**Joint China-WHO press conference of**

 **WHO-convened Global Study of Origins of SARS-Cov-2**

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Ladies and gentlemen, dear friends, good afternoon. Welcome to the joint China-WHO press conference of WHO-convened Global Study of Origins of SARS-Cov-2: China part. This is Mi Feng, the spokesperson of China National Health Commission.

Since COVID-19 became a global pandemic, WHO has been actively promoting the international cooperation in terms of the COVID-19 response. China has always been showing firm support to WHO in terms of unleashing the role of WHO in the leadership of the global COVID-19 response.

With the consensus based on negotiation between two sides, China and WHO have conducted joint research of the SARS-CoV-2 global origin tracing: China part. Since the arrival of international expert teams in Wuhan on January 14th 2021, the joint expert team has been working as three groups, respectively the group of epidemiology, molecular epidemiology and bioinformatics, animal and environment. The experts have been working in the forms of video conferences, on-site interviews and visits and data analysis, as well as discussions. They have conducted systematic and full-fledged research. The joint expert team have already concluded the China part of scientific research related to the origin tracing in Wuhan according to the original plan.

During this period, MR. Ma Xiaowei, the Minister of National Health Commission has been discussing and having extensive communication with Doctor Tedros, the Director General of WHO through telephone. They thoroughly exchanged ideas in terms of the scientific cooperation on the origin tracing.

For today's conference, we have guest participants on the podium with us from the joint expert team and they are Mr. Peter Ben Embarek, food safety expert from WHO, and Madam Marion Koopmans, member of the joint expert team and also team leader of the molecular epidemiology group. And also professor Liang Wannian from Tsinghua University. He is the team leader of the Chinese side of the joint expert team.

They will present the work that the joint expert team has done and introduce the public and the press to the updates and highlights of SARS-CoV-2 origin tracing of this joint study and also they are going to answer your questions. Consecutive interpretation will be offered in today's press conference. So journalists can ask question either in Chinese or in English.

First I would like to invite professor Liang Wannian, the team leader from the Chinese side to introduce relevant information of this joint study of origin tracing in Wuhan.

Dear friends from the press, good afternoon. On behalf of the team leader from the Chinese side of the China-WHO joint expert team of the SARS-CoV-2 origin tracing research, I would like to give you a brief introduction of the major research process and also the key findings of our endeavor in our recent joint study. With regards to the conclusions and future recommendations, these two parts will be introduced by the team leader from the WHO expert team, Doctor Peter Ben Embarek.

This joint research is the China part of the WHO-convened Global Study of Orgins of SARS-CoV-2. The joint research report is based on the relevant research, a crystallization from the Chinese and international scientists in the past. And the literature review of the previous research and the analysis will be also included in this joint report.

In May 2020, the 73rd World Health Assembly requested the Director General of the World Health Organization to work with the partners to identify zoonotic source of the causative virus of COVID-19, and the route of its introduction to the human population, including the possible role of the intermediate hosts. The aim was to prevent reinfection with the virus in animals and humans and prevent the establishment of a new zoonotic reservoir, as well as to reduce further risk of emergence and transmission of zoonotic diseases.

In July 2020, WHO and China began the ground work for the studies to identify the virus origins. The agreed terms of references or ToRs defined the scope of the studies, the main guiding principles and the main expected deliverables. These ToRs define an initial phase of short-term studies to better understand how the virus might have been introduced and started to circulate in Wuhan. The WHO Secretariat and the Chinese government have jointly set up an international multidisciplinary team to design, support and conduct these studies to contribute to the tracing of the origins of SARS-CoV-2 and the route of its transmission to human beings. The work of the joint international team was set it as the ground for origin tracing work in other parts of the world.

Therefore, the global origin tracing work will not be bound to any location and may evolve geographically as increasing amount of evidence is generated and science-based hypotheses keep evolving. The overall results and findings will help to improve global preparedness and effective response to SARS-CoV-2 and emerging zoonotic diseases of similar origins.

The joint international team comprises 17 Chinese experts and 17 international experts from ten other countries. And they represent WHO, World Organization of Animal Health, partners in the Global Outbreak Alert and Response Network (GOARN). The joint study team carries out a research over a 28-day period from January 14th to February 10th 2021 in Wuhan.

The joint expert team, through its three working groups, reviewed and discussed together the progress made by Chinese experts in phase one studies in the following three areas: epidemiology, animals and environment, molecular epidemiology and bioinformatics.

In addition to the three working groups, the joint international team received detailed presentations on relevant topics to help inform its work, and undertook a series of site visits and interviews with key informants.

Now I would like to give you a brief introduction of the key findings of our joint study. The first part of my introduction will be the result of the molecular epidemiology study.

As most of the emerging viruses have their origins in animals, in order to gather more insights of the process of virus spill-over and global spread, it is necessary to understand the diversity and evolution of viruses in an animal reservoir, the interactions between animals, environment and humans, and relevant factors contributing to the efficient human-to-human transmission.

Generally speaking, a virus causing global pandemic must be highly adaptive to human environment. Such adaptation may occur unexpectedly or may have evolved through multiple steps with each step driven by natural selection.

Consequently, the research for the origins of SARS-CoV-2 therefore needs to focus on two phases. The first phase involves viral circulation in animal hosts prior to zoonotic transfer. During this evolutionary process, various animal species may serve as reservoir hosts.

Progenitor strain of SARS-CoV-2 may have acquired an enhanced ability to infect humans during their circulation. The discovery of viral sequences with high homology to SARS-CoV-2 suggests that SARS-CoV-2 may have originated from zoonotic transmission, but the reservoir hosts remain to be identified.

