Ladies and gentlemen, dear friends, good afternoon. Welcome to the press conference of joint expert team of China WHO SARS-CoV-2 origin research. 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 two-sides negotiation, China and WHO have conducted joint research of the SARS-CoV-2 global source-tracing including the China parts since the arrival of international expert teams in Wuhan from January 14, 2021. The joint expert team has been working from three groups, respectively, the group of epidemiology, molecular research, animal and environment. The experts have been working in the forms of video conferences, onsite interviews and visits, and also discussions. They have conducted systematic and full-fledged research. They have already concluded the China part of the source-tracing in Wuhan according to the original plan.

During this period, Mr Ma Xiaowei, the minister of China National Health Commission, has been discussing and having abundant communication with Dr Tedros, the Director-General of WHO, through telephone. They have fully exchanged their ideas in terms of the scientific cooperation in the origin source-tracing.
For today’s conference we have the participants from the joint expert team and they are Mr Peter Ben Embarek, WHO’s food security expert, and also Madam Marion Koopmans, member of the joint expert team and also the team leader of the molecular and epidemiological research group, and also Professor Liang Wannian from Tsinghua University. He’s the team leader of the Chinese team of the joint expert team.

The participants from the joint expert team are going to introduce to the public and to the press of the relevant situation of the SARS-CoV-2 origin-tracing in China and also they are going to answer your questions. This press conference will have consecutive interpretation, so press can ask your question either in Chinese or English.

First I would like to invite Professor Liang Wannian, the team leader from the Chinese side, to introduce the relevant achievements in this source-tracing in Wuhan.

LW  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 research, I would like to give you a brief introduction of the major research process and also the key findings of our endeavour in our recent mission as regards for the conclusions and future recommendations and plans. These two parts will be introduced by the team leader from the WHO expert team, Dr Peter Ben.

This mission in Wuhan from January to February 2021 are based on the original mission that is convinced by WHO in terms of the global source-tracing research of the SARS-CoV-2. This part is the first part, China part, and also the joint research report is based on the relevant research crystallization from the Chinese and international scientists in the past and also the literature review of the previous research and also the analysis will be also included in this joint report.

In May 2020, the World Health Assembly requested the Director-General of the World Health Organization to work with the partners to identify zoonotic source of SARS-CoV-2, 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 reservoirs as well as to reduce further risk of emergence and transmission of zoonotic diseases.

In July 2020, WHO and China began the grant work for the studies to identify the virus origins. The agreed terms of references or TOR defined the scope of the studies, the main guiding principles, and the main expected deliverables. These TORs envisaged 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 government of China together established 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 a grant for origin-tracing work elsewhere.

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The global origin-tracing work would therefore not be bound to any location and may evolve geographically as evidence is generated and science-based hypotheses evolve. The overall results and findings would benefit improved global preparedness and response to SARS-CoV-2 and emerging zoonotic diseases of similar origin.

The joint international team comprise 17 Chinese experts and 17 international experts from ten other countries. Also they represent WHO, World Organization of Animal Health, partners in the Global Outbreak Alert and Response Network. The joint study team was conducted over a 28 period [sic] research from January 14 to February 10, 2021 in Wuhan by having a lot of onsite research.

The team through its three working groups reviewed the progress made by Chinese experts in phase-one studies in the areas of the following three parts, epidemiology, animals and environment, and the molecular epidemiology and bioinformatics.

In addition to the three working groups, the international team received detailed presentations on relevant topics to have informed 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 in our joint mission. The first part of my introduction will be the results of the molecular epidemiological study.

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As most emergent viruses originate from animals, understanding the process that may lead to a spill-over and global spread requires a deep analysis of both the diversity and evolution of viruses in an animal reservoir, the interactions between animals, the environment, and humans, and the factors contributing to the efficient human-to-human transmission.

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

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

Progeny testing of the SARS-CoV-2 may have acquired an increased 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 transfer. 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 for efficient onward transmission. Such early spill-overs may go undetected. Once viruses with pandemic population evolve or spill over, this would enable their spread, resulting in substantial clusters of viruses with adaptive mutations in different geographical human populations and hence causing the pandemic of COVID-19.

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

In addition to these findings, the high susceptibility of mink and cats to SARS-CoV-2 suggests that there may be additional species of animals, for example, those belonging to mustelid or feline family as well as other species, that act as potential reservoirs. Comparison of the data from sequenced databases with those from surveys of potential reservoir species shows that these possible reservoirs are massively under-sampled or this research is not adequate enough.

