Jiangxi Province, Xiamen of Fujian Province, Yunnan Province, Chongqing and other places have all detected positive for the virus [27]. The products have been strictly tested and timely destroyed, thus the virus did not

spread on a large scale like the case of Wuhan. It can be seen that this is very possibility that the virus outbreak in the South China Seafood Market in Wuhan was introduced to China from imported seafood frozen food.

Another important result of this investigation is that it completely ruled out the possibility of virus leak from Wuhan Institute of Virology, Chinese Academy of Sciences. However, it is worth noting that all investigations were carried out in Wuhan, so the conclusion that “it is extremely unlikely that the virus is from laboratories” only rules out the laboratories in Wuhan, not the laboratories in the United States or Europe. Therefore, in the paper published by Professor Baric and others in scientific journals in March 2021, the attempt to use the World Health Organization report to convince the public that the COVID-19 virus does not come from their laboratory is extremely unpersuasive, the report can only prove that Chinese laboratories are innocent, and such report cannot be used to prove that American laboratories are innocent.

2.7 Tables and mathematical calculations

The production and spread of viruses are two different events. Natural viruses may be artificially transmitted, and artificially manufactured viruses may also be transmitted by natural hosts or frozen food. Therefore, the zoonotic source of the virus and the source of frozen seafood as determined by the investigation report published by the World Health Organization can only explain the later transmission process of the virus, and these processes have nothing to do with the origin of the virus. The original source of related viruses can only be determined between natural and artificial origin, and artificial origin here is equivalent to laboratory origin.

Table 1. probabilities of different source of COVID-19

Type	Source	Code	Probability	Evidence
Natural source	Natural evolution	A	Less than 0.1%	Possibility of RNA natural evolution
	Natural chimerism	B		Probability of virus natural chimerism
Laboratory source (Artificial source)	Chinese laboratories	D	0%	World Health Organization report
	U.S. laboratories	E	Greater than 99.9%	Undisclosed and uninvestigated
	Laboratories of other countries	F		

Note: The code of "laboratory source" is C

Based on the calculation result:

$$PB(\text{Manmade})=0.9899999999$$

And $PB(\text{Manmade})=PB(D)+PB(E)+PB(F)$ According to the WHO conclusion, $PB(D)=0$, then $PB(\text{Manmade})=$

$PB(E)+PB(F)$, that is, the possibility of the virus leaking in the laboratory of the University of North Carolina, or the Fort Detrick laboratory, or other national laboratories outside of China is about 99.9%, this conclusion is based

on fine mathematical calculations and facts.

3. Results and discussion

3.1 Relationship analysis and reasoning

Biological and chemical technology is one of the foundations for the rapid development of the United States in contemporary times. After the Second World War, the domestic political and economic environment in the United States was stable, which has attracted a large number of technical talents for the country. On the basis of fully absorbing and integrating the biotechnological achievements of European countries, former Soviet Union, and the experimental results of the Japanese (formerly) Unit 731, biological science research of the United States has made considerable progress.

The development of biotechnology in the United States is the result of the hard work of scientific practitioners, and it is also the result of the joint promotion of capital and policies. From the perspective of development, the U.S. biotechnology is open to global cooperation on the basis of strictly retaining the core technology on its land. Open cooperation around the world is also one of its characteristics. Therefore, the current situation in the development of biotechnology in the United States is: policies promote capital, capital invests in enterprises, and enterprises conduct biotechnology research and development with universities. R&D experiments and core processes are carried out in domestic laboratories in the United States, products are developed, produced and

delivered to overseas military bases stationed in various countries through cooperation between enterprises and governments (or the military). These bases have both military functions and are account for the test of new drugs (or to test the virus manufactured to verify the new drug), the residents around the bases may participate in the relevant experiment with or without notification. When both the internal experiment and the external experiment have been completed and the design goal is reached, the relevant product will be finalized. If an unexpected problem occurs during the experiment, the product will be returned to the laboratory for reassessment and improvement.

