NIH lifts suspension of EcoHealth Alliance and reinstates grant to study bat coronaviruses in China

Part two

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This is the second part of a two-part article. Read part one here.

One of the key issues that has been raised in the right-wing attack on EcoHealth Alliance (EHA) is the laboratory work conducted by EHA in collaboration with the Wuhan Institute of Virology in 2017-2018 with bat coronaviruses. None of this work by either organization, contrary to the conspiracy theories about "gain of function" research, involved making coronaviruses more likely to infect human beings or more dangerous to their health.

On the contrary, this work, with viruses known not to cause disease in humans, has in fact provided considerable data that proved valuable when the viciously infective and lethal SARS-CoV-2 emerged in mid-November 2019. In short, they clearly understood the threat they were working diligently trying to prevent.

Dr. Peter Hotez, molecular virologist and dean of the National School of Tropical Medicine at Baylor University, told *Los Angeles Times* columnist Michael Hiltzik, "People don't understand the importance of the hard work EHA is doing and how unique and critically important it is. There are not many groups doing the granular grunt work needed to understand how these viruses emerge and transfer to humans."

The study of the mechanism of zoonotic transfer into human populations has been set back by the same forces who have used pseudo-scientific and disproven constructs to claim that because there are gaps in understanding this mechanism, the virus must have been created in a lab and set loose through incompetence or by nefarious design.

Former NIH director Harold Varmus, who has been a staunch defender of Peter Daszak's work, told Hiltzik, "It is impossible to say what would have been accomplished if the hiatus in funding did not occur. Restoring the grant cannot restore the three years in which [EcoHealth] was deprived of support for such critical work at a critical time."

The recent discovery of raccoon dog DNA in stalls contaminated with SARS-CoV-2 genetic material in the western stalls of the Huanan Seafood Market in Wuhan has only provided further confirmation of the central role this market had in the outbreak that began in mid to late November 2019, according to estimates based on genetic analysis of the early lineages of the SARS-CoV-2 virus conducted by Dr. Michael Worobey and colleagues.

These findings on raccoon dogs substantiate reports published in leading scientific journals that close to 50,000 wild animals and 38 different species had been sold between May 2017 and November 2019 at the Huanan market.

Damning to the argument of the Republican-backed COVID origin report that declared the outbreak started as early as September is the the World Health Organization's (WHO) 2021 origin study conducted in China, which found no evidence of heightened rates of influenza-like illnesses in Wuhan, Hubei province or the surrounding provinces before the reported outbreaks that occurred in December of 2019 in the massive metropolis of over 12 million people. Additionally, serological analysis of blood banks from September through December did not find one case of SARS-CoV-2 antibody in the tens of thousands of specimens evaluated, corroborating the WHO's results.

The entire argument by US officials and various media sources, brought in as a pseudo-scientific cover for their allegations that Chinese laboratories were unsafe and plagued with technical incompetency, was fabricated. The full text of the January 19, 2018, American Embassy in Beijing cable titled "China Opens First Bio-Safety Level 4 laboratory" demonstrates that "following two years of effort, which is not unusual for such facilities, the WIV lab was accredited in February 2017 by the China National Accreditation Service for Conformity Assessment."

It is not uncommon for international assistance in training technicians and scientists to safely operate high-containment laboratories. For instance, the University of Texas Medical Branch in Galveston, which has a well-established Biosafety Level-Four lab, was collaborating closely with the WIV.

As the cable concludes, the report makes some very critical observations that challenge the prevailing false conceptions that are being promoted:

> The ability of WIV scientists to undertake productive research despite limitations on the use of the new BSL-4 facility is demonstrated by a recent publication on the origins of SARS. Over a five-year study, … (and their research team) widely sampled bats in Yunnan province with funding support from NIAID/NIH, USAID, and several Chinese funding agencies.
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> The study results were published in PLoS Pathogens online on Nov. 30,2017, and it demonstrated that SARS-like coronaviruses isolated from horseshoe bats in a single cave contain all the building blocks of the pandemic SARS-coronavirus genome that caused the human outbreak. These results strongly suggest that the highly pathogenic SARS-coronavirus originated in this bat population. Most importantly, the researchers also showed that various SARS-like coronaviruses can interact with ACE2, the human receptor identified for SARS-coronavirus.
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> This finding strongly suggests that SARS-like coronaviruses from bats can be transmitted to humans to cause SARS-like disease. From a public health perspective, this makes the continued surveillance of SARS-like coronaviruses in bats and study of the

animal-human interface critical to future emerging coronavirus outbreak prediction and prevention. WIV scientists are allowed to study the SARS-like coronaviruses isolated from bats while they are precluded from studying human-disease-causing SARS coronavirus in their new BSL-4 lab until permission for such work is granted by the NHFCP.

Additionally, Worobey, a professor of ecology and evolutionary biology at the University of Arizona, who has seriously taken on the lab-leak versus market origin question, explained that two lineages of SARS-CoV-2 emerged around the same time centered around the Huanan market and not some other place in the city. Of note, WIV is located miles away to the west of the market.

