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Written Testimony of
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# PRINCIPLES FOR OUTBREAK INVESTIGATION: COVID-19 AND FUTURE INFECTIOUS DISEASES

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Chairman Foster, Ranking Member Obernolte, and Members of the Subcommittee, thank you for calling this hearing, and inviting me to participate. My name is Suzan Murray, and I am the Director of Smithsonian's Global Health Program, based out of the National Zoological Park and Conservation Biology Institute. This program utilizes experts in wildlife medicine, human medicine, public health, conservation biology, epidemiology, virology and molecular biology to study and respond to issues emerging at the human/animal interface. Recognizing that human health, wildlife health, and environmental health are inextricably linked, we utilize a multidisciplinary approach to investigate emerging infection diseases that threaten both human and animal life, and we build in country capacity and train the next generation of health specialists.

Determining the origins of a virus is difficult, but ongoing identification of novel viruses can improve and expedite the process. With a robust sample collection, we can more precisely determine how the virus in question is genetically related to known variants. This can tell us much about the geographic location, host species, and time period over which the virus may have evolved. We learn a great deal of information from the data collected from free-ranging species – particularly bats, primates and rodents – and expanding this data set exponentially is the most critical opportunity we have to better understand the origins of a particular virus. Over the past decade, as part of a larger consortium, we have worked in more than 30 countries and discovered over 100 novel mammalian viruses. Analysis of these viruses has determined that they represent less than 1 % of existing viruses. While this is a critical data set, to more fully understand the origins and evolution of these viruses, continued sampling at an increasing rate is needed to round out this data set.

If genetic quality of virus extracted from samples is sufficient, and the virus maps genetically to other well-sampled viruses, it is sometimes possible to conduct a 'time-scaled' phylogenetic analysis, allowing an estimation of the period of time over which the virus is likely to have evolved.

Which species is the most likely to be the reservoir host is a complicated question. From previous research we know that bats, primates, and rodents are the most likely to harbor emerging viruses of zoonotic potential, but they are not the only species able to do so. In fact, domestic livestock are responsible for most cases of zoonotic viral transfer to humans.

The genetic analysis described above, along with geographic information collected from the outbreak, can guide targeted bio surveillance in animals. In addition, the advent of new machine learning techniques may be able to help elucidate the proximal host species in which the virus may have evolved. Additionally, virus culture and experimental infection studies under laboratory settings can be used to determine the host range outside of humans.

Determining where a spillover occurred and from what species is only part of the story. Did the spillover occur directly from the wildlife reservoir species to humans? or was another intermediate species (e.g., livestock) involved? Often, another host that is not necessarily a 'reservoir' for the pathogen will be responsible for direct transmission to humans. Since the pathogen may not have evolved within this 'bridge' host, genomic methods are not always sufficient to identify the species responsible for direct transfer to humans.

Wild animals don't seek out human interaction, so we must also determine the human-drivers that brought people into contact with a new virus. Possible examples include wildlife trade, habitat destruction and encroachment, and other practices.

The variety of factors underscores the need to develop a multidisciplinary, systematized, transparent and cooperative community that includes not only wildlife veterinarians, physicians, virologists, but ecologists, human behavioralists and public health leaders among others, who must work hand in hand to develop and analyze approaches to data collection and protocols for sharing critical information. Some of this work is already underway now between multiple agencies and organizations. Additional coordination could further improve our ability to react to the next pandemic.

Orchestrating this kind of coordination is not easy. Managing across governments, researchers, and impacted communities is a huge undertaking with no one organization charged with ensuring that coordination. Even where there is commitment to work together, differences in how different places operate can add difficulty. Principles for transparency and data access range and vary from community to community based upon several factors including but not limited to shared trust on how data will be interpreted, utilized, and credited. In addition, there are costs to consider to the groups that spent the time and resources to collect the data up front.

These are complex systems to navigate and even more difficult when such efforts cross work groups, communities, or national borders. There are obvious reasons why data is most useful when shared openly and rapidly and there should be a strong focus on developing protocols in which all parties are encouraged and incentivized to contribute to shared data sets prior to the initiation of data collection, perhaps by engaging a neutral third party to coordinate and promote transparent and rapid sharing of laboratory-based and epidemiological data within and across national boundaries.

Even in a scenario where all the necessary global treaties are in place to enable timely and accurate data sharing, that will not matter if we cannot collect good data on the ground. This is only achieved through the committed and ongoing work to build trust with the communities in spillover hotspots. In addition to trust, creating and supporting the in-country communities with which we work presents a real opportunity to not only address the current pandemic but avoid future outbreaks. Our international exchange training and capacity building programs bring together experts from different countries to facilitate shared knowledge exchange and provide an avenue to have a more robust and sustainable impact.

We have learned a great deal - from the current pandemic and other epidemics - about what is working well and areas in which we must improve. We have developed invaluable partnerships with many countries, forming a strong and growing "One Health Workforce" to build upon the foundational work in areas of wildlife bio-surveillance, concurrent human syndromic surveillance, viral discovery, laboratory protocol development and implementation, rapid response units as well as sharing critical data with scientific counterparts. Over the past decade, our work has shifted from primary disease surveillance to investigating and better understanding the drivers of disease emergence. In this process, we have increasingly incorporated such essential practices as modeling, data sharing, and the role of human behaviors, cultural norms and outreach. Further, we are recognizing that science is strongest and most impactful when it draws upon these multidisciplinary assets while being inclusive and contextualized for affected communities, cultures and broader societies.

We've also learned much more about how to fully leverage current technologies including artificial intelligence and computation, which allow us to make more data available to more key players, much more quickly. We've also learned to look for weaknesses and gaps more transparently so that they can be addressed more broadly to achieve better solutions. Finally, we've learned how critical it is to gather critical data; analyze it thoroughly and quickly; share across many platforms; and then develop interventions to not only neutralize current pandemics, but prevent future ones.

For instance, some of the most critical and inter-related drivers of disease emergence include land use shifts, human behaviors and education that can affect human behaviors. Recently, with internal partners from the National Air and Space Museum, the National Museum of Natural History, the Smithsonian's Occupational Health Program, and our Office of Communications and External Affairs along with outside partners such as the UBS Global Visionaries program, we are developing a more comprehensive approach to pandemic prevention by more fully utilizing Smithsonian historical collections and incorporating previously under-utilized techniques to assess high-risk interfaces more quickly and truth-find the data. This will ensure that our approach is iterative and always learning, while incorporating affected communities from the beginning and then throughout the process. This will also require that we conduct both human and animal syndromic surveillance concurrently, utilizing the most advanced data collection methodologies such as smart phone technology and field-based PCR machines. Not only will this better and more quickly inform scientists and Pharma companies, but it will ensure that the public is engaged and informed along the way.

The term "public" is used here in the broadest sense as we seek to increase and diffuse knowledge as widely as possible and appropriate. Knowledge of pandemic prevention, public health and vaccinology are helpful to all of us, from communities living at high risk of human-animal interfaces, to scientists who study viruses, to economists interpreting impacts on the global economy, to people visiting exhibits such as Natural History's Outbreak exhibit, to the general public reading and watching the news. Knowledge is power, and broadly shared knowledge is absolutely essential to our global health.

Thank you again inviting me to participate in today's hearing. I look forward to answering any questions you have.