

## **SCIO press conference on COVID-19 origin tracing**

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On July 22, the State Council Information Office (SCIO) held a press conference in Beijing on COVID-19 origin tracing.

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### **Speakers:**

Xu Nanping, vice minister of science and technology

Zeng Yixin, vice minister of the National Health Commission

Wang Chen, vice president of the Chinese Academy of Engineering, president of the Peking Union Medical College, and director of the National Center for Respiratory Medicine

Liang Wannian, team leader of the Chinese side of the joint expert team of WHO-convened Global Study of Origins of SARS-CoV-2

Yuan Zhiming, director of the Wuhan National Biosafety Laboratory, and researcher at the Wuhan Institute of Virology, Chinese Academy of Sciences

### **Chairperson:**

Shou Xiaoli, deputy head of the Press Bureau of the State Council Information Office (SCIO) and SCIO spokesperson

### **Date:**

July 22, 2021

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### **Shou Xiaoli:**

Ladies and gentlemen, good morning! Welcome to this press conference from the State Council Information Office (SCIO). The topic of the press conference is COVID-19 origin tracing. Today, we have invited Mr. Xu Nanping, vice minister of science and technology; Mr. Zeng Yixin, vice minister of the National Health Commission; Mr. Wang Chen, vice president of the Chinese Academy of Engineering, president of the

Peking Union Medical College, and director of the National Center for Respiratory Medicine; Mr. Liang Wannian, team leader of the Chinese side of the joint expert team of WHO-convened Global Study of Origins of SARS-CoV-2; and Mr. Yuan Zhiming, director of the Wuhan National Biosafety Laboratory, and researcher at the Wuhan Institute of Virology (WIV), Chinese Academy of Sciences. They will introduce the relevant information and take your questions.

Next, I will give the floor to Mr. Zeng.

**Zeng Yixin:**

Friends from the media, good morning. I'm very glad to see so many journalists present at this press conference regarding COVID-19 origin tracing, as this is a very specialized issue. Since the COVID-19 outbreak, all responsible countries and scientists have been eager to find out where the coronavirus came from. Solving the question will greatly help prevent similar pandemics. On March 30, the World Health Organization (WHO) released the joint study report "WHO-convened Global Study of Origins of SARS-CoV-2: China Part," marking a good start for the global study of the origins of SARS-CoV-2. Governments, scientists, media outlets around the world have paid great attention to the report. Over the past few months since the report was released, more and more scientific evidence has proved it is a valuable and authoritative report that stands the test of science and time. The conclusions of the report are scientific, as they were made on the basis of scientific principles.

First, let's review the background of the report.

Before the joint study, China had organized a multidisciplinary team to do a lot of work on origin tracing, despite arduous epidemic prevention and control tasks. It was on the basis of this work that our experts and the WHO experts to China discussed and jointly formulated the Terms of Reference (TOR) last July. Since then, China has carried out origin-tracing studies in strict accordance with the TOR.

At the beginning of this year, the WHO international expert team arrived in China and started the China part of the global study of the virus origins. China upheld the principles of openness, transparency, science, and cooperation, and gave full support to the expert team. Together with local governments, we have done our best to coordinate relevant organizations to meet the requirements of the experts. The experts visited a total of nine places they wanted to visit, including Jinyintan Hospital, the Huanan Seafood Wholesale Market, and the WIV. They talked with everybody they wanted to talk with, including medical workers, laboratory staff

members, researchers, market managers, merchants, residents, and recovered patients. The joint origin-tracing study involved a heavy workload, but the experts carried out careful and in-depth analysis into every question and every piece of data. They often worked around the clock, forgetful of their sleep and meals. We deeply admire their professionalism and spirit of science. On behalf of the Chinese government, I would like to express our heartfelt gratitude to the international experts.

Second, I would like to talk about the conclusions of the study.

The report is an account of the China part of the global study of the virus origins. The expert team reached the following conclusions. The coronaviruses found in bats and pangolins are most highly related to SARS-CoV-2 and share the highest homology with SARS-CoV-2 by sequencing. However, neither of the viruses identified so far from these mammalian species is sufficiently similar to SARS-CoV-2 to serve as its direct progenitor. Although the homology is high, there is still much difference. Based on research results in various fields, such as clinical epidemiology, zoology, and environmental testing, the joint study team assessed the likelihood of different possible pathways for the introduction of the virus. First, direct zoonotic spillover is considered to be a possible-to-likely pathway. Second, introduction through an intermediate host is considered to be a likely-to-very-likely pathway. To put it simply, this means the virus would have been transmitted from an animal reservoir to an intermediate host, followed by transmissions to humans. This is a likely-to-very-likely pathway. The third potential pathway is introduction through cold food chain products. Some sporadic outbreaks in many places last year showed that introduction through cold food chain products was possible. So, this is considered a possible pathway in the report. At last, introduction through a laboratory incident is considered to be an extremely unlikely pathway.

Third, let's talk about the next step for tracing the origin of the virus.

On the one hand, we have been actively supporting relevant departments and scientists to continue the tasks that need to be supplemented and improved, which are clarified in the China part of the joint report of WHO-convened global study of origins, and will give timely feedback to the WHO. In other words, we will complete the remaining tasks as soon as possible. On the other hand, the China part of the joint report has pointed out the direction for the next step of joint study of origins in various countries and localities under the global framework, and we should continue to move forward along this direction. I want to

emphasize that the China part of WHO-convened joint study on the origins of the COVID-19 is an excellent example of international cooperation. We worked with the WHO and jointly explored a set of effective working mechanisms and working methods for global origin tracing of emerging infectious diseases. WHO experts have established a sound cooperation mechanism with Chinese experts. The cooperation between the two parties has been very close, which is of great significance to promoting the global tracing of the origins of the COVID-19. The expert group has always upheld a scientific and rigorous professional attitude, repeatedly discussing and researching every specific issue. This is a very good model and mechanism. Therefore, we sincerely hope that the international team of experts who participated in this study on origins can continue to play a role in the next phase of relevant work and make full use of their valuable experience in the follow-up global tracing study, making contributions to get to the bottom of the origin of the COVID-19.

