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SARS-CoV-2 in Wildlife: Q & A with Alan B. Franklin

Alan B. Franklin

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SARS-CoV-2 IN WILDLIFE

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FIGURE 19.0 Viruses can be transferred from wild and domestic animals to humans in a process called zoonosis

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Welcome Dr Franklin and thank you for joining us to help social workers increase their knowledge about the interconnectedness of humans, other mammals and the environment. Let's begin with zoonosis.

Can you explain zoonosis to us and the process that leads to diseases like COVID-19?

Zoonosis is where a disease-causing pathogen is transmitted naturally between vertebrate animals and humans (adapted from Botzler & Brown, 2014; Wobeser 2006). Botzler and Brown (2014) further partition the definition of zoonoses into *zooanthroponoses* (pathogens are transmitted to humans where humans are a dead-end host) and *anthropozoonoses* (pathogens are transmitted from humans to non-humans where the nonhumans are a dead-end host). In both cases, dead-end hosts are where a species serves as a host for the pathogen but does not serve as a source of the pathogen for another host (Botzler & Brown, 2014).

Two types of hosts are of concern in zoonotic pathogen transmission: maintenance and bridge host. *Maintenance*, or reservoir, *hosts* are one or more epidemiologically connected populations where a pathogen is permanently maintained (Haydon et al., 2002). Bridge hosts provide a link between maintenance hosts and target hosts, where the target hosts can be human populations in the case of zoonoses. To be considered a *bridge host*, a species must be competent for the pathogen to replicate within it and it must have infectious contacts with the target host (Caron et al., 2015). Bridge hosts cannot maintain pathogen persistence without additional inputs from maintenance hosts and, therefore, must overlap in time and space with both maintenance hosts and target hosts to effectively link the two. Interspecies transmission from a maintenance host to a non-maintenance host, such as a bridge host, is referred to as *spillover* transmission, and the recipients or secondary hosts as spillover hosts. Such spillover can play important roles in pathogen dynamics (Power & Mitchell 2004) and non-maintenance hosts can ultimately become maintenance hosts if the pathogen evolves within the new host. Nugent (2011) also used the term *spillback* to describe transmission from non-maintenance to maintenance hosts but acknowledged that maintenance transmission in one set of circumstances might be defined as either spillover or spillback, depending on the situation.

There are 1,145 known infectious organisms that are pathogenic to humans, which include viruses, prions, bacteria, fungi, protozoans, and helminths (Taylor et al., 2001). Of these, 61% are zoonotic infectious diseases, making up most of the diseases affecting humans. Of the novel pathogens that have emerged since the 1940s, 75% have been zoonotic and most have emerged from wildlife (Jones et al., 2008). Oftentimes, the pathogens that cause diseases are relatively benign and do not cause disease in their natural hosts. However, when the pathogens jump to another species, these pathogens can become much more virulent in the new host, causing disease that can sometimes have devastating consequences.

What do we know so far about the origins of SARS-CoV-2?

In January 2021, the World Health Organization (WHO) convened a team of scientists to examine the origins of SARS-CoV-2. This team recently released their report (WHO, 2020), which examined four plausible scenarios. These scenarios were:

1. Direct zoonotic transmission where there was transmission of SARS-CoV-2 (or a closely related progenitor) from an animal reservoir host to humans, which was followed by direct person-to-person transmission.
2. Introduction of SARS-CoV-2 from an animal reservoir host to an intermediate animal host, where it then spread among the intermediate host, which was then followed by zoonotic transmission to humans.
3. Similar to scenario 1 or 2 above, BUT introduction of SARS-CoV-2 to humans is through the cold/food chain; cold chain food products serve as the vehicle of introduction and transmission among humans.
4. SARS-CoV-2 is introduced to humans through a laboratory accident where release of the virus is from an accidental infection of laboratory staff by SARS-CoV-2.

Of these scenarios, only scenarios 1 and 2 were considered to be likely, with scenario 2 being assessed as likely to very likely while scenario 1 was considered possible to likely. The other two scenarios were considered to be possible (scenario 3) to extremely unlikely (scenario 4) by the WHO team (WHO-China Study Team, 2021).

