
Virtual Press conference
30 March 2021

Speaker key:
TJ   Tarik Jasarevic
PBE  Dr Peter Ben Embarek
TF   Professor Dr Thea Fisher
JW   Professor John Watson
MK   Professor Dr Marion Koopmans
DD   Professor Dr Dominic Dwyer
VD   Vladimir Dedkov
HNV  Dr Hung Nguyen-Viet
FL   PD. Dr. med vet. Fabian Leendertz
PD   Dr Peter Daszak
FAL  Dr Farag El Moubasher
KM   Professor Dr Ken Maeda
IS   Isabel Sacco
JL   Jérémie Lanche
DY   Du Yang
SN   Sarah Newey
Hello, good evening, good afternoon or good morning to everyone. My name is Tarik Jasarevic, and I'm welcoming you to our press conference regarding the publication of the report that was looking into origin of SARS-CoV2 virus. The report itself has just been published on our website. We have sent the link to the webpage where the report is placed, as well as the press release and opening remarks by Dr Tedros at today’s meeting with member states where the report was presented.

The report, as I said, describes the findings of the Wuhan field visit that took place from January 14th to February 10th, and that was conducted by a group of international scientists and Chinese scientists, as mandated by the World Health Assembly Resolution that was adopted in May last year. So, here today, we are to present those findings to the members of the media. We have with us, I hope, all ten of international experts, and I will read their names.

Here with me in WHO studio is Dr Peter Ben Embarek, who was a Team Lead for the Wuhan field mission, and who is our expert at the WHO for Food Safety and Zoonotic Diseases. So, the full names and affiliation of international experts, you can find on our website if you just look for WHO origin of the virus, but I will read just their names.

We have with us Professor Thea Fisher. We have Professor John Watson, Professor Dr Marion Koopmans, Professor Dr Dominic Dwyer. We have Vladimir Dedkov, Dr Hung Nguyen. We have Professor Dr Fabian Leendertz, Dr Peter Daszak, Dr Farag El Moubasher, and Professor Dr Ken Maeda.

Before we start with the opening remarks, I will just remind journalists to be short with their questions, and we will take, really only one question per journalist. So, if you ask many, I will have to decide which one I like. Also, we will send, after the press briefing, all the audio and video material, and if necessary, some other material that Dr Ben Embarek may be using in his opening remarks. With that, I will give the floor to Dr Ben Embarek, and then we will hear from other team members. Dr Ben Embarek?

Thank you, Tarik, and welcome to all of you for this press conference. Sorry for this. Small hiccups. So, again, thank you, Tarik, and welcome to this press conference on the result and outcome of the joint study into the origin of the virus that was conducted in Wuhan, China in January and early February 2021. As you know, we went there as part of a long process that started last
summer where we agreed on the series of studies to be conducted, to help us in the process of better understanding the origin of the virus.

00:04:05
And that was including a series of epidemiological studies looking into the human side of the start of the outbreak, looking at the earlier cases in December 19, trying to find earlier cases than the one we knew, and also looking at other data available prior to December samples kept from that time, data from surveillance systems of different syndrome and diseases that could give us clues about the possibility of having earlier cases than December 2019.

We also looked at the market where the first cases were linked to, the Huanan Wholesale Seafood Market in Wuhan, and we also looked at many studies that were conducted in the past few months in China on different animal species, trying to find or have a better idea of whether some animal species would be harbouring this virus. We looked at all these studies. We received a lot of data, raw data, processed data, results of studies and analysis done locally, and we processed that all together with our Chinese counterpart.

We also looked at molecular and genetic data available to help us link all the other pieces together. We looked at, and analysed and all the genetic sequences of the viruses coming from different sources in December 19 and January 2020 to try to give us a better picture of what we could find about the start of this event. In terms of key data we looked at on the epidemiology side, we looked, among other things, into data coming out of different surveillance systems, in particular, surveillance systems looking at cases of fever, cases of unspecified pneumonia, ILI and RE systems, which are respiratory syndromes that are picked up by different health facilities.

00:06:25
So, we looked at more than 76,000 cases of these symptomatic individuals in the months before December to try to look if anything there could look like COVID cases that had not been picked up before, but at the end of the day, we didn’t find anything. But this is only a first set of studies, and among other things in our recommendation is to look back in more detail into many of these data sets.

We also look at the data around the confirmed cases in December 2019, the 174 cases we know were confirmed at that time in Wuhan. And there, clearly, during the second half of December, we could see a surge of cases, both among the ones linked to the market, but increasingly, as we move towards the end of December, increasingly, cases not linked with the market, indicating that the disease was already at that time spreading outside in the different part of Wuhan.

And therefore, the more we move into the second half of December, the less relevant the market itself becomes, because then the disease is spreading around. We also look at data from mortality statistics to see, could we see any excess mortality, any sign of an excess number of deaths in the period before December 2019 in and around Wuhan and also elsewhere in the province. And we could not, there, see anything happening before December, and clearly, looking at this type of data, we could see that an upsurge of mortality
in the numbers of deaths somehow in January, towards the start of January 2020 in Wuhan, compatible with the fact that the number of cases was growing already at the end of December in the city.

00:08:36

And we also could see that outside Wuhan, this increase in mortality came a little bit later, indicating again that the event, at least, in the province, started in Wuhan and then moved more and more outside Wuhan.

We also looked, of course, at the market, the Huanan Market. We went there, and it’s a closed market now for more than a year, but it was still very interesting to see the setting, to see the state of the physical environment, in which these events unfolded more than a year ago. And we also were able to map the entire market. It’s a huge market, with more than 1,500 vendors and shops, and mapping all of them with the different type of product they were selling, different type of meats, poultry, seafood, wild animal meat, etc, and could link that with the most positive environmental samples that were found in different surveys in the market, but also with the human cases, particularly in the early days of December.

And by putting all this data together with the sequencing data, we could show that the virus was circulating in the market as early as the beginning of December 2019. But there were also cases not related to the market, outside the Huanan market with slight differences in the genetic makeup of the virus these cases had, showing that there was probably some circulation in different part of the city unrelated to each other.

