



# Maintain a Voucher Sample! The Importance of Including Natural History Collections in Research on Infectious Diseases

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## Abstract

In order to fully comprehend and mitigate the effects of emerging zoonotic diseases, this most fundamental information is essential. We suggest that researchers studying host-pathogen interactions adopt vouchering techniques and work with natural history collections to permanently archive host and microbiological samples. Utilizing vetted specimens and associated samples enables large workforce biodiversity scientists to assist in pandemic preparedness and provides both repeatability and extension to host-pathogen studies. We look at a few well-known examples of successful integration of natural history collections with host-pathogen research. In such studies, vouchering, on the other hand is still underutilized. We evaluated vouchering methods utilized in host-pathogen research by microbiologists, such as bacteriologists, parasitologists, and virologists, through an online survey. Microbiological samples are permanently archived by a much larger percentage of respondents than host specimens are archived, and less than half of respondents offer host specimens from which microbiological samples were lethally collected. We offer suggestions for integrating vouchering methods and archiving of microbiological samples into host-pathogen studies to encourage collaborations between microbiologists and natural history collections.

**Keywords:** Bio repositories, Coronaviruses, Extended specimen, Holistic specimen, Museums, Zoonosis

## INTRODUCTION

In recent decades, it has been observed a significant increase in the spread and emergence of infectious diseases attributed to novel pathogens that spread from animal populations, including domesticated and wild taxa (Boni MF, 2020). COVID-19's causative agent has demonstrated that a pathogen that was previously unknown can emerge from wildlife species and pose a threat to global public health within months. SARS-CoV-2 is a member of a group of beta coronaviruses that have been found in pangolins and Rhinolophus bats. Despite mitochondrial cytochrome b sequences identifying the bats sampled as least horseshoe bats elsewhere in the same publication, SARS-CoV-2 was initially recognized as similar to viruses previously reported from intestinal tissue of Chinese horseshoe bats, Rhinolophus

sinuous. However, the precise animal source of the SARS-CoV-2 spread to human populations is still unknown (Latinne A, 2020). Coronavirus diversity in bats and other wildlife species is still understudied, despite numerous studies of SARS-CoV-2. Prior to the SARS outbreak in 2002, only 19 coronaviruses had been identified. Following that, a number of research groups conducted surveys of wildlife populations to look for SARS-CoV, the virus that causes SARS in humans. Unfortunately, none of these studies included the deposit of vouchered SARS-CoV host specimens in natural history collections. As a result, we are unable to further investigate the diversity, distribution, and fundamental biology of the viruses that transmit SARS and SARS-like viruses to humans and wildlife, as well as the evolutionary processes by which viruses with the potential to spread a pandemic evolve in their reservoir hosts. Our ability to respond to the COVID-19

pandemic has been hampered by a lack of basic biodiversity infrastructure in the form of vouchered specimen collections. However, this infrastructure is essential for gaining a deeper comprehension of other zoonotic pathogens that have the potential to spread worldwide (Andersen KG, 2020). Host vouchering has essentially been absent from the majority of recent studies on zoonotic pathogens, including those that are relevant to comprehending the origins of over 300 horseshoe bats that were euthanized and necropsied while screening for coronaviruses. However, no host voucher specimens or archived tissue samples were reportedly preserved.

## METHODS

### Contribution of Natural History Collections to Research on Host-Pathogen

As more natural history collections have adopted the concept of the "holistic" or "extended" specimen, collaborations between microbiologists and biodiversity scientists have increased over the past few decades. Even though the host and parasite specimens and associated cryopreserved tissues and microbiological samples are collected at different times under this paradigm, bioinformatics links them all together (Lau SKP, 2007). The fact that these holistic collections naturally encourage more integrated science has numerous benefits. As it becomes increasingly recognized as an essential component of zoonotic disease surveillance, the incorporation of the "extended specimen" idea into research on host-pathogen interactions is just getting started. The various roles that environmental change plays in the emergence of novel zoonosis would likely be better understood if natural history collections were better integrated into infectious disease research. Human-caused disturbances of this kind make it more likely that pathogens can spread between host species, putting public health at risk. However, risk assessment is hard because we don't know much about how pathogens and hosts naturally interact (Ge X-Y, 2013). Targeted risk management of potentially zoonotic pathogens is likely to be more effective than retroactive efforts to eradicate zoonosis after they have spread to human populations (Lelli D, 2013). However, understanding the ecology and evolutionary history of host species in host-pathogen systems, as well as their historical and contemporary distributions, is necessary for rigorous and effective prevention strategies (Lin X-D, 2017).

### Ebola viruses

Ebola viruses are a group of pathogens for which it has been difficult to identify potential reservoir hosts due to a lack of high-quality vouchered specimens across time scales. Although bats have been suggested as reservoir hosts for the Reston Ebola virus, the Bombali Ebola virus, and the Zaire Ebola virus see Leendertz Caron the identification of both reservoir host populations and susceptible host populations, which range from insects to antelopes, remains

largely unknown (Rihtaric D, 2010). A lack of centralized repositories of historical and contemporary voucher specimens, particularly for mammal species, across the Afrotropics limits the ability to identify Ebola virus hosts in wildlife. The virus's widespread distribution, particularly in the vast and remote Afrotropics and the virus's highly unpredictable persistence in a host are related to obstacles in the detection of Ebola virus hosts (Tao Y, 2019). Specifically, the prevalence of Ebola viruses in populations of putative hosts, such as bats, can fluctuate greatly over short periods of time and is frequently lower than the prevalence of other viruses whose hosts have been identified more quickly using voucher specimens. Additionally, the Afrotropics represent a hotspot of evolutionary diversity for mammals, which have been the most targeted Ebola virus hosts thus far. A recent study predicts at least 122 undiscovered species (Gouilh MA, 2011). In addition, recent phylogenetic studies using voucher specimens from natural history collections have shown that the bat genus *Miniopterus*, which is thought to be a reservoir host for the Zaire Ebola virus, has a lot of cryptic diversity.

## CONCLUSIONS

The COVID-19 pandemic has highlighted the necessity of switching to an integrated One Health approach for addressing EIDs and exposed numerous flaws in the current public health approach to zoonotic spillover events. The need for a more integrated approach to surveillance and mitigation of EIDs is particularly highlighted by the critical importance of determining a definitive host for SARS-CoV-2 and the unprecedented potential of current molecular techniques to reinvestigate historic natural history collection material. The human immunodeficiency virus genome was recovered from samples collected in 1966, prior to the discovery of acquired immunodeficiency syndrome (AIDS). One of the most efficient ways to get around this obstacle is to verify host specimens and the tissue that goes with them in natural history collections. Natural history collections, on the other hand, need to expand at an exponential rate over the coming decades in order to fulfil their promise of significantly contributing to the study of infectious diseases. They also need to make investments in the development of methodology and infrastructure in accordance with best practices in order to get the most out of the specimens and samples that are deposited for use in future research projects. Natural history collections can last for centuries with proper care, serving as a physical record of current and future pandemics.

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