Research Report

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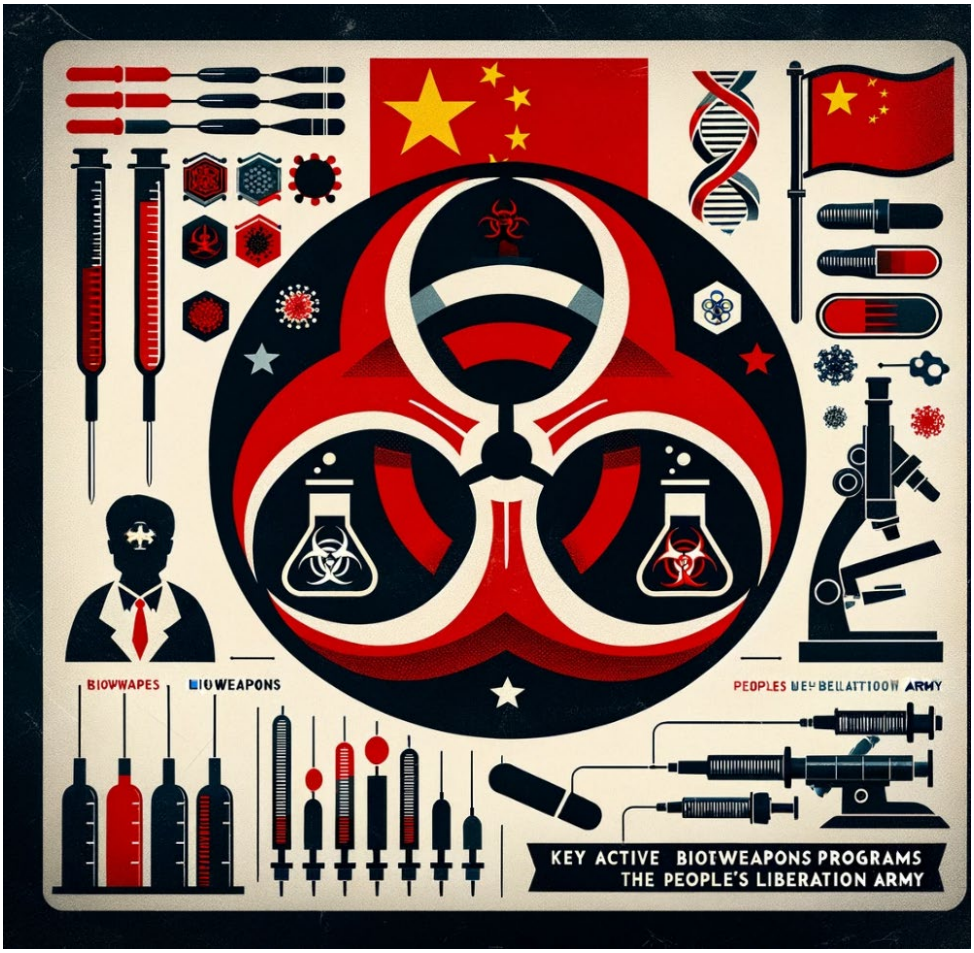
Current State of Key Active Bioweapons Programs of the Chinese Communist Party and People's Liberation Army[1]



[1] A full strategic net assessment of the full spectrum of these programs can be found in Ryan Clarke, Xiaoxu Sean Lin and LJ Eads, *China's International Military-Civilian Virology Fusion: High-Risk Pathogen Research, Global Linkages and Strategic Implications*, Broad Publishers, Taipei, April 2023.

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Unconventional Weapons: Core Elements of the CCP's Standard Order of Battle

The Chinese Communist Party (CCP) and its People's Liberation Army (PLA) views biological warfare as a core component of its asymmetric warfare strategy against the United States and its Allies. The PLA is ambitious in developing biological weapons as it is regarded as one core approach under the Unrestricted Warfare Doctrine. In 2015, then-president of the Academy of Military Medical Sciences (AMMS) He Fuchu (贺福初) argued that biotechnology will become the new 'strategic commanding heights' of national defense, from biomaterials to 'brain control' weapons.[2] In addition, the 2017 edition of Science of Military Strategy (战略学), a textbook published by the PLA's National Defense University that is considered to be authoritative, debuted a section about biology as a domain of military struggle, mentioning the potential for new kinds of biological warfare to include 'specific ethnic genetic attacks.'[3]

Bioweapons are part of the CCP's standard order of battle; not an unconventional set of capabilities only to be used under extreme circumstances. This represents a fundamental difference in strategic thinking regarding these domains in Beijing. This is not a hypothetical point. There was a sharp statistical increase in Chinese military activity in the South China Sea, East China Sea, Taiwan Straits, and along the Sino-Indian border during the most acute phases of the COVID-19 outbreak in 2020 and 2021.[4]

However, the CCP's weaponization of biology extends well beyond viruses (such as SARS-CoV-2), as well as beyond the scope and understanding of classical bioweapons. Their new landscape of bioweapons development includes the entire synthetic biology spectrum; from human genome editing of soldiers, genetic manipulation of bacteria to using human-computer interface to control entire populations. These research programs are not obscure 'moonshots'; they are core strategic focus areas that are designed to be utilized over the near-term and within current state strategic circumstances, such as in Taiwan. Any breakthrough in this dual-use research would provide unprecedented tools for the CCP to forcibly establish a new world order, which has been Xi Jinping's lifelong goal.

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[2] Elsa Kania and Wilson Vorndick, 'Weaponizing Biotech: How China's Military Is Preparing for a 'New Domain of Warfare', Defense One, 14 August 2019.
The Science of Military Strategy 2017, National Defense University, People's Liberation Army, Beijing, 2017.
Tianliang Xiao [肖天亮], eds., *The Science of Military Strategy* [战略学]. PLA National Defence University Press, Beijing, 2015.
Jieming Wu [吴杰明] and Zhifu Liu [刘志富], *An Introduction to Public Opinion Warfare, Psychological Warfare, [and] Legal Warfare* [舆论战心理战法律战概论], PLA National Defence University Press, Beijing, 2014.
Academy of Military Science Military Strategy Research Department [军事科学院军事战略研究部], eds., *The Science of Military Strategy* [战略学]. Military Science Press, Beijing, 2013.
Qiao Liang and Wang Xiangsui, *Unrestricted Warfare: Two Air Force Senior Colonels on Scenarios for War and the Operational Art in an Era of Globalization* [超限战], PLA Literature and Arts Publishing House, Beijing, February 1999.
Baocun Wang and Fei Li, 'Information Warfare', *Liberation Army Daily by Federation of American Scientists*, June 1995.
[3] Elsa Kania and Wilson Vorndick, 'Weaponizing Biotech: How China's Military Is Preparing for a 'New Domain of Warfare', Defense One, 14 August 2019.
The Science of Military Strategy 2017, National Defense University, People's Liberation Army, Beijing, 2017.
[4] For example, please see Ryan Clarke, 'Is China Converting COVID-19 Into a Strategic Opportunity?', EAI Background Brief No. 1545, National University of Singapore, 9 July 2020.

For example, these capabilities can 'fit' into the CCP's anti-access/area denial strategy in the Indo-Pacific. Imagine genetically immunized PLA troops being inserted into a geography where a specific weaponized bacterial strain has been released prior to their entry to prepare the ground and eliminate points of resistance. Any remaining sources of resistance on the ground are then dealt with through neurobiological weaponry that instill intense fear and/or other forms of cognitive incoherence resulting in inaction.