Origin tracing is a complex scientific matter that involves many disciplines and experts in many different fields. It is also a global problem. The origin tracing of diseases such as AIDS, Ebola, Middle East Respiratory Syndrome, SARS in 2003, and avian flu in 2009 all proved to be very difficult, and some of their origins still remain undiscovered. Therefore, for the next phase, the origin tracing work should be conducted under the overall planning and coordination of the WHO and based on the first phase of study. Outstanding experts from multiple countries should be organized to carry out further studies. It is necessary to ensure that scientists must be the main actors in the research. We also call for strengthening exchanges, cooperation and information sharing. We should scientifically carry out the work of tracing the origin.

That's all for my opening remarks. Thank you!

**Shou Xiaoli:**

Thank you, Mr. Zeng, for the introduction. Now the floor is open to questions. Please identify your news outlet before raising questions.

**CCTV:**

As mentioned earlier, tracing the origin of a virus is a long-term complex scientific issue. Relevant origin tracing work was carried out on the 1918 flu pandemic, 2009 H1N1 pandemic, and the global AIDS epidemic. This time, the inquiry into the origin of the COVID-19 has also been carried out globally. What is its significance and the reasons for it? Thank you.

**Wang Chen:**

Let me answer this question. This is a very important and necessary scientific and health matter. There are three important issues of an infectious disease. The first is the source of infection; the second is the transmission route; and the third is who is likely to be infected, the so-called susceptible groups. These three issues are important scientific links and scientific elements for us to understand the infectious disease. Origin tracing is related to the issues of source and transmission route. Therefore, by clarifying the issue of origins, we can answer the question of where the pathogen of this infectious disease came from. It holds important value not only for this infectious disease, but also has reference significance for the prevention and control of other infectious diseases in the future. The scientific community around the world is deeply interested in this issue, and it is a key matter that we need to focus on and explore. Therefore, this matter is worth exploring. But as Mr. Zeng said just now, we must realize that it is complex, and we need to hold a particularly objective and scientific attitude when probing into origins of a virus.

**Asahi Shimbun:**

I have two questions. First, the WHO proposed last week to conduct a second phase of the study into the origin of COVID-19 in China, including an investigation into Wuhan's seafood markets as well as audits of relevant research institutions like the WIV. They expect China to support this process in a spirit of transparency. How do you comment on this? Will China welcome the second phase of the COVID-19 origin probe? Second, in a report released in March on the China Part of the global study of the origins of COVID-19, the WHO said it was extremely unlikely that the virus escaped from a laboratory. However, some scientists have voiced their views in an article published in Science magazine this May, saying that consideration should be given to both a natural spillover and a lab accident. Two countries initially reported the COVID-19 outbreak. Do you think the virus was caused by natural spillover or human factors? Thank you.

**Zeng Yixin:**

I'll take the first question. Thanks for asking this question. I would like to express my thoughts on the WHO's plan to conduct the second phase of the study into the origin of COVID-19. Honestly speaking, I was rather shocked over the news, because the plan has listed the hypothesis that China's breach of laboratory protocols caused the virus to leak as one of

the research priorities. From this point, I can feel that the plan showed disrespect for common sense and arrogance toward science.

First, rumors including one about three WIV staff falling ill and the other one about the WIV conducting so-called "gain of function" experiments on the virus were dispelled long ago. They are pure lies.

Second, RaTG-13, the most similar coronavirus that the WIV collected from bat specimens, shares only 96.2% homology with SARS-CoV-2.

Moreover, some have wondered if the SARS-CoV-2 is a man-made virus. Some Indian researchers published a preprint scientific manuscript saying that they have found similarities between SARS-CoV-2 and HIV, speculating that the SARS-CoV-2 was man-made. The authors withdrew the paper after being criticized by their international peers. As many other viruses also show similar sequences, we cannot infer simply from this point that the SARS-CoV-2 was man-made. Based on thorough analyses, many experts concluded that there are not any traces of modification in the virus. It's common knowledge to genetic engineers that the artificial modification of a virus will definitely leave traces. But SARS-CoV-2 doesn't have any such traces, which totally rules out the theory that it was man-made.

So far, none of the staff or post-graduate students at the WIV have ever contracted SARS-CoV-2, nor has the WIV conducted any gain-of-function research on coronaviruses. There is no so-called man-made virus there. Then how could it happen that the virus leaked from the laboratory due to violations of lab procedures? Therefore, the "lab leak" theory goes against the common sense and scientific law. More importantly, the WHO sent an expert team on a field trip to the WIV and arrived at the conclusion that a lab leak was extremely unlikely. The experts, selected by the WHO, were authoritative in their respective fields and were rich in research experience. We should respect their conclusions. Therefore, the WHO's plan on the second phase of the study into the COVID-19 origin, as you mentioned, demonstrates a disrespect for common sense and goes against science in some respects. We cannot accept such a plan.

The COVID-19 origin tracing is definitely a scientific issue. The Chinese government has long supported the science-based investigation of the COVID-19 origins, but opposes politicizing the issue. We believe the second phase of origin tracing should be an extension of the first one, guided by the Resolution WHA73.1 and conducted after thorough discussions and negotiations among all WHO members. What was done

in the first phase of origin tracing, especially by those that have reached a clear conclusion, should not be repeated. What should be carried out is the origin tracing of early cases, molecular epidemiology, and intermediary hosts in multiple countries and regions based on extensive consultations among WHO members.