Under scenario 1, viruses very closely related to SARS-CoV-2 have been found in insectivorous bats of the genus *Rhinolophus* in China, where COVID-19 was first detected (Lau et al., 2020). However, other wild animal reservoir hosts have been implicated such as the Malayan pangolin (*Manis javanica*) or a member of the weasel family (Mustelidae). The latter potential host is based on the susceptibility of farm-raised mink (*Neovison vison*) to SARS-CoV-2 and their ability to transmit the virus to humans (Oude Munnink et al., 2021).

Scenario 2 also involves a wild animal host but genetic evidence suggested that an intermediate animal host may have been involved because the evolutionary distance between the viruses found in bats and SARS-CoV-2 was estimated to be several decades (Lau et al., 2020). This scenario, where there has been an intermediate amplifying host has been seen in other emerging viruses, such as the original SARS-CoV, MERS-CoV, and Hepinaviruses (Cui, Chen & Fan, 2017). Candidate species for the role of intermediate host include the Malayan pangolin, mustelids and cat (felid) species, which could have been from wild animal farms that supply wet markets in China (WHO-China Study Team, 2021).

Although most agree that SARS-CoV-2 had a wildlife origin, there is some dispute whether it came from direct animal to human transmission or whether a laboratory accident was involved (Bloom et al., 2021). The dispute centres

around the Wuhan Institute of Virology, where virologists worked on bat viruses with genetic similarity to SARS–CoV-2. In addition, the Wuhan Centre for Disease Control (CDC) laboratory moved to a new location near the Huanan Market in Wuhan, China, where SARS–CoV-2 was first detected. Bloom et al. (2021) argue that the scenario of an accidental release from a laboratory (scenario 4 above) should have been investigated more heavily by the WHO team and was discounted too readily. Regardless, evidence suggests that SARS–CoV-2 came from wild animals, most likely bats, but how it entered the human population is still largely conjectural and unknown. From the perspective of public health officials, however, understanding how the virus entered the human population is still critical information because it defines how mitigation measures would be shaped to deal with future pandemics.

It seems the process is rather circular, as people have also infected other animals with SARS–CoV-2 – lions in zoos, orangutans in Sumatra, and in mink farms, and we've even infected our pets – but it is said that pets can't give us the virus back? What is the explanation for these transmission paths?

The evidence for spillover of SARS–CoV-2 from humans into novel animal hosts has become increasingly well-documented. For example, whole genome sequencing identified similar strains of SARS–CoV-2 in farmed mink and human workers on those farms, indicating that transmission occurred and the initial introduction from a human worker to the farmed mink was suspected. Human workers on these captive mink farms were subsequently infected from mink carrying SARS–CoV-2 (Oude Munnink et al., 2021).

Spillback of the virus from animals, such as domestic pets, has not been well-documented but could be likely depending on the pet. Such infections will probably be few and very localised because most pets are isolated from others outside their households and would not likely serve as dominant sources of infection other than within their households. For example, the likely scenario is that an infected owner might transmit SARS–CoV-2 to their pet but would also serve as the source of infection to other human members of the household. Thus, pets would serve a very minor role in SARS–CoV-2 infections because the human sources of the infection would infect everyone else within a given household. Therefore, humans would play the dominant role as SARS–CoV-2 sources of infection and household pets serving a minor role. One exception to this would be where pets congregate, such as pet shops, animal shelters and veterinary clinics, where an infected pet can infect other pets from different households and subsequently spread the virus. This may partly explain why one-way transmission from humans to domestic dogs and cats is mostly observed. In coronaviruses similar to SARS–CoV-2, transmission from domestic dogs to humans was recently documented (Vlasova et al., 2021). However, SARS–CoV-2 appears to replicate poorly in domestic dogs, while domestic cats appear to be competent hosts for the virus and are also susceptible to airborne transmission of the virus

(Shi et al., 2020). Thus, Burkholz et al. (2021) and Sharun et al. (2021) argue that viral transfer from humans to farm animals and pets needs to be closely monitored to prevent the establishment of novel viral reservoirs for potential future zoonotic transfer.

Is it true that we can never prevent zoonotic infection and a better focus is on addressing the earliest pathway of transmission?