The net result of such a scenario would be the PLA establishing absolute control over a geography such as Taiwan while simultaneously blunting any American strategic options to intervene and physically insert personnel into the theater. This would effectively negate and render inert America's overwhelming conventional superiority with very few (if any) near-term remedies. This scenario is based on known existing CCP research programs and what the clear strategic aims of those programs are.

There Are No Civilian Labs in China Under the CCP

The Civil-Military Fusion Law, which was exercised by the PLA during the COVID-19 pandemic, renders any institution, private company, or non-governmental organization vulnerable to forcible takeover by the state at any time. In addition, high-risk pathogen research that is being conducted at various Chinese virology institutes is under the direction of the CCP and, in some cases, the PLA. This represents a fundamental difference in the system between China under the CCP and the select few other nations that have the demonstrated capability to work with dangerous pathogens. It should also be noted that while the PLA continues to lag far behind the United States and its Allies in the Indo-Pacific, the bioweapons domain is the one key area where China is currently 'upstream' and has clearly assessed that this provides the CCP with asymmetric options.

Harbin Veterinary Institute (HVRI) and the Doherty Institute at the University of Melbourne: Combining Human and Avian Influenza Viruses

The former mentor and long-time scientific collaborator of HVRI's Chen Hualan (China's leading Avian Influenza Gain-of-Function specialist) is Dr. Kanta Subbarao of the Doherty Institute at the University of Melbourne. Subbarao has a well-established track record of high-risk research on avian influenza viruses and has jointly produced multiple such studies with Chen. Chen and Subbarao have a particular demonstrated focus on combining elements of different avian influenza and human influenza viruses to produce new chimeric viruses. For example, in 2003 they conducted an experiment where they combined H1N1 and H3N2 human influenza viruses with genes from the H9N2 avian influenza virus, an event that would have been highly unlikely to have occurred in nature. Chen and Subbarao claimed that combining the genes of human and avian influenza viruses would help to develop a human vaccine. No such vaccine has been developed to date.[5]

[5] Kanta Subbarao, Hualan Chen, et. al., 'Generation and Characterization of an H9N2 Cold-Adapted Reassortant as a Vaccine Candidate', *Avian Diseases*, Vol. 47, No. s3, September 2003.
Please also see Kanta Subbarao, Hualan Chen, et. al., 'Generation and characterization of a cold-adapted influenza A H9N2 reassortant as a live pandemic influenza virus vaccine candidate', *Virology*, Vol. 305, Iss. 1, 5 January 2003.
Kanta Subbarao, Hualan Chen, et. al., 'Evaluation of a Genetically Modified Reassortant H5N1 Influenza A Virus Vaccine Candidate Generated by Plasmid-Based Reverse Genetics', *Virology*, Vol. 305, Iss. 1, February 2003.

Chen and Subbarao went on in 2006 to conduct additional experiments with H3N2 human influenza viruses to make them more transmissible between ferrets via respiratory droplets. They also combined H5N1 (the most lethal known avian influenza virus) genes with H3N2 and noted that this reassortment greatly enhanced H5N1 viral transmissibility. Chen and Subbarao had demonstrated how to make the world's most dangerous avian influenza virus much more transmissible between humans via reverse engineering techniques.[6]

International Bat Coronavirus Gain-of-Function (GoF) 'Breakthroughs' in 2010-2016: Wuhan Institute of Virology (WIV) Leads the Way

Under WIV leadership, joint Sino-US-Australian teams[7] published several GoF studies in leading scientific journals such as *Nature* and *Archives of Virology* in 2010, 2013, and 2015. These studies showed how a bat coronavirus can directly infect human cells without the need for an intermediate mammalian host.[8] Additional experiments enabled these researchers to make these lab-modified bat coronavirus more transmissible than bat coronaviruses found in nature.[9] These experiments sparked major debates within the scientific and security/defense communities.

However, the points made in opposition to these experiments were ignored by this transnational network of bat coronavirus GoF researchers. They continued their work openly at various institutions in China, Australia, and the United States, amongst others. The clearest evidence of this disregard is a subsequent 2016 study in which the same group of lead researchers clearly crossed into bioweapons research. In this study, Shi Zhengli and her team at WIV along with Peter Daszak from EcoHealth Alliance used reverse genetics method to constructed a full-length infectious cDNA clone of a SARS-like bat coronavirus strain (called SL-CoV WIV1 or rWIV1) and a related mutant clone called rWIV1-GFP-ΔX. The SL-CoV WIV1 strain contained the Open Reading Frame X (ORFX) gene, while rWIV1-GFP-ΔX strain deleted the ORFX gene.[10]

By comparing the functions of these two recombinant strains of viruses, they found that ORFX could inhibit interferon production and activate NF-κB. Their results demonstrated for the first time that the unique ORFX in the WIV1 strain is a functional gene involving

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Kanta Subbarao, Hualan Chen, et. al, 'Generation and characterization of a cold-adapted influenza A H9N2 reassortant as a live pandemic influenza virus vaccine candidate', *Vaccine*, Vol. 21, November 2003.

[6] Kanta Subbarao, Hualan Chen, et. al., 'Lack of transmission of H5N1 avian– human reassortant influenza viruses in a ferret model', *PNAS*, Vol. 103, No. 32, 8 August 2006.

[7] The Australian Centre for Disease Preparedness, Australia's BSL4 lab in Geelong (outside of Melbourne) have refrained from making comments so far, despite the fact that extensive research was conducted on bat coronaviruses in this facility with Dr. Shi even spending time there as a visiting scientist in 2006.

[8] See Shi Zhengli, Ralph Baric, et. al., 'A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence', *Nature Medicine*, Vol. 21, No. 12, December 2015.
Joanna Mazet, Peter Daszak, Shi Zhengli, et. al., 'Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor', *Nature*, Vol. 503, No. 28, November 2013.
Fang Li, Linfa Wang, Shi Zhengli, et. al, 'Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SARS-CoV entry', *Archive of Virology*, Vol. 155, 22 June 2010.

[9] See Shi Zhengli, Ralph Baric, et. al., 'A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence', *Nature Medicine*, Vol. 21, No. 12, December 2015.
Joanna Mazet, Peter Daszak, Shi Zhengli, et. al., 'Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor', *Nature*, Vol. 503, No. 28, November 2013.
Fang Li, Linfa Wang, Shi Zhengli, et. al, 'Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SARS-CoV entry', *Archive of Virology*, Vol. 155, 22 June 2010.

[10] Shi Zhengli, Peter Dazsak, et. al., 'Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response', *Journal of Virology*, Vol. 90, No. 14, July 2016.

modulation of the host immune response. In other words, this study demonstrated how to reverse engineer infectious clones of SL CoV and how a viral gene can modulate its pathogenicity.[11] And the rWIV1-GFP-ΔX is a mutant clone that has higher pathogenicity than its parental strain of rWIV1, since it replicates efficiently and does not have this ORFX gene that exists between ORF6 and 7. It is interesting that no more journal publications about any further study of the ORFX gene could be found since then. In addition, the sequence of the small protein expressed by ORFX gene (Genbank: ATO98224.1) could not find any homology with any known protein in the Genbank search. Where did this gene come from? Why was the ORFX gene never found in any other bat coronavirus strains collected in WIV or globally?