The WHO-China joint research, conducted in the first phase of origin tracing, fully demonstrated that the scientific and rational approach is to conduct work after the WHO and the host country reach consensus on origin-tracing research. The approach not only demonstrates respect to sovereign states, but also promotes origin-tracing work to be conducted in an orderly, smooth, high-quality, and efficient manner. It is necessary to summarize and absorb the successful experience of phase-one work and carry out the next phase based on it. Therefore, on July 4, the Chinese expert team proposed its recommendations on the second-phase origins study to the WHO and exchanged views with WHO experts. In the proposal, we voiced our concerns and core points. We hope the WHO can carefully consider the concerns and advice of Chinese scientists, take investigating the origin of the COVID-19 virus as a scientific issue free from political interference, and proactively and properly conduct sustained investigations into the origin of the virus in multiple countries and regions around the globe. We also call for strengthening international cooperation and exchanges in origin-tracing research, finding the most likely source of the virus as soon as possible and preventing the next pandemic like COVID-19 from happening again by every possible means. Our aim is to better understand the source of SARS-CoV-2, in order to handle the virus effectively and prevent similar pandemics from happening again. Therefore, we must equip ourselves with science-based principles, and promote origin-tracing work in line with scientific rules. This is the attitude adopted by the Chinese government. Thank you.

**Yuan Zhiming:**

The WIV has responded many times to the coronavirus lab leak rumors. Right now, Mr. Zeng elaborated on the same issue, and now I would like to add something.

It has become an academic consensus that the COVID-19 virus evolved in nature. On July 5, 2021, 24 leading experts from around the world published an article again in The Lancet medical journal, noting that the coronavirus Chinese lab leak theory remains without scientifically validated evidence. On July 7, 2021, scientists from the United States, the United Kingdom and Australia released a preprint paper in Zenodo, a research data sharing platform in Europe, in which they wrote, "There is

currently no evidence that SARS-CoV-2 has a laboratory origin. There is no evidence that any early cases had any connection to the WIV, ... nor evidence that the WIV possessed or worked on a progenitor of SARS-CoV-2 prior to the pandemic." A few days ago, in a joint paper published in the journal Science China: Life Sciences, 22 Chinese and overseas scientists applied a classic evolutionary theory to elaborate why SARS-CoV-2 could only come from nature, rather than being man-made. Using scientific evidence, they refuted the lab leak conspiracy theory on the origin of the virus.

I have also noticed that some media have paid great attention to the safety of the Wuhan P4 lab. As a laboratory with the highest level of biosafety, precaution and protection, the Wuhan P4 lab has never seen any laboratory leaks or human infections since it began operating in 2018. Designed, constructed and run in line with both international requirements and domestic standards, the Wuhan P4 lab has stable and reliable biosafety precautions in place, and has established a set of complete biosafety management systems and a professional team to bolster, manage and maintain its operation. I can assure you that the infrastructure, management, team composition and working protocols at the Wuhan P4 lab are the same as other P4 labs in operation around the world. There were media reports that three researchers at the WIV went to the hospital in November 2019 with all the same symptoms as COVID 19. These reports were created out of thin air. It would have been very simple for us to know the truth if the reporters had provided us with the names of these alleged researchers. In fact, we have long proposed the solution, but received no response to date.

What I want to emphasize is that first, before December 30, 2019, the WIV didn't come into contact with, preserve or study SARS-CoV-2; second, the WIV never designed, manufactured or leaked the virus; third, none of the WIV staff members and graduate students have ever been infected with the virus so far.

Facing the sudden outbreak of the COVID-19 epidemic, the WIV, leveraging its long-accumulated advantages in platforms, technologies and talent, quickly identified the virus as a new coronavirus and isolated the virus strain. The institute also sequenced the whole genome of the virus and submitted the genome sequence to the WHO under the United Nations on January 12, 2020. These important research results have provided bases for global respiratory pathogen testing, antiviral drug screening and vaccine research, and bought time for the global fight against the pandemic. After the virus strain was isolated, we organized tasks of antiviral drug screening, vaccine research and animal model

construction, which effectively supported the scientific and technological response to the pandemic.

Certainly, due to its location in Wuhan and its work in fighting the epidemic, the WIV has attracted global attention and been embroiled in various kinds of rumors. These rumors have exerted great pressure upon the researchers at the institute, interfered with some of our normal scientific research, and brought negative impacts on normal academic exchanges and sci-tech cooperation in the international academic community.

Facing the still raging pandemic, no country can stay immune. Only global cooperation and coordinated action can effectively contain the spread of the virus and restore prosperity and harmony to people around the world. Adopting the attitude of openness and transparency, the WIV is ready to keep working with scientists to contribute to the fight against COVID-19. Thank you.

**Liang Wannian:**

I would like to add something. During January and February this year, the WHO-China joint expert team, while studying the origins of the virus, put forward four different possible or potential pathways for the introduction of the virus, one among which was through a laboratory incident. The four pathways were proposed based on our past experience and understanding of viruses, especially the coronavirus-related diseases. The four routes include the direct introduction from a natural host to humans; the introduction through wild animals and an intermediate host to humans from a natural host; a cross-border long distance introduction through cold chains; and an introduction through a laboratory incident. All the four routes are called "potential introduction pathways." How did we assess them? At that time, the whole study was centered on these four routes to collect materials, including carrying out interviews, literature reviews and field inspections.

I will focus on laboratory-related hypotheses. At the beginning, after discussion, the expert team basically thought that laboratory incidents may occur most likely in two cases. One is artificial synthesis, which scientists explicitly find impossible. The other is leakage and the most important point in this regard is whether the laboratory had the virus or not. The answer is that the WIV didn't engaged in such research before, as Mr. Zeng and Mr. Yuan clearly explained just now. The scientific community and the Wuhan side have made it clear as well. However, for further validation, the expert team specially went to the WIV to get

details, and conducted field inspections with relevant researchers and management staff. We obtained information particularly about the institute's implementation of standard processes, management and security systems, and about research projects the institute was and is engaged in. Then, we came back and discussed again. We talked about evidence that supported the lab incident and evidence that didn't. The detailed information is recorded in the report on the joint WHO-China study of COVID-19 origins, which was published on the official website of the WHO on March 30. The details about our inspection to the WIV are also included in this report. You are welcome to read it. We finally concluded that the introduction through a laboratory incident was "extremely unlikely."