Professor Baric has been in this field of research for nearly 40 years, in line with the development of biotechnology in the United States. He has written more than a hundred of papers and books. This paper focuses on the analysis of the papers and patents of his team, including the main researchers in various scientific research projects and their working institution, as well as the joint owners of the patents. At the same time, this paper is not limited to using the literature method to analyze the relationship of the papers, but also conducts a sufficient research on social news, stock market transactions and urban economic structure through investigation methods.

After investigating without presupposing any positions and opinions, the author of this article has drawn a graph of the main relationships of this event (as shown in Figure 2.).

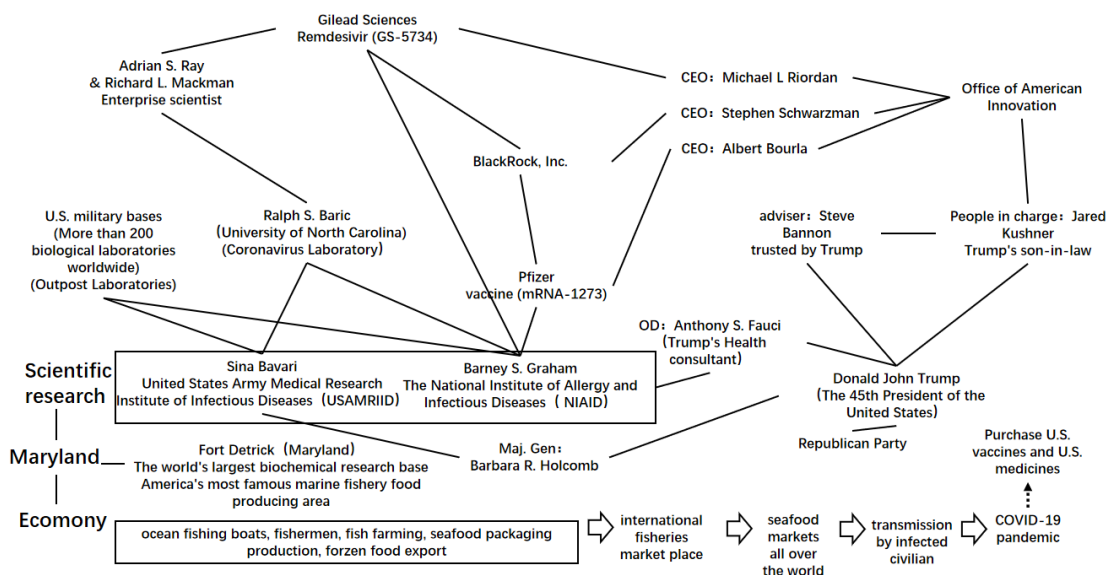


Figure 2. COVID-19 related people and organizations

Description:

(1) The patents related to viral RNA modification and chimeric virus development applied by Professor Baric are co-invented with the staff of Fort Detrick. The U.S. military can use the patent without authorization to transform and develop viruses [28];

(2) Many of Professor Baric's senior postgraduates work in U.S. Army research institutes, and various U.S. military research departments also provided support for a number of Professor Baric's research projects. Therefore, it was identified that the two parties are in close cooperation;

(3) Baric has cooperated with Adrian S. Ray, Richard L. Mackman and others to identify the therapeutic effects of GS-5734 drugs on various viruses for many years. At the same time, Gilead Sciences has provided Baric with funds that lasted for many years and covers multiple subjects;

(4) Baric was introduced by Barney S. Graham to identify the efficacy of Mrna-1273 vaccine;

(5) The declassified documents released by U.S. government show that U.S. military bases stationed overseas have cooperated with multi-drug testing, sample collection, and virus collection of the country;

(6) The stock transaction data shows that BlackRock Investment Company has invested in Gilead Sciences and Pfizer, and the actual controllers of the three companies are all contacts of the Office of American Innovation;

(7) The purpose of the Office of American Innovation is to "make recommendations to the President on policies and plans to improve government operations and services, improve the quality of life of Americans and create job opportunities now and in the future." The office is run by Jared. Kushner (Trump's son-in-law), he is a senior adviser to President Trump;