In addition, the SARS-CoV-2 genome also does not have this ORFX gene. Does the absence of ORFX have anything to do with the pathogenicity of SARS-CoV-2 if this virus was a natural or engineered derivant of bat coronavirus? It should be noted that the infection by wild type SARS-CoV-2 virus leads to severe multi-organ failure and at the same time around 40% of all confirmed COVID-19 infections were asymptomatic.[12]

WIV GoF Research on Nipah Virus: High-Probability Bioweapons Research With (At Least) International Awareness

World-renowned physician, vaccine developer, and biomedical scientist Dr Steven Quay recently testified in a U.S. Congressional hearing that his team have identified evidence that WIV was conducting dangerous experiments on Nipah virus. Nipah is a BSL4-level pathogen and US Centers for Disease Control and Prevention (US CDC)-designated Bioterrorism Agent.

Dr. Quay made this detection in raw RNA-Seq sequencing reads which were deposited by WIV itself produced from five December 2019 patients infected with SARS-CoV-2. Research involving Nipah infectious clones has never been reported to have occurred at the WIV and these patient samples were also reported to contain reads from several other viruses: Influenza A, Spodoptera frugiperda rhabdovirus and Nipah. Other scientists erroneously interpreted the presence of these virus sequences as indicative of co-infections of the patients in question by these pathogens or laboratory contamination. However, Quay's analysis clearly demonstrates that Nipah genes are actually encapsulated in synthetic vectors, which was specifically designed for the assembly of an infectious Nipah clone. Quay and his team also note that contamination of patient sequencing reads by an infectious Nipah clone of the highly pathogenic Bangladesh strain could indicate a significant breach of BSL4 protocols.

Quay documents the presence of Nipah sequences, Bangladesh strain, interpreted as likely for assembly of a Nipah infectious clone, found in raw sequencing reads by WIV from five patients infected with SARS-CoV-2 sampled by the Wuhan Jin Yin-Tan Hospital at the

[11] Shi Zhengli, Peter Dazsak, et. al., 'Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response', *Journal of Virology*, Vol. 90, No. 14, July 2016.
[12] Daniel Oran and Eric Topol, 'Prevalence of Asymptomatic SARS-CoV-2 Infection', *Annals of Internal Medicine*, 1 September 2020.
Qiuyue Ma, et. al., 'Global Percentage of Asymptomatic SARS-CoV-2 Infections Among the Tested Population and Individuals With Confirmed COVID-19 Diagnosis: A Systematic Review and Meta-analysis', *JAMA Network Open*, Vol. 4, No. 12, 14 December 2021.

beginning of the COVID-19 outbreak.[13] The Bangladesh strain of Nipah virus was often associated with high levels of oral shedding and is one of the most transmissible and pathogenic strains of Nipah viruses. The five patients experienced COVID-19 illness onset between 12 December 2019 and 23 December 2019 and were admitted to intensive care between 20 December 2019 and 29 December 2019 with all BALF (bronchoalveolar lavage fluid) sampling conducted on 30 December 2019 and 10 January 2020. BioProject PRJNA605983 containing the analyzed samples was actually registered by WIV with GenBank on 11 February 2020 and consists of nine RNA sequencing (RNA-Seq) BALF datasets. NGS (next-generation sequencing) was undertaken at the WIV using BGI MGISEQ-2000 and Illumina MiSeq 3000 sequencers.[14]

Some mistakenly interpreted [15] the presence of these virus sequences as indicative of co-infection of early Wuhan COVID-19 infected patients with these microbes. However, Quay analyzed the presence of a sequence H7N9 Hemagglutinin A segment 4 gene and found in a synthetic vector in these COVID-19 patient samples. He concluded that contamination was the likely cause while his colleague Dr Zhang Daoyu[16] identified the presence of a Nipah infectious clone in the datasets.

Nipah was designated a priority research area at WIV.[17] However, after a search using Google Scholar and Pubmed, only two publications by WIV-affiliated authors were found in the 2018-2020 year period: a general overview of phylogeny, transmission and protein structure[18] and an article relating to rapid detection assay research, but which only concerns N gene pseudotyped Nipah virus, rather than a fully assembled Nipah infectious clone.[19] Interestingly, WIV Chief Biosafety Officer Yuan Zhiming is on public record openly stating that WIV is working on synthetic biology studies to manipulate the proteins of Nipah viruses as well as Ebola that involve animal models.[20]

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[13] Peng Zhou, Shi Zheng-Li, et. al., 'A pneumonia outbreak associated with a new coronavirus of probable bat origin', *Nature*, Vol. 579, 12 March 2020.
[14] Peng Zhou, Shi Zheng-Li, et. al., 'A pneumonia outbreak associated with a new coronavirus of probable bat origin', *Nature*, Vol. 579, 12 March 2020.
[15] For example, see Sandeep Chakraborty, 'There was a simultaneous outbreak of the zoonotic Nipah henipavirus in Wuhan - 4 out of 5 patients have the virus in Jinyintan Hospital, along withSARS-Cov2, in their metagenome - which seems to have resolved by itself', OSF, 1 October 2020.
Mohammed Abouelkhair, 'Non-SARS-CoV-2 genome sequences identified in clinical samples from COVID-19 infected patients: Evidence for co-infections', *PeerJ*. 2 November 2020.
[16] Steven Quay, Daoyu Zhang, et. al., 'Vector sequences in early WIV SRA sequencing data of SARS-CoV-2 inform on a potential large-scale security breach at the beginning of the COVID-19 pandemic', *Zenodo*, 19 September 2021.
[17] Shi Zheng-li, 'Inter-nation collaboration Sino-French NiV taskforce 2019', Nipah Virus International Conference, 9-10 December, Singapore.
https://cepi.net/wp-content/uploads/2020/06/2019-Nipah-Conference-Proceedings.pdf
[18] Bangyao Sun, et. al., 'Phylogeography, Transmission, and Viral Proteins of Nipah Virus', *Virologica Sinica*, Vol. 33, No. 5, 2018.
[19] Liping Ma, et. al., 'Rapid and specific detection of all known Nipah virus strains' sequences with reverse transcription-loop-mediated isothermal amplification'. Frontiers in Microbiology, Volume 10, Article 418, March 2019
[20] 'U.S China Dialogue and Workshop on the Challenges of Emerging Infections, Laboratory Safety, Global Health Security and Responsible Conduct in the Use of Gene Editing in Viral Disease Research', Draft Version 4, Harbin Veterinary Research Institute – Chinese Academy of Agricultural Sciences, 8-10 January 2019. This document was obtained via a Freedom of Information request from the University of Texas System.

Over the course of Dr. Quay's Nipah-focused investigation he and his team detected other contaminating sequences, including HIV, Simian Virus and Woodchuck Hepatitis Virus that are all synthetic vector-related and not related to primary patient infection. These findings converge with previous findings on significant contamination at Wuhan sequencing facilities was previously documented by Dr. Zhang Daoyu[21] Middle Eastern Respiratory Syndrome (MERS) and SARS-CoV-1 genomes recovered from agricultural sequencing datasets. Those sequences are consistent with an infectious Nipah clone and numerous other synthetic sequences[22] were found in samples from the earliest sequenced COVID-19 patients in Wuhan. Quay notes that this could indicate serious contamination problems at WIV. Quay fundamentally assesses that the finding of Nipah gene sequences attached to synthetic vectors (presumably for assembly as a full length infectious Nipah clone of the highly pathogenic Bangladesh strain) in datasets of the earliest sequences COVID-19 patients in Wuhan is potentially a significant breach of BSL4 protocols. [23]

Galveston National Laboratory/UTMB: From American BSL4 Capacity Builder and GoF Research Partner to Abrupt Access Denial in Kunming

Recently legally obtained email communications between Dr. James LeDuc at UTMB in Galveston and Chinese Academy of Medical Sciences (CAMS) reveal that the Institute of Medical Biology (IMB – a constituent units of CAMS) houses a BSL4 lab. This lab appeared to be engaging in joint high-risk virology research with UTMB that is made only available to a select few Chinese scientists.[24] Previously, many analysts assumed that China only had two BSL4 labs, one at WIV and one at HVRI.