When we were assessing the possibilities, we adopted a five-scale system. Because it's not easy to tell whether there is a possibility or not. It is not easy to determine whether a possibility absolutely exists or absolutely doesn't. So, we adopted a semi-quantitative method to conduct this assessment by utilizing continuous variables, in which we graded the virus' four possible pathways of introduction with the five rankings of 'very likely,' 'likely,' 'possible,' 'unlikely,' and 'extremely unlikely.' As for the possibility of a lab leak, our experts reached a final consensus that it is 'extremely unlikely.' As we were discussing the issue and finalizing the joint report, we offered relatively clear advice and recommendations for further studies regarding other possible pathways of introduction of the virus, including direct zoonotic transmission, introduction through an intermediate host followed by zoonotic transmission, and introduction through the cold food chain. This advice and recommendations include the objectives, emphases, and methodologies for further studies. However, we think that introduction through a laboratory incident is 'extremely unlikely,' therefore, it is no longer necessary to continue to devote energy and resources to study this hypothesis. Of course, we don't exclude the possibility of new evidence emerging. In that case, further studies can be conducted. If certain countries need to do further studies on this aspect, we suggest, from the point of view of the Chinese experts, that the studies be conducted in countries that haven't undergone lab inspections like the ones conducted in Wuhan, to at least gain more understanding of possible leaks there, which actually gives rise to safety issues. Together, our experts carried out a relatively thorough exploration and inspection of the Wuhan lab and reached the conclusion that it is 'extremely unlikely' to be the pathway of introduction of the virus.

That's all I want to add, thank you.

**Phoenix Satellite Television:**

Previous reports say that several miners fell ill inside a mine in Tongguan town, in Mojiang county of Yunnan province in 2012. According to what the experts know, is there a connection between these miners and the bat coronavirus RaTG13 or SARS-CoV-2? Thank you.

**Yuan Zhiming:**

In July and October 2012, the WIV team received 13 blood serum samples belonging to four of the miners from Tongguan town, which were collected by the First Affiliated Hospital of Kunming Medical University and sent by the Guangzhou Institute of Respiratory Health. We didn't detect any bat coronavirus in the miners' blood serum samples after conducting multiple nucleic acid tests, antibody tests, and genome sequencing. This also shows that these cases are not connected to SARS-CoV-2 at all.

The RaTG13 coronavirus that you just mentioned is a viral sequence detected by the WIV team from the biological samples collected from Mojiang county in Yunnan province in 2013 and was not discovered from the blood serum samples of the sick miners that we received in 2012. So there is no evidence that the RaTG13 coronavirus and similar bat coronaviruses have any connection with the cases of the sick miners from Mojiang county in 2012.

Of course, the WIV has made several public responses regarding the origin and distinctive features of the RaTG13 coronavirus and its difference from SARS-CoV-2. On July 24, 2020, the Science magazine published an interview with Professor Shi Zhengli, which disclosed that the evolutionary distance between the RaTG13 coronavirus and SARS-CoV-2 ranges from 20 years to 50 years. If you are interested in this, you can read the related content of that interview in the Science magazine. Thank you.

**Reuters:**

Recently, the WHO discussed concerns over information transparency. Is China willing to provide raw data that might reveal the early transmission of COVID-19 in Wuhan? If not, can you explain the reason? The virus database managed by the Wuhan Institute of Virology went offline in 2019. Has the institute published all the genome sequences it has collected since the outbreak? The joint report by the WHO and China said that scientists conducted tests on thousands of animal samples — will China do any more tests? Will China carry out studies on more venues and facilities that are used for breeding animals? How many more bat communities can be studied? Thank you.

## **Liang Wannian:**

I will answer the first and third questions. When our joint team of experts conducted the study in January and February, we had sufficient discussions over the issue of providing early-stage raw data. At that time, we said that since this is an international joint research team launched by the WHO, the 17 foreign scientists and the 17 Chinese scientists should be acting as a whole and all the members should be highly integrated and conduct the research work as a team. We followed four common principles to complete the origin-tracing task initiated by the WHO. We had been following the principles of making research plans together, conducting on-site inspections together, analyzing data together, and presenting our study report and results together.

The most important thing in the origin-tracing work is the early information and data. Mr. Zeng just explained that following the outbreak of the epidemic, Chinese scientists carried out extensive and in-depth origin-tracing work under the leadership of the Ministry of Science and Technology, the National Health Commission and other relevant departments before the joint research launched by the WHO. Among this work, we were very concerned at the time with the data related to animals and early cases. I have also noticed that regarding the data of early patients, some foreign voices have said that we didn't provide them, especially the data of the first 174 COVID-19 cases. In fact, these patients' data were all displayed and shared during our stay in Wuhan. However, China has relevant standing regulations regarding patients' clinical data, including epidemiological survey data and laboratory test data, which involves personal privacy. If the data is completely released, this will violate the relevant regulations. At the time, we did a lot of work to centralize these databases, and conducted analysis and research together with foreign experts, including on what to analyze, what patterns could be seen in the end, and the conclusions drawn in the final report — we did this work together. It is only because we need to guard the patients' privacy, that we did not agree to give away the original data, nor did we allow them to copy it or take photos. At the time, international experts also fully understood and believed that this was international routine, not only in China. Later, we also explained many times why we were not handing over the original data. In fact, this is a rough concept. First, what does it mean to say we "did not provide" the data? In fact, we showed it to you and we analyzed it together. We thought it was provided; it's just that we didn't let you take the data away. Second, what is the "original data"? Was it the data we finally analyzed after sorting and analysis, or the raw data, every single data point? There are big

differences in understanding. I remember that when we were conducting research, our team of experts had no problem on this point, and thought that the data provided by China was for joint research. I want to explain this a little bit: It's not true that we deliberately didn't provide the data; neither was it because we didn't give the data away to the foreign experts, that the conclusions drawn in our research report were said to be one-sided. You can understand this when you look at our detailed research report.

