Kaiyuan Sun

Behind the Mask

November 20, 2023

Barr: Good morning. Today is November 20, 2023. My name is Gabrielle Barr, and I am the Archivist with the Office of NIH History and Stetten Museum. Today, I have the pleasure of speaking with Dr. Kaiyuan Sun. Dr. Sun is a Research Scientist in the Division of International Epidemiology and Population Studies (DIEPS) at the Fogarty International Center. Today, he will be speaking about the many COVID-19 studies and research projects he has been a part of. Thank you very much for being with me.

Sun: Thank you. Glad to be here.

Barr: To begin, how did you first learn about the initial cases of SARS-CoV-2 back in early 2020? How did you convince your department at NIH that the disease was important to track even before it became a worldwide problem?

Sun: Actually, I was in China in early 2020. I was visiting home back in China. At that time, I saw the news and that there was a cluster of a pneumonia cases with an unknown etiology in Wuhan. It was quite concerning. What was more concerning at that point in the early days was that they started to report cases outside China. They had travel-associated cases in Thailand and surrounding countries. That was a big warning sign for me, because I was working on basically understanding the diffusion of pandemics when I was doing my Ph.D. When you saw the international cases, you could back-calculate the size of the epidemic at the epicenter. Based on what we saw, it seems like that should be larger than what was being reported already, so that's really a warning sign. When I flew back to DC, in early January, I talked to my supervisors at DEIPS and convinced them that this was a really important matter to work on. During that time, many other modeling teams around the world started to raise concerns as well because of this travel pattern. That's how we got on the problem.

Barr: Will you speak about one of the first COVID-19 studies that looked at epidemiological data from January 13, 2020, to January 31, 2020, using social media accounts? How did you select which social networks to assess and the timeframe of your analysis? It's a very unique study—just using social media and news for modeling.

Sun: Right. One of the unique things about early reports of COVID-19 in China is that they were highly detailed. This is rarely seen, actually, for other outbreaks. Local governments start to report case information at the case level. Basically, for each case, at a local CDC [Centers for Disease Control and Prevention], local health authorities will report how many cases they're having that day. And for each case, it will tell you the sex and their ages. Later on, they will follow up with the outcome of their case—whether they are recovered or were being hospitalized or were eventually deceased. This is actually quite rare—and is really, as a technologist, very valuable information, that in the past has been really difficult to get your hands on. I thought this was very

valuable information. What's more exciting is that in China, there's many websites that are doing this, but I think one that really stands out is dxy.cn. That's a community website for healthcare professionals and doctors or people who work in public health. This would be comparable to a U.S. website for doctors. This is a community that is for the professionals. They gathered information and then put it in a centralized website. For me it'll be easier to see and to get all the cases from across China. Unfortunately, all the information is in Chinese, but I thought this could be very important information for the [scientific] community across the world. What I did is basically spent my nighttime translating those long lists of case information from Chinese to English and putting them in an Excel file—and then sharing it on Twitter, so that the whole research community across the world can have access to this valuable information in real time. That's what I was focused on at a very early stage of the pandemic—mostly sharing information.

Barr: That's really interesting. Will you discuss the findings of a modeling project that looked at the effect of travel restrictions on the spread of COVID-19 in the early weeks of the pandemic, and were you at all surprised by the numbers?

Sun: Yeah, so this is a collaboration. When you see the cases traveling outside of China, and you do the back-calculation, you figure out that this could be your concern. The study is in collaboration with my Ph.D. advisor, Alessandro Vespignani at Northeastern University. He is really the expert in understanding how mobility drives the diffusion of infectious disease on a global level. His group has really high-resolution data of air travel, and it is updated in real time, so you do see how people were traveling right at the eve of this pandemic. He's using this highly detailed, agent-based, data-driven model to simulate how large the epidemic could be at the epicenter to see those travel patterns and those travel related cases distributed in different countries. I can't say I'm surprised because I trained to work on this type of problem when I was a Ph.D. candidate. My intuition aligned with my Ph.D. advisor, but that's a paper that really pinpointed the technical details of the problem.

Barr: While I'm obviously not an expert, by the time all of the countries put in place their travel restrictions, there was already so much spread—it was already out there. I thought that was really interesting. I did not realize how the infection was really out there and that was going to be very hard to control. That was very fascinating.