The point person between the Galveston lab and CAMS was Dr. Shi Pei-Yong. Shi has conducted research involving the manipulation of spike proteins of the SARS-CoV-2 virus to make the pathogen more infectious than the variants that were circulating naturally.[25] This may have represented a common interest with his counterparts in Kunming. Shi has also worked extensively with the PLA's AMMS and CAMS on other infectious disease projects that involve the manipulation of viruses, such as chimeric Zika vaccine development and Zika GoF studies using mouse models.

One of Shi's key collaborators, Qi Chen, is the director of the Virology Lab at the Institute of Microbiology and Epidemiology (BIME – a constituent unit of AMMS).[26] Despite these

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[21] Steven Quay, Daoyu Zhang, et. al., 'Vector sequences in early WIV SRA sequencing data of SARS-CoV-2 inform on a potential large-scale security breach at the beginning of the COVID-19 pandemic', *Zenodo*, 19 September 2021.
Daoyu Zhang, et. al., 'Unexpected novel Merbecovirus discoveries in agricultural sequencing datasets from Wuhan, China', *ArXiv* 6 June 2021.
[22] Steven Quay, et. al., 'Contamination or Vaccine Research? RNA Sequencing data of early COVID-19 patient samples show abnormal presence of vectorized H7N9 hemagglutinin segment', *Zenodo*, 3 July 2021.
[23] Steven Quay, et. al., 'Contamination or Vaccine Research? RNA Sequencing data of early COVID-19 patient samples show abnormal presence of vectorized H7N9 hemagglutinin segment', *Zenodo*, 3 July 2021.
[24] These email conversations were voluntarily shared with Ryan Clarke by Gary Ruskin.
Please also see Yuan Zhiming, 'Current status and future challenges of high-level biosafety laboratories in China', *Journal of Biosafety and Biosecurity*, Vol. 1, Issue 2, September 2019.
[25] For example, please see Pei-Yong Shi, 'Spike mutation D614G alters SARS-CoV-2 fitness', *Nature*, Vol. 592, 26 October 2020.
[26] Qi Chen, Chao Shan, Shi Peiyong, et. al., 'Treatment of Human Glioblastoma with a Live Attenuated Zika Virus Vaccine Candidate', *mBio*, Vol. 9. Iss. 5, September/October 2018.

well-established linkages, the UTMB team was shut out of the BSL4 lab in Kunming that they helped develop. Dr. Chao Shan also held simultaneous dual appointments at WIV[27] and on LeDuc's team at UTMB in Galveston.

Chao has several joint publications with Shi and others demonstrating GoF research. In one 2020 PNAS study, Chao, Shi and colleagues took a pre-epidemic Asian Zika virus strain (FSS13025 isolated in Cambodia in 2010) and inserted the 'V473M' substitution that significantly increased neurovirulence[28] in neonatal mice and produced higher viral loads in the placenta and fetal heads in pregnant mice. This E-V473M mutant strain was further studied in competition experiments in cynomolgus macaques. The results showed that this mutation increased Zika's fitness for viral generation in macaques, a clear demonstration of GoF that was based on the reverse genetics techniques that had been used in other high-risk studies.[29]

CAMS Researchers Create a Non-Human Primate Host for Previously Low-Risk Middle Eastern Respiratory Syndrome (MERS) with Dutch Assistance

The MERS virus that emerged from Saudi Arabia's Eastern Province in 2012 generated modest outbreak clusters across the Middle East and limited clusters in Southeast and South Asia, as well as South Korea in 2015. Although there were human-to-human transmissions in nosocomial outbreaks in hospitals, the MERS virus was not well adapted for continuous human-to-human transmission. It is listed on the WHO Priority Pathogen list; however, its pandemic potential remains limited. MERS-CoV has been identified in dromedaries in several countries in the Middle East, Africa and South Asia. The origins of the virus are not fully understood but, according to the analysis of different virus genomes, it is believed that it may have originated in bats and was transmitted to camels sometime in the distant past.[48]

A group of CAMS researchers infected non-human primates with the MERS coronavirus in a study in 2014. In the study titled, 'An animal model of MERS produced by infection of rhesus macaques with MERS coronavirus', Yao Yanfeng, Bao Linlin, Deng Wei and Qin Chuan from CAMS set out to determine whether monkey models were effective to study the pathogenesis of MERS infections. In this CAMS study, the research team sourced its MERS samples from Dr. Ron Fouchier in Erasmus and utilized them to directly infect the lungs of Rhesus Macaques and observe their physiological responses. The researchers reported that infected monkeys showed clinical signs of disease, virus replication, histological lesions and neutralizing antibody production. They also reported that they could confirm that the monkey model supports viral growth, and manifests respiratory and generalized illness along with

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Xiao Feng I, et al., 'Development of a chimeric Zika vaccine using a licensed live-attenuated flavivirus vaccine as backbone', *Nature Communications*, Vol. 9, No. 673, 2018.
Chao Shan, et. al., 'An Infectious cDNA Clone of Zika Virus to Study Viral Virulence, Mosquito Transmission, and Antiviral Inhibitors', *Cell Host Microbe*, Vol. 19, No. 6, 8 June 2016.

[27] For additional information on high-risk pathogen research at the Wuhan Institute of Virology and its transnational linkages, please see Ryan Clarke and Lam Peng Er, 'Coronavirus Research Networks in China: Origins, International Linkages and Consequences', Center for Non-Traditional Security Studies, May 2021, Singapore.

[28] Neurovirulence refers to infection of the brain.

[29] Chao Shan, et. al., 'A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission', *PNAS*, Vol. 117, No. 33., 18 August 2020.
For additional GoF work conducted by Galveston/UTMB's Pei-Yong Shi and colleagues at AMMS involving Zika viruses in mice, please see Ling Yuan, et. al., 'A single mutation in the prM protein of Zika virus contributes to fetal microcephaly', *Science*, Vol. 17, No. 358, 17 November 2017.

tissue pathology. These CAMS researchers claim to have conducted similar experiments on mouse, ferret and guinea pig models but decided not to publish the data.[30]

Although the animal model studies will benefit the studies on vaccine, antiviral as well as viral pathogenesis, the adaptation of MERS-CoV in primates has intrinsic risks of obtaining viral variants that have enhanced transmissibility in primates. Then, whether these variants also have higher transmissibility in humans, causing more efficient human-to-human transmission, becomes a great concern and bioethics issue. Dr. Bao Linlin is of particular interest in this MERS study as well as her multiple studies on H7N9 and other GoF research on avian influenza viruses. Bao operates under Institute of Laboratory Animal Sciences (ILAS) at CAMS and conducts GoF research that is virtually identical to the research conducted by Ron Fouchier[31]. Both Bao and Fouchier have engineered avian influenza (H7N9 and H5N1) viruses that could transmit between ferrets via droplets.[32] However, while Fouchier's research was criticized and has periodically ceased under EU regulations related to weapons of mass destruction, Bao's research has continued with no apparent restrictions.