The third question you just mentioned was regarding the research into animals. We believe that the introduction pathway of animal origin, especially from natural hosts to intermediate hosts to humans, has gone from "more likely" to "very likely." Therefore, we particularly suggested that in the future more energy should be invested, and even that the top priority of the work should be concentrated in this direction. Chinese scientists have done a lot of work in this regard. When we went to work on site in Wuhan, the Chinese side had already demonstrated some results of tests on animals in markets. Just now, Mr. Zeng introduced in detail that there were no positive findings from the tests of animals in markets. Also, we had the comprehensive tracing of their upstream farms, and no positive results were found. The scope was then further expanded. We had conducted virus antibody or nucleic acid testing for more than 38,000 livestock and poultry samples, and more than 41,000 samples of wild animals collected from 31 provincial-level regions across the country from 2018 to 2020, yet still no positive results were found. All such detailed data, including the animal species, sources, testing methods and testing results, was reflected in detailed tables and graphs in the joint report. Actually, in brief, whether it was in markets or the upstream of the markets, or in the broader areas of the country, whether it was livestock and poultry, or wild animals that Chinese scientists can find, we have carried out tests on them all, and no positive results have been found in terms of antigens or antibodies.

In fact, Chinese scientists have also done a lot of research on bats and collected a large number of samples. At that time, compared with other countries, we believed that China had led the world in the breadth and depth of bat research and done more. As Mr. Zeng and Mr. Yuan just mentioned, viruses quite similar to SARS-CoV-2 were found through our research, but there are still differences. Scientifically speaking, it is certain that no SARS-CoV-2 has been isolated from China's large number of bat samples. Similarity does not mean the same. Secondly, there are many kinds of bats that live widely in the world. As we know that there has been no systematic study on bats in many parts of the world. Studies

on bats, as parts of studies on wild animals, should be a focus when tracing origins of COVID-19, according to the basic conclusions of scientists and the results of our first-phase origin tracing. Bats are so widely throughout the world, and they are very likely to be an intermediate animal, so the research should not be limited only in China but also encouraged on a larger scale, such as in countries and regions with a bat distribution.

Studies on origins of COVID-19 in animals should be the focus of next phase. This is the most worthwhile thing to do. The natural evolution of a pathogen is the most worthwhile topic of our attention. Our study should not only be limited on wild animals such as bats, but also related animals, such as pangolins, civets, minks and more. It is valuable to study the possible origins and distribution of these intermediate hosts, which have been proved able to carry or possibly carry pathogens through researches carried out by scientists of various countries. Of course, further research on markets that have had outbreaks, including the upstream and downstream chains of farms, is also valuable. I know that Chinese scientists have been working very hard in this regard even after the global study on the coronavirus origins. We have also been expecting that scientists around the world will do this work, focusing on natural evolution and animals. That's all I have to say.

**Yuan Zhiming:**

Just now, the reporter mentioned the database of the WIV, which is a preliminary framework established by the team of the institute. The structure and content of the database are still being improved. Considering the large number of malicious attacks on the institute's website and the work and private email addresses of many of its staff, including Shi Zhengli's team, the database is currently shared within the WIV.

The project team will analyze and systematically sort out the original data of the database and publish research results in the form of papers, which will also be displayed and retrieved in a visual way on the database. As we know, it is the usual practice that the original data of scientific research is published in the form of papers after being analyzed and collated and the database will then be opened to the public. The institute will strictly follow the rules of the sci-tech community in displaying and sharing our scientific data.

The WIV has always insisted on timely sharing of the information on scientific research. We have submitted to the WHO the whole genome

sequence in a timely manner after we obtained the preliminary results of the pathogen identification. As early as Feb. 3, 2020, the research team, led by Shi Zhengli, published a paper in Nature linking the origin of COVID-19 to nature. After we found that several drugs had antiviral activities at the cellular level, we published our research results in international magazines on Feb. 4. Meanwhile, the WIV also actively took part in international video and audio academic conferences, organized by the WHO, the United States National Academy of Sciences, the French National Institute of Health and Medical Research and the Russian Academy of Sciences, to share our research results in the establishment of animal models, the selection of antiviral drugs, and the development of inactivated COVID-19 vaccines with our international counterparts.

Running the laboratory, we have long upheld a set of management principles which feature openness, shared benefits, and transparency. Over the past four years, we have continuously organized workshops concerning lab-based biosafety management and technologies, and helped some countries train groups of personnel in the fields of infectious diseases prevention and control and biosafety management. We proactively participate in the global and regional system of high-containment biosafety labs, and become one of the designated labs under the UN Secretary-General's Mechanism (UNSGM) and a member of the Group of High-containment Laboratory Directors (GOHLD), and share with global colleagues our management experience and technological progress. Some of our staff have also received biosafety training and relevant qualifications in France, Australia, Canada and the U.S. In the meantime, we have invited biosafety experts from France, the U.S., Germany, the U.K., and Canada to our labs and they provided on-site guidance and exchanged experience with us, so as to jointly promote the safe and stable operation of high-containment laboratories around the world. That's all. Thank you.

**Bloomberg:**

Since the WHO team concluded its field mission in China, research published in June showed that animals that could've carried the coronavirus were being sold live at markets in Wuhan, including at the Huanan market. Was this known when the WHO team visited Wuhan? If not, why? And what investigation of these animals has taken place? Additionally, what communication has there been between China and the WHO about these animals? Second question, what progress has been made in checking for SARS-CoV-2 antibodies in the stored blood of Hubei residents collected in 2019? Thank you.