00:10:23

And remember, the cases we picked up in December 2019 were only the severe cases at that time. A COVID case was a case of severe pneumonia. All the mild cases were missed, because at that time, we didn’t know that there were many mild cases or even asymptomatic cases. So, all these other cases were never picked up, and of course, they could help us get a much better understanding of the start of the epidemic if we have access or could detect these cases.

We were also able, for each of the interesting vendors in the market, to trace back their suppliers, in particular, the shops selling farmed wild animals of much interest in our work. We could detect or identify the suppliers they were using, all the way back to the farms providing and raising these animals in different provinces of the country, and in particular, in some provinces where we know that bat populations of interest are also there. So, clearly pointing into interesting new studies to be conducted in the coming months.

So, again, this is only a first start. We’ve only scratched the surface of this very complex set of studies that need to be conducted, and we have pointed to many additional studies that should be conducted from now on. We were also able to do a lot of analysis on the genetic sequences of the virus that were isolated in December and early January at the start of the epidemic and being able to see how these sequences were linked in evolution, meaning helping us to understand, and try to understand, where and when the start of the presence of the virus could be related to. And we will see that in the report,
there is a lot of very detailed information and useful information that, again, points towards the need for very specific new studies.

00:12:35

Chinese counterparts, ahead of our coming, were also conducting a large number of surveys on animals, different types of animals, wild animals, animals from zoos, animals from farms, domestic animals, etc. Dozens of thousands of animals were tested and all negative, so, again, showing the difficulty of picking up a particular species as a potential intermediary host.

And in the process of helping us to prioritise our recommendations and prioritise studies to be conducted, we also looked at what are the different possible pathways for this virus entering the human population back in 2019. And that helped us organise our thoughts and prioritise our recommendations. And there we looked at four possible pathways for the introduction of the virus. One was a direct introduction from the host animal, from the reservoir, and that could be a bat or another animal where the virus had been initially present, directly into the human population.

Then we looked at this scenario together with an intermediary host, meaning the virus would have first jumped into an animal, adapted into that animal population and then jumped and adapted to the human population. And then we also looked at the possibility of frozen food products or contaminated products being a vehicle for the virus, allowing the virus to enter the particular Wuhan area from further away, and there this interesting lead into frozen farmed wild animal products, present and sold in the market, in Huanan Market, are very interesting and warrant further studies to explore that type of disease.

00:14:36

And the last one, of course, was the possibility of laboratory accident or leak. And in doing so, we looked at all the arguments for and arguments against we had for each of these hypotheses or each of these pathways, and we tried to stay to what are the arguments we have, the hard facts we have. We tried to stay away from suspicions, ideas, theories and so on, because we couldn’t really use that in a systematic way for all the hypotheses to help us, moving forwards.

And there in that process, we then assessed the likelihood of each of these possible pathways and organised our recommendation towards the ones that were, as an outcome of our work, the most interesting to continue with. And in particular, with regards to the current joint group, the joint group of experts between Chinese experts and international experts, where and how this group can best, and in the most useful way, conduct the necessary additional studies in better, again, exploring certain of these hypotheses and improving our understanding of the source of the virus.

In closing, I will just say that it has been an incredible experience. We really learned a lot. You will see, if you dig into the report, it’s a huge report, and I can understand the challenge of going through that in a short period of time, but it’s a huge report with a lot, a lot of new knowledge, a lot of data, a lot of new information. And, I think, a lot of work will continue to come out of these initial studies.
We also, of course, have to thank hundreds and hundreds of people who made this work possible, both in the host country, in China, facilitating all our work, gathering data, generating data together with us, but also a huge logistical challenge to get us to Wuhan and stay there for a month. As you know, travelling these days is not easy. Bringing an entire team from the outside is not easy, so it has been a really challenging time for the whole team to get there, do the work and come out again.

So, on this, I would like to thank you all and give the floor over to Tarik. Tarik, over to you, please.

TJ Thank you very much, Peter. Just two technical things. First is, Dr Ben Embarek has used some slides that those who are on Zoom were able to see, but those following as through broadcasters or through social media were not able to see, and we may send these slides for everyone to be able to see them after the press conference. I also understand that for journalists who are on Zoom, they have missed the introduction that I made, so I’ll just briefly repeat that the report has been posted some 15 minutes before the beginning of the press briefing at the webpage, and we have sent the link to that webpage alongside with a press release to our media list.

You may contact mediaenquiries@who.int if you have not received any of that. Just to repeat that we have ten scientists with us, and I will read one more time the names, for journalists who have not heard me the first time.

So, Professor Dr Thea Fisher, Professor John Watson, Professor Dr Marion Koopmans, Professor Dr Dominic Dwyer, Vladimir Dedkov, Dr Hung Nguyen, Professor Dr Fabian Leendertz, Dr Peter Daszak, Dr Farag El Moubasher, and Professor Dr Ken Maeda. Their affiliation and places they work normally you can find on our website. So, after these opening remarks from Dr Peter Ben Embarek, we will go to the three co-chairs of subgroups. So, first we will start with Dr Thea Fisher who was co-leading the group on epidemiology. Professor Dr Fisher, the floor is yours.

TF Thank you very much, and thanks so much for a very strong presentation made by the entire team, but presented by our Team Lead. It’s a pleasure to reach this day with the final publication of the report. And I think, Peter has already really worded it very well. So, from the Epi side, I would just like to underscore the main findings. They are all preliminary findings, of course, as this is just a very first step on an expectedly long trip to find the origin.

But we have managed to come quite far with the joint work. And you have to remember, this is based on 28 days of international travel to Wuhan, of which only two weeks, 14 days, were working, actually, jointly together in the various teams and in the entire team.

So, from the Epi side, we have been reviewing thousands and thousands of data points. We have reviewed data points of respiratory surveillance data. We have reviewed data points of mortality data. We have looked at
pharmaceutical data, and we have looked specifically and zoomed in on the already known early cases from December 2019 in Wuhan.

**00:20:39**

All in all, trying to get as much information as we could, looking for early cases, looking for previous smaller epidemics that were not yet identified. We have looked, really scrutinised the respiratory data, and so far, we have not been able to document any substantial transmission of SARS coronavirus in the months preceding the outbreak in December. However, we cannot exclude that there have been milder cases, and there might have been smaller epidemics that have gone under the radar, as with our current knowledge of COVID-19, some of these cases, and that’s actually the vast majority, they might only have mild symptoms.