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

For the cases detected in Wuhan, China, data was linked with the epidemiological background to select samples from cases with illness onset before December 31. The final analysis showed that several of the cases with exposure to Huanan Market had identical virus genomes, suggesting these can be part of a cluster.

However, the sequence data also show that some diversity of viruses was already present in the early phase of the pandemic in Wuhan, suggesting unsampled chains of transmission beyond the Huanan Market cluster. There was no obvious clustering by the epidemiological parameters of raw meat exposure or exposure to fur animals.

Finally, according to the relevant literature review concerning the research on the data, it suggests that early circulation of SARS-CoV-2 from unpublished studies was also a very important part of our review. These studies from different countries suggest that SARS-CoV-2 circulation preceded the initial detection of cases by several weeks. Some of the suspected positive samples were detected even earlier than the first case reported. This indicates the possibility of the missed reported circulation in other regions.
So this kind of omission or report of the cases or the underreporting of those kind of cases are highly related to the disease course and also the symptoms of those illness. So this is basic judgment that we can achieve after the review of the global data and the relevant literature of the global research community.

The second part of my introduction will be the source-tracing work conducted by the 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 mobility or the causative agent of COVID-19 in the month before the outbreak of COVID-19.

Sentinel surveillance data from ILI from one hospital in Wuhan and SARI surveillance data from provincial hospital in Hubei Province was reviewed. The full name for SARI is severe acute respiratory illness. The findings indicated that there is no substantial unrecognized circulation of SARS-CoV-2 in Wuhan during the latter part of 2019.

In retrospective testing of a convenient subset 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 and it did not provide a useful indicator of early community SARS-CoV-2 activity.

Also during the period of July to December 2019, we have conducted review of the surveillance data on all-cause mortality and pneumonia-specific mortality from Wuhan City and the rest of Hubei Province. It produced little evidence of substantial unexpected fluctuations 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 76,000 episodes presenting one of the four conditions, respectively, fever, acute respiratory illness, influenza-like illness, and all unspecified pneumonia, in the period of October 1 to December 10, 2019.

We have also reviewed the testing of the blood obtained from the relevant data bank and also tested the antibodies in the blood samples. All were inactive. Also, it was followed by the multidisciplinary clinical review 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 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.

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Substantial transmission of SARS-CoV-2 infection occurred in the population of Wuhan in December 2019 with most cases reported in the second half of that month. Many early reported cases were associated with Huanan Market, indicating that it was one of the focus of the transmission. Nevertheless, transmission was also occurring elsewhere in Wuhan at the same time.

It is not possible on the basis of the current epidemiological information to determine how the SARS-CoV-2 was introduced into the Huanan Market. Substantial transmission of SARS-CoV-2 infection occurred among the population of Wuhan in December 2019.

While some of the early cases had an association with the Huanan Seafood Market, others were associated with other markets and other cases have no market association at all. It is likely that Huanan Seafood Market acted as a focus for transmission of the virus, but there are also transmissions appearing to have the occurrence elsewhere in Wuhan at the same time. This is our basic judgment. It is not possible on the basis of the current information to determine how SARS-CoV-2 was introduced into the Huanan Market.

The third part of my introduction will be the research of the animal environment group, the third group of our joint mission. Coronaviruses that phylogenetically relate 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.

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

According to this research, all the samples related to the animal products or animals were all negative. For the cold-chain products and relevant testing, the research is on the ongoing stage.

SARS-CoV-2 can persist in conditions found in frozen food, packaging, and cold-chain products. In these cases, in 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. So further research of the virus in terms of its persistence in the low environment and also in the temp environment where the humidity is relatively high will be under further research.

In Huanan Market, a substantial number of stores sell cold-chain products, but it is unclear how well the initial cases in people associated with the market
can be mapping or corresponded to the stores that sell these products. We need further research in this area.

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So this is my introduction of our major findings of the three groups of the joint mission.

MF Thank you, Professor Liang Wannian. Now I would like to invite Dr Peter to give an introduction.

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

I am here this afternoon with Marion Koopmans from the Erasmus Centre in the Netherlands. She’s one of the members of the international team that came here a month ago together with colleagues from WHO and OIE. She’ll represent here the entire team who unfortunately cannot sit with us in the room and we will share a question later on together.