I am not sure we can never predict zoonotic infection with known pathogens but predictions for most future events are difficult. Nils Bohr, the pioneering physicist, jokingly commented "Prediction is difficult – especially about the future" (Petticrew et al., 2007, p. 106). Especially with unknown pathogens, such as ones that have never been discovered in wild animal hosts, there is a high degree of unpredictability in when, where, and how a zoonotic infection of humans will occur. Pathogen discovery alone will not solve the problem because understanding the host dynamics for those pathogens is critical to assess risk of spillover. Some have developed systems that follow a probabilistic framework to assess the risk of zoonotic spillover for emerging pathogens. For example, Grange et al. (2021) developed a risk assessment framework for 887 wildlife viruses in terms of their potential for spillover into humans. Although imperfect, such a framework can be revised and adjusted as new information becomes available. In addition, such frameworks identify lack of knowledge and can guide where focussed research is needed. However, others argue, and demonstrate to a certain degree, that zoonotic risk assessments are largely inaccurate because of the paucity of data, the uncertainties around current data, and biases in focussing on certain wildlife and domestic animal species (Wille, Geoghegan & Holmes, 2021). For example, ferrets (*Mustela putorius furo*) were found to be competent hosts of SARS-CoV-2 based on experimental inoculations with the virus (Shi et al., 2020). However, there may be genetic barriers for transmission of SARS-CoV-2 from infected humans to ferret (Sawatzki et al., 2021). These contradictory lines of evidence make it difficult to rely solely on studies of host competency but also require transmission studies to develop a complete picture of the process.

Wille, Geoghegan and Holmes (2021) argue that pathogen surveillance of people is required at the human–animal interface, such as people working with raising and slaughtering domestic animals, hunting animals such as bushmeat, to better assess zoonotic transmission. This is similar to focussing on the earliest pathway of transmission from animals to humans. I argue that both approaches have merit and the combination of both would provide increased prevention coverage than each approach considered separately. In addition, surveillance for pathogens of concern in wildlife populations are possible, given political will and financial commitment. An example of large-scale surveillance of wildlife pathogens affecting human and agricultural health is under the National Wildlife Disease Program in the United States (https://www.aphis.usda.gov/aphis/ourfocus/wildlifedamage/programs/nwdp); avian influenza viruses in waterfowl are tracked through a targeted, designed surveillance program that covers the entire US (Bevins et al., 2014).

Thus, it is unlikely that a single approach will prevent future zoonotic pandemics but a combination of approaches in a unified framework will mitigate, but probably not eliminate, the unpredictability of zoonotic outbreaks and pandemics. In all of these and other approaches, the COVID-19 pandemic has spotlighted the need for multi-disciplinary approaches that require collaboration among the human, animal, and environmental sectors (Belay et al., 2017).

A lot of waste goes into sewerage systems including prescribed and illegal drugs. Sewage analysis has been used to detect diseases such as polio or COVID-19. Does this in turn affect marine life and other wildlife?

Even in the most modern countries with sophisticated wastewater treatment plants (WWTP), there are issues with pathogen pollution from sewage. This is more of a problem in developing countries where raw sewage from municipalities is often dumped directly into natural waterways. One example of pathogens from sewage affecting wildlife is infection of southern sea otters (*Enhydra lutris nereis*) with the *Toxoplasma gondii* parasite originating from domestic cat faeces in cat litter that was flushed down toilets, passed through WWTP, and was discharged into the ocean where it subsequently infected sea otter populations (Jessup & Miller, 2011). Avian influenza viruses and some coronaviruses can be detected in effluent from WWTP that is being discharged into the environment (Wigginton, Ye & Ellenberg, 2015). Global surveillance for SARS–CoV-2 in municipalities now includes monitoring of sewage for SARS–CoV-2 RNA, where COVID-19 outbreaks are often detected prior to reports in human individuals (Medema et al., 2020). The basis for this surveillance is that infection with SARS–CoV-2 in humans also causes gastrointestinal symptoms, and the virus is passed through in faeces, which is subsequently detected in wastewater (Kitajima et al., 2020). Based on this, Franklin and Bevins (2020) hypothesised that SARS–CoV-2 released from WWTP had the potential to spillover into wild mammals using aquatic habitats near where WWTP effluent was discharged into the environment. One issue with this hypothesis is whether SARS–CoV-2 remains infective after undergoing the wastewater treatment process. However, a substantial amount of raw sewage is discharged into the environment through accidental spills or when WWTP are overwhelmed during natural disasters, such as hurricanes and floods (Franklin & Bevins, 2020). Such events have the potential to release infective SARS–CoV-2 and other pathogens into the environment where they can theoretically become established in wildlife hosts.