**Liang Wannian:**

I'll take your questions. Regarding the information mentioned in your first question, we knew nothing about this situation when the WHO and China joint team were doing their jobs in January and February. At that time, the WHO and China joint team had spent half a day conducting an on-site investigation in the Huanan Seafood Market and discussed and communicated with relevant shop owners and management staff. The joint team went into detail about the situation in the Huanan Seafood Market, including the distribution of booths, the types of items on sale, the composition of shop owners, management details, and certain regulations, to name a few. At that time when we visited the Huanan Seafood Market, it was shut down and all the businesses were closed. We got inside the market and spent hours communicating and discussing. Therefore, we have presented all the information that we know about Huanan Seafood Market, such as those concerning the composition and situation of sales staff and customers, as well as the products being sold. This information was jointly studied and discussed by the experts of the team. Thus, we did go to the Huanan Seafood Market. In fact, since the foreign experts of the joint team left Wuhan on Feb. 10, Chinese experts have maintained good communication and contact with them, because lots of scientific issues require further discussions after the field work was finished.

As you may have noticed, the WHO and China joint team held a press conference in Wuhan on Feb. 9, and the final joint research was published on the WHO's website on March 30. During this period of time, we communicated with 17 global experts almost on a daily basis in order to improve the report, since many issues required to be stated in a more precise manner. Since the research was published on March 30, we have still maintained good relationships and built sufficient communication with foreign experts. For example, Chinese experts have kept close contact with their foreign counterparts concerning follow-up works and some scientific issues. Just now, Mr. Zeng also mentioned that Chinese experts gathered and conducted research on the WHO's plan for a second phase of the study of origins of COVID-19 -- based on the experience of the first phase of such a study, especially the report of the joint study of the first phase. Experts of both sides have taken a responsible attitude. We have drafted a proposal from the perspective of Chinese experts on the WHO's plan for a second phase of the study of origins of COVID-19. During the drafting process of the proposal, we discussed and communicated with relevant WHO experts. We also hope that they could put forward relevant suggestions for the WHO from their own perspective,

so as to provide a basis for better carrying out the global study of origins of COVID-19. In fact, throughout the whole COVID-19 origin-tracing process, scientists have upheld the spirit of seeking truth regarding scientific issues. We have maintained very good relationships. This is my answer to your first question.

Your second question is about blood samples. This is a very good question. Regarding the origin-tracing of the virus, apart from the early epidemiological studies, testing of early samples, especially the blood samples, if any pertinent evidence found through tests, will be conducive to tracing the earliest COVID-19 case. According to China's research, the earliest case reported in China was on December 8, as said in our research report. But the earliest reported case is an index case at most, and doesn't mean it is the primary case. The primary case refers to the first human who was infected at the moment when the virus jumped from an animal to a human. The person is also called the "patient zero." Our research and the previous related research papers of Chinese scientists fully suggest that the case reported in Wuhan on December 8 is probably not the primary case. There might be other cases that occurred before. But where did these cases come from? This is another question. The region where cases were first reported doesn't necessarily mean it is the region where the virus jumped the species barrier from animals to humans. Of course, it's better to test the blood samples. We had made our proposals in Wuhan, and invited experts from the Wuhan Blood Center to have a full discussion.

Experts from the Wuhan Blood Center told us that they had kept blood samples, but the samples were kept for the use of responding to possible medical disputes and lawsuits due to blood transfusion. Such a sample is called a "blood braid." A small amount of plasma and serum is kept in the pilot tube of a blood bag, which is sealed at both ends. In accordance with the Article 31 of the Measures for the Administration of Blood Stations, the term of preservation of a blood sample shall be two years after the whole blood or the component blood is used. A quite small amount of blood is preserved during the period and it can only be available for use when there is a medical dispute or lawsuit. For example, a donor has donated blood to a patient, and then the patient is diagnosed with Hepatitis or AIDS. The disease is probably transmitted through blood transfusion and samples are kept to determine whether the disease was caused by blood transfusion. So, samples are usually kept for two years at least, and kept in the pilot tube of the blood bag. The amount of blood serum is quite small. We believed that it was necessary for us to conduct the test. I remember that we and the experts from the Wuhan Blood

Center and the WHO spent an afternoon discussing it. The issue was then specifically referred to in our report, which will be our future research work in the next stage. Once the blood from the Wuhan Blood Center is used and after the two-year validity term, meaning the samples meet the requirements stipulated in the Measures for the Administration of Blood Stations, we will carry out relevant works. In fact, the Chinese side is organizing related experts and institutions to make preparations for the work. So far, we have made several assessments and evaluations on the testing methods and action plan, which will be implemented after the expiry. Related institutions from the Chinese side also express that, once they have the results, they will deliver them to both the Chinese and foreign expert teams. Thanks.

**China Daily:**

According to the WHO expert team for origin tracing of SARS-CoV-2 this February, COVID-19 introduction through an intermediate host is "likely-to-very-likely", and introduction through cold chain products is "possible." What's your take on that? Thanks.

**Wang Chen:**

The role the cold chain plays in spreading infectious diseases is a new phenomenon. I am an expert in respiratory diseases. Respiratory infectious diseases are a dominant type of infectious diseases. The transmission route of respiratory viruses, including the cold chain, is indeed a new phenomenon that deserves our full attention. In summary, first, in terms of epidemiology, we have found associations between the cold chain and the disease. That is to say, through epidemiological investigations, we found that the possible cause of some COVID-19 infections could be traced to touching the surface of cold chain products. The close associations can be seen from the COVID-19 flare-ups in Beijing's Xinfadi Market and Qingdao. The infected people were exposed to the cold chain, and no other possible sources of the virus were since found, except the cold chain.

