

# Did a Review of Samples Collected from a Mineshaft Cause the COVID-19 Pandemic?

This is a compilation of circumstantial evidence to support the theory that SARS-CoV-2, the virus that causes COVID-19, leaked from a Wuhan laboratory.

Several Wuhan laboratories have conducted research into SARS or SARS-related coronaviruses in the years prior to the pandemic. These include facilities at Huazhong University, the Wuhan Center for Disease Control (WHCDC), the Wuhan Institute of Virology (WIV) and Wuhan University (WU).

This research focuses on a project connecting these institutions and presents information supporting a potential spillover event due to mishandling of a sample or specimen stored at the WIV in late 2019. This is proposed to have taken place during a well-documented review of samples and specimens collected under the multiyear project that identified the closest known virus to SARS-CoV-2.

## Evidence of a COVID-19 outbreak before December 2019

Evidence suggests that SARS-CoV-2 had been circulating in Wuhan months before the outbreak was reported publicly:

- Satellite images show that Wuhan hospitals had been overcrowded [from September 2019](#), supported by anecdotal evidence [in November](#).
- One Wuhan-based PhD student was warned of a pneumonia outbreak [in September 2019](#), followed by a major pneumonia outbreak in November that was concealed.
- The earliest independently verified classified Chinese government data showed that one patient contracted the virus [on 17 November](#), weeks before the virus reportedly spread at the Huanan Seafood Market.
- Evidence within the virus itself indicates that it had already adapted to human-human transmission [before being detected in December](#).

## Hospitals were told to stop isolating virus specimens from respiratory disease patients testing negative for influenza in November 2019

In the weeks before the COVID-19 outbreak was announced publicly, Chinese authorities were preparing for a dangerous respiratory disease epidemic.

[On 13 November 2019](#), China's National Health Commission (NHC) [issued new influenza guidance](#) instructing hospitals to check the [blood-oxygen levels](#) of patients with respiratory disease-related pneumonia and to look for what are also COVID-19 symptoms. These included: pneumothorax and mediastinal emphysema; [acute](#)

[necrotizing encephalopathy](#); and multifocal brain damage, including of the bilateral thalamus and white matter around the ventricle.

The 2019 plan reversed previous guidance on testing by telling hospitals to [stop isolating virus specimens from patients who test negative for influenza](#), and said that a negative antigen test cannot rule out influenza.

The SARS-CoV-2 outbreak was made public by the [isolation of viral specimens from patients testing negative for influenza](#), against the recommendation of the 2019 influenza guidance. The results of this specimen isolation were shared with Dr Li Wenliang, who shared the results with others who shared them with the world.

The influenza plan and medical staff handbook were drafted by [an expert group](#) under China's NHC, headed by Wang Chen with Zhong Nanshan is a consultant. Other members include respiratory disease specialists from various institutes.

The social vaccination idea [later encouraged by the WHCDC](#) was promoted at [the group's press conference](#). It encourages frequent handwashing, avoiding touching the face and wearing a mask. This concept was supported by guidance from the Hubei CDC, which on 20 December [issued instructions](#) encouraging frequent handwashing, avoiding crowded places, outdoor physical exercise and advising those with flu-like symptoms to wear masks to prevent transmission to other family members, and seek medical attention if symptoms continue to develop.