Early cases, both with and without connection to the market, infected with both lineages, have been linked geographically to Huanan to a remarkable statistical significance. This means that in a lab leak scenario it would require two people at the WIV, without knowledge of becoming infected by two different versions of the virus, to have then traveled to Huanan without causing anyone else to get infected and cause a chain of infections to sustain itself into an outbreak. Statistically, this would be extremely unlikely and implausible. Yet the US intelligence apparatus and Democrats and Republicans want the public to believe this precise scenario.

Worobey recently remarked in a lecture at Arizona State University, “Lab leak proponents cling to the contention that the presence of a lab that studies viruses and the emergence of a coronavirus pandemic in the same city can’t possibly be coincidental. But my colleagues and I showed in 2021 that this virus wasn’t going to emerge just anywhere in China: It took a city.”

He added, “Simulations indicate that when a virus with the properties of SARS-CoV-2 jumps into a human in a sparsely populated rural area, it will fail to cause an outbreak 99 percent of the time. But take that same virus into a huge city like Wuhan, and about a third of animal-to-human transmissions will result in an epidemic.”

Notably, every major hub in China has academic institutions studying viruses, bacteria and other pathogens. It is precisely in a place like Wuhan where pandemics emerge and not because they have an institute of virology but because they are densely packed with new hosts for viruses that can support their transmission. Inevitably, Worobey notes, had the outbreak occurred in Beijing, lab-leak conspiracists would have made the same allegations.

It is worth noting that Peter Daszak was part of the WHO’s R&D Blueprint group which met in early 2018 and coined the term Disease X, defined as a novel pandemic pathogen originating in animals, which “would emerge somewhere on the planet where economic development drives people and wildlife together.” His work has documented that spillover of SARS-like viruses is common in Southeast Asia and portends new pandemics in the near future, given the current political climate.

A recent report by scientists working at the Chinese Center for Disease Control has identified two beta coronaviruses that contained furin cleavage sites, implying these evolutionary mechanisms are not uncommon among coronaviruses. This is contrary to the allegations of the conspiracy theorists who claim that the presence of a furin cleavage site in SARS-CoV-2 suggests that it was engineered rather than developing by natural evolution.

Another recent paper on research conducted in rural Myanmar found that between 2017 and 2020, approximately 12 percent of the people tested had at some point been infected with a diverse range of sarbecoviruses, of which SARS-CoV-1 and SARS-CoV-2 are two notable coronaviruses, meaning zoonotic spillovers have become far more common than previously anticipated.

Professor David Robertson from the University of Glasgow’s Centre for Virus research, remarked, “These spillovers in rural areas tend to not spread as there’s unlikely to be a large enough population to sustain chains of transmission. That’s why a city like Wuhan was so significant for being the start of the pandemic, as there’s lots of opportunity for further human to human spread.”

EHA’s restoration victory remains uncertain because the same House committee that asked the National Academy of Medicine to expel Daszak from membership has called the reinstating of EHA’s grant “beyond outrageous.” Chair of the Energy and Commerce Committee Cathy McMorris Rodgers wrote Christi Grimm, the Inspector General of the Department of Health and Human Services, on May 8, 2023, asking her “to assist our understanding about how the audit was conducted and the basis for not recommending debarment of EcoHealth … please provide the work papers of the audit of the NIH grant to EcoHealth to the Committee no later than May 22, 2023.”

Conclusion

There is not a single verifiable fact that could suggest a lab-leak scenario at the WIV or any other facility in Wuhan. There is growing evidence of the epidemiologic picture on the ground in and around Huanan seafood market in November and December 2019. There has been robust molecular analysis showing a natural origin for SARS-CoV-2, and long experience with the overwhelming biological preponderance of bat coronavirus with potential zoonotic transmission capacity in Southeast Asia. Given all these scientifically incontrovertible factors, one must ask why US authorities, both Republicans and Democrats in Congress and the Biden administration, are so determined to denounce and bankrupt EHA and their critical work in preventing the next pandemic?

The two decades of work by EHA are a byproduct of the extensive collaboration across national borders which characterizes the best of modern scientific inquiry, where trust and respect develop out of a collective effort to address urgent questions that could affect the wellbeing of the world’s population.

Coronaviruses and other deadly pathogens are biological organisms that lack consciousness. In an evolutionary process, they react to their environments in order to propagate their genetic codes. When their natural habitats are impacted, the mechanisms they possess to replicate give one or another form of the pathogen an evolutionary advantage in adaption. This advantage can mean becoming more infectious, more resistant to antibodies or more destructive to their host, depending on the circumstances. It also means they find new hosts to infect–humans.

This is the evolutionary logic behind the many previous pandemics that have left their marks on human civilizations, with deadly consequences if they are ignored and allowed to take hold.

In the struggle against such pandemics, mankind has developed numerous tools and highly specialized disciplines, particularly relating to public health and disease prevention. In its initial three years of success with the Zero-COVID strategy, China invented nothing new. It simply carried out systematically and rigorously the time-tested measures of quarantine and isolation that were being abandoned by all the major capitalist countries and eventually by China itself, at the end of 2022, with tragic consequences.

The COVID-19 pandemic has made clear that for the capitalist ruling elites, the enforcement of their manic needs to extract ever more surplus value from the working class means the complete rejection of well-established principles of public health and disease-fighting and the

advances made in scientific inquiry and the technology that supports this work. Clearly, EcoHealth Alliance became collateral damage in this process: its work no longer aligned with the dictates of the capitalist mode of production.

Concluded