Sun: This is the tricky part of containing an epidemic—sometimes you only need one person in your country to establish an outbreak. The travel restriction really only works when you capture all the infections that are coming into your country. For SARS-CoV-2, as we now know, many of the cases are asymptomatic or they're transmissible before they show symptoms, so it's impossible to screen all the infections through travel. You will find infections landing in your country and then at some point it will trigger outbreak. That's why I think travel restrictions will not be very efficient for diseases that have very high asymptomatic rates and where those asymptomatic cases contribute to transmission.

Barr: Will you discuss your role in a study that looked at the evolving epidemiology and transmission dynamics of COVID-19 outside the Hubei province in China?

Sun: I'm not the major contributor. I published one in Lancet Digital Health that used the online data we collected and translated. This is sort of a step-up of that study. Basically, this is in collaboration with Professor Hongjie Yu at Fudan University. They really have a big team over there, so basically, they were able to really gather all the information across China in high detail. That's a more refined database. They use that database to analyze and to characterize key ecological parameters, like the serial intervals and the generation intervals for SARS-CoV-2—which are very important at the beginning. Those parameters will define policies like how long you need to quarantine for travelers when they are traveling from high-risk countries, and if they're impacted, how long they need to be isolated to make sure that they don't transmit the disease to other people when they're out.

Barr: Will you discuss, in a similar vein, the heuristic method you and your colleagues developed for addressing biases that arise from neglecting changes in serial intervals, and how you applied the method to serial interval-based estimates of the R value for the COVID-19 outbreak in China in the Hubei province?

Sun: I'm actually not the expert at addressing this. When I was seeing the data, I did realize that the epidemic was growing. In that case, in order to look at serial intervals or competence intervals, you have to wait for the outcome of another person to know whether they're infected or not. But when you have a growing epidemic, you're not seeing all the outcomes. If you just naively calculate the serial intervals based on the data you're seeing, you're creating a selection bias. Whoever shows up early will end up in the database earlier. In that sense, what you're seeing is likely shorter than the actual value. I raised this question, and I was very lucky to find collaborators that are experts on this—in particular, Sang Woo Park from Princeton and Professor Jonathan Dushoff from McMaster University in Canada. They have been working on this problem for a very long time. They have very precise mathematical models to address this issue. I had the data and then I reached out to them, and we started a collaboration. They helped me resolve this problem using their mathematical framework.

Barr: Will you talk about your efforts as part of a team that assessed the case fatality risk of the initial COVID-19 wave in China, and how COVID compared to the 2009 H1N1 outbreak? How did this study impact other models and global policy? For the audience, could you define what "fatality risk" is, because I don't know if everyone listening to this interview knows what that is.

Sun: Yes. I think the better metric to use for COVID-19 is the infection fatality rate—the risk of having a severe outcome in terms of fatalities, or the risk of deaths, given that you are infected. And for COVID-19, what we find is, this parameter really depends on age—so the burden of the disease. This is a parameter that we use to characterize the burden of disease giving infection. For COVID, what we find that is truly unique is that you're heavily dependent on age. For a younger population, when you get infected, the risk of severe outcome is really low. But as the age increases, you see the burden of the disease increasing in exponential form. This is really a hallmark feature for SARS-CoV-2. The other thing is that if we look at the overall infection fatality rates, we should look at the overall burden to the human population—and this is actually quite high. It's between 1-1.5 per every 100 infections. This is actually very high compared to flu. We were able to assess this in the early phase of the pandemic. This really changed how people react to the disease. Because of the really high burden

of disease for this virus, many countries eventually have to face the reality and adopt to more aggressive control policies like lockdowns or try to contain it at the beginning. In terms of the process of recovering and discovering this disease burden, actually, this is the most important study that we did from the data that were collected on the internet. This is really thanks to the health authorities in China that, when they share the data, follow up on the case and tell you the outcome—so we know for a given faction why this person will be hospitalized and when they will be hospitalized. And furthermore, if the person is deceased, we know the outcome in the end. I can actually use those data and do a very preliminary calculation of very early on in the pandemic. And actually, we're not the only group to analyze and discover this pattern. We share the data on Twitter, and there are many groups across the world analyzing this data, and they show this pattern in real time. That's very helpful in terms of informing the research communities.

Barr: You used this data to look at the transmission in Hunan, China in the early part of the pandemic, also looking at the ancestral strain in the initial Beijing outbreak?