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

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

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 of course in the report of this mission that will 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. So 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? 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 the two broad, large objectives we had and all our studies and work and discussion and visits were trying to get better understanding of these two pictures.
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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, and 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 a very detailed and profound search for other 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 wider circulation of the virus in December. It was not just only a 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 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, among others, that happening in the Huanan Market.

These early clusters are usually, also in this case, the way one detects the first cases, the first sign of these emerging diseases. That’s what happened during the month of December 2019.

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When mapping all the initial cases of the time throughout December, combining that with location and mapping of some of them in the markets, in the front [?] part of the markets, and combining that with genetic sequences and genetic information from some of these cases, we could see that picture becoming more and more clear of the spread within the market and spread outside the market. Initially very few cases and then more and more cases as we moved into January 2020.

The data and the information we got from the very large amount of looking retrospectively through different studies of mortality data, of surveillance disease data, etc. and also reanalysing a large number of the initial genetic sequences identified in the early days of the event in early January, all these data feed perfectly and very well in comforting us in the picture I just described.

Then we embarked on trying to better understand how the virus was introduced in Wuhan and where 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, a 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 introduce the virus in particular in the Huanan Market.
The market was dealing primarily with frozen product, in particular frozen animal product and mainly seafood, but there were also vendors selling products from domesticated wildlife, farmed wild 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 frozen and other processed and semi-processed form or raw form.

There was also a large amount of testing for the coronavirus responsible for COVID-19 in many different animal species throughout the country in a large number of samples of both domestic animals, farmed animals, wild animals in many different provinces. Through these studies it has not been possible to pinpoint any animal species as a potential reservoir for this disease and 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.

So the search for the possible route of introduction of the virus through animal species and the specific reservoir is still work in progress. So what we did after looking at our findings and combining the information that we could extract from this finding... We then sat down and told 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? So we looked at all the possible pathways for the introduction of the virus into the human population and 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 groups 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 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 search 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 through 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 of course using an extensive search of the literature for useful scientific arguments.

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

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

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

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

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

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

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

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There we are 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 setting 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 to explain introduction of the virus into the human population and therefore is not a hypothesis that will imply to suggest future studies into our work to support our future work into the understanding of the origin of the virus.

So this discussion on the different hypotheses and how they will help us direct our future studies was extremely helpful and 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 the 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. So the plan we developed in July 2020 is still valid. It has been extremely helpful in guiding our work and the recommendations we are making at the end of these missions are in line with that approach.
So we have identified and we propose in our report a large number of valuable recommendations and ideas for future studies, but here I will just mention some of the key studies and key recommendations we are making.

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

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

In our search to still try 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 analysed that is still available from that time. A lot of this material has been already looked at and we heard the many studies that have been conducted over the past weeks and months, but we have identified potential new sources of valuable material that could be analysed 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 other cities and provinces of interest but also use that material elsewhere where there are initial reports and indications that perhaps the virus was also present in individuals in other places and other countries. 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 analysed 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 all samples for traces of the presence of the virus at that time. There we need new approaches and new ways of doing that.

Of course, we can continue exploring the potential that the 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 with targeted, in-depth studies of some of these cases that 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.

For the studies to better explore the hypothesis that an intermediate 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 neighbouring countries in the sub-region and in other parts of the world. There there is an under-survey because not much has been done in many of these countries in terms of surveying bats and there we may have some interesting studies as well.

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We also have to do much more into understanding the possible role of the cold-chain frozen products in the introduction of the virus over a distance. We know that the virus can persist and survive in conditions that are found in these cold and frozen environments, but we don’t really understand if the virus can then transmit to humans and under which conditions this could happen. It would be interesting to explore if a 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 environments could be conducive to a rapid spread of the virus in such an environment. So a lot of work needs to be done to better understand these 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. 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. See if we can go further back in terms of identifying interesting clues in the farming environments in the species being raised in these farms and where they were potentially coming from before that. So that’s another area we’re 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 reasons is that a possible path 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.

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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 the dots, connect the different pieces of information to try to get a better understanding of this whole picture, again not limiting ourselves to any preconceived ideas and just following all the leads, following the science, following well-designed and conducted studies.

I 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 and before and trying to give you a picture of all our findings and conclusions. I would now give the floor back to Dr Mi Feng. Thank you.

MF 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 are 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.

01:33:08

QU   Hello there. My name is Josh Horwitz. I’m a reporter with Thomson Reuters in Shanghai. I’d just like to see if we could drill down with a bit more specificity about the likelihood for these hypotheses that were presented. So I want to know if it’s possible for each of the three of us actually to give a percentage of the likelihood to which we think that the virus either originated from wildlife and subsequently transitioned to a human or through some form of frozen food.