The second phase involves evolution of SARS-CoV-2 during its spread in human populations, following zoonotic transmission. The likelihood of animal-human spill-over increases with increased frequency and intensity of animal and human contact. Spill-overs may be occurring repeatedly, if the genomic of the virus in the reservoir requires further adaptation to efficient onward transmission. Such early spill-overs may go undetected. Once viruses with pandemic potential evolve or spill over, which would enable their spread, it results in substantial clusters of viruses with adaptive mutation in different geographical human populations, and hence causing the pandemic of COVID-19.

Evidence from surveys and targeted studies so far have shown that coronavirus most highly related to SARS-CoV-2 are found in bats and pangolins, suggesting these mammals may be the reservoir of the virus that causes COVID-19, due to the high similarity in genetic sequences between the sample virus and SARS-CoV-2. However, the viruses identified so far from neither of these two species are sufficiently similar to SARS-CoV-2 to serve as direct progenitor of the SARS-CoV-2.

Apart from these findings, the high susceptibility of minks and cats to SARS-CoV-2 suggest that there may be additional species of animals, for example those belonging to mustelidae or felidae family as well as other species, as potential reservoir. Comparison of the data from sequence databases with those from surveys of potential reservoir species shows that these possible reservoirs are massively under-sampled and the research in this area is not sufficient.

The joint team reviewed data collected through China National Center for Bioinformation in their integrated database, containing all the available coronavirus sequences and meta data.

For the cases detected in Wuhan, China, by linking the sequence data and epidemiological background, cases with illness onset before December 31st , 2019 were selected for in-depth analysis. The final analysis showed that several of the cases selected with exposure history to Huanan market had identical virus genomes, suggesting these several cases may be part of a cluster.

However, the sequence data also showed that some diversity of virus was already present in the early phase of the pandemic in Wuhan, suggesting the possibility of unsampled chains of transmission outside the Huanan market cluster. There was no obvious cluster of cases by the epidemiological parameters of raw meat exposure or exposure to fur animals.

Finally, according to the relevant literature review on the data of early circulation of SARS-CoV-2 from published studies, these studies from different countries suggest that SARS-CoV-2 circulation was possibly several weeks earlier than the initial detection of cases. Some of the suspected positive samples were detected even earlier than the first case reported in Wuhan. This indicates the possibility of the missed diagnosis of cases in the early circulation in other regions.

These kinds of missed diagnosis and diseases are highly related to the features of SARS-CoV-2. This is a basic judgment that we can make after the review and analysis of the global data from global research community.

The second part of my introduction would be the origin tracing work conducted by epidemiological group. Surveillance of influenza-like illness or ILI and Severe Acute Respiratory Illness, SARI, with appropriate laboratory confirmation, is a standard measure of the impact of influenza and other respiratory viruses in the community to determine the possible impact of morbidity or the causative agent of COVID-19 in the month before the outbreak of COVID-19. Adult sentinel surveillance data from ILI from one hospital in Wuhan and SARI surveillance data from one hospital in Hubei province was reviewed. The full name of SARI is Severe Acute Respiratory Illness. The finding indicated that there was no substantial unrecognized circulation of SARS-CoV-2 in Wuhan during the latter part of 2019.

Origin tracing of stored lab samples. In retrospective testing of stored samples of more than 4,500 research project samples from the second half of 2019 stored at various hospitals in Wuhan, the rest of Hubei province and other provinces, no SARS-CoV-2 was identified.

Analysis of retail pharmacy for the purchase of the antipyretics, cold and cough medications have also been conducted. It did not provide a useful indicator of early community SARS-CoV-2 activity.

And also, we have conducted review of the surveillance data on all cause mortality and pneumonia-specific mortality during the period from July to December 2019 in Wuhan city and the rest of Hubei province. There was no evidence of substantial unexpected fluctuation in mortality that might suggest the occurrence of the transmission of the SARS-CoV-2.

There is no indication of the transmission of the SARS-CoV-2 in the population in the period before December 2019. There is not enough evidence either to determine whether SARS-CoV-2 infection had spread in Wuhan before December 2019.

We have also conducted research among 233 health institutions in Wuhan by searching the records of more than 70,000 cases presenting one of the four conditions or symptoms, including fever, acute respiratory illness, influenza-like illness or unspecified pneumonia in the period from October 1st to December 10th, 2019.

We have reviewed the testing of the blood obtained from the relevant data bank, and also tested the antibodies in the blood samples. All were negative. And it was also followed by the multidisciplinary clinical review and screening of those cases, which determined that none were compatible with SARS-CoV-2 infection.

Retrospective search for potential earlier cases in Wuhan in the two-month period prior to the outbreak detection in December 2019 has not revealed clear evidence of the occurrence of the clinical cases of the SARS-CoV-2 infection. Based on analysis of this and other surveillance data, it is considered unlikely that any substantial transmission of SARS-CoV-2 infection was occurring in Wuhan during those two months.

It is not possible to determine how the SARS-CoV-2 was introduced into the Huanan market or other markets on the basis of the current epidemiological information. There was a possibility of transmission of SARS-CoV-2 infection among the population of Wuhan in December 2019.

Although there was an association with the Huanan Seafood Market in some of the early cases, others were associated with other markets, and the other cases had no market's association at all. It is likely that an outbreak occurred at Huanan Seafood Market. But there are also transmission appearing to have the occurrence elsewhere in Wuhan at the same time. This is our basic judgment. It is not possible to determine how SARS-CoV-2 was introduced into the Huanan Market based on the current information.

The third part of my introduction will be the research of the animal and environment group, the third group of our joint study. Coronaviruses that are genetically related to SARS-CoV-2 have been identified in different animals, including horseshoe bats and pangolins. Sampling of bats in Hubei province, however, has failed to identify evidence of SARS-CoV-2 related viruses, and sampling of wildlife in different places in China has so far failed to identify the presence of SARS-CoV-2.