Sun: The Beijing study is another interesting study. At the beginning of the pandemic, different countries had different approaches, right? Some countries adopted a mitigation approach—they're not aiming to control or to eliminate to the virus, but to suppress the spread of the virus so that it doesn't overwhelm the healthcare system, but then there are other group of countries, including China, that pursued containment policies. They want to eliminate all the infections through lockdowns and the contact tracing, so that, at least within the border, there was no circulation of the virus so they can reopen up the society. The Zengcheng outbreak containment was a valid example of this policy. At that stage, China was finally able to ramp up the testing capacity—so different from the early stages. In addition to contact tracing, they could also do mass testing, basically testing millions of people in a short period of time to find all the infections in the high-risk population. This is for the ancestral strain. At that stage, the virus was not as infectious as we're seeing right now with the Omicron strain. The infectiousness of the virus may be quadrupled at this stage. Omicron also is an immune-evasive variant as well, so it's really hard to contain. But if we look back, the ancestral strain is actually containable. It's not an easy job to do, but it is containable. We use mathematic modeling to simulate how fast you need to find new infections through contact tracing, and how fast you need to isolate the infection you discover, and then we use a mathematical model to assess the feasibility of containing the virus. We find that is doable. It's a lot of work, but it's doable.

Barr: In addition to looking at China, you also looked at South Korea. Can you speak a little bit about your role in a study that looked at potential social distancing in mitigating the spread of COVID in South Korea in the early months?

Sun: Right. I was not in a leading role for this study, so this is also in collaboration with Dr. Samuel Park at Princeton, who is a Korean Canadian. He's really interested in looking at how non-pharmaceutical interventions disrupt transmissions in South Korea. Since I have some experience from China, I was helping him by interpreting the data. But eventually, it is a similar story to mainland China. South Korea also pursued a containment policy. The data shows that the non-pharmaceutical interventions were successful in terms of

really cutting off the transmission chains and eliminating the virus in the early days of the pandemic in South Korea.

Barr: A very different type of study, but how were you involved in a study that focused on CT [scans] and clinical assessment in asymptomatic and pre-symptomatic patients with early SARS-CoV-2 in outbreak settings?

Sun: My supervisor David Spiro actually made that connection with Dr. Brad Wood at NCI [National Cancer Institute]. For the early diagnostics of SARS-CoV-2, one of the methods they were looking at was doing scans of the lungs—because at the beginning it was really the pneumonia that was the hallmark feature of the disease form of SARS-CoV-2. Dr. Brad Wood at NCI was interested in whether there was a way with CT scans to see the progression of disease in the lungs. Even when there is not, the question was really to see whether you can see the disease in the lungs using CT before physical symptoms showed up. Many studies have shown that is actually the case. You might start to see the blur of your lungs even before you have very severe symptoms. In that case, when other testing methods were not quite ready yet, especially PCR [polymerase chain reaction] tests—we had a lot of trouble getting PCR tests in the early days—maybe using CT scans to look at pneumonia at the very beginning to help identify infections in the early stage and for severe cases could be helpful for planning for treatment at an early stage. Certain treatments at the beginning are really where the timing matters a lot, where we want to use it before it progresses to severe disease. We are just contributing from an ideological perspective, in terms of understanding the progression of disease and how it relates the timing of symptoms to finding patterns in the imaging of the lungs.

Barr: You also did a lot of modeling with the variants. Will you talk about a study you were a part of that evaluated the transmission dynamics and epidemiological characteristics of the SARS-CoV-2 Delta variant in Hunan Province in China?

Sun: This is also in collaboration with Professor Hongjie Yu at Fudan University. He has a connection with the Hunan CDC and has access to their contact tracing data in Hunan. Interestingly, China, before Omicron, pursued this zero-COVID policy, so there were not many prior infections—the population is relatively naive. At that time, a certain amount of the population had been vaccinated by the active vaccine developed in China, but we can still find a certain proportion of population that aren't vaccinated. It's interesting to look at this population in a way that we can characterize the exact margin of Delta in the relatively immune naive population. We do find through contact tracing of Delta that it is much harder to contain compared to the wild type. We do see that there is an increased transmissibility of the virus. This is actually a warning sign. SARS-CoV-2 is constantly evolving, so what worked in the past may not be working as well in the future. We will see this later when Omicron emerges and overwhelms the containment policies in China in early 2023.