Engineering Synthetic, Replicative SARS-CoV-2 Viruses at the Christophe Merieux Laboratory (CML) of the Institute of Pathogen Biology (CAMS)

While most of the daily flow of clinical, laboratory, research and educational activities within Institute of Pathogen Biology (IPB) can be classified as standard, there is high-risk research being conducted, some of which with international cooperation. In October 2021, researchers from the IPB-controlled CML in Beijing developed their own synthetic SARS-CoV-2 virus in

[30] Yao Yanfeng, et. al., 'An Animal Model of MERS Produced by Infection of Rhesus Macaques With MERS Coronavirus', *Journal of Infectious Diseases*, Vol. 209, No. 2, 15 January 2014.

[31] For example, please see Ron Fouchier, et. al., 'Airborne transmission of influenza A/H5N1 virus between ferrets', *Science*, 22, 336:6088, June 2012.
Ron Fouchier, et. al., 'The Potential for Respiratory Droplet–Transmissible A/H5N1 Influenza Virus to Evolve in a Mammalian Host', *Science*, 22;336:6088, June 2012.
Martin Enserink, 'Flu Researcher Ron Fouchier Loses Legal Fight Over H5N1 Studies', *American Association for the Advancement of Science (ScienceMag)*, 25 September 2013.
https://www.science.org/content/article/flu-researcher-ron-fouchier-loses-legal-fight-over-h5n1-studies,

[32] For example, please see Linlin Bao, et. al., 'Novel Avian-Origin Human Influenza A(H7N9) Can Be Transmitted Between Ferrets via Respiratory Droplets', *Journal of Infectious Diseases*, Vol. 209, Issue 4, 15 February 2014.
Linlin Bao, et. al., 'Transmission of H7N9 influenza virus in mice by different infective routes', *Virology Journal*, Vol. 11, Article No. 185, 2014.
Ron Fouchier, et. al., 'Airborne Transmission of Influenza A/H5N1 Virus Between Ferrets'.
Ron Fouchier et. al., 'Gain-of-Function Experiments on H7N9', *Science*, 3 August 2013.
Ron Fouchier, et. al., 'The Potential for Respiratory Droplet–Transmissible A/H5N1 Influenza Virus to Evolve in a Mammalian Host'.
Martin Enserink, 'Flu Researcher Ron Fouchier Loses Legal Fight Over H5N1 Studies: Dutch court confirms that export license is needed to publish certain influenza paper', *Science*, 25 September 2013.
Robert Roos, 'Fouchier study reveals changes enabling airborne spread of H5N1', Center for Infectious Disease Research and Policy, University of Minnesota, 21 June 2012.
Jocelyn Kaiser, 'EXCLUSIVE: Controversial experiments that could make bird flu more risky poised to resume: Two 'gain of function' projects halted more than 4 years ago have passed new U.S. review process', *Science*, 8 February 2019.
Martin Enserink, 'Scientists Brace for Media Storm Around Controversial Flu Studies', *Science*, 23 November 2011.

the lab, which they refer to as the 'SARS-CoV-2-GFP replicon', with the logic that experimentation on this synthetic virus would more fully inform treatment options.[33]

As the SARS-CoV-2 replicon generated by this synthetic virus does not have functional structure genes and NSP-1 gene, this replicon is not infectious, even though it can replicate and produce reporter proteins efficiently in their experiments.[34] While this work aimed to avoid high-risk experiments of producing infectious SARS-CoV-2 clones in the BSL-3 labs, it is just one step away from generating full length infectious clones via adding back missing genes using the same reverse engineering methods.

This work on SARS-CoV-2 shares fundamental similarities with some of the work that was done by Ralph Baric in 2002 when he was developing synthetic SARS-CoV-1 viruses in his lab at UNC - Chapel Hill. Baric filed US Patent Number US 7,279,327 B2 on 19 April 2002. The first case of the SARS-CoV-1 outbreak in China was in Guangdong province in November 2002.[35]

The April 2002 US patent describes the bioengineering work as producing an infectious, replication-defective coronavirus that was specifically targeted for human lung epithelium – a literal description of SARS-CoV-1. This patent lays out the fact that these researchers knew that the ACE receptor, ACE2 binding domain, the S1 spike protein and other elements could be synthetically modified in laboratory settings. This could be done using existing gene sequencing technologies (even back in 2002) to utilize computer code to turn this genetic sequence into a pathogen or an intermediate host of a pathogen.[36]

This 2021 study conducted by IPB, CAMS, and CML used a different version of the strategies: generating assembly-defective replicon, but not replication-defective replicon as used by Dr. Baric's group. But in principle, once a scientist has mastered the reverse engineering methods to produce SARS-CoV-2 cDNA clones, it is straightforward to obtain full infectious viral clones if no bioethics committees are blocking the effort.

High-Risk Virology Studies Identified on SARS-CoV-2 and African Swine Flu Virus at AMMS

In 2021, researchers from WIV and the Chinese Communist Party Central Military Commission Joint Logistic Support Force (CCP CMC JLSF, which AMMS is subordinated to) published a study describing a high-risk serial passaging experiment with a SARS-CoV-2 virus.

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[33] Bei Wang, Chongyang Zhang, Xiaobo Lei, Lili Ren, Zhendong Zhao and He Huang, 'Construction of Non-infectious SARS-CoV-2 Replicons and Their Application in Drug Evaluation', *Virologica Sinica*, Vol. 36, No. 5, October 2021.

[34] Bei Wang, Chongyang Zhang, Xiaobo Lei, Lili Ren, Zhendong Zhao and He Huang, 'Construction of Non-infectious SARS-CoV-2 Replicons and Their Application in Drug Evaluation', *Virologica Sinica*, Vol. 36, No. 5, October 2021.

[35] Ryan Clarke, 'Emerging Global Pandemic Risks Come from Engineered Viruses in Chinese Labs, Not the Jungle or Bat Caves', Epoch Times, 5 September 2021.
Please also see Kristopher Curtis, Boyd Yount and Ralph Baric, United States Patent, Patent No: US 7,279,327 B2, Date of Application: 19 April 2022, Date of Patent Grant: 9 October 2007.
https://patentimages.storage.googleapis.com/a8/c0/6a/0584dd67435ef2/US7279327.pdf.

[36] Ryan Clarke, 'Emerging Global Pandemic Risks Come from Engineered Viruses in Chinese Labs, Not the Jungle or Bat Caves', Epoch Times, 5 September 2021.
Please also see Kristopher Curtis, Boyd Yount and Ralph Baric, United States Patent, Patent No: US 7,279,327 B2, Date of Application: 19 April 2022, Date of Patent Grant: 9 October 2007.
https://patentimages.storage.googleapis.com/a8/c0/6a/0584dd67435ef2/US7279327.pdf.

One of the key scientists involved in this study was WIV's Shi Zhengli.[37] To further investigate the genetic susceptibility of SARS-CoV-2 during serial passage (a clear GoF technique) on different cells, this team identified nine cell lines (human, non-human primate, and swine) susceptible to the SARS-CoV-2 virus. These nine cell lines were then serially passaged with increasingly virulent variants of the SARS-Cov-2 virus and monitored to identify the most transmissible combinations.[38] There is no identifiable biomedical application for this type of research.