Environmental sampling in Huanan market from the point of its closing revealed widespread contamination of surfaces with SARS-CoV-2, compatible with possible introduction pathways of the virus through infected people or contaminated cold-chain products, animals and animal products.

According to this research, the testing results of all the animal related samples from Huanan market were negative. The cold-chain products have not been tested yet.

SARS-CoV-2 can survive in conditions found in frozen food, packages and cold-chain products. Recent outbreaks in China have been linked to the cold chain. Studies have shown that the virus can survive for a long time, not only at low temperatures, but also at refrigerator temperature, indicating that it can be carried long distance on cold chain products. More attention should, therefore, be paid to further research of the virus in terms of its persistence in the low temperature environment and also in the damp environment where the humidity is relatively high.

In Huanan market, a substantial number of stores sold cold-chain products. But it is unclear so far how well the first confirmed cases in Huanan Market can be corresponded to the stores that sold these products or not. We need further research in this area.

This is my introduction of our major findings of the three groups of the joint study.

Thank you, professor Liang Wannian. Now I would like to invite Doctor Peter to give an introduction.

Thank you, Mr. Mi Feng and Professor Wannian for the introduction and for presenting our findings and also how we have conducted our work.

I'm here this afternoon with Prof. Marion Koopmans from the department of Virology of the College of Medicine of Erasmus University in the Netherlands. And she's one of the member of the international team that came here a month ago together with colleagues from WHO and OIE. We have the presence of Marion, but it is unfortunate we cannot invite all the members of the joint team on the podium together. We will answer your questions later on together.

I would like to start by thanking you who are here in the room today and those joining us remotely. We have followed many of you in the past few weeks. I would also like to thank those who we have seen every day following us on cold days for long hours in the rain and bad weather, and we really thank you for following us. It has provided us with constant reminding of the importance of this work and focus that the world is putting on this work. So thank you for following us.

And the international team would like to recognize the impact of epidemic on the city of Wuhan from the individuals affected, the communities affected, both from the government officials, the citizens, the scientists and the health workers in particular who fought the disease last year here, in particular. Thank for the engagement of my colleague Professor Wannian, who spent several months here last year on the front line. Thank you for that.

So you have heard the many findings that we have detected out of our studies and work in the past few weeks and they will be detailed in the report of this mission that would be released later on. I would like to concentrate on some of our key conclusions from these findings. We came here with two goals, two objectives. One was to try to get a better understanding of what happened at the beginning of the event in December 2019. This was the starting point for our work, but also the starting point of the initial outbreak. We've focused on trying to understand what happened during that period and trying to see if that period had a previous history, could we move the history of the start of the outbreak further down the line in earlier weeks of 2019. And then in parallel, we also embarked on trying to understand how it happened, how did the virus emerge and at some point, jumped and was introduced in the human population. So these were two broad objectives we had and all our studies and work and discussion and visits were trying to get better understanding of these two pictures.

So in terms of understanding what happened in the early days in December 2019, did we change dramatically the picture we had beforehand? I don't think so. Did we improve our understanding? Did we add details to that story? Absolutely. You heard some of the key findings from Professor Wannian on this picture.

In trying to understand the picture of December 2019, we embarked on the very detailed, profound search for all the cases that may have been missed, cases early on in 2019. And you heard the detail from Professor Wannian. The conclusion was that we did not find evidence of large outbreaks that could be related to cases of COVID-19 prior to December 19 in Wuhan or elsewhere.

We can also agree that we have found evidence of why the circulation of the virus was in December. It was not just only the cluster outbreak in the Huanan market, but the virus was also circulated outside of the market.

The picture we see is a very classical picture of the start of an emerging outbreak where we start with a few sporadic cases early on in the month of December. And then we start to see small outbreaks where the disease starts to spread in clusters and we have seen it further that was happening in the Huanan market.

And these early clusters are usually and also in this case, the way one detects the first cases, the first sign of these emerging disease and that's what happened during the month of December 2019.

When mapping all the initial cases of the time throughout December, combining that with location and mapping of some of them in the market, in different parts of the market, and combining that with genetic sequence and genetic information from some of these cases, we could see that a picture becoming more and more clear of the spread within the market and spread outside the market. Initially there were very few cases and then more and more cases as we moved into January 2020.

And the data and information we got from the very large amount of looking retrospectively to different studies of mortality data, of surveillance disease data, etc., and re-analyzing a large number of the initial genetic sequences identified in the early days of the events and early January, all these data fit perfectly and very well, confirming us in the picture I just described.

Then we embarked on trying to better understand how the virus was introduced in Wuhan, the way it came from.

All the work that has been done on the virus and trying to identify its origin continue to point towards a natural reservoir of this virus and similar viruses in bat population.

But since Wuhan is not a city or an environment close to these bat environments and direct jump from bats to the city of Wuhan is not very likely. Therefore, we have tried to find what other animal species were introduced and moving in and out of the city that could have potentially introduced or contributed to introducing the virus, in particular, in the Huanan market.

The market was dealing primarily with the frozen product, in particular frozen animal product and maybe seafood. But they were also windows selling products from domestic agents -- wildlife, farmed fur animals and their products.

So the joint team in their studies have identified the vendors who were trading this type of products, identified the suppliers of these vendors, identified the farms from where these products were coming from, and they were coming from different parts of the country and some of the products were also imported products, of course. So there is the potential to continue to follow this lead and further look at the supply chain and animals that were supplied to the market in the frozen and order process.