MF   Thank you for your question. Dr Peter, over to you. Thank you.

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

MK   Yes. Thank you very much. So this is a very tough question. So what we really did is develop the figure that was shown to help structure our thinking but be systematic about it. So what that does is, it lists from literature, from studies where there’s evidence for or against and where there’s uncertainty. That is what we then have used to assess, what do we think is more or less likely? I think going into exact percentages is really overstating what can be done.

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It’s really developed to help us structure our thinking and also structure the discussions somewhat because these are very complex questions and there’s 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 and 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 entry pathways change?

Maybe a last point is, in our complete report we will list all the elements that were used in that assessment, so the literature, the studies, all the aspects that we included to make that assessment.

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

LW   I applaud the view offered by Dr Marion and actually there will be more detailed introduction of the methodologies and more abundant evidence that are going to be demonstrated in the first 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 endeavour. We have tried our best to provide an evaluation of the possible hypotheses and also other kinds of possibilities in a scientific way by unleashing the joint wisdoms [?] from the experts of the two sides based on the existing, available evidence.
This is the teamwork. Also, we have not used the whole quantitative nor the whole qualitative method either, as it was introduced by Dr Marion. 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 possibility to put them into different measures to have a comprehensive consideration and evaluation.

Next question, please.

I’m with CGTV [?]. I have one question related to Huanan Seafood Market. Is 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 and what are those possible early transmission routes? Is Huanan Seafood Market the earliest outbreak source of the Wuhan epidemic?

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 Markets. 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 who were linked to the market.

So we have a picture of where the cases worked, 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. All that tells us that there was a spread among people in the Huanan Markets 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. We know that there was also spread among individuals who were not linked to this market. They were linked to other markets. They had no links to markets. So the picture is not clear in that respect.

For the introduction part, it’s part of the discussion we’re having and the work we are planning ahead of us through this hypothesis evaluation, is to understand how I was introduced. 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 another person in the market. That could be the 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 were frozen farmed wild animals and some of these species are known species susceptible to these 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 markets were detected or had their onset of symptoms in the first two weeks of December. That indicating 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.

MF Any additional comment from Professor Liang?

LW I would like to offer additional comment. First, according to the current research conclusion of this joint research team, Huanan Market may not be the first place that had the outbreak and it is not 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 8, 2019. Also, the earliest confirmed case that has association with Huanan Seafood Market was December 12. Actually, according to our research from the epidemiological group, the case with the onset date on December 8 and actually have no relationship or association either with Huanan Seafood Market.

The second point I would like to explain is, why do we attach so much importance to Huanan Market in terms of the consideration 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 aetiology of the virus and the disease as well. At the beginning, we detected this pneumonia-like disease and actually it can occur on the cluster base. So that is why we focus our early research in Huanan Market and relevant cases that have association with Huanan Seafood Market.

For the earliest cases with the suspected pneumonia or the PUE, pneumonia of unknown aetiology, 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 better and much improved testing capacity and also with the improvement and development with different kinds of the testing tubes or test kits, we have greatly increased our understanding of the virus. So when we conduct the retrospective study related to the early cases, in the earlier confirmed cases a majority 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. Actually, we have also conducted the 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 intermediate hosts or from the cold-chain transmission or introduction. So we are having full exploration of these possible introduction pathways and this will be also a highlight of the future research.

MF Next question, please.
TC    Tom Cheshire, Sky News. Of the four hypotheses, the only one you decisively rejected was the laboratory incident. Can you explain the evidence or the reasoning for discarding that hypothesis?

MF    Dr Peter, thank you.

PE    Thank you. We evaluated this hypothesis in the same way we evaluated the other hypothesis with the method described by Marion. So we looked at, what are the arguments for and against such a hypothesis? So in short, you will see in the report the more detailed evaluation of these hypotheses, but in short, it’s about, yes, accidents do happen. Unfortunately we have many examples from many countries in the world of past accidents. Of course, 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 had been no publication, no reports of this virus, of another virus extremely linked or closely linked 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 they’re looking and discussing with them these hypotheses as well. He’ll wring from them how their staff health monitoring programme or how their audit programme, for example, are conducted, and what this revealed in the past months and years.