(8) Steve Bannon is Trump's special adviser, his office is next to Jared Kushner's, and they are colleagues and close friends;

(9) Anthony S. Fauci was Trump's national health adviser. He is the direct leader of Barney S. Graham and the director of the National Institute of Allergy and Infectious Diseases (NIAID);

(10) Trump led the United States Army Medical Research Institute of Infectious Diseases (USAMRIID) through Major General Barbara R. Holcomb (female). Sina Bavari is a senior researcher at the institute and a senior co-author of several papers with Baric;

(11) The Fort Detrick Institute of Biological Weapons is located in Maryland, USA. Maryland is the state with the

least proportion of the poor population in the United States and the largest proportion of wealthy population. The state has more than 400 biological technology and supporting enterprises. Another major source of income in the state is freshwater fish farming and deep-sea fishing. The residents of Maryland, as operators of ocean-going fishing boats, can directly pack and quick-freeze the fish caught on board and trade them on the high seas for export. The fishery companies in Maryland export to Canada, China, India, Mexico, Europe and other places.

To sum up, after analyzing and displaying the relationship of the various figures shown in this section, it can be clearly found that during the outbreak of the novel coronavirus (COVID-19), the 45th President of the United States (Donald John Trump) has sufficient control of microbiological research, virus research, and drug research in the United States. At the same time, there are many channels to learn the harm of the viruses. This paper maintains an objective, scientific, and rigorous position on the cause of the COVID-19 pandemic, it does not presuppose a conclusion. However, when the relationship diagram is established, it will undoubtedly make all the public, including the author of this article, question the original intention of Trump, during his presidency, why he called for the public not to wear masks and maintain intensive gatherings.

3.2 Potential security risks

Scientific research is accompanied by risks, and the risks may come from many aspects, such as economic risk for experimental failure, safety risk for laboratory accidents, social risk for the release of experimental results, policy risk of experimental process, etc. Therefore, both scientific research in biological science industry and computer industry must strictly abide by the corresponding industry rules, regulations and ethics. The success of an experiment does not mean that the subsequent experiments will always succeed. Once the experimenter fails to follow the relevant rules, the possible disasters are likely to be devastating, and far beyond what the experimenter can afford.

In the process of studying the daily scientific research of Baric, we found that there are many security risks in his laboratory, which will be analyzed in this section and suggestions will be made accordingly.

Experiments on microbiology, especially virus research experiments, are extremely dangerous experimental processes. In the process of studying Baric

team's research results, the author discovered that the team did not strictly implement the experimental safety rules. In a widely circulated photo, Professor Baric's office is messy. The kits used in experiments are randomly placed on the desk, the experimental supplies marked as red biological

pollutants are directly exposed to the air, and the chemical reagents are randomly placed without caps and express deliveries are piled on the office floor. All of these behaviors obviously violated the safety regulations of biological laboratories.



Figure 3. professor Baric's working environment

During the time this article was written, the basic properties of SARS-Cov-2 (COVID-19) are well known. The transmission capacity of this coronavirus is extremely strong. It can be spread by contact, droplets, or even by aerosol.

However, before the large-scale outbreak of the virus, no one had evaluated the spread capacity of the virus. If Baric's team actively or accidentally generated the first virus template through virus chimeric experiment, it would be a high probability event that the laboratory personnel get infected. It is a reasonable result that laboratory personnel can spread the virus to family members and passers-by after getting off work.

Scientific researchers and scientific teams should have their own professional ethics. They should never provide scientific research results to terrorist forces, nor provide dangerous technologies to the military and violent machines, because such behavior is inhumane and violates the U.N. international spirit and international consensus related to the prohibition of biological weapons and chemical weapons research and development.

Professor Baric's team has not only received long-term support from the U.S. military to provide research services for Fort Detrick Military Biological Weapons Research Base, and even shared the patented

technology developed by its own laboratory with the U.S. military. This behavior will make the latest scientific research results of the scientific community into war machines, and the war machines can conduct biological weapons research through the technology and personnel obtained in the process, which can lead to a humanitarian crisis. Knowing for long that the U.S. military has biological weapons research and development program, Professor Baric not only failed to strictly observe scientific ethics, but also provided the virus chimeric method that was originally applied to benefit mankind to the U.S. military biological weapons laboratory. What a shame for the scientific field of the world.