There was also a large amount of testing for the coronavirus responsible for COVID-19 in many different animal species throughout the country in large number of samples of both the domestic animals, farmed animals, wild animals in many different provinces. To these studies, it has not been possible to point any animal species as a potential reservoir for this disease. They indicate that currently and also back in 2019, it doesn't look like there was wide circulation of the virus in any animal species in the country.

The search for the possible route of introduction of the virus to different animal species and the specific reservoir are still under working progress. What we did after looking at our findings and combining the information that we could extract from this finding and we then sit down and say to ourselves -- okay, the next step is, let's look at the future. What are these conclusions telling us and how are we going to move forward in our search for the start of the story? Look at all the possible pathways for the introduction of the virus into the human population. You will have the details in the report, but it's basically a very simple illustration of different pathways coming from wild animals into different environments where human and animals and products can interact.

Out of that exercise, we then identified four main hypotheses or group of hypotheses on how the virus could have been introduced in the human population. We decided to take that approach to really cover all the possible pathways, initially without any value and without any assessment or a judgment, but purely to make sure that we would cover all the possible pathways for the introduction of the virus in the human population.

Once we identified these four key hypotheses, we also did a literature research to make sure that we would not have missed some valuable options that others could have come up with. Then we sat down and went to these different hypotheses, one by one, and assessed their likelihood by putting forward arguments for and arguments against such hypotheses. And then assessing the likelihood of each of them in a systematic way, in a rational way, using scientific arguments and combining all the information that we had collectively collected in the past four weeks, and also using an extensive search of the literature for useful scientific arguments.

So the four main hypotheses that we evaluated, identified and re-evaluated are first, a direct zoonotic spill-over that is a direct transmission from an animal reservoir or animal species into the human population. So a direct jump from an animal to a human.

The second hypothesis was through the introduction of the virus, through an intermediary host species, meaning another animal species potentially closer to humans, where the virus can potentially adapt, and then circulate and then jump to humans.

The third one was the food chain, in particular, meaning the potential for food, frozen products in particular, acting as the surface for the transmission of the virus into the human population and all the food-related route of transmission.

The last one was the possibility of a laboratory-related incident.

As I have said, we took a systematic approach to look at all these hypotheses, putting arguments for and against, and assessing the likelihood using the standardized set of parameters. Each of them was then used to help us plan in a useful direction to help us continue our way forward into a better understanding of the virus origin.

Our initial findings suggest that the introduction to an intermediary host species is the most likely pathway and one that we require more studies and more specific targeted research.

Similarly and connected to this hypothesis is also including the possibility of transmission through the trade of frozen cold-chain products.

Then we were making the difference between the introduction of the virus into the human population and the possibility of the circulation of the virus through long distance and through different settings, or the introduction of the virus into a particular city, like a market, for example.

Then the hypothesis of a direct spill-over from an original animal source into the human population is also a possible pathway and is also generating recommendation for future studies.

However, the findings suggest that the laboratory incident hypothesis is extremely unlikely, and to explain the introduction of the virus into the human population. Therefore, it is not a hypothesis that implies to suggest future studies into our work, to support our future work into the understanding of the origin of the virus.

So the discussion on the different hypotheses and how they will help us direct our future studies was extremely helpful. We have been able to then develop a series of recommendations for future studies, future work in line with the plan we had outlined last July in terms of reference for how we would go about understanding the origin of the virus and what type of sequence in the studies that would be needed, was developed. The plan we developed in July 2020 is still valid, has been extremely helpful in the guiding our work. The recommendations we are making at the end of this mission are in line with that approach.

So we have identified and we're proposing our report a large number of valuable recommendations and ideas for future studies. But here I would just mention some of the key studies and key recommendations we are making.

One of them is to expand existing integrated data basis that connect epidemiological, clinical and molecular data on cases, in particular, and extremely useful as well, genetic sequences. So all that information can be possible and connected through integrated databases, and that should be done at the global level to facilitate the analysis and connection of data coming from a different part of the world in helping us understanding better and connecting better all the data and information that comes from many of these research projects.

And that will also include data from animal surveys, from environmental surveys and enable us to integrate all these information and make the best use of many of our studies.

In our search of still trying to identify earlier cases, because that will help us better understand the start of the event, we would recommend to continue some of the good work that has been initiated in looking for material that can be analyzed, that is still available from that time. A lot of this material has been already looked at and we heard that many studies that have been conducted for the past weeks and months. We have identified potential, new sources of valuable material that could be analyzed and help us perhaps move forward in that direction. One of them, just to give an example, is blood samples from blood banks and not only here in Wuhan and all the cities and provinces of interest but also use that material else where there are initial reports and indication that perhaps the virus was also present in individuals, in other places and other countries. And that kind of study would help get a better picture of the initial days of the event potentially if some of them turn back positive. So we have to continue our search for material that can be analyzed and give us clues on what happened in the early days of the event.

We should also explore new approaches and new ways of exploring and reinforcing the use of serological tests in some of the material that have already been tested. Here we're talking about tests that allow us to look in old sample for traces of the presence of the virus at that time. And there we need new approaches and new ways of doing that.

And of course, we can continue exploring the potential that early cases have. Even if memory fades, if people are less present and accessible and if clinical material is also less and less available，there is still value we had targeted in the studies of some of these cases can potentially yield more useful information. But a lot has already been done in trying to extract all the information that we could extract from these early cases in December 2019.

And for the studies to better explore the hypothesis that an intermediary animal species or an original animal species was involved in the introduction, here we need to conduct more surveys into certain animal species that could be the reservoir or act as a reservoir and of course including more sampling and more studies of bat population, not only in China because already a lot has been tested in terms of bats in China, but we know that some of the similar species found in China are also found in neighboring countries in the sub-region and in other parts of the world. And there is under-surveyed because not much has been done in many of these countries in terms of surveying bats. But there we may have some interesting studies as well.