During the course of this serial passaging experiment, the viral loads of SARS-CoV-2 increased exponentially along with increased transmission fitness driven by evolutionary adaptations gained from serial passaging. These scientists note that human tissue (including lung, liver, colon, larynx, and skin), monkey (kidney), and swine (testicle) were most susceptible to SARS-CoV-2.[39] The key 'discovery' made by these scientists in this 2021 study is that the SARS-CoV-2 virus replicated most efficiently in human cell lines (classified as Huh-7, Calu-3, Caco-2 in this paper) and non-human primate cells (classified as Vero E6 in this paper) but less so in swine cells. The specific verification that the Vero E6 cell line is suitable for viral amplification is presented as a primary 'scientific breakthrough'.[40]

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[37] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.
For a more in-depth discussion on Shi Zheng-Li's high-risk pathogen research, see Ryan Clarke and Lam Peng Er, 'Coronavirus Research Networks in China: Origins, International Linkages and Consequences', Center for Non-Traditional Security Studies, May 2021, Singapore.

The following studies conducted at WIV demonstrate, in aggregate, how to engineer a bat coronavirus to directly infect humans without the need for an intermediate mammalian host for the first time in history:

Shi, Zheng-Li, Baric, Ralph et. al., 'A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence', *Nature Medicine*, Vol. 21, No. 12, December 2015.
Mazet, Jonna, Daszak, Peter, Zheng-Li, Shi et. al., 'Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor', *Nature*, Vol. 503, No. 28, November 2013.
Li, Fang, Wang, Linfa, Shi, Zheng-Li, et. al, 'Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SARS-CoV entry', *Archive of Virology*, Vol. 155, 22 June 2010.
[38] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.
Additional scientific evidence demonstrating the clear GoF implications of this study for both animals and humans of this study can be found in:
Zheng-Li Shi, Yufei Zheng, et. al., 'SARS-CoV-2 rapidly adapts in aged BALB/c mice and induces typical pneumonia', *Journal of Virology*, Volume 95, Iss. 11, June 2021.
Li-Teh Liu, et. al., 'Isolation and Identification of a Rare Spike Gene Double-Deletion SARS-CoV-2 Variant From the Patient With High Cycle Threshold Value', *Frontiers in Medicine*, 6 January 2022.
[39] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.
Additional scientific evidence demonstrating the clear GoF implications of this study for both animals and humans of this study can be found in:
Zheng-Li Shi, Yufei Zheng, et. al., 'SARS-CoV-2 rapidly adapts in aged BALB/c mice and induces typical pneumonia', *Journal of Virology*, Volume 95, Iss. 11, June 2021.
Li-Teh Liu, et. al., 'Isolation and Identification of a Rare Spike Gene Double-Deletion SARS-CoV-2 Variant From the Patient With High Cycle Threshold Value', *Frontiers in Medicine*, 6 January 2022.
[40] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.
Additional scientific evidence demonstrating the clear GoF implications of this study for both animals and humans of this study can be found in:
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Li-Teh Liu, et. al., 'Isolation and Identification of a Rare Spike Gene Double-Deletion SARS-CoV-2 Variant From the Patient With High Cycle Threshold Value', *Frontiers in Medicine*, 6 January 2022.

These researchers also noted their surprise that none of the tested bat cell lines supported SARS-CoV-2 replication. This finding appears to directly conflict with their own assertion in the introduction of their own paper that SARS-CoV-2 is natural in origin and entered the human population via bats.[41] This lack of viral replication in bat cell lines was also observed by scientists from the University of Hong Kong in a 2020 study that was published by the US CDC.[42]

This lack of SARS-CoV-2 replication in bat cell lines could also contradict the official position of Beijing that SARS-CoV-2 and the subsequent COVID-19 pandemic is the result of a zoonotic spillover event. How can the SARS-CoV-2 virus be reliably determined to originate from bats when the virus does not actually replicate in bat cells? Interestingly, this lack of transmissibility of the SARS-CoV-2 virus in bat cells is consistent with other leading researchers who have claimed that this virus is uniquely adapted to directly infect and transmit amongst human cells, not other animal species.[43]

Qi Chen is the Director of Virology at the Institute of Virology and Microbiology (IVM) under AMMS. Qi has a well-established track record of conducting high-risk pathogen research with Chinese counterparts from WIV and CAMS as well as international collaborators at UTMB in Galveston.[44] In July 2021, Qi and colleagues published a study on an experiment that involved direct intranasal inoculation of virus in the olfactory system of humanized mice[45] and demonstrated rapid viral replication, massive cell death, and neurological damage.[46] Although SARS-CoV-2 infections primarily impact the respiratory system (and the lungs in particular), olfactory dysfunction is actually one of the most predictive and common symptoms in COVID-

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[41] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.
Additional scientific evidence demonstrating the clear GoF implications of this study for both animals and humans of this study can be found in:
Zheng-Li Shi, Yufei Zheng, et. al., 'SARS-CoV-2 rapidly adapts in aged BALB/c mice and induces typical pneumonia', *Journal of Virology*, Volume 95, Iss. 11, June 2021.
Li-Teh Liu, et. al., 'Isolation and Identification of a Rare Spike Gene Double-Deletion SARS-CoV-2 Variant From the Patient With High Cycle Threshold Value', *Frontiers in Medicine*, 6 January 2022.
[42] Susanna Lau, et. al., 'Differential Tropism of SARS-CoV and SARS-CoV-2 in Bat Cells', *Emerging Infectious Diseases*, Vol. 26, No. 12, December 2020.
[43] Nikolai Petrovsky, et. al., 'In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin', *Scientific Reports*, Vol. 11, 24 June 2021.
Steven Quay, 'A Bayesian analysis concludes beyond a reasonable doubt that SARS-CoV-2 is not a natural zoonosis but instead is laboratory derived', *Zenodo*, 29 January 2021.
Steven Quay and Angus Dalgleish, *The Origin of the Virus: The hidden truths behind the microbe that killed millions of people*, Clinical Press Ltd., September 2021.
Steven Quay and Richard Muller, 'The Science Suggests a Wuhan Lab Leak: The Covid-19 pathogen has a genetic footprint that has never been observed in a natural coronavirus', Wall Street Journal, 6 June 2021.
Birger Sørensen, Andres Susrud, and Angus Dalgleish, 'Biovacc-19: A Candidate Vaccine for Covid-19 (SARS-CoV-2) Developed from Analysis of its General Method of Action for Infectivity', *QRB Discovery*, Volume 1, 29 May 2020.
[44] For additional information, please see Ryan Clarke, Lam Peng Er, and Lin Xiaoxu, 'High-Risk Virology Research at the Chinese Academy of Medical Sciences and Peking Union Medical College', EAI Background Brief No. 1642, National University of Singapore, 24 March 2022.
[45] Humanized mice used in this study were mice that are genetically modified to have lungs that are genetically identical to humans. Humanized mice are used in multiple biomedical domains to most closely simulate how disease pathogenesis occurs in humans.
[46] Qi Chen, et. al., 'SARS-CoV-2 infection in the mouse olfactory system', *Cell Discovery*, Vol. 7, No. 9, 2021.
Please also see Qi Chen, Chao Shan, Shi Peiyong, et. al., 'Treatment of Human Glioblastoma with a Live AttenuatedZika Virus Vaccine Candidate', *mBio*, Vol. 9. Iss. 5, September/October 2018.

19 patients. Therefore, this research has its unique merit to confirm that humanized mice is an appropriate model for further examine the mechanism for olfactory dysfunction upon COVID-19 infection.