3.3 Conducting research in violation of government order

On October 17, 2014, the Obama administration issued a notice with the U.S. Department of Health and Human Services: "U.S. Government Gain-of-Function Deliberative Process and Research Funding Pause on Selected Gain-of-Function Research Involving Influenza, MERS, and SARS Viruses", the experiment being conducted by Professor Baric's team fell within the scope of the 18 dangerous experiments.

The US Health and Human Services defines the

experimental nature of GOF as “Gain-of-Function”, which refers to any modification of biological agents that confers new or enhanced capacity. Typically, researchers mutate or change genes and examine the effects of these modifications on specific attributes or characteristics of organisms. For example, some researchers can modify influenza viruses by enhancing its pathogenicity and/or transmissibility in order to better understand the origin and nature of these traits and their pathogenesis in susceptible hosts at the molecular level. As influenza viruses continue to evolve in nature, these GOF studies may help predict whether these viruses can naturally evolve over time to obtain these new or enhanced characteristics, and if so, how the viruses may affect the hosts and the possible medical countermeasures. Some GOF studies may involve biosafety and biosecurity risks, requiring unique risk assessment and mitigation measures.

According to this definition, combined with the research content of Professor Baric's team described in section 3 of this paper, it can be seen that Baric's research fell within the scope of the suspended funds. This funding suspension measure is to suspend scientific research activities in this direction, and Baric didn't take it into consideration nor stop its research activities, but continued to conduct chimeric experiments and published many papers.

In addition, according to a ABC news report, this type of experiment has been banned by the order [29], the author of this paper did not find the original text of the White House order in the process of retrieving the content, and some pieces of news have obvious signs of being deleted. If the facts are as stated in the news, Baric's research behavior has violated the law.

3.4 Reasonable inference

Based on the security risks mentioned earlier, combined with the basic characteristics of the SARS-Cov-2 virus, it is possible to reasonably infer its subsequent impact and the occurrence of incidents. However, the Baric's team could not predict all of the possibilities in advance, some of the security risks are unavoidable:

(1) The purpose of Baric team's was to try the effect of HIV vaccine on SARS-Cov, and the two viruses were contaminated, accidental chimerism occurred in their laboratory environment. In 2015, HIV vaccine was used by Baric's team to test the vaccine's protective effect against MERS-COV chimeric viruses [30]. The chimeric virus

surpassed the cognition of the experimenter and infected the laboratory operator first. The operator left the laboratory without showing symptoms, and transmitted the virus to people outside the laboratory;

(2) In the process of applying Baric's chimeric virus patent method, the American researchers in Fort Detrick, who were not systematically trained, carried out the RNA chimeric experiment of HIV and SARS-Cov type coronavirus, and the transmission capacity of the chimeric virus surpassed the cognition of the experimental staff, and firstly infected the laboratory operator. The operator left the laboratory without showing symptoms, and transmitted the virus to the people outside the laboratory;

(3) In the process of applying the patented method of Baric's chimeric virus, the researchers of Fort Detrick laboratory carried out the RNA chimeric experiment of HIV and SARS-Cov type coronavirus. The experiment was extremely successful. The researchers used the laboratory water to clean the experimental vessels, and the virus entered the wastewater treatment system. It happened that the wastewater treatment system failed. The virus escaped in the water and spread to nearby residents;

Fact A: On July 12, 2019, ABC reported that a deadly respiratory disease broke out in Greenspring, a retiree community in Virginia. 54 people developed fever, cough and weakness, and 2 died.

Fact B: In July 2019, the US Centers for Disease Control (CDC) issued a letter to stop and terminate the operation of Fort Detrick Laboratory of the US Army Institute of Infectious Diseases. The reason was that the leakage accident was caused by the failure of the wastewater treatment system. At this time, research on antibody-based therapies against four deadly viruses has been ongoing for many years. This plan is just one of the many ongoing projects led by scientists of United States Army Medical Research Institute of Infectious Diseases (USAMRIID).