We also have to do much more into understanding the possible role of the cold-chain frozen products in the introduction of the virus and over a distance. We know that the virus can persist and survive on conditions that are found in these frozen environments. But we don't really understand if the virus can then transmit to human and on which conditions this could happen. It will be interesting to explore if frozen wild animal that was infected could be a potential vehicle for the introduction of the virus or the viruses into market environments, where we know that the temperature, the humidity, the environment could be conducive to a rapid spread of the virus in such environment. So a lot of work needs to be done to better understand this interesting pathways.

We should also look further back in tracing the source of the products and the source of the animal products in particular that were in Huanan market in December 19, and go back and see if we can find products that were produced at that time and that are still available to also look at the suppliers to these vendors in the market, and see if we can go further back in terms of identify interesting clues in the farming environment in the species being raised in these farms and where they were potentially coming from before that. This is another area worth exploring.

What was important for us when we developed our hypotheses was to make sure that they were not geographically bound because since the beginning we have taken an open approach in terms of not limiting ourselves in this manner. One of the clear reason is that the possible paths from whatever original animal species, all the way through the Huanan market could have taken a very long and convoluted path, involving also movements across borders, travels, etc., before arriving in the Huanan market. Therefore, it's also very interesting to follow up on every one of these clues and preliminary reports and indications that perhaps here and there in other places in the world. There were individuals who were infected and try to follow up on these and connect again dots, connect the different pieces of information to try to get a better understanding of this whole picture and again, just following all the leads, following the science, following well-designed and conducted studies.

Apologize for these two lengthy introductions, but we feel it was necessary to present you with a clear picture of all the work that we have conducted in the past four weeks before and trying to give you a picture of all our findings and conclusions. And I would now give the floor back to Doctor Mi Feng. Thank you.

Thank you, Dr. Peter. Just now we have listened to the introduction from the team leaders from both sides. They have been introducing the major content and highlights of the joint report. Now we would like to take your questions. Before you raise your question, please introduce yourself by telling us which news agency you're with. In order to provide more chances to different journalists, one question from one journalist, please. Thank you. Now we are glad to take your question.

Hello, there. My name is Josh, reporter with Thompson Reuters in Shanghai. I'd like to see if we drill down with a bit more specificity about the likelihood for these hypotheses that were presented. So whether it is possible for each of the three of us actually give a percentage of the likelihood to which we think that the virus either originated from wildlife and subsequently transmitted to a human or through some form of frozen food.

Peter over to you. Thank you.

Thank you. And I will ask Marion to try to give you an answer.

Yes, thank you very much. So this is a very tough question. What we really did is to develop the figure that was shown to help structure our thinking, but be systematic about it. What that does is it lists from literature, from studies, various evidence for or against and various uncertainty. And that is what we then have used to assess what we think is more or less likely. I think going into exact percentages is really overstating what can be done. It's really developed to help us structure our thinking, also structure the discussions somewhat， because these are very complex questions and there are many different potential routes that you can think of. That's the key use of it. So we’ve gone as far as broad categories, most likely, less likely. And that’s how I think for the time being, we will use this. What we also discussed is that whenever new information becomes available and that could be any time, because there's ongoing studies in different parts of the world, we can take this again and say with this new information, does our assessment of these different pathways change.

And maybe in our complete report, we will list all elements that were used in the assessment, including the literature, the studies, all the aspects that we included to make that assessment.

I would like to invite Professor Liang Wannian to offer additional comment.

I applaud the view offered by Dr. Marion. Actually, there will be more detailed introduction of the methodology and more abundant evidence that are going to be demonstrated in the full joint report and also in the future recommendations and suggestions for the research orientations. Actually one of the deepest impressions for me is that as regards for the question you are asking, it requires a lot of daunting and demanding efforts. We have tried our best to provide an evaluation of the possible hypothesis and also other kinds of the possibilities in a scientific way by unleashing the joint wisdom from the experts of the two sides based on the existing available evidence. This is a teamwork. And also we have not using the only quantitative nor only qualitative method either, as it was introduced by Dr. Marion. And we were using the semi-quantitative method to conduct the relevant research. We have stratification of five levels and to match each evaluation of different kinds of the possibility, to put them into different matrix to have a comprehensive consideration and evaluation.

Next question，please.

I'm with CGTN. I have one question related to Huanan seafood market. Is the Huanan seafood market the source of the COVID-19 epidemic in Wuhan? What are the possible infection sources of the cases related to Huanan seafood market? How was the virus introduced to Huanan seafood market? What are possible early transmission routes and what kind of role did Huanan market play in the early stage of epidemic in Wuhan? Thank you.

Dr. Peter over to you.

Thank you for some very well thoughts and detailed questions. These are exactly the same questions we have ourselves, so you should join us next time on the team. We don't know the exact role of the Huanan market. We know that there was spread among people who were and lived and worked and visited the Huanan market throughout December. How it was introduced and spread within the market is still unknown. We have a map and we have mapped over time the spread of the virus, among the earlier cases we were linked to the market. So we have a picture of where the cases were, for example, in the market. We have also genetic sequences for some of these cases that we can use to help us to understand this picture. And all that tells us that there was a spread among people in the Huanan market in December. And therefore, the market probably was a setting where that kind of spread could happen easily. But it's not the whole story and we know that there was also spread among individuals who were not linked to this market. They were linked to other markets. There had no links to market. So the picture is not clear in that respect. And for the introduction part, it's part of the discussion we are having and the work we are planning ahead of us through this hypothesis, evaluation is to understand how it was introduced. And as of today, we are still working with the hypothesis that it could have been introduced by a person who was infected and then spread it to other persons in the market. And that could be one of the traders. It could be a visitor, but it could also be through the introduction of a product. As I mentioned, among the more interesting products where frozen farmed wild animals and some of these species are known species susceptible to this kind of viruses. So these are providing clues and providing direction for the next round of studies. We have a lot of good material now to further explore many of these avenues and hopefully some of them will provide us with a good direction afterwards.