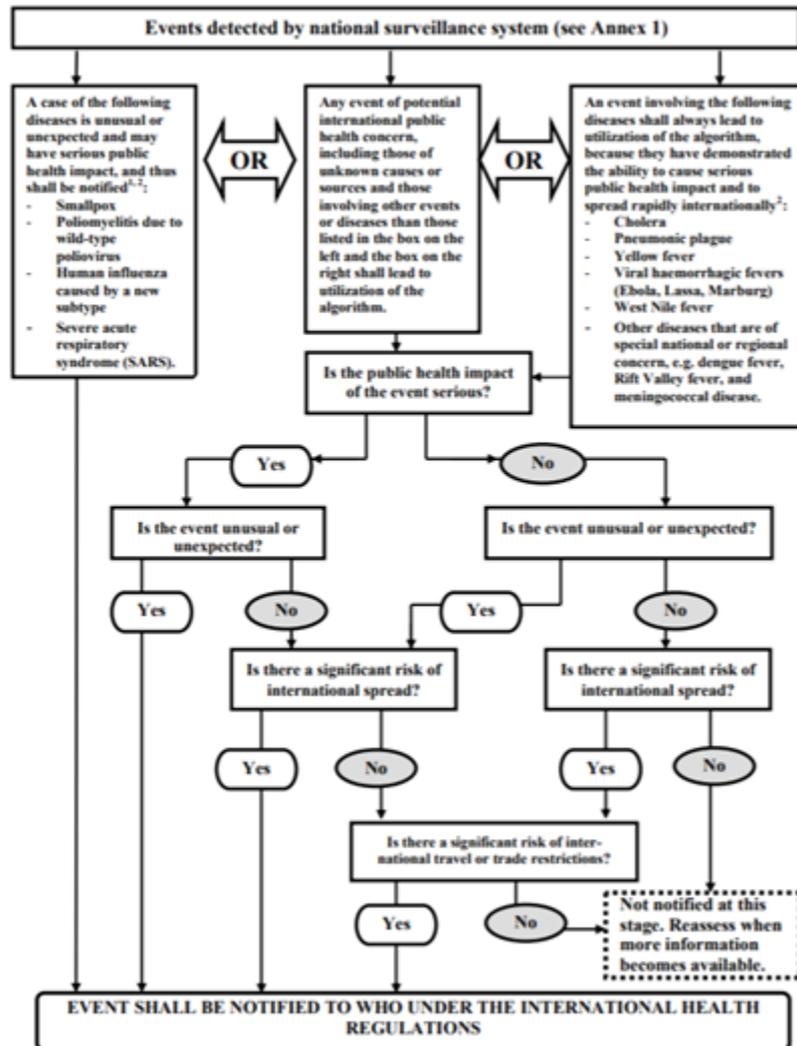
The change to not recommending virus specimen isolation in China's 2019 plan is not consistent with equivalent guidance from the US CDC, which recommends it for novel virus identification ([1](#), [2](#), [3](#)).

The 2019 and 2018 medical guidance both state that [virus specimen isolation is used to identify novel viruses](#) and for virus mutation analysis. By changing the guidance to say that virus specimen isolation is not recommended for respiratory disease patients testing negative for influenza, China's NHC appears to have discouraged detection of novel viruses and made clinical misdiagnosis of COVID-19 as influenza more likely.

Soon after this guidance was issued, pneumonic influenza outbreaks and overcrowded hospitals were reported in Hubei and across China, ([1](#), [2](#), [3](#), [4](#), [5](#), [6](#), [7](#), [8](#), [9](#), [10](#), [11](#), [12](#), [13](#)) and the WHCDC publicly [refuted rumours of an influenza outbreak](#) on 20 December. This was during an unusually [large and early spike](#) in officially reported influenza cases.

Knowing when authorities knew about the epidemic is important. As a signatory to the 2005 International Health Regulations, the Chinese government has an obligation under Article 6 to assess an event within 48 hours and then report it to the WHO [within 24 hours](#). The WHO was informed of the outbreak on 31 December 2019 by its own country office, and by China's government on [3 January 2020](#).

ANNEX 2  
**DECISION INSTRUMENT FOR THE ASSESSMENT AND NOTIFICATION  
 OF EVENTS THAT MAY CONSTITUTE A PUBLIC HEALTH EMERGENCY  
 OF INTERNATIONAL CONCERN**



<sup>1</sup> As per WHO case definitions.

<sup>2</sup> The disease list shall be used only for the purposes of these Regulations.

Notification decision making tool of the 2005 International Health Regulations

There are reasonable grounds to independently investigate a violation of the Regulations. The Chinese Communist Party (CCP) routinely covers up evidence of epidemics: Chinese censors had [instructed social media platforms](#) to cover up reports of a pneumonic plague outbreak on 12 November 2019, and had been [censoring discussion of the COVID-19 outbreak](#) from at least 31 December 2019, three days before notifying the WHO of the outbreak.