(4) The emergence of community transmission has caused more and more Maryland residents to be infected with the virus. Doctors in general hospitals have begun to come into contact with the cases. Some professional medical practitioners believe that it was a common coronavirus influenza (such as HCoV-HKU1 virus). However, according to clinical experience, HCoV-HKU1 is very unlikely to cause severe lung infections, so the disease was attributed to the patient's e-cigarette smoking, and the pneumonia was called "e-cigarette pneumonia." At this

time, all the departments that can determine whether the coronavirus is SARS-Cov virus or HCoV-HKU1 virus are related parties of the leak (see Figure 2);

Fact C: From July to August 2019, some American military athletes was trained in Maryland. These people would participate in the 7th Military World Games in Wuhan, China from October 18th to 27th, 2019.

Fact D: Authoritative medical expert Aleksandr Kalininskiy and others published a paper called *E-cigarette*,

or vaping, product use associated lung injury (EVALI): case series and diagnostic approach [31], which determined the diagnosis process of e-cigarette pneumonia and common cold. Since then, various hospitals started to follow this process. However, this process lacks the RNA detection for the virus, and patients with the novel coronavirus will be diagnosed as e-cigarette pneumonia in this process.

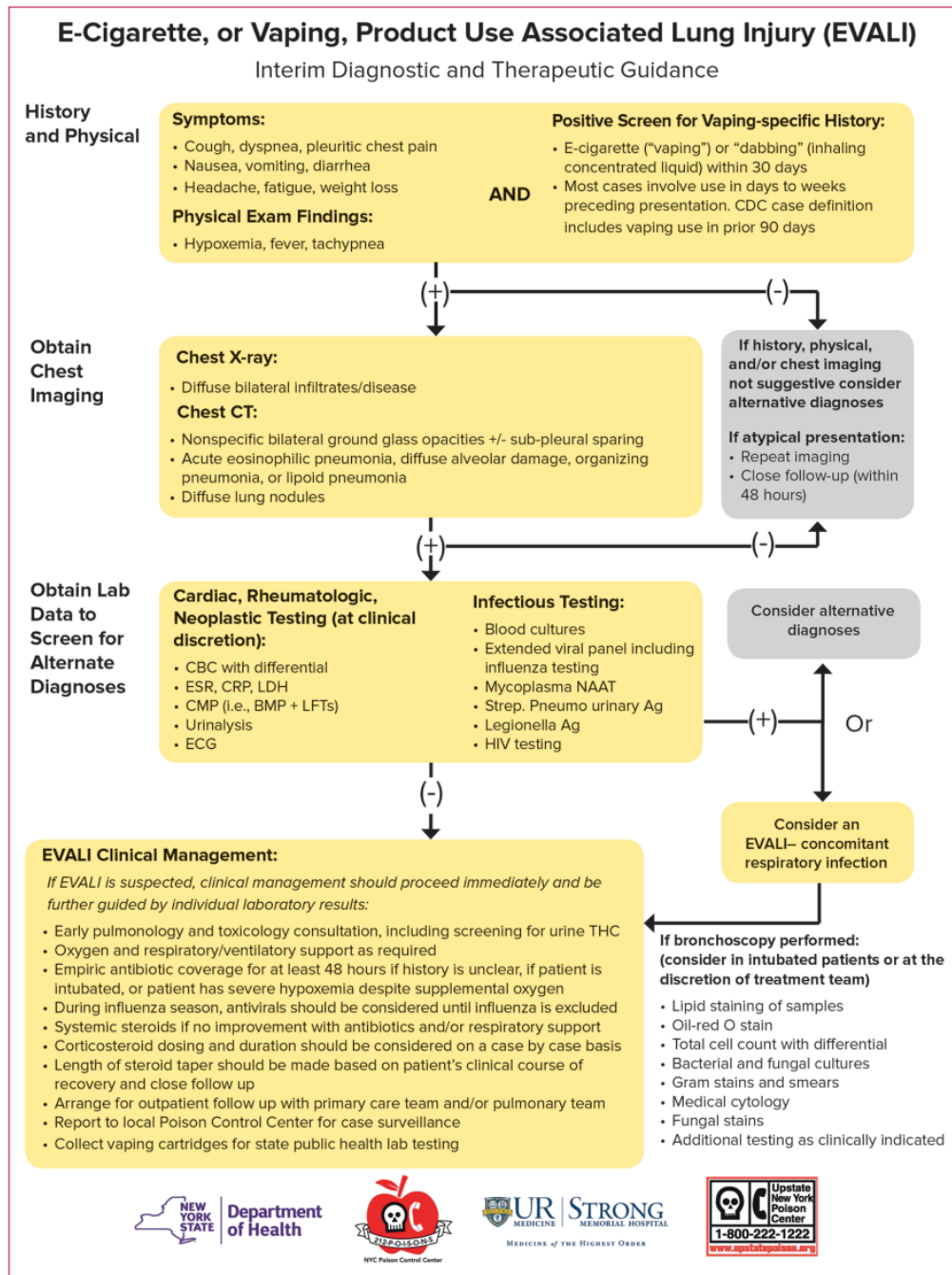


Figure 4: Clinical algorithm for the workup of e-cigarette, or vaping, product use associated lung injury (EVALI)
Reproduced with permission from New York State Department of Health and the University of Rochester Medical Center © 2019.

Figure 4. The diagnosis process of e-cigarette pneumonia implemented by U.S. hospitals

(5) When evaluating the impact of the virus leak, scientists found that there was no model could be used for reference, so they called on more scientists from all over

the world to evaluate the impact and come up with countermeasures. The military organization believes that the scientists' proposal is unfounded and worrying.

Although they reluctantly agreed to organize a meeting, they did not agree to disclose the specific details of the leak, so the meeting was only conducted in the form of sand table deduction;