Second, in terms of detection of the nucleic acid of the virus, positive results have been found on cold chain goods. During the outbreak in Qingdao, in particular, the RNA of SARS-CoV-2 was detected on the surface of cold chain goods, and the virus was isolated and cultured, proving the fact that living virus existed on the surface of cold chain goods. Given the two points above, the chain of evidence has become complete. Moreover, there is a circumstantial evidence for the exploration of the scientific issue, which is that the virus can survive and remain

infectious for a longer period in a cold and relatively dry environment. It can even survive for 21 days in winter. Therefore, when the virus emerges in a place, and if the cold chain products get the virus, the virus can be transmitted from one place to another in a low temperature during transportation, leading to cross-regional transmission accordingly. The cold chain transmission is a new feature that we have found in the COVID-19 pandemic, which is worthy of attention, and the chain of evidence for the transmission has become relatively complete.

To further trace origins of the virus, we suggest that the cold chain should be taken as a key clue. Given the circumstances of international trade, with the exchange of people and goods around the world, the items-to-human transmission in the cold chain environment has made pathogen transmission more complicated, which is particularly worthy of investigation and studies.

**Xinhua News Agency:**

Since the outbreak of the pandemic, scientific research has played a very important role. Could you talk about the work of the Ministry of Science and Technology in terms of the scientific research on origins of COVID-19? What achievements have been made? Thank you.

**Xu Nanping:**

Thank you for your question. There are a lot of journalists today, and everyone looks very serious. It shows that everyone recognizes the importance of the origin tracing of COVID-19. We should realize that origin tracing is substantially a scientific matter, so scientific research has played a crucial role in searching for origins of the virus. The Chinese government attaches great importance to the scientific research on the origin tracing of the virus. After the outbreak, China made five priorities for scientific research, and origin tracing of the virus is one of the priorities which has been considered as very important. The Chinese government called on the scientific research community to follow the principle of "open, transparent and responsible" and put the utmost effort to find out "where the virus came from." Responding to this call, the Ministry of Science and Technology has organized research groups from the Chinese Academy of Sciences, the Chinese Academy of Medical Sciences, the Chinese Center for Disease Control and Prevention, and universities to carry out scientific research on the origin tracing of the virus on a number of priority areas, including animals, humans, molecules and the environment. Some progress has been achieved.

I'd like to name some examples. I think everyone is concerned about the first one. After human-to-human transmission was detected, we wondered where the virus came from; whether it was the animals around us which might have transmitted the virus to humans; or whether it could spread from people to animals. All these regard tracing animal origins. We conducted nationwide viral tests over wild animals, poultry and livestock in 31 provinces, municipalities and autonomous regions soon after the epidemic broke out. The tests covered dozens of species, such as pigs, cattle, sheep, chickens, ducks, geese, pigeons, turkeys, wild rabbits and wild boars. We tested more than 80,000 samples over a short period of time, and no COVID-19 antibodies or positive nucleic acid test results were detected. After that, we further conducted COVID-19 challenge trials on animals around us in the lab, and classified them into groups according to their susceptibility to COVID-19 infection, such as highly susceptible, not susceptible or resistant. By doing so, we further understood the situation, and it was also helpful for us to determine the priorities in terms of tracing animal origins.

Second, in order to define the origin of the virus, bat was one of the animals we focused on. In the wake of the COVID-19 outbreak, we organized several groups to conduct research on the coronavirus carried by bats to identify its similarity with SARS-CoV-2. As several experts said just now, bat coronavirus RaTG13 has a 96.2% genome homology with SARS-CoV-2. Yet further research found it shows only 89.3% amino acid homology in the receptor-binding domain (RBD), meaning that its infectiousness is to some extent very low. Our further experiments showed that the infectiousness of RaTG13 differs greatly from SARS-CoV-2 when infecting different species. As such, experts have concluded based on a comprehensive study and judgement that RaTG13 has a remote evolutionary relationship with SARS-CoV-2.

Apart from bats, researchers also found other animals carry SARS-CoV-2-related coronavirus. For instance, scientists detected multiple strains of coronavirus in smuggled pangolins seized by customs. Among them, the highest genome homology with SARS-CoV-2 is 92.4%, lower than RaTG13, but one strain of the pangolin coronavirus shows 96.9% amino acid homology with SARS-CoV-2, higher than RaTG13's 89.3%. Through those studies, scientists concluded that pangolin coronavirus may have played a role in the evolution of SARS-CoV-2.

Our research groups have done lots of other work such as molecular tracing. The origin-tracing work has made solid progress due to joint efforts with overseas scientists. By July 19, Chinese research groups and their overseas counterparts from the U.S., the U.K. and other countries

had jointly published 225 articles related to tracing origins of the COVID-19 virus, and Chinese research groups had published 352 articles. That shows our origin-tracing work is highly international. During this period, Chinese and U.S. medical scientists held six dialogues via video link on prevention and control of COVID-19. On top of that, we have beefed up efforts on data and information sharing regarding scientific research, and established the 2019 Novel Coronavirus Resource database for global sharing under the China National Center for Bioinformation. By July 19, the database had garnered and shared more than 2.53 million collections of worldwide SARS-CoV-2 genome sequences, and offered access to almost 300,000 users from 177 countries and regions.

More than one year of effort has made us realize that tracing origins of the virus is a scientific question full of uncertainties, so there is a long and arduous way to go. At the same time, we should realize that origin-tracing work is very important, and we should give a good answer to the serious and fundamental question about where the virus comes from. With responsibilities falling on us and difficulties lying ahead, we must firm up our confidence and adopt a science-based approach. Only by basing the origin-tracing work on scientific attitudes, scientific methods and scientific facts can we uncover the truth. Thank you.

**CGTN:**

Recently it was reported that Chinese researchers last year deleted some genome sequences of cases from the early stage of the outbreak, which had been uploaded on to the database maintained by the U.S. National Center for Biotechnology Information (NCBI). It was speculated that China has concealed some information about the origin of the virus. How would you respond to this issue? Thank you.