In terms of time and place, what we know is that some of the first cases that could be linked to the market, where detected symptoms in the first two weeks of December. And that indicated that they were probably infected around the start of December or late November. But we can't go into more details with the information we have looked at and that we have studied in detail. Thank you.

Any additional comment from Professor Liang?

I would like to offer additional comment. First, according to the current research progress of this joint research team, Huanan Market may not be the first place of the outbreak. It may not be the place that witnessed the earliest case, either, as it was also introduced by Dr. Peter. The onset date of the earliest case in this joint research was December the 8th, 2019 and also the onset date of the earliest confirmed case that had association to the Huanan seafood market was December the 12th. And actually, according to our research from the epidemiological group, the case with the onset date on December the 8th actually have no relationship or association either with Huanan seafood market.

The second point I would like to explain is that why have we attached so much importance to Huanan Market in terms of the considering whether Huanan Market is one of the earliest places of the outbreak or even the source of the outbreak? Because at the beginning, we have very limited knowledge concerning the properties and features and the etiology of the virus and the disease as well. We noted that this kind of pneumonia-like disease actually could occur on the cluster base. So that is why we focused our early research in Huanan Market and relevant cases that have association with Huanan seafood market for the earlier cases with the suspected pneumonia or PUE, Pneumonia of Unknown Etiology. And actually, in the research of those early cases, a large number or a high proportion of those early cases had association or have market exposure history with Huanan seafood market. But later, when there have been enhanced and improved testing capacity and also with the improvement and development with different kinds of the testing tools or test kits, we have greatly increased our understanding of the virus. So when we conducted the retrospective study related to the early cases, in the earlier confirmed cases, some of those earlier confirmed cases actually did not have any market exposure history with Huanan seafood market. It was also mentioned by Dr. Peter previously and actually we have also conducted relevant research of the possible introduction of the virus transmission of the Huanan seafood market from several possible introduction pathways either directly from animal to any intermediary hosts or from the cold-chain transmission or introduction. So we are having full exploration of this kind of possible introduction pathways. This will be also a highlight of the future research.

Next question, please.

I am Tom Cheshire, Sky News. Of the four hypotheses, the one you decisively rejected was the laboratory incident. Can you explain the evidence of the reasoning for discarding that hypothesis?

Dr. Peter, thank you.

Thank you. We evaluated this hypothesis in the same way we evaluated the other hypotheses described by Marion. We looked at what are the arguments for and against such a hypothesis. So in short, you can see in the report the more detailed evaluation of these hypotheses, but in short, it's about yes, accidents do happens. Unfortunately, we have many examples from many countries in the world of the past accidents. So this is not impossible. It happens once in a while. We also in terms of arguments against, look at the fact that nowhere previously was this particular virus researched or identified or known. There has been no publication, no reports of this virus or another virus extremely linked or closed to this, being worked with in any other laboratory in the world. We were also discussing with the managers and the staff of many of the relevant laboratories in the region and looking and discussing with them these hypotheses as well, and hearing from them how their staff health monitoring program, how their audits program, for example, are conducted and what this revealed in the past months and years. We also looked, for example, at the Wuhan Institute of Virology, P4 level laboratory and the states of that laboratory. And it was very unlikely that anything could escape from such a place. And we also know that when lab accidents happened, they are extremely rare. If you look at the history of lab accidents, these are extremely rare events. So this is not the first thing that happened on or would happen on a regular basis. So many of these evaluations and the arguments were put for and against and helped us take a rational approach to assessing the likelihood of such an event happening. As I said, we looked both at the arguments against but also the arguments for to make sure that we are not biased in our approach. And again, in terms of arguments for the fact that, as I said, past accidents have happened all over the world. There was the fact that some of the laboratories were in the city of Wuhan and all these arguments were put for and against each other in helping us making this assessment.

For us, it was important to develop a system to evaluate all these hypotheses where we could take a rational approach and look at fact and evidence in a rational way and try to move away from the situation that has been around for the past year where all of us and many people around the world have all come up with. There are personal views and feelings, wanted to move away from "I think it is this way" or "I believe it is this way". And try to move away from that and put rational facts on the table that everybody can then look in a systematic way. We felt that was a much more useful approach than to put personal views, feelings, etc., are looking at only half of the arguments. Thank you.

Professor Liang?

I agreed with the answer offered by Dr. Peter. The hypothesis of lab leak is put into the matrix of extremely unlikely as a conclusion of the research outcome of the joint team. On the basis of a serious discussion and very diligent research, we have reached the extremely unlikely conclusion. As regards for the hypothesis of lab leak, there are two possible pathways if there was one. First, virus was engineered by humans, but this hypothesis has already been refuted and rejected by the whole scientific community around the world. Second, there may be a leak of the virus from the lab. But in terms of the leaking of the virus, it should be leaking of existing or known virus. However, in all the laboratories in Wuhan, there is no existing virus of SARS-CoV-2. If this virus does not exist, there would be no way that this virus could be leaked. In addition, for all the laboratories in Wuhan, including WIV, they uphold a very stringent and high quality management system. And also proceeding from the current evidence, we regard the lab leak hypothesis is extremely unlikely. Thank you.

Mi Meng: Next question, please.

From Hubei Radio Network. The number of the confirmed patients has already been cleaned to zero in Wuhan 9 months ago. In terms of the origin tracing in Wuhan, how do the joint expert team members conduct this kind of origin tracing, including the identification of the early cases?