So, this is indeed a possibility that we cannot exclude, based on the current findings, and we have made a substantial amount of recommendations. Some of the data we will recommend to revisit and re-review jointly, and that will be the next step forwards. And in addition to that, some of the very important recommendations are also that we will jointly undertake a serology study, looking at blood donors who are otherwise healthy people and look for any traces of SARS coronavirus antibodies in these populations in the months preceding the outbreak.

So, all in all, many important first preliminary findings, many important joint recommendations for the next steps, and we welcome the questions you will have to the work we have, today, presented here, both in the presentation and in the report on the joint Epi and the joint International team. Thank you.

**00:22:33**

TJ Thank you very much, Professor Fisher. Now we will go to Professor Dr Marion Koopmans, who was co-leading a subgroup on Molecular Epidemiology. Dr?

MK Yes, thank you, Tarik. Also, very briefly, so just to emphasise that part of the work in the Molecular Epi team has been, trying to see what we can learn from bringing together virus genomic data. We’ve all learned in this pandemic how important genomic data can be. We are seeing that used every day now, so we’ve really done an effort to look at the earliest available data, bring that together from different laboratories and going back to the original data and re-analysing them to see, what are the golden sequence data from that first episode and what can we learn from that.

And that may seem like a very simple endeavour, but in reality, it is not, because molecular data are generated in laboratories, and they are released, for instance, through the Global Database at GSH, but then they are not linked with the patients that they came from. So, that was a piece of work that was needed, in order to really see how the molecular data could help reconstruct the early phase of the pandemic in Wuhan.

And the key conclusion there supported already the findings from the epidemiology, that the market in Huanan has been an important amplifier event, but that there also, already at the time of those early cases, was some
virus diversity, telling us there were some chains of transmission missed. So, we have to dig back a little bit further.

00:24:39

And then there’s also this, so what was summarised is, all the genomic data that is out there now also from animal surveys before 2020 and since, and what we can learn from that about plausible hypotheses for reservoir species. And all of that is described. So, I will leave it at that.

TJ Thank you very much, Professor Koopmans. And now we will go to Dr Peter Daszak who was co-leading the subgroup on Animal and Environment. Dr Daszak?

PD Thank you very much. Just briefly, two points. First of all, as you read through the report, you’ll see quite a significant amount of work that’s been conducted since, really, the very beginnings of this outbreak in China, to try and trace back the animal origins, including over 900 swabs in the Huanan Seafood Market. Tens of thousands of samples of animals collected, tested around China. Different types of wild animals and livestock, bats in the province, Hubei Province where Wuhan is.

And the second thing is to put the animal work in the context of both the human epidemiology and the molecular work that you see in the report. It all collects together in a true One Health way, and what we do see are some clear links, some clear pathways this virus could have taken that all of the evidence suggests are plausible and some that are less plausible. And I think, that’s how you read the report, and I look forward to answering every question you have on this issue. Thanks.

00:26:20

TJ Thank you very much, Dr Daszak. So, now we will open the floor for questions, and we have many of them. So, please, if you can introduce yourself and ask only one question. As you know, for this press briefing, we don’t have a translation interpretation available, so it will have to be in English, although many languages are spoken here. But let’s try, for others to be able to understand. So, let’s start with Isabel Sacco from Spanish news agency, EFE. Isabel, unmute yourself, and please go ahead.

IS Good afternoon. Thank you, Tarik. The report mentions the possibility of circulation of missed SARS-CoV-2 in other countries even before the first case was detected in Wuhan. So, how, Dr Embarek, do you assess the possibility that the origin of this new coronavirus was somewhere else but not in China? Thank you.

PBE Thank you for your question. We don’t think that the possible findings of indication of earlier circulation elsewhere outside China is incompatible with the current scenario. It is perfectly possible that you would have earlier sporadic cases circulating in and around Wuhan before December, let’s say, in November and, potentially, also October 2019. And potentially, that some of them were also travelling abroad and seeding and transmitting the disease abroad, again, in a sporadic way elsewhere during November and earlier December.
And so, that could be possible. Don’t forget that Wuhan was a major international hub at that time with direct flights every day to most parts of the world and most big capitals of the world. So, that earlier move of the virus outside of the area could, potentially, be explained that way. This being said, until we have more data, more firm information or results pointing into that direction, the current thinking is still that we are looking at a start in and around Wuhan and moving backwards, trying to find out how it came there.

And whether it came from another part of China or elsewhere, that will depend on the further studies and research. But because of the strong suspicion of certain bat species being the host of this virus, and having found other relatively close virus strains to SARS-CoV-2 in the region, also in Southeast Asia in general where these bats are living, is a strong indication that that’s where the source is. But we are still working on finding the exact traceback of the virus before Wuhan. Thank you.

TJ Thank you very much, Dr Peter Ben Embarek. I understand, Professor Koopmans would like to add something.

MK Yes. So, maybe to add that, so there is, of course, the plausibility of bat viruses in geographically neighbouring countries, but there are also two pieces of information that really also why this recognition is there. One is that if you look at the earliest sequences, there are already clusters of identical viruses in two other provinces in China.

And the second is that there is some literature from outside of China, particularly in Europe, that is suggestive of earlier circulation, although the methodologies there really need some scrutiny. But because of that literature, we have said, well, we need to keep an open mind and be sure that those types of pieces of information are also explored further.

TJ Thank you very much, Professor Koopmans, for that, and we will now go to the next question, and that’s Radio France Internationale, Jérémie Lanche. Jérémie?

JL Yes, thank you, Tarik. I’d like to know more about the missing data that you’re looking after. How confident are you that China will transmit those data to upcoming missions to Wuhan, if they ever happen? And would you say it is likely, possible to likely, possible, or extremely unlikely that China did try to hide some data from you?

PBE Thank you for this question. Yes, as we said, the amount of data generated all the way up to our arrival, and while we were in quarantine, in fact, colleagues in China were still generating data as the follow-up to some of our initial questions. So, there was an incredible amount of data being generated. We got access to quite a lot of data in many different areas, but of course, there are areas where we had difficulties getting down to the raw data, and there are many good reasons for that.