Barr: Will you share your experience being part of a team that devised an age-structured stochastic compartmental susceptible-latent-infectious-removed-susceptible model of SARS-CoV-2 transmission calibrated on the initial growth phase for the 2022 Omicron outbreak in Shanghai to project COVID-19 burden under hypothetical mitigation scenarios? What were some of the factors applied to this model, and how did the model correlate with what actually ended up happening?

Sun: This is a modeling study we did in Shanghai. You may recall that in the early months of 2022, Shanghai had its Omicron outbreak. This was one of the largest outbreaks during China's zero-COVID policy. It was one of the hardest to contain, so the whole city was basically put under lockdown for more than three months. The entire population of Shanghai has been tested by PCR—multiple rounds. This is really where we saw the power of Omicron. The idea is that we have collaborations with South Africa, where Omicron first emerged. I've been doing quite a bit of analysis with collaborators in South Africa to characterize the epidemiology of Omicron. And we find a very significant increase in terms of transmissibility, even compared to Delta, and we find that Omicron is immune-evasive and can evade immunity conferred by prior infection or vaccination—so we bring that information in. We also collaborate with teams at Hong Kong University, where they actually have the severity data for people who were administered the active vaccine, and people who are naive. Because Hong Kong also had a very large outbreak just a bit earlier than Shanghai, and they have similar immunological backgrounds, we can really use their data to understand how harmful Omicron is in a naïve population, and then attenuate the severity of Omicron. We sort of bridged those data together, put it in the mathematical model, and tried to simulate what [would happen] if the containment doesn't work and what the burden of Omicron will be if China opened up at that stage. And we found that, because at that stage the older population vaccination rate was not ideal in China, if the society opened up at that point, you are bringing pretty high fatality rates in China. Later on—this is a few months later—many other provinces start to have Omicron outbreaks as well, and it becomes very difficult to sustain that zero-COVID policy. And China eventually opened up. We don't really have very good fatality data for the Omicron wave since China started reporting that information inconsistently as the healthcare system has been overwhelmed. But there were hints suggesting that our projection was not too far away from the reality. The Zhejiang province published their excess mortality data during the Omicron wave, which is pretty close to our projection.

Barr: Why was Shanghai hit so hard with Omicron so much earlier than other major metropolitan areas in China?

Sun: Shanghai, for one, is really an international transportation hub. Secondly, it has very strong connections with Hong Kong. Hong Kong, prior to Shanghai, had a very large outbreak of Omicron. What we believe is many of the initial infections in Shanghai were connected to the Hong Kong outbreak, and since they have very close ties in terms of air transportation, that's probably one of the primary reasons why Shanghai was hit by Omicron so early compared to other locations in China.

Barr: During the same time, you were also part of a descriptive study that looked at epidemiological characteristics and transmission dynamics of the outbreak of Omicron in Shanghai. Was there anything in particular that you gleaned from that study?

Sun: Right. I think the China Study was less interesting in Shanghai. Maybe we could talk about the South Africa study.

Barr: Will you expound upon how you went about analyzing infection and serological data in South Africa? What were the mathematical models you created to see the fitness of the Omicron variant and epidemic trajectory?

What was learned from these models, and how do they provide a framework for contending with future variants?

Sun: For just the South Africa study, I would like to set the clock a little bit earlier. This is a really unique cohort, right? This is a cohort pioneered by Professor Cheryl Cohen from South Africa, who has a long-term collaborative relationship with Fogarty. She really started the first study design prior to the pandemic. The design of the study was to have this very intensive cohort population followed. They do PCR testing for those populations repeatedly, at very high frequency—in this case, a day of testing twice per week, and for the entire epidemic season. They are collecting blood draws also, at a very high frequency as well, to try to see all the infections that are circulating in the community. It was designed for understanding flu and RSV [respiratory syncytial virus] transmission in South Africa. They had been running the study prior to the pandemic—three years ahead of 2020. During the COVID pandemic, they thought it would be very important to adopt that study design to understand the transmission of SARS-CoV-2, so they created a new cohort and started to follow-up intensively. This was for a population of around 1,000 at two sites in South Africa in the middle of the first epidemic wave in South Africa—which was driven by the wild type through the Beta wave, which first emerged in South Africa—then the Delta wave, and then the Omicron, BA.1, BA.2, BA.4, and BA.5 waves.