### First publicly shared SARS-CoV-2 sequence collected under new program

On 11 January 2020, a team of scientists led by Professor Zhang Yongzhen of the Shanghai Public Health Clinical Center published the full SARS-CoV-2 genome sequence. This had reportedly been collected by the team from the Wuhan Central

Hospital and the WHCDC on 26 December 2019, but not delivered to the Shanghai lab until [3 January 2020](#). It was then fully sequenced and submitted to the Chinese NHC on 5 January. The WIV had submitted a similar sequence on 2 January. Another lab had reportedly submitted a SARS-CoV-2 sequence to the Chinese Academy of Medical Science's Institute of Pathogen Biology [on 27 December](#).

After waiting for days without the authorities publishing the sequence, on 11 January Professor Zhang's team published it in full, allowing the world to begin research. China's government [shut the Shanghai lab down the following day for "rectification"](#).

Professor Zhang had said that the samples were collected from patients as a part of the team's long term cooperation with the WHCDC and the Hospital under the program ["Scientific survey of the principal natural viral pathogen resources in China"](#). One of Professor Zhang's team later said that this [had been going on for many years](#).

This Ministry of Science and Technology program had recently gone through [a tendering process](#) over 11 July-13 September 2019. Winners were required to identify five major novel viral pathogens from wild animals including bats, and carry out biosecurity risk assessments by testing them on small animals. Its assessment indicators were to:

- 1) Submit a report on the lineage, genetic characteristics and geographical distribution of viral pathogen carriers such as bats, birds, mosquitoes, rodents and ticks in key regions of China;
- 2) Obtain genomes of more than 100 novel viruses / strains;
- 3) Isolate, identify, collect and preserve 50 major viral pathogens;
- 4) Analyse the pathogenic characteristics of 10 major novel viruses / strains, including at least five major novel viral pathogens, based on a biosecurity risk assessment at the cellular and small animal level; and
- 5) Establish a standardised viral pathogen resource library and shared database.

The project [was awarded to Professor Zhang's team and then suspended](#). As the project was not running at the time of the collection of these virus samples, Professor Zhang's team likely referred to another very similar project led by the WIV.

### **The WIV's viral pathogen program**

The WIV had been running a program very similar to the program under which Professor Zhang's team obtained SARS-CoV-2 for years. The program, "Investigation of viral pathogens of major natural hosts and vector insects in China" (2013FY113500), launched in [May 2013](#) and was being reviewed around the time of the outbreak.

It carried out extensive research into viral pathogen vectors and was already running a database very similar to that described in the new program, containing data on arthropod, bat and rodent viruses.

Under this program, the WIV investigated the main natural virus hosts and vectors in China, [taking samples](#) from bats, birds, mosquitoes, rodents and ticks. The WIV had collected [over 15,000](#) such samples from bats, [over 1,400 live viruses](#) and over 60,000 strains.

Data from [over 20,000 samples and specimens](#) collected on such trips were stored on an WIV database, and the samples themselves were stored at -80°C.



Viral pathogen vectors investigated by the Wuhan Institute of Virology, *Virologica Sinica* Volume 33 Issue 1, February 2018

### **Mojiang mine-related unknown pneumonia outbreak**

The WIV [collected samples containing BtCoV/4991](#), later known as RaTG13, under the program. The partial BtCoV/4991 sequence published in 2016 is a [98.9% match to SARS-CoV-2](#). When the WIV sequenced the full RaTG13 genome after the COVID-19 outbreak, the published results show a [96.1% match](#). This is by far the closest known match.

According to WIV research, similar SARS-related coronaviruses appear to [cluster geographically](#). This means that SARS-CoV-2 may have been present in the same area that RaTG13 was collected from.

RaTG13 was identified from samples collected on trips to investigate a [mineshaft associated with a deadly outbreak of unexplained pneumonia](#) in Tongguan, Mojiang, Yunnan, China. The mine had been associated with an outbreak that killed three

miners, whose deaths were suspected to be connected to a SARS-related coronavirus. Four of the miners were shown to have [carried SARS antibodies](#).

These cases were [not reported in China's unknown pneumonia statistics](#), despite the PhD thesis being supervised by now head of China's CDC George Gao, and samples being sent to SARS expert Zhong Nanshan's laboratory. It is unclear whether the outbreak was reported to the WHO under the 2005 International Health Regulations.

The WIV appears to have [continued to work on RaTG13 for years](#), publishing sequences dated June 2017 and September-October 2018. The [RaTG13 amplicon sequences dated from before the outbreak](#) and uploaded afterwards differ significantly from the full sequence also uploaded after the outbreak, likely due to the sequencing method used.