In China, like in many other countries, there are restrictions and privacy laws that forbid the sharing of data, including private details to outsiders, in particular if the data are moving out of the country.
That would be exactly the same in most countries in the world. If we were going there to do any studies, and we’ve done many studies in the past, and we always face the same challenges, how much and how can we share critical data with outsiders? But also because there was a large amount of data, don’t forget that some of these data sets, the one looking at 76,000 individuals, these were generated by hundreds of different healthcare centres, by thousands of medical staff. And just the fact of being able to extract and put all this data in a way that you could have easy access to the raw data is a challenge in itself.

So, therefore, where we did not have full access to all the raw data we wanted, that has been put as a recommendation for future study. So, the idea is that because we didn’t have time or because certain authorisation needed to be given before we could get access to the data, all that will be, and could be, done in the second phase of the studies. And then for the likelihood, I think, it’s clear that, for us, we are engaging in discussion. We got access to a lot of data. We were asking a lot of questions. They were, as I said, challenging for sharing some type of data, and we are working towards finding solutions on how we can get access and share this data in phase 2 studies.

So, I see that, again, as a continuum in working closely with our Chinese counterparts on making best use of all the data that is out there. Thank you.

TJ Thank you, Dr Ben Embarek. I understand, we have two team members who would like to add a few points. Let’s start with Dr Hung Nguyen.

HNV Thank you very much. I agree fully with our team leader, Peter, on this point. I just want to add that people might need to realise that this is very short mission, and we, as the team between WHO expert and China, we clearly try to come up with some conclusion on the current status of knowledge. Actually, we can wait more and more to have more data, like Peter said, to come up with more conclusion. But I think that in this mission, we really, at the end of the mission, working from both sides, [unclear] in a qualitative risk assessment of different scenarios and pathway of likely transmission.

And with different types of data you can see from three [unclear], and Peter mentioned before, we came up with this ranking of likelihood. So, in short, I think that is very important, us, as scientists, really to come up with something, with the availability of data, to really respond to the urgent situations that we want to know about these diseases. Over.

TJ Thank you. Maybe last comment from Dr Peter Daszak?

PD Briefly, I think, if we look at the amount of information, new data that’s in the report, and just thinking about the animal side, tens of thousands of samples tested. They’ve never been published yet. Over 900 swabs from the Huanan Seafood Market. The data’s not been published anywhere else yet. And in the process of doing this work, we did go backwards and forwards with the China team and ask for them to do further analyses, provide more evidence, more information, and they did that. So, I don't think it will be a problem to continue this momentum.
If we look at the recommendations, China has agreed to follow those recommendations, and we really look forward to continuing that work. If the current report is anything to go by, we should expect to see significant new amount of information coming out in the future.

TJ  Thank you very much to all three team members on this answer. Now we will go to Xinhua News Agency, and we have a Du Yang with us, if I’m not wrong. Can you please unmute yourself and go ahead?

DY  Yes, can you hear me?

TJ  Yes.

DY  Okay, thank you for taking my question. What would WHO comment on the cooperation from the Chinese professionals and colleagues during the mission in Wuhan? Is there any plan from WHO to further the study on the animal source of the SARS-CoV-2 virus or to send a mission to countries or regions other than China for this study? Thank you.

PBE  Thank you very much for this question. I think, the size of the report and the amount of material and results and analysis and data in the report speaks for itself, in terms of how the collaboration went. There would never have been anything like that if we did not have a very strong and good collaboration with our colleagues in China. We would then have ended up with a very small report with very few results, very few studies presented. So, I think, this speaks for itself, and just look at the amount of results there. That will tell you everything about the depth and intensity of the collaboration between the entire whole members of the team.

This being said, it’s clear that there is still a lot of work to do. There are still a lot of studies and good leads that are in the recommendation of this report. This is a set of recommendations that comes out from the joint team from both sides, from all the members of the team. Everybody stands behind these recommendations, and we anticipate that many of them, if not all of them, will be followed through and will be implemented in the coming weeks and months, hopefully, because we owe to the world to find, or to get a better understanding of the origin of this virus. This virus has really created havoc on the planet and a crisis we have never experienced before, any of us, and really, this is the minimum we can do, to try to understand what happened, how it did happen, why, and try to prevent something similar happening again. Thank you.

TJ  Thank you. Professor Koopmans, would you like to add something?

MK  The question was addressed to WHO, but maybe as part of the External Scientists team, it’s good to explain how that collaboration came about. So, we were starting online in many meetings before the departure, then had a lot of online meetings during our quarantine, and then had two weeks where we were able to meet in a big room, face to face. And that’s, of course, what you need to really get to know each other better and to work better. So, I think, it’s really important for everyone to realise that it takes time
to build up a collaboration, a spirit, in any project, whether that’s in this situation or in a new project that you run at home.

00:40:30

And given those limitations, I personally think we’ve come very far in the collaboration. And then your question about studies in other countries, I think, that already came across earlier in one of the questions. So, what we said, we need to follow the leads. We cannot just go on speculation, but we need to follow the leads. If there’s a lead from a supply chain, tracing back to another country with, let’s say, wildlife products, that would be a potential lead. Then, yes, that would guide where to go for those studies.

TJ  Thank you very much. We will now go to Sarah Newey From Telegraph. Sarah?

SN  Hi, thanks for taking my question. I’ve seen the comments from Dr Tedros to member states this lunchtime, or earlier today, and he talks about the investigations into the lab not being extensive enough. I just wonder what your reaction is to that, and is that theory still going to be explored in future studies? Thank you.

PBE  Thank you for your question. As you know, the team put together to do joint studies into the zoonotic origin of this virus, as per the World Health Assembly resolution of last May in collaboration with our partner agencies, and this is what we put together and initiated, starting last July, and will continue in the coming months. We looked at the different hypotheses, as I outlined earlier, among others, the lab incident possibility. This is the first time that we have been able to discuss openly this possibility. Initially, it was just speculations all over the place, as you’ll remember throughout 2020.

00:42:41

Now we have a process to discuss it. We’ve put it in our report. It has been assessed. And of course, since this was not the key or main focus of the joint studies, it did not receive the same depth of attention and work as the other hypotheses. Also, because that was the assessment, that it was not something where we could see strong indication that that was something we should look into, and therefore, it was ranked as the least likely, so to speak, of the four possible pathways.