**Zeng Yixin:**

After it was reported, we immediately conducted an investigation. The report mentions the deletion of SARS-CoV-2 sequences, which is relevant to a paper 'Nanopore target sequencing for accurate and comprehensive detection of SARS-CoV-2 and other respiratory viruses' published by researchers from Wuhan University in the international scientific journal 'Small.' According to the title, we can tell the paper was about a sequencing method. When they made a submission last March, the sequencing results were needed. That means when a sequencing method is created, the results are needed to assure its accuracy and reliability. Therefore, the researchers uploaded their concrete sequencing results of the virus onto the database of the National Center for

Biotechnology Information (NCBI), a branch of the National Institute of Health (NIH).

On June 9, 2020, the journal sent back the researchers the proofread paper where they found the information about where they had uploaded the sequencing results of samples from confirmed cases had been deleted. The researchers thought that since the information about the sequencing was deleted, it was unnecessary to keep those sequencing results on the NCBI.

Therefore, they sent an email to the NIH to request the removal of the data on June 16, 2020. The NIH followed the protocol and deleted the data without notice. When the researchers requested the removal, the data was automatically removed without notifying the researchers. The researchers were not informed, and hence they ignored this. So it is clear that the researchers had absolutely no need, or intention, to hide or conceal any information. Recently, they uploaded all 244 pieces of sequencing data of 61 COVID-19 samples onto the GSA database built by the China National Center for Bioinformation, which is open to global researchers.

As far as we know, the earliest sampling in the case was done on Jan. 30, 2020, some time after the initial outbreak, so the sequences cannot count as early ones and thus have limited value or information regarding the study of SARS-CoV-2 origins. However, a U.S. researcher, Jesse Bloom, with the Fred Hutchinson Cancer Research Center, fabricated the conspiracy theory that this was an attempted cover-up, without any confirmation from the Chinese researchers and with absolutely no understanding the background context of the matter. His actions deviated from science and violated scientific ethics, having not only smeared the Chinese researchers, but also causing a negative effect on relevant international public opinion. After the publication, his paper has been criticized by experts from various countries for its violation of scientific ethics. During this epidemic, the public is deeply concerned about and highly sensitive to the words and deeds of professionals, especially scientists. Therefore, researchers should understand they have their own responsibility to society. Especially during the pandemic, people are highly sensitive to opinions about the disease, so we professionals should not speculate in a deceptive and unrealistic manner. This could cause bad influence on the whole society's control and prevention of the pandemic. We should instead make contributions and correctly guide public opinion. Here, I want to remind every expert to learn the lesson that experts are more than just experts; they have a responsibility to the society. This deserves recognition. Thanks.

## **Global Times:**

At present, the start point of the global spread of the coronavirus continues to go further back. Some have proposed studies to be conducted in multiple countries and regions around the globe within the framework of the WHO. The United States, in particular, should also be subject to investigation. What are your opinions of that? Thank you.

## **Liang Wannian:**

I'd like to take this question first before having the other experts share their opinions. Results of ongoing studies into the origin tracing by scientists in various countries showed that this coronavirus emerged in multiple places in the world before the time we knew about its existence. Here are some examples.

Samples from November 2019: A SARS-CoV-2 in situ hybridization reaction detected at multiple parts on skin biopsy of an Italian woman.

Samples from November 27, 2019: Coronavirus genetic materials detected in wastewater collected from a Brazilian city.

Samples from December 13, 2019-January 17, 2020: Check-ups of donated blood samples for archive in nine U.S. states found that 106 blood samples tested positive for coronavirus antibodies.

The early gene sequences collected from Iran, Brazil and Italy on December 24, 2019 uploaded to national databases.

The mid of December 2019: The prevalence of neutralizing antibodies reportedly increased in France.

Sample from December 27, 2019: A throat swab of a French patient with hemoptysis tested positive for coronavirus RNA in RT-PCR detection.

Samples from January 2020: Waste water samples collected in Barcelona of Spain tested positive for coronavirus.

Samples from January 2, 2020-March 18, 2021: Nine of 24,079 blood samples from 50 U.S. states tested positive for coronavirus antibodies.

These examples come from recent studies of scientists from around the world, which show that Wuhan might not have been the first place of SARS-CoV-2 inception. The spread of the virus could be complex, with a cyclical infection chain from a human or an animal host to an object, and then to humans and later back to objects. Just now, Mr. Wang Chen

talked about the importance of the studies into cold chains. In fact, the studies into the entire transmission pattern of the virus, including its origin tracing have offered us a new vision and a new issue, as well as a new scientific proposition to solve. As for the modes of transmission and circulation, how the virus jumped from animals to people, including from animals to objects and then to people? what is the logical relationship between them? What are their roles and interface points? All shed lights on new research ideas.

Next, studies into early cases, biological samples, genetic sequences, natural hosts, intermediate hosts and cold chains should be conducted with joint efforts in multiple countries and regions around the globe. To explore trans-species infections and viruses' global spread, research work ought to be done on the diversity of viruses and their evolution in animal hosts, on the interaction among animals, environment and humans, and on the factors affecting virus infections among people. This is what we need to do in the future.

Viruses are a common enemy of mankind; and in both prevention and treatment, we must unite. The critical, complicated and difficult scientific mission of tracing origins of viruses requires cooperation of scientists across the world, of governments and of all people. Thank you.

**Wang Chen:**

I want to share a view that the findings just mentioned by Professor Liang have also been recognized by the international scientific community, which suggest the possibility of multiple sources. The origin-tracing work is so complex with diversity. If we really want to find the origins, we should not be restricted in our vision but rather broaden it. It is an important issue of direction for the world to make systemic studies of origin tracing in multiple regions and multiple orientations.

**Shou Xiaoli:**

Thank you, to our speakers and journalists from the media. Today's briefing is hereby concluded. Goodbye.

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