The screenshot shows the NCBI Sequence Read Archive interface. It displays a list of reads for the accession SRR11806578. The reads are listed with their IDs, names, and member information. A sequence alignment plot is shown below the list, displaying the sequence of the reads and various annotations such as Quality Score, Base#, Density, and Comments. The plot shows a partial sequence of RaTG13 dated 14 October 2018.

A partial sequence of RaTG13 dated 14 October 2018

The question of whether RaTG13 is a result of a passage experiment of SARS-CoV-2 published after the outbreak as a diversion is beyond the scope of this research. The presence of [weak matches to mus musculus](#) in its amplicon sequences may be explained by in lab contamination as well as by passage. The results of the SARS-CoV-2 reference genome compared to the RaTG13 reference genome are below.

Blast Results				
SARS-CoV-2 Reference Genome	T	C	G	A
<b>RaTG13 Reference Genome</b>	<b>C</b>	<b>T</b>	<b>A</b>	<b>G</b>
<b>Mismatches</b>	350	331	136	127

## **The missing WIV bat virus database containing unpublished virus sequences**

Data on these samples and others were stored in a WIV database, which has been taken offline. The database was expanded as part of a long term effort to investigate the link between bat viruses and vectors for the [Ministry of Science and Technology](#).

Version 2 of the database was [released in June 2019](#). It improved on other databases like DBatVir by including information on seasonal epidemics of viruses crossing the species barrier into other wild animals, based on samples taken by the WIV in the field. This version had a [password protected section for as yet unpublished novel virus sequences](#).

It presents a HKU9 virus as an example of its contents, sampled on WIV trips to Yunnan, including to [Mojiang in 2013](#). BtCoV/4991 (RaTG13) was sampled by the WIV in Mojiang in 2013.

Its description was [amended significantly in the update to Version 4 on 30 December 2019](#), replacing references to wild animals with those to bats and rodents. Dr Shi Zhengli was the administrator and busy at a conference on that day until reportedly being informed of the novel coronavirus outbreak at 19:00.



Landing page of the Wuhan Institute of Virology's Wildlife-borne Viral Pathogen Database, June 2019

The [database was accessed](#) on a near daily basis from 10 April until it was taken offline in the early hours of [12 September 2019](#). The database does not appear to have been accessed via its portal since then, despite the 30 December edits removing keywords related to the COVID-19 epidemic from its description. Records show it being [online intermittently](#) without recorded visits from outside of the WIV until early 2020.

6.4GB was downloaded from the 61.5MB SQL database in June 2019 from [within the China Science and Technology Network \(CSTN\)](#), mainly [in Beijing](#). By September it was accessed almost entirely [by the WIV and non-CSTN users](#). This indicates that the WIV were accessing data on viral pathogens from the program that identified RaTG13 well into September 2019.

This fits with the proposed research direction recommended by WIV researchers in March 2019 [to investigate cross-species transmission](#) and human pathogenesis of bat SARS-related coronaviruses. WIV job postings on [18 November](#) and [24 December 2019](#) indicate that such work was taking place.

This public database and its password protected section with unpublished virus sequences are no longer available publicly, and even the pages describing it have now been taken offline. Related Chinese virus databases have also been taken offline ([1](#), [2](#)).

The purpose of this database is to provide information on the cross-species transmission of pathogens including bat SARS-related coronaviruses collected by the WIV in Yunnan. It has been made unavailable to the scientific community at the time when the world needs it most.

### **Inspections of samples from the program that identified RaTG13**

To understand why the database may have been taken offline on 12 September 2019, it is worth examining what was happening at the WIV at that time, when the program that identified RaTG13 was being reviewed.

The reviews included a financial and management audit by an [approved auditor](#), [spot checks](#) including [on-site inspections of samples and specimens](#) collected under the program and a review of data accumulated under it, including that relating to [samples and specimens](#).

The WIV were told that spot checks of samples and specimens collected under the program such as those containing RaTG13 may occur at any time during the review. Inspections of the WIV had previously also looked at [model animals](#) used in experiments.

On-site [inspections of such projects across China](#) were carried out by the Ministry of Science and Technology's Basic Research Department. The Department had visited the WIV in March 2019 and discussed construction of its biosafety level four (BSL-4/P4) lab, expressing hope that this would [improve biosafety standards](#).