Not saying that it was impossible, but not the one we would start initially going deeper into, and focusing our attention on. But this being said, of course, if others, and if there is a need to further explore this and, potentially, other hypotheses, of course, we will continue to look into this hypothesis. We have also, all along, said that as soon as there is new data, new evidence, new information for any of these hypotheses, we will put that into the assessment and re-evaluate any of these hypotheses.

So, it should not be seen as a static product. It’s a dynamic product. It will be fed by the result of new studies, of new evidence coming up, by new analysis, and therefore, it’s important that the entire world is supporting this work, is contributing constructively into the analysis, into the studies, supporting them, etc, so we collectively can get through it and get to the bottom of these events and better understand the origin of this virus. Thank you.
TJ Thank you very much, Dr Ben Embarek. Let’s go to next question. we have NBC and Kier Simpson [sic]. Kier?

KS You can hear me?

TJ It’s a bit broken. Can you try again?

KS Can you hear me now?

TJ Yes.

KS Okay, great. Kier Simmons at NBC News. One question just about the report you’ve published. It refers to appendices, to annexes. Have you published those, and can you help just us navigate where to find those? And then a question substantially about the report. The report has very few clear-cut conclusions, so why would you not maintain an open mind about what is worth investigating?

TJ Thank you very much. On annexes, I think, we have not published them yet, but we will do. Please check on the website. If it has not been, it should be, because we were really trying to publish as soon as possible and to meet the deadline that we promised to you. Peter, would you like to take the question?

PBE Yes. No, apologise if the appendixes are not there, but they should be very soon up there, together with the core report. They are almost as big, if not bigger than, the report itself and contain a lot of information as well in it. So, yes, in terms of conclusions and keeping an open mind, I think, reading the report, you will see that throughout the report, there are many conclusions on the different studies and the different data sets being looked at and analysed.

So, there are conclusions throughout the documents, and we, of course, said it immediately, and have, I think, said it throughout the course of the past month, that nobody would expect that this mission would have come up with the final answer and that we will have showed up at end of the mission holding whatever animal in our hands and say, here is the culprit. That was never the intention or the expectation.

This is work in progress again, and we all have to be patient and, again, support the logic of our work, which is to start from where the first cases were identified, detected in Wuhan, and looking at that event, that phase, that environment and then expanding the environment and the studies, starting from that point and radiating out of it, following the leads that individual studies will give us.

We could, of course, all of us and others, go out and start testing and looking everywhere for the virus in nature, in the environment, in old samples, etc. That would be a total waste of resources. These are expensive studies, and they need to be targeted and led by previous studies, led by science, led by logic, otherwise we will never have a chance to get there. So, that’s why we also, because of that, keep, constantly, an open mind and say, until we have a firm lead that leads us in one direction, we are not closing the other doors. We
keep them open to enable us to not miss even a weak indication, a weak link to an interesting pass.

00:48:33

So, it’s a very slow process and is very complex, and therefore, it really demands that we don’t jump too early to conclusions and that we pace ourselves, keep an open mind and really look at what science and data tells us. Thank you.

TJ Thank you very much. Let’s go now to NHK Japanese Media, and we have our friend Shoko. Shoko, please unmute yourself, and before I give you the floor, I’m just hearing from colleagues that annexes are being formatted and will be uploaded soon by our web team. Shoko?

SH Hi, Tarik. Can you hear me?

TJ Yes.

SH Oh, okay. Thank you for taking my question. So, Peter, you mentioned, there is still a lot of work to do, but is the team planning to go back to Wuhan or some other places in China sometime near future for further studies? Thank you.

PBE That will depend how we organise the phase 2 studies, how we plan them. And some of that can be done quickly and with little resources and manpower. Others will demand more time to be well-planned, well-resourced, and therefore, it’s difficult to tell you if and when we will go where next, but I think, there is a consensus that these new studies need to be undertaken, preferably as soon as possible, but in a proper way, again well-planned and well-organised.

00:50:12

And I believe, speaking on behalf of the entire team, that the whole team is still eager to continue working on these studies, but of course, that will depend on where and how the next studies are planned. But we hope that these will start very soon and that we will... We know that some of them are already ongoing, so we’re not just staying and waiting for new studies to be done. Some are already ongoing. Some are continuing from where we left in early February in Wuhan and elsewhere.

And we know that other researchers around the world are also contributing by initiating new studies in support of this work. So, it’s a very large body of work that is in the pipeline, and it’s a very dynamic environment, and as, I think, Peter and others said earlier, we expect to see a lot more new useful and exciting information coming up of these many studies. Thank you.

TJ Professor Koopmans, would you like to add something?

MK Yes. May be good to understand that, so there is ongoing work like the work that has been evolving, but some of our recommendations really require development of a full protocol, get funding, get assay set up. So, it’s also important to realise that that will take time and that this team is dedicated on helping to get those studies established, but it will require some time to get there.
TJ Thank you. We have Professor Dominic Dwyer who would like to add something.

DD Oh, look, I just wanted to make the point, in all these questions about the data and what was available and what we reviewed and so on, and also in the context of future studies, I think, it’s worth remembering that this outbreak was an extremely difficult thing for the people and the medical system and the community to handle in Wuhan at that very early stage of the pandemic. I think, we’ve got to remember how hard it was for them and how they were operating in a system without any information.

We can argue the toss about data and what it’s shown and what it meant, but at the end of the day, there are people at the end of all of this data, and I think, we need to bear that in mind. And I think that, certainly, us as an international team, very much respected the difficulties that people had during this time. So, I think, that’s an important point to remember in all these questions. So, thank you.

TJ Thank you, Dominic. Indeed, important point. We will go to next question, USA Today, and we have Karen Weintraub with us. Karen, sorry if I’m mispronouncing your name.

KV Close enough. Thanks so much. I was hoping you could go into a little more detail about the theory that this was a leak from a lab. Some have said that you didn’t have a mandate or access to the granular lab records, data, personnel, to the extent that would allow you to confidently evaluate the hypotheses.

00:53:33

Do you feel like you have adequately evaluated these? Do you feel like you need...? That other people need to be involved in other data? Much other data needs to be considered for this?