01:56:28
We also looked, for example, at the Wuhan Institute of Virology, a BSL-4-level laboratory, and the state of that laboratory. It was very unlikely that anything could escape from such a place and we also know that when lab accidents happen, they are of course extremely rare. If you look at the history of lab accidents, these are extremely rare events. So this is not the first thing that would happen on a regular basis. So many of these evaluations and arguments were put for and against and helped us taking a rational approach to assessing the likelihood of such an event happening.

Of course, as I said, we look both at the arguments against but also the arguments for to make sure that we were 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 of course the fact that some of these were in the city of Wuhan. Of course, all these arguments were put forth and against each other in helping us making these assessments.

For us it was important to develop a system to evaluate all these hypotheses where we could take a rational approach and look at facts 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 their personal views and feelings. We wanted to move away from, I think this is this way, or, I believe it is this way, and try to move away from that and put rationale and facts on the table that everybody can then look in a systematic way. We felt that that was a much more useful approach than to put personal views, feelings, etc. or looking at only half of the arguments. Thank you.
I agree 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 expert team on the basis of 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, a virus was engineered by humans, but this hypothesis has already been refuted by the whole scientific community around the world.

Second, there may be a leak of the virus from that lab, but in terms of the leaking of the virus, it should be leaking of an existing or no virus. However, in all the laboratories in Wuhan, there is no existing virus of SARS-CoV-2. If there is no existence of this virus, there will be no way that this virus would be linked. In addition, in all the laboratories in Wuhan, including WIV, they upheld a very stringent and high-quality management system. Also proceeding from the current evidence, we regard the lab leak hypothesis as extremely unlikely.

Thank you.

Thanks. Next question, please.

From Hubei Broadcast TV Network [?]. My question is, actually the numbers of the patients has been coming to zero in Wuhan nine months ago. So in terms of this source-tracing in Wuhan, how do the joint expert team members conduct this kind of source-tracing including the identification of the early cases? Thank you.

So maybe I can start. What was done was a series of studies. So of course there were reports of non-cases from later December and 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. You’ve seen in other countries that 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 record by clinical teams from... I think it was 233 healthcare centres in Wuhan and so they have... With their knowledge of now what COVID cases look like, have looked back in their records to see if they found evidence for earlier cases.

So that is what has been done. So what all the studies then showed was a number of recorded cases in December with the first people that were mentioned just there by Professor Wannian. So that’s how that was done. So we cannot, by that process, 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. So that’s what the studies conclude.
Additional introduction of the methodologies that we have been adopting in this joint research. Actually, in our joint research, it covers three kinds of methodology. First, we conduct ample and abundant retrospective study. 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 kind of methodology is that we tried to connect the dots by analysing from a full-fledged manner different associated factors by pricing in as many factors as we can in a highly integrated and systematic manner.

So in our research, our diversified and multi-prong approaches on methodologies can allow us to have different kinds of comparative study and also to better draw the influence from those kinds of causal relationship analysis. So apart from those kind of multi or broad-spectrum analysis, we also provide description of the current situation. So these all-encompassing research methodologies can allow us to reach a more comprehensive conclusion portfolio.

We are already having two and five hours sat 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’s ever been confirmed what exactly those animals were and you mentioned that some are known to carry coronaviruses. Have you identified some that are therefore of greater interest to you as potential intermediate hosts? Have you identified ones that maybe were in the market earlier but had left by the time inspectors arrived, by the time the market was closed?

In terms of the following the trail and trying to identify the trades and the farms and the sources of those animals, you go into a bit more detail about how far you’ve got, what’s the stumbling block, what needs to be done yet? 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 ask for and obtain information, data, samples regarding any gain-of-function experiments that might have been done at Wuhan’s Institute of Virology, which might have been working with one type of enhancing it through genetic manipulation? Thank you.

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

So the question about animals. I think first it is important to emphasize that testing did not reveal any positives, but the full trace-back that was done, a very extensive trace-back of all the animals and products on the market, showed that there was some animal species that have been confirmed as susceptible like rabbits or that could be suspected to be...
susceptible like ferret badger or bamboo rats. So the way that is interpreted is to really say, well, if they were there then, then maybe they could have been similar animals earlier?

So it is an entry point for a trace-back investigation 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 raised some interest is also that some of the trace-back was in farms or in traders in regions that are known to harbour bats with the closest-related viruses. So it is really seen as an entry point for rationale, for taking the next step of surveys in animals on farms. That’s how we’ve looked at that.