How do changes in climate such as drought and global warming, deforestation, agricultural practices and eco-tourism affect zoonotic transmission from wildlife?

This is a very broad area of interest with some specific examples that all of these factors have contributed to transmission of zoonotic pathogens and increased geographic spread of zoonotic pathogens. For example, climate change has been implicated in the northward geographic expansion of tick-borne zoonotic

Borrelia burgdorferi, the pathogen causing Lyme disease (Brownstein, Holford & Fish 2005), deforestation has been implicated in decreasing wild mammalian species diversity and increasing the prevalence of the zoonotic parasite causing Chagas disease in the remaining small mammal hosts (Vaz, D'Andrea & Jansen 2007), and changes in agricultural practices were considered responsible for the emergence of Nipah virus in human populations (Epstein et al., 2006). A classic example of emergence of a novel zoonotic pathogen in response to anthropogenic changes is with Nipah virus in Malaysia (Epstein et al., 2006). The emergence of Nipah virus from fruit bats (*Pteropus* spp.) coincided with agricultural intensification (Pulliam et al., 2012) that included combining fruit trees with pig farms and where bats feeding on fruits in trees above pig pens dropped partially eaten fruit contaminated with infected saliva into the pig pens (Epstein et al., 2006). Pigs became infected after consuming the virus-contaminated fruit and subsequently infected workers on the farm and in slaughterhouses (Epstein et al., 2006).

In a review of 305 scientific articles, Gottdenker et al. (2014) found that over 56% of the studies documented increased pathogen prevalence and/or transmission in response to human-caused changes. Most of the positive responses were from viral and protozoan pathogens and the principal land use changes associated with those responses were deforestation, agricultural development, and urbanisation. Most of the studies were observational with only seven experimental studies. Thus, inferences about cause and effect were not possible in most cases. However, proposed mechanisms included modified niches for pathogens and/or hosts, changes in host community composition, altered spatial distribution of species, and socio-economic factors that altered human exposure and risk of pathogen transmission. Land use–induced spillover of zoonotic pathogens is considered vitally important to understanding zoonotic disease pandemics (Plowright et al., 2021).

How might we include a planetary health perspective to prevent the emergence and spread of infectious disease and what do we humans need to do differently?

We need to better understand the systems that spawn zoonotic pathogens, such as SARS-CoV-2. Currently, we focus on understanding what species zoonotic pathogens emerge from but pay scant attention to the ecological systems from where these pathogens emerged. This bias is probably because medical and veterinarian scientists initially promoted the concept of *One Health*, which focussed primarily at zoonotic diseases at the human-domestic animal interface. It has since expanded more broadly to include wildlife ecology, with a more encompassing definition for One Health as "… a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for people, animals and the environment" and "A collaborative, multisectoral, and transdisciplinary approach (working at the local, regional, national, and global levels) with the goal of achieving optimal health outcomes recognizing the interconnection between people, animals, plants, and their shared environment" (Gibbs, 2014). Thus, One Health attempts to tie together the disparate

disciplines that deal with zoonotic diseases into a single collaborative framework. Currently, there is a large effort to incorporate One Health into global programs under the WHO, the Food and Agriculture Organization of the United Nations (see www.fao.org/one-health/en/).

Alan B. Franklin (1 June 2021)

References

Belay, E. D., Kile, J. C., Hall, A. J., Barton-Behravesh, C., Parsons, M. B., Salyer, S. J., & Walke, H. (2017). Zoonotic disease programs for enhancing global health security. *Emerging Infectious Disease*, 23(13), S65–S70.