Maybe I can start. What was done was a series of studies. So there were reports of known cases from later December. There was a series of studies to try and find if there was evidence for earlier circulation. That was done by a systematic analysis that is in the report of different registrations. One is a registration that lists the number of people with fever with respiratory symptoms in a wider region that was looked at to see if there was evidence for earlier increase in the number of people with flu-like symptoms, for instance, that was seen in December, but not before that.

The same was done looking at mortality statistics. And we've seen in other countries that correlates very well with activity of SARS-CoV-2. So that again showed increase, a peak that said there was considerable circulation in December, second half of December, but not really much before that.

The third element was a very extensive review of patients and patient records by clinical teams from, I think, 233 health care centers in Wuhan. They have with their knowledge of now what COVID-19 cases look like, have looked back in their records to see if they found evidence for earlier cases. That is what has been done. What all the studies then showed was there was a number of recorded cases in December with the first people that were mentioned by Professor Liang. That's how that was done. We cannot say there was absolutely no circulation and there were no cases before December because that's not what you can do by this approach. But what we can say is there's no evidence for widespread circulation much earlier. That's what the studies conclude.

Professor Liang.

Additional introduction of the methodology that we have been adopted in this joint research. And actually, in our joint research, it covers three methodologies. First, we conduct ample and abundant retrospective study. And second, by reviewing the accumulated or existing information or material, we tried to generate literature review and also to have some relevant analysis in a comprehensive manner of those existing material or information. The third methodology is that we tried to connect the dots by analyzing different associated element in a holistic manner by pricing in as many factors as we can in a highly integrated and systematic manner. So in our research, our diverse and multi-prong approaches can allow us to have different kinds of comparative studies and also to better draw inferences from those causal relationship. So apart from those kinds of broad-spectrum analysis, we also provide description of the current situation. This kind of all-encompassing research methodology can allow us to reach a more comprehensive conclusion portfolio. Thank you.

We are already having two and half hours together in this press conference. Due to the interest of time, last question, please.

Thank you, from the Wall Street Journal. I was wondering if you could talk a little more about the animals that were found alive or dead at the Huanan Market. For example, I don't think it has ever been confirmed what exactly those animals were. And you mentioned that some are known to carry coronaviruses. Have you identified some of greater interest to you as potential intermediate hosts? Have you identified ones that maybe were in the market earlier, but it had left by the time that inspectors arrived, by the time the market was closed? And in terms of following the trial and trying to identify the traders and the farms and the sources of those animals, could you go into a bit more detail about how far you've got and what's the stumbling block? What needs to be done next?

And then a quick follow-up on the Wuhan Institute of Virology. You mentioned that there were no coronaviruses in Wuhan that matched SARS-CoV-2, but did you obtain that you ask for and obtain information, data, samples regarding any gain of function experiments that might have been done at Wuhan Institute of Virology, which might be working with one type of coronavirus and then enhancing it through some genetic mutation. Thank you.

Dr. Peter.

Thank you, I will let Marion start with the first part of the question. Thank you.

The question about animals. I think first, it is important to emphasize that the testing did not reveal any positives, but the full trace-back that was done was very extensive. Trace-back of all animals and other products on the market showed that there were some animal species that have been confirmed as susceptible, like rabbits, or that could be suspected to be susceptible, like ferret badger, bamboo rats. The way that is interpreted is to really say if they were there, then maybe they could have been similar animals earlier. So it is an entry point for a trace-back research because that's the step that we're now looking for. We have a deeper understanding of the early situation -- where would you go for a next step of these origin studies. The reason why that raise some interest is also that some of the trace-back was in farms or in traders in regions that are known to harbor bats with a closely-related viruses. So it is really seen as an entry point for rational, for taking the next step of surveys in animals, on farms. That's how we've looked at.

Then I will take the second part of your question about the Wuhan Institute of Virology. We went there and we have also received the visits of some of the staff here. They have participated in further discussion and worked with us. We've had over the weeks quite substantial interaction with the staff there. During the visit, we first had the visit of the place, the institute, the different laboratories. And then a very long frank open discussion with the management and the staff of the institute. First, they gave us a description, very detailed description of their research, both present and past, all the projects involving the studies with bats and coronaviruses and so on, and also some of the more advanced projects. And then we engaged in the discussion with them on the different lab-related hypotheses, because they have been on the front line of the discussion around this hypothesis for the past year. And it was very interesting to hear directly from them how they are thinking in terms of how can we explain this one, how can we dismiss this one, are we using the wrong arguments, are we providing the wrong evidence or are we answering questions in the wrong way. So we had a very interesting discussion on their views, on all these hypotheses involving their lab. And we discussed how to improve that communication, how to provide the right arguments in the future for better explaining their position, explaining their views. And of course, they are the best one to be able to dismiss any of these claims and provide answers to all the questions that are out there around it. So we also feel that by again taking our detailed and rational approach, we will help to better clarify some of these claims around specific studies, gain of functional working with samples directly from bats, etc. You will also have in the report the minutes of our different visits and meetings with different individuals and this one will also be in the report. Thank you.

Professor Liang.

I would like to cite a few numbers for joint animal research study. First and foremost, we have conducted testing of the serum samples, numbering 11,000 from different species of animals like pig, cow, goat, chicken, duck and goose as a kind of testing sampling from the livestock and poultry from 31 provinces in China from 2019 to 2020. And the testing results of those 11,000 samples of SARS-CoV-2 antibody were all negative. We have also done the testing related to the 12,000 swap samples and animal tissue samples from different kinds of animals in terms of PCR testing. The testing results were all negative as well. In addition, from 2019 to 2020, we have conducted PCR testing for 26,800 samples generated from different kinds of animals that are distributed in 24 provinces in China. Again, the PCR testing results were all negative.