The first study we did was really trying to see the evolving etymology of SARS-CoV-2 with the emergence of variants. We were able to compare transmission and shedding of SARS-CoV-2 Beta compared to the wild type, and the Delta compared to the wild type, using high resolution PCR data. For Omicron, and since we have this highly detailed characterization of all the infections circulating in this cohort, we can reconstruct their infection history. This is important for SARS-CoV-2 because natural infections also confer protective immunity, and we have been showing that they were actually quite protective against the pre-Omicron variants. We have this immunological landscape prior to the emergence of Omicron, and we have very good serological data for the Omicron phase, so we can infer how many infections were occurring in this cohort at an individual level. Through that, we can look at the total impact of Omicron—so how many people were getting infected irrespective of their symptoms. We're seeing that more than half of the population were getting infected because Omicron is so infectious—and we can compare how much more infectious Omicron was compared to Delta since they have a very good record of Delta transmission as well. We can do a quantitative comparison between the two. We found that Omicron is even more infectious than Delta, taking out the immune-evasive property. Lastly, we were able to show that Omicron is a very immune-evasive variant, so prior immunity doesn't confer as good of protection as it did for the pre-Omicron variants. Putting all this together, we're showing that the virus changed so much when Omicron become dominate and started to overtake other variants in South Africa and then later on dominated the entire globe. This is connecting back to the studies in China, showing that what works in terms of containment policy for older strains may not work for the newer strains. The virus is really constantly evolving and changing, so the policy has to adapt to what is circulating and to the latest variant. The policy has to be up to date with the evolution of the virus. This is a very important lesson we should learn through this pandemic.

Barr: Can you talk a little bit about how you and your team have continued to monitor the virus both in South Africa but also other places in the world?

Sun: Right. In South Africa, the study is still continuing, but now, since we're pretty much out of the pandemic phase, we have other questions that we do want to address. One of the important questions is immune correlator protection for SARS-CoV-2. We want to understand if we can identify an immunological marker, the level of which can be associated with protection. One of the studies we're working on right now is to look at neutralizing antibody titers in the blood to try to see how it correlates with protection for the Delta wave and for the Omicron wave. We're trying to see if our correlator protection is different when we have different variants of concern, and that is very valuable information to inform the design of vaccines. Once you identify reliable correlators of protection, you can use that to do immunological bridging for the licensure of new vaccines. If you want to improve the efficacy of a vaccine, if you have correlator protection identified, we can look at the immunological marker the vaccine induced, and if the vaccine was able to induce reliably high levels of that marker, we can use that to bridge that advocacy of the vaccine. This is very important if we want to have next generation vaccines approved because it's very difficult, and very expensive, to run another vaccine trial, for SARS-CoV-2. This is a topic we have been working on right now. The other topic we're working on is going back to look at the returning circulation of other respiratory virus, like influenza and RSV. We're participating in scenario projections of RSV in the in the United States. We're also looking for correlator protection studies in other countries like South Korea. Those are the things we're focusing on right now.

Barr: Will you speak about your work as part of the RESPIRA Study Group which has looked at COVID outbreaks in places like Costa Rica?

Sun: Yes. This is a study that is in collaboration with Dr. Rebecca Prevots at NIAID [National Institute of Allergy and Infectious Diseases] at the NIH, and Professor Rolando Herrero at ACIB [Agencia Costarricense de Investigaciones Biomedicas] in Costa Rica. The idea of this study is to really to look at the behavioral factors that could drive transmission within the household—and if there are effective protective measures you can take when you know somebody is sick within a household. The very unique part of this study is that Dr. Prevots designed the questionnaires to really ask those highly detailed behavioral questions. When you see your house members identified as a case of SARS-CoV-2, do you try to avoid sharing bathrooms with that person? Is the index case wearing a mask or do the household members wear a mask when they know that there is an infection within the household? Other questions include how much time you spend with the infected person per day when he or she was identified, or whether you share meals or eat meals together. It is actually quite interesting that we find transmission, even within the household, is highly heterogeneous, and your behavior does matter in terms of transmission. For example, wearing a mask. If the index case is wearing a mask, it can reduce transmission to other household contacts. This is what we know as the source control of transmission reduction—so basically, if the index case wears a mask, it is likely to reduce shedding of the virus into the environment and in essence, reduces the risk of transmission to other household members. The other thing we find is that avoiding sharing the same bedroom with the infected person can significantly reduce transmission as well, especially in the early phase of the pandemic, or when we don't have protection from vaccination. Taking those precaution measures within the household can reduce the risk of transmission. This is especially important for individuals who are at high risk of SARS-CoV-2 outcomes, like the elderly or people with comorbidities. That's really a unique or very important point from this study.