Bevins, S. N., Pedersen, K., Lutman, M. W., Baroch, J. A., Schmit, B. S., Kohler, D., . . . DeLiberto, T. J. (2014). Large-scale avian influenza surveillance in wild birds throughout the United States. *PLoS One.* https://doi.org/10.1371/journal.pone.0104360

Bloom, J. D., Chan, Y. A., Baric, R. S., Bjorkman, P. J., Cobey, S., Deverman, B. E., . . . D. A. Relman. (2021). Investigate the origins of COVID-19. *Science*, 372(6543), 694–694.

Botzler, R. G., & Brown, R. N. (2014). *Foundations of wildlife diseases.* Oakland, CA: University of California Press.

Brownstein, J. S., Holford, T. R., & Fish, D. (2005). Effect of climate change on Lyme disease risk in North America. *EcoHealth,* 2(1), 38–46.

Burkholz, S., Pokhrel, S., Kraemer, B. R., Mochly-Rosen, D., Carback, R. T., Hodge, T., ... Rubsamen, R. (2021). Paired SARS-CoV-2 spike protein mutations observed during ongoing SARS-CoV-2 viral transfer from humans to minks and back to humans. *Infection, Genetics and Evolution*, 93,104897. https://doi.org/10.1101/2020.12.22.424003

Caron, A., Cappelle, J., Cumming, G. S., de Garine-Wichatitsky, M., & Gaidet, N. (2015). Bridge hosts, a missing link for disease ecology in multi-host systems. *Veterinary Research*, 46(1). https://doi.org/10.1186/s13567-015-0217-9

Cui, J.-a., Chen, F., & Fan, S. (2017). Effect of intermediate hosts on emerging zoonoses. *Vector-Borne and Zoonotic Diseases*, 17(8), 599–609.

Epstein, J. H., Field, H. E., Luby, S., Pulliam, J. R. C., & Daszak, P. (2006). Nipah virus: Impact, origins, and causes of emergence. *Current Infectious Disease Reports*, 8(1), 59–65.

Franklin, A. B., & Bevins, S. N. (2020). Spillover of SARS-CoV-2 into novel wild hosts in North America: A conceptual model for perpetuation of the pathogen. *Science of the Total Environment*, 733,139358. https://doi.org/10.1016/j.scitotenv.2020.139358

Gibbs, E. P. J. (2014). The evolution of One Health: A decade of progress and challenges for the future. *Veterinary Record*, 174(4), 85–91.

Gottdenker, N. L., Streicker, D. G., Faust, C. L., & Carroll, C. R. (2014). Anthropogenic land use change and infectious diseases: A review of the evidence. *EcoHealth*, 11(4), 619–632.

Grange, Z. L., Goldstein, T., Johnson, C. K., Anthony, S., Gilardi, K., Daszak, P., . . . Mazet, J. A. K. (2021). Ranking the risk of animal-to-human spillover for newly discovered viruses. *Proceedings of the National Academy of Sciences,* 118(15). https://doi.org/10.1073/pnas.2002324118

Haydon, D. T., Cleaveland, S., Taylor, L. H., & Laurenson, M. K. (2002). Identifying reservoirs of infection: A conceptual and practical challenge. *Emerging Infectious Diseases*, 8(12), 1468–1473.

Jessup, D. A., & Miller, M. A. (2011). The trickle-down effect: How toxoplasmosis from cats can kill sea otters. *The Wildlife Professional*, 5, 62–64.

Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, 451, 990–994. https://doi.org/10.1038/nature06536

Kitajima, M., Ahmed, W., Bibby, K., Carducci, A., Gerba, C. P., Hamilton, K. A., Haramoto, E., & Rose, J. B. (2020). SARS-CoV-2 in wastewater: State of the knowledge and research needs. *Science of the Total Environment*, 739. https://doi.org/10.1016/j.scitotenv.2020.139076

Lau, S. K. P., Luk, H. K. H., Wong, A. C. P., Li, K. S. M., Zhu, L., He, Z., . . . Woo, P. C. Y. (2020). Possible bat origin of severe acute respiratory syndrome coronavirus 2. *Emerging Infectious Diseases*, 26(7), 1542–15.

Medema, G., Heijnen, L., Elsinga, G., Italiaander, R., & Brouwer, A. (2020). Presence of SARS-Coronavirus-2 RNA in sewage and correlation with reported COVID-19 prevalence in the early stage of the epidemic in the Netherlands. *Environmental Science & Technology Letters*, 7(7), 511–516.