The WIV were instructed to ensure that samples and specimens including those collected from the Mojiang cave were stored appropriately ready for inspection.

The process of physically going through samples and specimens from this project is the proposed means by which a spillover event occurred.

### **Poor lab safety record of institutions involved in the program that identified RaTG13**

According to a September 2019 paper, biosafety-related supervision at laboratories studying pathogens [is inadequate across China](#).

The WIV's high security BSL-4 lab has well-publicised [safety issues](#). However, it is not the only Wuhan lab with such issues. Wuhan University (WU) also worked on the program that identified RaTG13. WU operates its own [ABSL-3 facility](#) for studying SARS coronaviruses in [animals](#) and had been researching a [SARS vaccine](#).

Along with Huazhong Agricultural University, which had also been involved in SARS research, and the Wuhan Institute of Technology, WU facilities were [being inspected in late 2019](#).

The WU inspections were intended to check that [problems announced on 12 June 2019 following inspections](#) had been rectified. [These problems](#) included: hazardous waste being exposed; no separation of the experiment area; students not wearing lab coats; no eyewash; a crowded experiment area cluttered with cardboard boxes; and there being no laboratory-specific safety guidelines.

The issue of laboratory safety was particularly important in 2019. Several Wuhan universities issued strict guidelines on lab safety measures during the 18-27 October Military Games. WU labs were inspected again [over 24-25 September](#), and [again in October](#) to rectify problems before the Games.

The concern with lab safety at the time of the COVID-19 outbreak was part of an overall effort to improve the inadequate system. The Ministry of Education, responsible for the WU inspections, had [issued new guidelines on lab safety](#) on 25 September. It had issued a circular on institutions inspecting their own labs [on 18 April](#), and [another](#) on 22 May on strengthening lab security. The Wuhan government had issued guidance on lab inspections in the healthcare industry [on 5 September](#).

The facts that WU staff worked on the same program that identified RaTG13, and WU had such a poor track record of lab safety adds to the plausibility of a WIV staff member on the program mishandling a sample or specimen.

The WIV filing [their only patent for a device to protect against accidental virus transmission in a biosafety laboratory](#) on 15 November 2019 shows that accidental transmission was a concern at the time of the outbreak.

### **WIV disciplinary meetings and rectification**

Criticism and disciplinary procedures are to be expected, though the WIV's [records](#) indicate that significant mistakes were made in 2019:

- [12 November 2019](#): The WIV Communist Party met to discuss a recent in-depth investigation of the Wuhan BSL-4 laboratory staff, the problems found and ways to improve the laboratory management team.
- [19 November 2019](#): Training of all WIV safety officers to address common problems in the safety management of laboratories.

One WIV security officer presented on the problems found during the safety inspection of the WIV over the past year, and the serious consequences of safety

hazards, emphasising that personnel should rectify the problems by implementing safety regulations.

A CAS representative presented on recent large-scale accidents in China and abroad, based on practical experience of the CAS.

The presentation covered instructions on safety from the Communist Party leadership. Proposals to implement such instructions involved taking responsibility, operational planning, emergency planning, in-depth analysis of hidden problems and an assessment of the complexity and danger involved.

It covered common problems in the management of laboratory safety, technology safety, student safety, campus safety and network safety. The CAS plan to improve safety management included: strengthening understanding of political doctrine; clarifying powers and responsibilities and promoting their implementation; coordinating as a unit and strengthening management and control; and strengthening scientific and technological security risk research and construction of an early warning monitoring system.

- [25 November 2019](#): The WIV Communist Party Disciplinary Committee discussed accountability and correcting mistakes, and measures to take after cadres make mistakes.
- [11 December 2019](#): WIV training for 20 new hires discusses confidentiality and safety, including recent cases of confidentiality violations.
- [19 December 2019](#): WIV Disciplinary Committee discusses identification of problems in audit.
- [3 January 2020](#): WIV disciplinary meeting discusses mistakes made when archiving materials in 2019. The discussion covered the importance of safety, ensuring a safe and accident free archiving process, strengthening the implementation of safety responsibilities, and strengthening the rectification of hidden hazards.
- [14 January 2020](#): CAS and WIV issue 2020 guidelines for a project to improve biosecurity at the BSL-4 lab.
- [16 January 2020](#): WIV invites bids for artificial intelligence lab monitoring system to be installed at high level biosafety labs.