However, the authorship of this publication indicated that the authors like Chen Qi and Cheng-Feng Qin are from Beijing Institute of Microbiology and Epidemiology (BIME), which appears to be civilian research institute. However, BIME is actually the same institute of Institute of Microbiology and Epidemiology under AMMS, Academy of Military Medicine. Therefore, the connection of this study to military research institution was covered up by using the name of BIME.

Therefore, it is important to question whether this study also has the potential of dual-use applications. For example, a key finding of this study is that SARS-CoV-2-infected humanized mice experienced a damaged olfactory system, degradation of immune cell function, and impaired olfactory function. Robust viral replication and direct antiviral responses were only detected in the olfactory systems of the infected humanized mice and not in other parts of the brain.[47] Then, the next step would be to further engineer or conduct serial passage of the viruses so that it will infect or only infect other parts of the brain, using the same humanized mice model.

In 2020, Qi and colleagues artificially created a 'pseudorabies virus (PRV)' that expressed the CD2v protein of African Swine Flu (ASFV) and evaluated its effectiveness and safety as a vaccine candidate in mice.[48] No similar experiment has been conducted outside of China and it was well established for over a decade that the CD2v protein actually plays a key role in enhancing the replicability and transmissibility of ASFV virus in pigs.[49] The virulent effect of CD2v was tested by lethality, tissue pathology, expression of inflammatory factors and tissue inflammation in the mice infected with various artificially created PRV strains. The viral genome DNA was detected in all tissues in PRV-infected mice while viral nucleic acid was detected in the brain and lungs of mice infected with certain PRV strains.[50] Qi and team also stated that specific PRV strains have the now-demonstrated ability to reduce immune system function in the early stages of infection, specifically the initial generation and proliferation of adequate T-cells. One key conclusion of this study by these scientists is that this experiment proves that CD2 is actually safe for use in mice and is therefore a viable component of a vaccine candidate. It should be noted that all mice in this study that were directly infected with any of the artificial PRV strains died.[51]

Qi and colleagues did not address any other unique reason why mice were chosen for study of a swine virus AFSV; besides it is more convenient to handle mice in the lab conditions for vaccine study. Qi has also previously conducted experiments on pigs to study the Porcine

[47] Qi Chen, et. al., 'SARS-CoV-2 infection in the mouse olfactory system', *Cell Discovery*, Vol. 7, No. 9, 2021.
[48] Qi Chen, at. al., 'The recombinant pseudorabies virus expressing African swine fever virus CD2v protein is safe and effective in mice', *Virology Journal*, Vol. 17, No. 180, 16 November 2020.
[49] For example, please see Daniel Pérez-Núñez, et. al., 'CD2v Interacts with Adaptor Protein AP-1 during African Swine Fever Infection', *PLOS ONE*, 27 April 2015.
Rebecca Rowlands, et. al., 'The CD2v protein enhances African swine fever virus replication in the tick vector, Ornithodoros erraticus', *Virology*, Vol. 393, Iss. 2, October 2009.
[50] Qi Chen, at. al., 'The recombinant pseudorabies virus expressing African swine fever virus CD2v protein is safe and effective in mice', *Virology Journal*, Vol. 17, No. 180, 16 November 2020.
[51] Qi Chen, at. al., 'The recombinant pseudorabies virus expressing African swine fever virus CD2v protein is safe and effective in mice', *Virology Journal*, Vol. 17, No. 180, 16 November 2020.

Deltacoronavirus.[52] Therefore, Qi's lab did have the capacity to study AFSV directly on pigs. How did they address the concerns that the experiment of AFSV in mice might make the virus adapted to be transmitted in mice and create an additional animal reservoir for this virus, a dangerous virus that causes hemorrhagic disease of swine? The decision to experiment with the CD2v protein is also curious. CD2v has the proven primary function of increasing viral load and transmissibility of the AFSV virus. Therefore, any experimentation of the type that Qi and colleagues conducted would facilitate the emergence of AFSV strains with enhanced pathogenic functions or host range expansion. The 'discovery' of vaccine-related utility (if any) of CD2v would be a secondary discovery at best.

August 2022 LayV Outbreak: PLA in Command (Via Front Organizations) With Evidence of Human Experimentation

The discovery of Langya Henipavirus (LayV) in Shandong and Henan provinces of China has quickly attracted the attention of medical experts around the world.[53] LayV is a type of zoonotic henipavirus and 35 people have been identified to be infected with this pathogen since 2019 in these two provinces in China. Among all the patients, 26 people were infected with LayV only while nine others were co-infected with other pathogens at the same time. All 26 patients with the LayV infection have experienced fever with their probability of suffering from anorexia, coughing, weakness, muscle pain and leukopenia are as great as 50 percent. In addition, liver function impairment, thrombocytopenia, and headaches are also common symptoms of LayV infection.[54]

This report also mentioned that a live LayV sample was isolated from an infected patient and that the full genome sequence was characterized. The phylogenetic analysis based on the L gene homology indicated that LayV was more closely related to the Mojiang Virus, not Nipah or Hendra virus, the two more commonly known henipaviruses.[55] This surprised and confounded many experts.

The Mojiang virus was found in an infamous abandoned mine in Mojiang County in China's Southwestern Yunnan Province. This mine in Yunnan first attracted attention in 2012 when six miners working inside it contracted severe pneumonia of unknown origin and three of them died.[56] Researchers at the time claimed that the Mojiang Virus originated from rats in the mine.[57] In 2013, Shi Zhengli from WIV discovered the coronavirus RaTG13 from bats in the Mojiang mine, which is the official closest known relative to the new coronavirus SARS-CoV-

[52] For example, please see Qi Chen, et. al., 'Pathogenicity and pathogenesis of a United States porcine deltacoronavirus cell culture isolate in 5-day-old neonatal piglets', *Virology*, Vol. 482, August 2015.
[53] 'A new virus that can infect people has been discovered', Health Commission of Hebei Province, 9 August 2022.http://wsjkw.hebei.gov.cn/wbcz/390125.jhtml
Linfa Wang, Liu Wei, et. al, 'A Zoonotic Henipavirus in Febrile Patients in China', *New England Journal of Medicine*, Vol. 387, 4 August 2022.
[54] Linfa Wang, Liu Wei, et. al, 'A Zoonotic Henipavirus in Febrile Patients in China', *New England Journal of Medicine*, Vol. 387, 4 August 2022.
[55] Linfa Wang, Liu Wei, et. al, 'A Zoonotic Henipavirus in Febrile Patients in China', *New England Journal of Medicine*, Vol. 387, 4 August 2022.
[56] Xavier Fernández-Aguilar, et. al., 'Novel Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012', *Emerging Infectious Diseases*, Vol. 20, No. 6, June 2014.
[57] Diego Cantoni, et. al., 'Pseudotyped Bat Coronavirus RaTG13 is efficiently neutralised by convalescent sera from SARS-CoV-2 infected patients', *Communications Biology*, Vol. 5, No. 409, 3 May 2022.

2 (with a 96 percent genetic similarity between the two) and the Mojiang mine gained additional attention from researchers in China and their international collaborators.[58]

This mine in Mojiang resembles a 'cave of viruses' harboring these two dangerous viruses in different hosts: Coronaviruses in bats and Mojiang Virus in rodents. However, there are still many questions that remain unanswered about this mysterious cave: what happened to the other three miners who had unknown pneumonia but did not die? Did they have any other coinfection with other viruses? After the Mojiang Virus was identified, did those miners' samples get retested for any potential zoonotic infection from the Mojiang Virus? What is unique in this cave that makes it such a unique hub of emerging pathogens?