Meanwhile, as regards for the testing of the samples from wild animals, the samples collected during the period from November 2019 to March of 2020 were taken. We have conducted testing of 1,914 serum samples from 35 different species of wild animals. The testing results of antibody testing from the serum samples were all negative. And also before and after the COVID-19 outbreak, we have increased our sampling scale from Huanan seafood market, Wuhan municipality and other cities in Hubei province and also the neighboring provinces of Hubei, and collected 50,000 samples of the wild animals covering 300 different species. With the PCR testing of those more than 50,000 samples, the testing results were again negative again. Thank you.

Dr. Peter expressed that he would like to take one more question.

Thank you. I'm from AFP. I'd like to ask. So the Chinese government and the Chinese media have highlighted various reports of virus cases in countries such as Italy and other places abroad that appeared in late 2019 with the implication that the virus originated from overseas. How likely do you think this is and do you think there's a possibility that they were passed on to the sort of seemingly unrelated places across the world from undetected mild cases traveled to Wuhan? Do you think that because there's obviously substantial spreading we had at the time with several concurrent clusters, in addition to Huanan Market.

Sorry. Would you please repeat your question?

Sure. Okay, so I'd like to ask, so the Chinese government and Chinese media have drawn attention to reports of several virus cases that appeared in other countries outside of China such as Italy in late 2019 with the implication that this virus originated from overseas. How likely do you think this is? Especially given that there were several clusters in Wuhan in December 2019 at the same time? Do you think it's likely that maybe a mild or asymmetric case traveled from Wuhan to these places in different places around the world that might have led to the clusters elsewhere?

What we have done is looking into that question also again in a systematic manner. So the focus here initially was on what exactly can we learn about the initial phase of the pandemic in Wuhan. That showed that there was clearly circulation in December. But as part of that work, we also reviewed what is available in the literature and also in the databases about viruses possibly circulating elsewhere. And that has found a couple of, a few publications that would suggest that, for instance, in Italy, there had been already circulation in December, may be late November, but difficult to know. Because the methods for that were not confirmatory. So they did not provide full evidence for that circulation, but these parts of information is part of what we collected, reviewed and included in our recommendations for the next step. So in the next step, what we say is we should really go and search for evidence for earlier circulation, wherever that is indicated, and indications like this can come from that kind of literature. So this is therefore in our recommendations for follow-up. Maybe to then say, could that mean that the virus had traveled from Wuhan to elsewhere? Again, here we take a step-wise approach. But looking at what evidence is there, what evidence could be found, it would be possible to get genetic information and then see what that tells us.

This is a very good question and also your question has explained the issue by itself -- why do we need to take an international perspective in terms of the origin tracing of SARS-CoV-2. That is also why we will need to have the joint endeavor from the international scientists to have this kind of research in a highly cohesive manner to identify the possible pathways and to identify the possible rationale behind. That is also an orientation that both from the joint research team and also different scientists around the world will try to follow in their future plans. Thank you.

Any final comment from Dr. Peter？

Thank you. Thank you all for all your very interesting questions. As you heard, many of them are exactly the same questions we asked ourselves over the past few weeks. And just to let you know that we have answered some of your question today, but the other members are not here and will be available for questions in the coming days and we will also organize more media access in the coming days for you and your colleagues. As we go back home, we will also have opportunities back afterwards in a few days.

And as I said, you're only facing three of us here, but we have been over the past four weeks and even before working closely with some 30 to 40 colleagues who were part of the joint team. And over the past few weeks, we have really had an intense and very productive work among that very special group. I would like to thank them all individually for all their contribution and efforts.

And beyond them, we were discussing that earlier today, there are probably more than 1,000 individuals who have contributed over the past four weeks in providing us with data, helping us analyze data, generating reports, and finding and helping us getting information and processing them. And it’s also here an opportunity for us to thank them all for that. So as you can hear, it's a huge, huge group and amount of work that is behind the outcome of this joint-study and robust and very numerous details that came out of this work.

And to go back to the work itself in my closing remark, I would like to point the detail that marked me, because before embarking on this work like probably many of you, I was thinking how will it be to actually be on the ground and trying to find answers around the first cases. And who are they? What information could they provide about the origin of the virus? It was in a way fascinating to realize that these people are not holding very exciting clues when we talk to one of the first cases who had symptoms in early December. When you talked to one of these cases, you immediately think they must have some very special habits, hiking in the mountains, having special wild pets at home. All these kinds of ideas pop up. And then you realize that they're very much like all of us, no special particular history of interest, spending most of their days on the internet or doing the same activities and sports and jobs of his work, type of jobs as many of us do. So it's also illustrating how complicated this work is and therefore it's not that easy to come up with all the answers after a few weeks of studies. Therefore, we have to understand that these are complex studies that need to be done systematically. And that's how we bit by bit can connect the dots and get all the information and we need to move forward. And that's the approach we have taken. That's approach we will continue to take in continuing this work together with our colleagues in China and in the international team. So again, thank you to my colleagues and thank you to my friend Liang.

I would like to express my appreciation to the three experts on the podium with us. COVID-19 global pandemic has been exerting unprecedented and profound impact to the whole human society and the future progress of the development of the global community. However, people from different countries never change their pursuit for the betterment of their life. As it was mentioned by Director General, Dr. Tedros of WHO, there will always be the light at the end of the tunnel. As long as we unite as one, we will achieve the ultimate victory. Chinese New Year, the year of ox, is coming soon. Here I would like to wish all of you happy Chinese New Year, good health and all the best.

That's the end of the press conference. Thank you.