The meetings to discuss problems at the WIV, a recent large scale lab safety accident in China, confidentiality violations and mistakes made when archiving materials support the hypothesis that the WIV was responding to a leak of SARS-CoV-2 due to an incident. The urgent need to improve biosecurity and monitor staff implies that the WIV were well aware of the need to rectify safety failings.

**No evidence of natural exposure to BtCoV/4991-like virus**

The rival theory of the COVID-19 pandemic emerging via natural zoonotic transmission uses seropositivity tests as evidence of natural spillover of SARS-related viruses. These include a study showing [6/218 people living close to Yunnan bat caves](#) with bats known to host SARS-related viruses were seropositive for SARS antibodies. The authors used patients in Wuhan as the control group, due to Wuhan's location over 1,000km away. Another study showed [9/1596](#) were seropositive. The four tested Mojiang miners were also seropositive for SARS antibodies.

While these studies involving small sample sizes are evidence of some natural exposure to SARS-related viruses, the authors state that "The low seroprevalence observed in this study suggests that bat coronavirus spillover is a rare event."

Such a rare event must be considered alongside the probability of spillover of a SARS-related virus with an RdRp only 1% different to BtCoV/4991, as well as the probability of this spreading undetected past China's extensive virus surveillance network and first being detected in the vicinity of the WIV while WIV staff were handling BtCoV/4991 and related samples.

## **Conclusion**

This research establishes the circumstances in which a spillover event may have occurred: the mishandling of a sample or specimen collected from Mojiang, Yunnan during the scheduled review.

This is based on the documentary evidence that WIV staff were handling samples and specimens containing BtCoV/4991 (RaTG13) and related viruses around the time of the outbreak.

Samples and specimens collected under the multi-year pathogenic bat virus research program that identified the virus closest to SARS-CoV-2 were being reviewed before a 30 September deadline, while applications for the successor program were due to be assessed. Labs at institutions involved in the program have a poor safety record, and the WIV's records indicate that there were problems at its facilities in 2019.

Proving how SARS-CoV-2 managed to infect humans may be impossible, owing to the [destruction of evidence](#) including [orders to destroy samples](#) and strict control on the flow of information. Investigation by researchers not under the influence of the CCP is essential, as [the Chinese government has decreed](#) that all research into the origins of SARS-CoV-2 in China must be reviewed by the government before publication.

Areas to further explore include:

- Accounting for the movements in late 2019 of WIV staff, looking for potential 14 day self-isolations, and the program [inspectors](#).
- The motivation behind the WIV taking databases associated with the program that identified RaTG13 offline and deleting traces of them.

- Any guidance similar to the [13 November 2019 instructions](#) issued to hospitals to look for COVID-19 symptoms in respiratory disease patients and to stop isolating virus specimens from them.
- Whether biosecurity legislation and regulations appear to have been drafted as a reaction to a lab leak spillover event or part of a [long term effort to overhaul China's inadequate biosafety standards](#).
- Assessing the type of viral pathogen research being carried out by the WIV based on [the types of files downloaded](#) from the now offline database until the early hours of 12 September 2019, and knowledge of the [research direction in 2019](#).
- Mapping which teams were accessing the database in 2019 using records of which [networks](#) accessed them from which [countries](#), [cities and provinces](#), and the movements of researchers.
- Mapping work on SARS-related coronaviruses done at the WIV's [ABSL-2 facility](#), its [BSL-2, BSL-3 and BSL-4](#) and other facilities at Zhengdian Scientific Park and its [BSL-3 facility](#) at Xiaohongshan Park, as well as at Huazhong University, the WHCDC and WU.

### **Credit**

Many thanks to [@BillyBostickson](#), [@franciscodeasis](#), [@luigi\\_warren](#), [@TheSeeker268](#) and others for publicly sharing your excellent research into Wuhan labs, early discussion of the Wuhan pneumonia outbreak and the pneumonia outbreak connected to the Mojiang mineshaft.

Many thanks also to [@schnufi666](#) for your correction relating to the publication date of the RaTG13 amplicon sequences in the [18 June 2020 version](#) of this article.