Another material issue related to the discovery of LayV in this recent study is the involvement of PLA medical entities. The two key Chinese scientists that have taken the lead in the analysis of LayV are Dr. Li-Qun Fang and Dr. Wei Liu, both of whom are part of BIME. However, BIME is actually the same entity of Institute of Microbiology and Epidemiology under AMMS and, by extension, the PLA. In addition, Supplementary materials related to this study clearly indicated that the PLA's 990 Military Hospital in Henan province was involved in this study. Interestingly, BIME reporting has indicated that 34 out of the 35 LayV patients were local farmers.[59] Why were the farmers' samples analyzed in a military hospital as a sentinel surveillance program?

BIME has also indicated that those 35 patients infected with LayV were identified during sentinel febrile illness surveillance (i.e., routine infectious disease surveillance) in 2020. Given the nature of LayV, it is very unusual to report the discovery and isolation of a live henipavirus with significant delay of three years. A new henipavirus is highly epidemiologically significant and should have been publicly reported in 2019 as soon as it was discovered. Meanwhile, among the 35 patients, 6 patients were found to be co-infected with Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) while 2 patients were found to be co-infected with Hantavirus.[60]

The SFTSV and Hantavirus are highly infectious viruses that could lead to severe viral hemorrhage and their outbreaks in China are relatively rare events. So, in this so-called 'sentinel febrile illness surveillance', this group of military scientists identified three dangerous pathogens at one time with some patients being co-infected with two rare pathogens. How likely would this happen in a natural situation? Also, in regular sentinel febrile illness surveillance, these viruses would not be included in the regular screening under normal circumstances.

LayV, SFTSV and Hantaviruses can also all infect rodents. SFTSV is a novel phlebovirus (in the Bunyaviridae family) and certain tick species have been demonstrated as a competent vector of SFTSV by experimental transmission study and field study.[61] Further, LayV and Hantavirus can infect humans if people encounter rodent droppings or feces. So, in order for

[58] Joanna Mazet, Peter Daszak, Shi Zheng-Li, et. al., 'Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor', *Nature*, Vol. 503, No. 28, November 2013.
[59] Supplementary Appendix to Linfa Wang, Liu Wei, et. al, 'A Zoonotic Henipavirus in Febrile Patients in China', *New England Journal of Medicine*, Vol. 387, 4 August 2022.
[60] Supplementary Appendix to Linfa Wang, Liu Wei, et. al, 'A Zoonotic Henipavirus in Febrile Patients in China', *New England Journal of Medicine*, Vol. 387, 4 August 2022.
[61] Yuan-Yuan Hu, et. al., 'Role of three tick species in the maintenance and transmission of Severe Fever with Thrombocytopenia Syndrome Virus', *PLOS Neglected Tropical Diseases*, Vol. 14, No. 6, 10 June 2020.

the patients to be co-infected with SFTSV and LayV, the rodents need to be infected by the ticks first to get SFTSV, and also their droppings and feces need to be touched by those farmers. How 'lucky' these scientists were to find all of these exceedingly rare co-infection cases from a single field case study under an official sentinel surveillance framework.

Although SFTSV and Hantavirus infections have become endemic in Shandong or Henan Provinces in recent years, it is still very unusual to see patients co-infected with these dangerous pathogens. In the BIME study, no patient died even though SFTSV and Hantavirus normally high mortality rates. Given these dynamics, his study appears to be a targeted surveillance project to look for certain pathogens' zoonotic infection risk to humans via transmission by rodents (with screening of different species of rodents).

Would it be possible that this study was a test of these dangerous pathogens and see which one was more prone to cause human infection? With the involvement of a military hospital and scientists from the PLA, would it be possible that this was a field release of multiple dangerous pathogens followed by field screening of rodents and potential human infections caused by infected rodents? The answer to this question is beyond the scope of this specific report, but these questions are reasonable speculation and should serve as an alarm for national security experts.

Strategic Implications and Near-Term Directions

All Chinese biomedical research institutions fall under the control of the CCP and the Civil-Military Fusion Law. As such, there is a possibility that any institution can be repurposed and directly controlled by the Chinese government under specific contingencies, including lab accidents.[62] The Civil-Military Fusion Law is an overarching legal framework within which all biomedical institutions must operate. However, despite this uniform structure, CAMS/PUMC and AMMS have nonetheless emerged as primary nodes in the Chinese virology research network. AMMS carries out high-risk experiments in its own right while also enabling other nominally civilian institutions in China. Displaced high-risk research that was previously conducted at other institutes, such as WIV, would have 'top cover' protection to be conducted, especially given Major General Chen Wei's status within the highest levels of the CCP. It should be noted that the 2021 SARS-CoV-2 GoF serial passaging study also involved Shi Zhengli from WIV.[63] This is unlikely to be purely coincidental.

CAMS meanwhile conducts nearly identical high-risk pathogen research that has been observed at WIV and HVRI while avoiding international scrutiny even as the respective capabilities of its constituent units accelerate. While CAMS is not formally organized under the PLA, its high-risk pathogen research network is demonstrably more diversified than even AMMS in terms of pathogen types and both its domestic and transnational linkages, specifically to UTMB in Galveston. CAMS also has demonstrated high-risk pathogen research capabilities that are at least on par with WIV and may actually exceed them. This has been accomplished while avoiding international attention almost entirely.

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[62] For additional analysis of the Civil-Military Fusion Law, please see 'Alibaba and Ant Group: Involvement in China's Military-Civilian Fusion Initiative', RWR Advisory Group, 2 October 2020. https://www.rwradvisory.com/wp-content/uploads/2020/10/RWR-Report-Ant-MilCiv-Fusion-10-2020.pdf For a more in-depth discussion, please see Ryan Clarke, 'Emerging Global Pandemic Risks Come from Engineered Viruses in Chinese Labs, Not the Jungle or Bat Caves', Epoch Times, 4 September 2021.

[63] Zheng-Li Shi, Ben Hu, et. al., 'Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells', *Virologica Sinica*, Vol. 26, 2021.

The aggregated capabilities of CAMS, WIV, HVRI, AMMS (and BIME in particular) demonstrate an ambitious and increasingly domestically-driven high risk pathogen research ecosystem. Unlike prior generations, these Chinese pathogen research institutes will maintain specific transnational linkages under CCP direction to ensure that China remains the world leader with an ever-increasing gap between 1st and 2nd place. The inherent dual-use nature of these experiments on SARS-CoV-2, ASFV, Zika, Henipah/Nipah virus have geostrategic implications. Any nation that can be the first to identify an emerging pandemic and take specific measures to protect its population will inevitably have strategic advantages over nations that do not.

Annex A: Additional Bioweapons Intelligence and Research Reports

Malevolent Matrix: Forging a Coherent National Biodefense Strategy — The CCP BioThreats Initiative

In the Shadows of Science: Unravelling China's Invisible Arsenals of Nanoweapons — The CCP BioThreats Initiative

Guardians of the Invisible Arsenal - Weapons Research at the Research Institute of Chemical Defense — The CCP BioThreats Initiative

State-Backed Synthetic Narcotics Trafficking Syndicates and the Vectored Threat to the Five Eyes — The CCP BioThreats Initiative

The International Frontier of the CCP's Bioweapons Program — The CCP BioThreats Initiative