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 and they have participated in further discussions and work with us. So we’ve had over the weeks such a 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 very detailed description of their research, both present and past, all the projects involving their studies with bats and coronaviruses and so on and also some of the more advanced projects. Then we engaged in a discussion with them on the different lab-related hypotheses because of course they have been on the front line of the discussion around these hypotheses for the past year. It was very interesting to hear directly from them how their thinking was in terms of, how we can explain this one? How can we dismiss this one? Are we using the wrong arguments? Are we providing the wrong evidence? 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. Of course, they’re 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 function, working with samples directly from bats, etc. You will also have in the report the minutes of our different visits and the meetings with different individuals. This one of course will also be in the report.

I would like to cite a few numbers or figures for the joint research related to animals. First and foremost, we have conducted testing of the samples numbering 11,000 from different kinds of animals like pig, cow, goat, chicken, duck, and goose in terms of the serum sample testing as a kind of testing sampling from the livestock and poultry from 31 provinces in China.
from 2019 to 2020. The testing results of those 11,000 samples of SARS-CoV-2 were all negative.

**02:27:48**

We have also done the testing related to the 12,000 swab samples from different kinds of animals in terms of PCR testing. The testing results were all negative as well and also 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 the wide animal, during the sample that were collected in the period of November 2019 to Match 2020, we have conducted testing of 1,914 serum samples from 35 different species of wild animals. The testing results of this antibody testing from the serological study were all negative. Also before and after the COVID-19 outbreak, we have increased our sampling sizes from Huanan Seafood Market and also we think Wuhan Municipality and other cities in Hubei Province and also the neighbouring provinces of Hubei. We have 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. Thank you.

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

QU Thank you. I’m from Agence France-Presse, 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 that this is? Do you think there’s a possibility that they were passed on to seemingly unrelated places across the world from undetected, asymptomatic, or mild cases who travelled from Wuhan? Do you think that, because there was obviously substantial spread in Wuhan at the time with several concurrent clusters in addition to Huanan Market, as you mentioned...

**02:31:32**

MK Sorry. Would you please repeat your question?

QU Sure. I’ll go slower. 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 other than China such as Italy in late 2019 with the implication that the virus originated overseas. How likely do you think this is, especially given that there were several clusters in Wuhan in December 2019 at the time? Do you think it’s likely that maybe a mild or asymptomatic case travelled from Wuhan to these places in different places around the world and that might have led to these clusters elsewhere?

So what we have done is look 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 is 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. That has found a couple or a few publications that would suggest that, for instance, in Italy there has been already circulation in December, maybe late November, but difficult to know because the methods for that were not confirmatory.

02:33:56
So they did not provide full evidence for that circulation, but this part 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 of earlier circulation wherever that is indicated. 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 travelled from Wuhan to elsewhere? Again, here we take a stepwise approach, but looking at what evidence is there, what evidence could be found, it wouldn’t be possible to get genetic information and then see what that tells us.

MF Dr Peter, any additional comments? So, Professor Wannian, over to you.

LW This is a very good question and also your question has explained by itself, why do we need to take an international perspective in terms of the source-tracing of SARS-CoV-2? That is also why we will need to have the joint endeavour 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 the joint research team and also different scientists around the world will try to research in their future plans.

02:38:13
MF Any final comment from Dr Peter?

PE Thank you and thank you all for all your very pertinent and interesting questions. As you heard, many of them are exactly the same questions we ask ourselves over the past few weeks. Just to let you know, we have answered some of your questions today, but the other members are not here and they will be of course 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.

As I said, you are only facing three of us here, but we have, over the past four weeks and even before virtually, worked closely with some 30 to 40 colleagues who were part of the joint team. Over the past few weeks, we have really had an intense and very productive work among that very special group and I would like to thank them all individually for all their contribution and effort. Beyond them, we were discussing that earlier today. Probably more than a thousand individuals have contributed over the past four weeks in providing us with data, helping us analysing data, generating reports, and helping us getting information and processing them. It’s also here an opportunity for us to thank them all for that.
So as you can hear, it's a huge group and amount of work that is behind the outcome of this mission and the robust and very numerous details that came out of this work. To go back to the work itself in my closing remark, I would like to point to a 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? Who are they and 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.

02:41:22
When we talked to one of the first cases who had onset of symptom in early December, when you talk 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 kind of ideas pop up. Then you realize that they are 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, office 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 study. Therefore we have to understand that these are complex studies. They need to be done in a systematic way and that's how we, bit by bit, can connect the dots and get all the information we need to move forward. That's the approach we have taken. That's the 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 Wannian.

02:46:27
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 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.