PBE Thank you, Karen, for the question. Yes, as you said, that has been a theory and a speculation floating there for a long time, and frankly speaking, that was probably the first reaction of everybody, at that time, early January. Has the lab role in this? Everybody who knew that there was a lab in Wuhan, or several labs, by the way. Even the staff in these labs told us, that was their first reaction when they heard about this new emerging disease. Oh, a new coronavirus. It is something coming out of our labs of work.

They all went back to their records and worked, tried to find out if there was a link, but nobody could find any trace of something similar to this virus in their records or their samples. So, it has, of course, been a logical natural speculation by everybody at that time, but apart from that idea that, yes, there is a lab nearby or several labs nearby in the same city, so there must be a link, apart from that, nobody has been able to pick up any firm arguments or proof or evidence that these labs or any of these labs would have been involved in a lab leak accident.

Lab accidents, of course, do happen once in a while. We’ve seen that throughout history in many places, so of course, it’s possible, and therefore, it’s also part of the conclusions in the report, that it’s not impossible.
That could have happened. But we haven’t seen or been able to hear or see or look at anything that would warrant a different conclusion from our side. But as you said, we haven’t done a full investigation or audit of these labs or any other labs around the world, for that matter, and therefore, it’s not something that we can conclude more than what we have concluded.

We have concluded our conclusions and recommendations, based on what we’ve told, based on hours of discussions with colleagues, with staff from these labs with this management of these labs. And again, we haven’t seen any, or been receiving any, documentation that would lead us to believe that there was something that we should explore further. And therefore, that was not the focus of our work, because we had so many other studies, so many other concrete and interesting leads to look at that, of course, naturally, that’s where we put our attention, our efforts and our future work.

If we had seen nothing elsewhere, if all the studies around would have led to nowhere, yes, maybe we would have then looked at the alternative options, including other scenarios in more details. But we have strong leads. We have strong indication that we should explore further, and therefore, it’s a natural way to go. And of course, if this, again, leads to nowhere, then we can reassess our evaluation. We can reassess our hypothesis, and as I said earlier, this is a dynamic process. Nothing is cast in stone. There are no firm conclusions, and I think, that’s how we should look at the whole outcome of this report and this work.

TJ Thank you very much, Dr Ben Embarek. Now, next question is for our dear friend, John Zarocostas from Lancet, who also works for France 24. John?

JZ Yes, good afternoon. I would just like to follow a bit on Dr Nguyen’s comments earlier and also on the lab. How did you decide on the rankings, 17 scientists from both sides? Are your individual’s estimates published somewhere? And, secondly, with reference to the laboratory, I understand, one, BSL-4 Laboratory is quite recent, not even three years’ experience in operating it. One of your participants, Dr Dwyer, has experience in a BSL-4 facility. Was he satisfied with the answers you got from the experts of the BSL-4 facility? Thank you.

PBE Thank you. I will take the first part and then let Dominic answer the second part. We reached out conclusions by consensus and by discussing among ourselves in the whole team of both Chinese scientists and international experts, so there was no... Of course, there was discussion back and forth like always in this type of discussion, and that’s why we brought this large group of individual experts with different backgrounds, experiences and so on, to hear all these different views.

It was extremely important from the onset that we had very diverse views, diverse experiences of different kinds, to make sure that we would not miss any angle, that we would not miss any diverging opinion or evaluations. And because of the diversity and complexity of the data and situation we will look
at during our studies, it was important that we had that diversity on both sides.

On both sides, we had very diverse groups. And we reached our conclusions just by consensus at the end, by arguing, by convincing each other. And where some of us were not convinced, they would express that. They would try to counterargue against that, and again, the final outcome was a series of individual consensuses on all the issues we discussed and put in our report, as always, in this type of work when you bring a group of scientists with different backgrounds. And at the end, what you want is a consensus opinion.

Of course, if, at the end of the day, we could not have reached consensus on some of the assessments and some of the conclusions, we would have ended up putting these different views on the table and in the report. But we were able, by using good arguments, by putting science on the table, by looking at the data in an unbiased way, to reach a consensus on all the issues. And I think, that’s, again, showing the strength of this report, the strength of the work, that we spent the time that was needed to reach this consensus and to find the right language, the right conclusions and the right recommendations.

It makes it much stronger than if we had had a report with two or three different sets of views here and there all over the place. That would not have been very helpful. Thank you.

TJ Thank you. Maybe we can hear from Dominic Dwyer. Professor Dwyer?

Yes, thank you very much. Look, I think, it's worth pointing out first of all that SARS-COVID-2 does not have to be worked out in a P4 biosecurity level and neither do the other coronaviruses, bat coronaviruses. SARS-CoV-2 can be handled in a biosafety level 3 laboratory, so that's important to remember. I think, in terms of visiting the Wuhan Institute of Virology, and indeed, the other public health laboratories that we visited in Wuhan, we did have the opportunity to discuss a number of issues with the laboratory.

For example, what were their biosecurity protocols, in terms of handling material, and also looking after the staff that work in those facilities. There are generally accepted methods of staff health and staff monitoring that are undertaken in P4 laboratories, and indeed in P3 laboratories as well. So, we were happy that they did have processes in place. We also discussed with them about some of the testing they did on blood that is normally routinely collected from people who work in high-level security laboratories.

And they had done testing for SARS-CoV-2 antibodies and found those to be negative, which is some indication. And we also had the opportunity to talk to the scientists in the laboratory about the type of work they were doing. And again, as we know from the report, the most closely related bat coronavirus 2, SARS-CoV-2, the so-called RaTG13, in fact, has not been isolated in the laboratory, but is, essentially, a genetic sequence. So, I think, with that information, we were satisfied that there was no obvious evidence of a
problem and that people had done the appropriate lookback to see how the laboratory had been functioning during that time.

01:03:32

A true forensic examination of a laboratory like one might do other types of forensic examinations is a much more complex process, and that’s not what we are there to do. So, I think, that’s important to remember.

TJ [Inaudible], Dominic. Now, we have time for two, maximum three questions, as we have another event from WHO Facebook Live, so our colleagues from the studio will have to prepare for that. Let’s then go to Anjalee from Yahoo Finance. Anjalee, unmute yourself, and please ask only one question.

