



# Comprehensive Knowledge of Reservoir Hosts is Key to Mitigating Future Pandemics

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**Coronavirus disease 2019 (COVID-19) and other epidemics (such as severe acute respiratory syndrome [SARS], Ebola, and H1N1) are stark reminders that knowledge of animal behavior and ecosystem health are key to controlling the spread of zoonotic diseases early in their onset. However, we have very limited information about the set of behavioral and ecological factors that promote viral spillover and the effects that has on ecosystem health and disease transmission. Thus, expanding our current knowledge of reservoir hosts and pandemics represents an urgent and critical tool in ecological epidemiology. We also propose to create an integrative database that ranks animal species in terms of their likelihood as hosts for specific infectious diseases. We call for a global and cooperative effort of field and laboratory scientists to create, maintain, and update this information in order to reduce the severity of future pandemics.**

**KEYWORDS:** SARS-CoV-2; reservoir hosts; database; human health

The coronavirus disease 2019 (COVID-19) has spread to over 189 countries and territories worldwide, resulting in more than 40 million confirmed cases and almost 1 million deaths. Although the natural reservoir of the virus has not been fully confirmed, a wildlife origin is strongly suspected.<sup>1</sup> Over the past several decades it has become clear that in addition to the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), many emerging infectious diseases are transmitted from wildlife to humans because natural barriers to human-animal contact have been eroded. For example, the human immunodeficiency virus type 1 (HIV-1) originated in chimpanzees (*Pan troglodytes*) and type 2 (HIV-2) originated in sooty mangabeys (*Cercocebus atys*), and likely were passed to humans through the unprotected butchering of wild animals or as part of the illegal pet trade.<sup>2</sup> The SARS-CoV was identified in Chinese horseshoe bats (*Rhinolophus sinicus*).<sup>3</sup> Finally, fruit bats (*Eidolon* spp.) are likely to be the primary reservoir for the Ebola virus.<sup>4</sup> Combined, these diseases have caused pathogenic death in tens of millions of humans worldwide.

## Gaps in Zoonosis, Zoology, and Ecology

Despite the critical roles that host behaviors and ecology play in the emergence of epidemic or pandemic diseases,<sup>5</sup> most of the ongoing studies and databases focus principally on pathogens in the context of disease. For example, two globally influential virus projects, the US Agency for International Development (USAID) Emerging Pandemic Threats (EPT) PREDICT and the Global Virome Project (GVP),<sup>6</sup> have as their main objective field sampling in order to identify unknown potentially zoonotic viruses with pandemic potential. Given a primary focus on viral identification, detailed information on host behavior, biology, life history, and ecology are generally absent from established meta-datasets. Similarly, zoological databases that focus on species diversity, behavior, and conservation have failed to include detailed information on pathogen diversity and disease. For example, the Catalog of Life<sup>7</sup> and the American Society of Mammalogists Mammal Diversity Database<sup>8</sup> represent important basic references of taxonomic hierarchy, description,

and distribution but do not contain information on microbes hosted by wild animals. Moreover, the information included in many animal pathogen and animal behavior databases is incomplete. For example, the Virus-Host DB lists 11 known viruses of the Chinese horseshoe bat, the species responsible for the origin of SARS-CoV. However, relevant data on the life history and ecology of this bat species, including home range, dispersal pattern, social system, inter-litter interval, population density, population trend, and interactions with humans, are not available (e.g., PHYLACINE, Anage, ADW, and Mammal diet).

In addition, once there is evidence of cross-species pathogen transmission, it is crucial to identify each of the key reservoir hosts of that pathogen; i.e., reconstruct the cross-species transmission route. This step largely relies on what we know about the natural behavior, ecology, and biology of putative hosts. Given that our current knowledge offers only a limited set of hypotheses to predict host-pathogen interactions that might cause future pandemics, flexible and integrated predictive models based on historical and current environmental and cultural conditions are needed to identify bounded estimates to evaluate the transmission processes. Thus, in the absence of a comprehensive and well-integrated database focused on both pathogens and animal hosts (both primary and secondary hosts), our understanding of the potential for viral spillover, disease transmission, and zoonotic and pandemic events remains limited.

## Establishing an Integrated Database

To bridge the gap between zoonosis and zoology, we propose the creation of a database that functions to provide comprehensive information on both hosts and pathogens that pose a likely threat to human health. This would require establishing an international committee or international panel of distinguished scientific experts in the fields of microbiology, zoology, ecology, genetics, epidemiology, tropical diseases, veterinary sciences, animal physiology, medicine, and public health. This panel could be under the auspices of the GVP, International Union for Conservation of Nature (IUCN), World Health Organization (WHO), or other respected international organizations. The required database can be built using a relational database management system and the variable host species would be used to unify the related information (Figure 1): i.e., (1) taxonomy (i.e., Kingdom, Phylum, Class, Order, Family, Genus, and synonymy); (2) hosted pathogens and their sequences; (3) associated zoonosis, clinical and epidemiological phenotype, agent of the disease, symptomatic and/or asymptomatic response of the host, vaccines, and vaccinations; (4) life history of hosts (e.g., time to sexual maturity, length of gestation and weaning periods, litter size, litters per year, inter-birth interval, basal metabolic rate, body mass); (5) demography and behavior (i.e., population history, population size, density, geographical distribution, home range area, distance traveled per day, habitat preferences, diet and feeding ecology, dispersal distance); (6) phylogeny and conservation status.

It is essential for the scientific panel to assess the completeness, sample size, and credibility of the data prior to integrating the information into the primary dataset. A number of intelligent techniques can be applied to facilitate data mining, including summarization, classification based on