Fact E: On October 18, 2019, multiple agencies in the United States organized a global pandemic exercise code-named "Event 201". The model in the exercise assumed that a coronavirus called CAPS is more deadly than SARS and spreads easily like a cold, but no vaccine had been developed. It could spread quickly and contributed to a global pandemic. Military personnel and senior CIA officials participated in the exercise, countries with experience in epidemic prevention and control were also invited.

(6) The epidemic in Maryland has further spread, and the movement of people and international exchanges have never stopped. While the virus continues to spread in Maryland, it has also been brought to all states in the United States and around the world. The novel coronavirus has an incubation period of 2-14 days. After the incubation period, it attacks. Different races have different proportion of ACE2 protein expression in the lungs, resulting in a serious illness rate of 5%-16% of each race, and the mortality rate is between 0.1%-2%. Therefore, in the time when the virus has not clearly confirmed as SARS-Cov-2, all patients were treated according to the treatment plan for severe cold, and patients who develop pneumonia were diagnosed as "e-cigarette pneumonia."

Fact F: The Military World Games was held in Wuhan from October 18th to 27th, 2019.

Fact G: American medical experts believed that "e-cigarette pneumonia" is contagious.

Fact H: On December 27, 2019, Zhang Jixian from the Hubei Provincial Hospital of Integrated Traditional Chinese and Western Medicine reported to the hospital the continuous admission of several unidentified pneumonia patients, and the hospital immediately reported it to the Jiangnan District Center for Disease Control. On the evening of December 30, 2019, the National Health Commission of China learned of the occurrence of "unidentified pneumonia" in Wuhan, and the pathological analysis and sequencing of the virus began. On January 9, 2020, China identified the novel coronavirus as the main pathogen causing the unidentified pneumonia and informed the WHO, and also shared with the international community. On January 11, 2020, China shared the virus gene sequence with WHO and uploaded the gene sequence

to the global influenza database. Countries around the world can produce diagnostic reagents based on this sequence.

Fact I: Italian media reported in March 2020 that the epidemic may have been spread to Italy in November 2019. In addition, Italian researchers said that in the last quarter of 2019, the number of severe pneumonia and flu cases in Lombardy was higher than usual. This may indicate that the novel coronavirus was spread in Italy earlier than in China.