Barr: What do you feel that you have learned from your COVID-19 experiences and studies that you would apply to other types of diseases that you study and work on?

Sun: Right. For SARS-CoV-2, one thing it really shows are the debates around non-pharmaceutical interventions or whether you should pursue a containment policy or mitigation policy. For SARS-CoV-2, what we find is that this can be assessed at a very early stage. We need to look closely at how the virus is shed over time, and that can be measured pretty consistently with current technology. We need to understand when the virus is transmissible and how it relates to their symptom onset. The other important dimension is the whole severity pyramid, right? What fraction of the population were asymptomatic when they got infected? And if they were asymptomatic, were they infectious? Those are key parameters highly related to the "containability" of the virus. You can be assessed very early on and that can really drive policy, like whether it is worth it to pursue a containment policy or not. We should really adopt the lessons we learn for SARS-CoV-2 and try to assess such policies for maybe a future influenza pandemic at some point or other emerging pathogens. The other important information is that evolution is really important for SARS-CoV-2, so we really need to keep track of the changing of epidemiological patterns with the emergence of a new variant, and we have to learn to adopt the non-pharmaceutical intervention policies and other mitigation policies in accordance with the features of SARS-CoV-2. Omicron can pretty much be compared to the wild type as almost a new virus. The transmission patterns and the immune escape capacities are totally different. If you're insisting on what works for the wild type and apply that to Omicron, unfortunately, that may not work. We see those lessons in the real world as well.

Barr: In addition to being a scientist, you're also an individual who has been living through the pandemic. What are some of the personal opportunities and challenges COVID-19 has presented for you.

Sun: In terms of opportunities—I'm a Chinese national, so I do speak the language of where the virus first emerged. I have the opportunity to see some of the epidemiological data firsthand from the very beginning of the pandemic. I was lucky to be able to work on the problem very early on, and very grateful to be able to contribute to the understanding of SARS-CoV-2 epidemiology, as well as being one of the first groups to do it. This is also a very personal experience for me. I'm lucky to be in highly collaborative environments, where scientists across the globe work together to find solutions to a common enemy. I'm really inspired by the collaborative environment that Fogarty was able to create. Not only can I bring my expertise and my connections from China, but I can also work with scientists from South Africa and other places, like South Korea, to solve this—and to have, in a way, multiple perspectives of the virus and find solutions to mitigate the impact.

Barr: And were there any challenges? You did so many studies in such a short amount of time. Or just other challenges related to the pandemic?

Sun: In terms of the challenges, I think, one is really the workload, right? During the pandemic, you really had to work nonstop. This is really the priority over anything else. I remember, especially in the early days, the information from China was coming out in their time [zone], so I had to stay up. I had to change my schedule in the United States. I would stay up the whole night, and then I would try to sleep during the day so that I could

translate that information and then share it, and then people can analyze it and look at it. Then I could go to sleep. That was pretty tough for me. Also, the pandemic really creates a lot of geopolitical conflicts between countries. That was not helpful in terms of scientists collaborating. In the future, we really need to have solidarity, or the entire human race working together. This is not just a problem for China or for the United States or for any other single country. This is a global issue. We really, really have to work together to solve this problem. Fingerpointing doesn't really contribute too much, really.

Barr: Is there anything else that you'd like to share about your COVID research or experiences?

Sun: Yeah, I do want to highlight my colleagues and my supervisors at Fogarty, especially the leadership. They have been super supportive of my work here and create collaborative opportunities for me. My mentors have been really great. I started at Fogarty as a postdoc (with Cecile Viboud) and was not a fully trained scientist, and my mentors really helped me refine my skills in terms of in terms of how to do science and how to write good papers. I felt like I grew a lot in the community of Fogarty. Also from a personal perspective, they're really warm and supportive people. This is a very difficult time for everybody, and I really felt supported at Fogarty. I do want to use this opportunity to thank my colleagues and collaborators at Fogarty and also in other places like in China, South Africa, and South Korea. It means a lot to me.

Barr: Definitely. Well, thank you so much for all that you have done. I wish you and your team only continued success going forward. Thank you for participating in this interview and getting the modeling and the Fogarty perspective into the history records.

Sun: Thank you so much for the opportunity, and it's really great to share my experience with you. Thank you.

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