Nugent, G. (2011). Maintenance, spillover and spillback transmission of bovine tuberculosis in multi-host wildlife complexes: A New Zealand case study. *Veterinary Microbiology*, 151 (1-2), 34–42.

Oude Munnink, B. B., Sikkema, R. S., Nieuwenhuijse, D. F., Molenaar, R. J., Munger, E., Molenkamp, R., . . . Koopmans, M. P. G. (2021). Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science*, 371(6525), 172–177.

Petticrew, M., Cummins, S., Sparks, L., & Findlay, A. (2007). Validating health impact assessment: Prediction is difficult (especially about the future). *Environmental Impact Assessment Review*, 27(1), 101–107.

Plowright, R. K., Reaser, J. K., Locke, H., Woodley, S. J., Patz, J. A., Becker, D. J., Oppler, G., Hudson, P. J., & Tabor, G. M. (2021). Land use-induced spillover: A call to action to safeguard environmental, animal, and human health. *The Lancet Planetary Health*, 5(4), e237–e245. https://doi.org/10.1016/S2542-5196(21)00031-0

Power, A. G., & Mitchell, C. E. (2004). Pathogen spillover in disease epidemics. *The American Naturalist*, 164, S79–S89. https://doi.org/10.1086/424610

Pulliam, J. R. C., Epstein, J. H., Dushoff, J. S., Rahman, S. A., Bunning, M., Jamaluddin, A. A., . . . Daszak, P. (2012). Agricultural intensification, priming for persistence and the emergence of Nipah virus: A lethal bat-borne zoonosis. *Journal of the Royal Society Interface*, 9(6), 89–101.

Sawatzki, K., Hill, N. J., Puryear, W. B., Foss, A. D., Stone, J. J., & Runstadler, J. A. (2021). Host barriers to SARS-CoV-2 demonstrated by ferrets in a high-exposure domestic setting. *Proceedings of the National Academy of Sciences*, 118(18). https://doi.org/10.1073/pnas.2025601118

Sharun, K., Dhama, K., Pawde, A. M., Gortázar, C., Tiwari, R., Bonilla-Aldana, D. K., . . . Attia, Y. A. (2021). SARS-CoV-2 in animals: Potential for unknown reservoir hosts and public health implications. *Veterinary Quarterly*, 41(1), 181–201.

Shi, J., Wen, Z., Zhong, G., Yang, H., Wang, C., Huang, B., . . . Bu, Z. (2020). Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS – Coronavirus 2. *Science*, 368(6494), 1016–1020.

Taylor, L. H., Latham, S. M., & Woolhouse, M. E. J. (2001). Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society of London, Series B. Biological Sciences*, 356(1411), 983–989.

Vaz, V. C., D'Andrea, P. S., & Jansen, A. M. (2007). Effects of habitat fragmentation on wild mammal infection by Trypanosoma cruzi. *Parasitology*, 134(Pt. 12), 1785–1793.

Vlasova, A. N., Diaz, A., Damtie, D., Xiu, L., Toh, T-H., Lee, J. S-Y., Saif, L. J., & Gray, G. C. (2021,). Novel canine coronavirus isolated from a hospitalized pneumonia patient, East Malaysia. *Clinical Infectious Diseases.* https://doi.org/10.1093/cid/ciab456

Wigginton, K. R., Ye, Y., & Ellenberg, R. M. (2015). Emerging investigators series: The source and fate of pandemic viruses in the urban water cycle. *Environmental Science: Water Research & Technology*, 1(6), 735–746.

Wille, M., Geoghegan, J. L., & Holmes, E. C. (2021). How accurately can we assess zoonotic risk? *PLoS Biology*, 19. https://doi.org/10.1371/journal.pbio.3001135

Wobeser, G. A. (2006). *Essentials of disease in wild animals.* Ames, IA: Blackwell Publishing.

WHO. (2020). *Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19).* Geneva, Switzerland: WHO.

WHO–China Study Team. (2021). *WHO-convened global study of origins of SARS-CoV-2: China Part.* Geneva, Switzerland: WHO.