Fact J: On May 7, 2020, the Albert Schweitzer Hospital in France issued a press release. The hospital conducted a retrospective study of 2456 CT images from November 1 to April 1, 2019, and found that a case of November 16, 2019 was diagnosed as the novel coronavirus patient.

Fact K: Michael Melham, the Mayor of Belleville, New Jersey, United States, stated that he was infected with COVID-19 pneumonia on November 21, 2019.

Fact L: After governments around the world began to pay attention to the epidemic prevention work, there have been multiple news reports that the novel coronavirus was imported from frozen seafood.

(7) After being notified by Chinese scientists and the World Health Organization, the Trump administration still maintained a negative attitude towards epidemic prevention. They neither controlled the movement of people nor promoted national testing, and allowed the virus to wantonly spread in the crowd, and eventually the American people were dragged into the disaster of the pandemic.

3.5 Summary

A scientific attitude is the foundation of scientific development. It includes both meticulous and rigorous scientific hypothesis and scientific verification process, as well as a scientific attitude towards work and life. A scientific research should be considered as comprehensive as possible, blindly pursuit for quick success may bring catastrophic consequences. This is especially true in the field of biology and microbiology. Little carelessness will have a catastrophic impact on human society. Observed from the current international epidemic situation, the novel coronavirus is likely to accompany mankind for a long time. I hope that Baric team and related teams working in Fort Detrick can abide by the bottom line of scientific research and strictly prevent safety risks, don't create new uncontrollable leaks.

4. Conclusion

This paper conducts the traceability analysis of the novel coronavirus with a scientific and rigorous attitude and without presupposing positions. The author first started from the natural mutation and natural sources of the virus, set up an RNA virus model, and calculated the probability based on this model, and concluded that the natural origin of the new coronavirus is close to 0%, and the probability of artificial chimeric virus is greater than 99.9%.

On the basis of this conclusion, the author further studied the frontier areas of molecular biology in the United States and the frontier areas of virology in microbiology. Taking the scientific research results of Professor Ralph S. Baric as a starting point, the author have downloaded and read more than 400 papers of the professor published during last nearly 40 years (from 1983 to the present), it is concluded that except for the United States, no countries have the capacity of virus chimerism.

Furthermore, through the analysis of Professor Baric's papers and the collection of reliable news, this paper has completed the investigation of the background and social relationships of all related parties, and constructed a relationship map centered by the 45th U.S. President Donald John Trump. Under the guidance of this map, the

author has reasonable doubts about the original intention and purpose of President Trump's passive epidemic prevention policies, including organizing gatherings, obstructing testing, and calling for no masks.

Furthermore, through the sorting and observation of multi-party materials, this paper discovered some of the violations of Professor Baric's team, and predicted and assessed the possible risks of these violations. In order to illustrate the actual possibility of these risks, this paper also introduces actual events as risky events to proof the correctness of this paper.

Science is a double-edged sword. When scientists wield this sword, they must be clear in our minds that they may bring happiness to mankind, or disasters. Professor Baric is one of the scientists that I admire. He devoted his entire life to the research of virus science. His original intention is probably to provide solutions for diseases that humans may encounter in the future, but his anxiety for success or theft conducted by military forces has eventually led to the disasters all over the world. This is a sad thing. His reputation was ruined. I hope that scientists in all industries take it as a warning, earnestly and strictly implement scientific experiment norms, abide by the moral bottom line, and treat every detail of their work with awe.

Appendix

Appendix A, Professor Baric's papers and research projects supported by Fort Detrick's Biological Weapons Laboratory and other departments of the US military, see: https://yunpan.360.cn/surl_yStpFeWgh7i (Extraction code: 38ce)

Appendix B, pdf files of reference papers, see: https://yunpan.360.cn/surl_yStpbyIfdTh (extraction code: 6445)

Appendix C, Presents of US which about GOF, see: <https://www.kuoso.com/zhuanli/>

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