AN Thank you. Yes, thanks, Tarik. Okay, so since I only have one question, I’ll just make it this. Speaking of the laboratory examination and everything else that you’ve been able to put into this, what level of confidence do you have that, going back, you’ll be able to look more into the idea of where the origin is? And is there any pressure to find an origin outside of China right now?

PBE Thank you for the question. We have a fairly high confidence that we can continue many of these studies, because we have a consensus on the recommendations, consensus on all these studies that are needed from now on. So, that, I think, is a good starting point. And with regards to where the origin might be and whether there’s pressure from one side or the other side or from China to look elsewhere, of course, nobody wants to have an origin in your backyard, but we are, again, following the science.

01:05:21

We’re following the leads. We are going step by step. And we already know that, and we have recommendation for studies to be conducted outside the borders of China because it’s relevant, looking at bat populations that are crossing the borders. And looking at them across the borders is a logical step, looking further into the initial reports of positive samples in other places elsewhere in the world is needed, is warranted, is again, continuing exploring the different leads, the different paths, the different information we get from previous studies.

So, again, open-minded, following the science, logical approach, step by step, that’s the way forwards, and we will see where that leads us. Thank you.

TJ Thank you very much. Let’s go to the next question. We have Christiane [unclear] from the German news agency, DPA. Christiane?

CO Thank you, Tarik, for taking my question. Dr Embarek, you have said in an interview with Science Magazine that politics was always in the room and that there were dozens of people on the Chinese side that were neither scientists, nor in the global public health sphere. Can you tell us what kind of pressure there was, if there was any, from the Chinese side, in the direction of the investigations, and also in the formulation of this report? Thank you.

PBE Thank you for your question, and, yes, I think, there was. That’s accepted by everybody.
There was a lot of attention, a lot of pressure on all this work. We also had the entire world following every move we made during our stay in Wuhan, whether during quarantine or after the first quarantine period. And, of course, there was a lot of interest from all sides. And I think, as you said, of course, there was political pressure from all sides, also outside China.

But I think, we were able to create a space for the science, a space for the two groups of scientists that were together. We had nothing to hide, so there was no problem working in an open environment and sharing our work and our discussions as we had them. We also attracted a lot of attention during our visits to different sites, of course, both from the media, but also from the local populations, from the staff of these places we visited, etc. And of course, there was a lot of attention from our host country to follow, and making sure that we were able to work, and interested, of course, in our discussion, in our work.

We were never pressured to remove a critical element in our report. As I said, the report is something that all the scientists on the joint team can stand behind and have supported. And we have all fought for our ideas and beliefs to be in this report, and I think, we have all contributed and can recognise our footprint in this report. So, personally, I’m very proud of this report, and like my other colleagues, we all stand behind it on both sides, despite all the interest and the pressure and the immense difficult environments that we have faced over the past few months.

But again, we are also extremely pleased to have seen this interest and this pressure, in a way, around us. It has made our work more interesting, more challenging, but also more dedicated, because we could feel that there was no time to rest. There was no time to even sleep. We were really interested in making every possible effort to get this work done in the best way possible. And I think, we have achieved that, thank you.

Thank you very much, Dr Ben Embarek. Let’s take a question from Robin Millard from Agence France-Presse. Robin?

Yes, thank you. If I could just ask, what did you think was the most interesting finding from your mission? And how confident are you that your work will eventually lead to identifying the source of the pandemic? Thank you.

It will be difficult to pinpoint one particular result. I think, there are so many exciting results coming out of this work that it will be difficult to pinpoint one. I will think that finding the suppliers, the farm supplying what frozen animal products to the market is an exciting lead, is an exciting finding, and I can’t wait for going back to these farms and their environment and trying to move forwards and find something there. I think, the genetic work linking the genetic sequences of all the strains of December 19 and seeing how these are linked and also seeing possible link to parts outside Wuhan is an exciting finding.

I think, all the findings on the Epi side around the early cases, to see how the different surveillance system data can be linked together, the data on excess
mortality contributing to understanding how the disease was spreading in December in Wuhan is exciting.

01:11:21

All the data from the animal side. New finding of related viruses throughout the region is an exciting new piece. The large number of animal studies that have been conducted is also extremely exciting, not mentioning all the science data on the virus, its persistence in environments. There are really a lot of very interesting leads and exciting results here. It's really interesting, in particular from a scientist’s point of view, to see how much there is to look at and how much we’ve discovered already. Thank you.

TJ Professor Koopmans wanted to add something.

MK Yes, of course, Peter said it all, but I’m excited by just the sheer size of this endeavour and how important it is to go from broad, so many of the studies now, as that is typical in an outbreak investigation, have been based on convenience sampling, have been casting quite a broad net, but have now provided us with a very deep dive into what happened, the early phase of this pandemic. And that really provides a solid basis for more detailed follow-up questions on the serology.

Where would we want to target this? What are the places with the earliest evidence of circulation from the genomic data? And that really will help us target the follow-up study. So, that’s what I’m really excited about, going from the wide-cast net to, okay, next-phase study. So, yes, I think, that’s what is really nice about this approach.

01:13:23

TJ Thank you, Professor Koopmans. Dr Daszak wanted, also, to add something.

DD Yes. From the animal side, first of all, how well our understanding of this, the events in Wuhan began to fit together when we looked at the molecular data, the epi data and the animal data. It all seemed to fit to form a big-picture story about what likely happened. And I think, that’s quite exciting. We went there with open minds. We all did. We didn’t know what we were going to find. We didn’t know what data we were going to be shown. From the animal side, it would have been incredible to have a bat with the exact same lineage of viruses. We didn’t see that yet. That will come in the future, I think.

What we did see on the animal side is clear evidence that the Chinese scientists showed us, they found this information out from the market, that there was a pathway into that market of animals that we know are coronavirus reservoirs or able to carry coronaviruses from places where the nearest related viruses are found. What that does is, it shows you right there and then, there is a pathway that this virus could have taken to move 800,000 miles from the rural parts of South China, Southeast Asia, into this market. That was exciting to see that. Thanks.

TJ Thank you, Dr Daszak. Let’s go to, maybe, last question because we are already well beyond one hour, closer to one hour and a half. I have Sara Jerving from Devex. Sara, the floor is yours.
SJ Thanks so much. What would say is the timeframe on how long it might take for more conclusive answers on the origin? Could this be a matter of years, or what are your thoughts on that?

PBE Thank you, Sara. That’s a very difficult question. It’s always difficult to predict the future. It will take some time, and it will also demand and be depending on a good portion of luck as always, but we are still optimistic that we will discover more. We will get closer to the final answer, but when and how long it will take, that’s very difficult to predict. So, be patient, and please continue to follow the exciting set of studies that, hopefully, will come into motion in the coming weeks and months. And again, it’s an exciting adventure.

I hope the whole world will continue to follow these studies and this work, because it’s a fascinating journey, and it’s a critical one, because it’s the only way we can understand what happened, and more importantly, try to prevent something similar from happening again, because if we don’t look into what happened, if we don’t understand what happened and don’t... We will risk again, and most certainly, we will again face something similar in the future, and that will be, again, a terrible result. Thank you.

TJ Thank you, Dr Ben Embarek. Dr Farag El Moubasher wanted to add something. Dr El Moubasher?

FAM Thank you so much, Tarik. I guess, one of the exciting points of this report is this, which is One Health. So, we are using animal, human, environment. I guess, the report itself, it is good to apply this methodology using science, and hopefully, we will have the confidence to have the origin. This is one of the exciting points. I guess, our respected journalists, they need to take a cup of tea and sit and read this comprehensive report. Thank you so much.

TJ Thank you very much. I hope all journalists will do exactly that, take a drink, whatever it is, and read the report. I would maybe now just turn to some final remarks from some of our team members. I will start with Hung Nguyen who wanted to have some final talks.

HNV Yes, thank you very much, Tarik. I think that I just would like to follow up the point of El Moubasher, who is in my team, to say that it’s not about the concept One Health alone that we have done, but I have to say that I am so happy to be part of this one One Health team, in terms of composition, because we have... I think that WHO and China have made up a very nice team that reflects, really, the One Health concept.

I don't know, if you look on this camera and this screen, but I can tell this One Health team proposed by, really, a medical doctor, epidemiologist, a biologist like me. You have veterinarians, and you have people working in the lab and to the field, both from international side and the Chinese side. And it was really a good experience for me. And I think, then and now is the complex issue of the pandemic, that COVID-19 really needs this One Health and One Health team, yes, not only us, but as the One Health team, they’re going to
work together, and that should be the way forwards, that we start sometime with the phase 2. Thank you.

01:19:14
TJ Thank you very much. I see that Professor Dr Fabian Leendertz would like to say something as well. Fabian, please?

FL Yes, thank you very much. I very much agree to the previous said. Perhaps for those people who are a bit impatient and wonder, why does this all take so long to find out the origin of that disastrous disease, please, read the literature. There are some excellent books on the origin of other zoonotic diseases. It always took many months or years, in some cases, 1,500 years, like when you look at the origin of measles, to find out what really happened. So, we understand the curiosity, and many scientists around the world, including this team, are trying to do what we can to find out what happened. Thanks, that’s all.

TJ Thank you very much, Fabian. Now, Professor John Watson would like, also, to add something. Professor Watson?

JW Look, thank you very much. Only a couple of words, because really, all that needs to be said has been said. I really just wanted to emphasise that this is a process. It will take time. We’ve come a long way as a result of collaboration, and in order to be able to take this further and get closer to that answer, we need to be able to continue that collaboration, that dialogue, with our colleagues in China. And so, we will certainly be pushing to be able to do that. So, thanks very much.

01:20:55
TJ Thank you very much, Professor Watson. Dr Peter Daszak, you would like to add something as well at the end?

PD Just a single point here. I think, what we’ve seen in this report, half of this team is missing, and it’s the China co-chairs of the Animal, Epi and Molecular group. It’s the China scientists who did a lot of the work that we sat down and went through. And I think, this report is a testament to how, even under very intense scrutiny and very difficult political circumstances, countries can come together to focus on the origins of emerging diseases. And viruses don’t think about national boundaries, and if we really want to defeat pandemics, we have to do this work.

We have to come together with other countries to focus on how they emerge and try and stop them for the future. So, I hope that spirit of goodwill continues, and I really look forward to that allowing us, allowing the world to really better protect ourselves in every country against pandemics. Thanks very much.

TJ Thank you very much, Dr Daszak. And, well, Dr Peter Ben Embarek, maybe you would like to say a few final remarks?

PBE Thank you, Tarik, and thank you, colleagues, for all your good words. And I will echo everything you have said. This has been an incredible collaborative work, and we should really thank all that have been involved in
making this possible. And we are talking about hundreds and hundreds of individuals throughout the world who made this possible.

01:22:37

In particular, I would like, at the end, to extend our collective sincere thanks to the population of Wuhan, which we disturbed again, and where we put back in their memory the difficult days of last year by putting Wuhan again, last month, into the headlines. They have accepted us. They have facilitated our stay, and they have borne with us while we were disturbing their daily life with our visits and our work. So, sincere thanks for them, and in particular, after having gone through that traumatic experience in 2020 last year.

And I would like to also thank our entire team, both the Chinese side and the international team, for their dedication, their hard work. We have really spent months together almost day and night, and that has been an incredible experience.

And, lastly, I want to extend our sincere thanks also for the media who followed us throughout our stay in Wuhan. In January, the weather, unfortunately, was not the best in Wuhan. It was wet, cold, misty, and still, many of you stand up every morning or the whole day, waiting for us and try to communicate with us and follow our work for months. And that shows the incredible dedication and interest from your side as well. And again, thank you for that. Thank you.

01:24:14

TJ Thank you very much, Dr Ben Embarek. Thanks to all the team members who were with us today, presenting their findings. Thanks also to all journalists who were with us today. You have seen, we had more than 300 people online. I apologise to all those whose questions were not taken, but don’t hesitate to contact us at WHO, or any of the team members directly. I’m sure, they will have a little bit more time now to answer your questions.

Before closing, just to remind you that we will send audio file very soon. We will also have a transcript. That transcript will be available not before tomorrow morning, and we may try also to send material that Dr Ben Embarek was using in his opening remarks. With this, I wish everyone a very nice rest of the day or evening. Goodbye.