PLOS PATHOGENS

REVIEW

Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats

Kevin J. Olival[1☯*], Paul M. Cryan[2☯*], Brian R. Amman[3], Ralph S. Baric[4], David S. Blehert[5], Cara E. Brook[6], Charles H. Calisher[7], Kevin T. Castle[8], Jeremy T. H. Coleman[9], Peter Daszak[1], Jonathan H. Epstein[1], Hume Field[1,11], Winifred F. Frick[10,12], Amy T. Gilbert[13], David T. S. Hayman[14], Hon S. Ip[5], William B. Karesh[1], Christine K. Johnson[15], Rebekah C. Kading[7], Tigga Kingston[16], Jeffrey M. Lorch[5], Ian H. Mendenhall[17], Alison J. Peel[18], Kendra L. Phelps[1], Raina K. Plowright[19], DeeAnn M. Reeder[20], Jonathan D. Reichard[9], Jonathan M. Sleeman[5], Daniel G. Streicker[21,22], Jonathan S. Towner[3], Lin-Fa Wang[17]

1 EcoHealth Alliance, New York, New York, United States of America, **2** US Geological Survey, Fort Collins Science Center, Ft. Collins, Colorado, United States of America, **3** US Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America, **4** Department of Epidemiology, University of North Carolina, Chapel Hill, North Carolina, United States of America, **5** US Geological Survey, National Wildlife Health Center, Madison, Wisconsin, United States of America, **6** Department of Integrative Biology, University of California Berkeley, Berkeley, California, United States of America, **7** Arthropod-borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology & Pathology, College of Veterinary Medicine & Biomedical Sciences, Colorado State University, Ft. Collins, Colorado, United States of America, **8** Wildlife Veterinary Consulting, Livermore, Colorado, United States of America, **9** US Fish and Wildlife Service, Hadley, Massachusetts, United States of America, **10** School of Veterinary Science, University of Queensland, Gatton, Queensland, Australia, **11** Bat Conservation International, Austin, Texas, United States of America, **12** Department of Ecology & Evolutionary Biology, University of California Santa Cruz, Santa Cruz, California, United States of America, **13** US Department of Agriculture, National Wildlife Research Center, Ft. Collins, Colorado, United States of America, **14** School of Veterinary Science, Massey University, Palmerston North, New Zealand, **15** One Health Institute, School of Veterinary Medicine, University of California Davis, Davis, California, United States of America, **16** Department of Biological Sciences, Texas Tech University, Lubbock, Texas, United States of America, **17** Programme in Emerging Infectious Diseases, Duke-National University of Singapore Medical School, Singapore, **18** Environmental Futures Research Institute, Griffith University, Nathan, Australia, **19** Department of Microbiology & Immunology, Montana State University, Bozeman, Montana, United States of America, **20** Department of Biology, Bucknell University, Lewisburg, Pennsylvania, United States of America, **21** Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow, Scotland, United Kingdom, **22** MRC-University of Glasgow Centre for Virus Research, Glasgow, Scotland, United Kingdom

☯ These authors contributed equally to this work.
* olival@ecohealthalliance.org (KJO); cryanp@usgs.gov (PMC)

Citation: Olival KJ, Cryan PM, Amman BR, Baric RS, Blehert DS, Brook CE, et al. (2020) Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. PLoS Pathog 16(9): e1008758. https://doi.org/10.1371/journal.ppat.1008758

Editor: Seema Lakdawala, University of Pittsburgh, UNITED STATES

Published: September 3, 2020

Funding: This work was supported in part by the USGS John Wesley Powell Center for Analysis and Synthesis, National Institute of Allergy and Infectious Diseases of the National Institutes of Health (Award Number R01AI110964), and the US Department of Defense, Defense Threat Reduction Agency (HDTRA11710064). Funding for DTSH was provided by a Royal Society Te Aparangi grant RDF-MAU1701. Funding for DGS was provided by a Wellcome Trust Senior Research Fellowship (217221/Z/19/Z). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Abstract

The COVID-19 pandemic highlights the substantial public health, economic, and societal consequences of virus spillover from a wildlife reservoir. Widespread human transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) also presents a new set of challenges when considering viral spillover from people to naïve wildlife and other animal populations. The establishment of new wildlife reservoirs for SARS-CoV-2 would further complicate public health control measures and could lead to wildlife health and conservation impacts. Given the likely bat origin of SARS-CoV-2 and related beta-coronaviruses (β-CoVs), free-ranging bats are a key group of concern for spillover from humans back to

Competing interests: The authors have declared that no competing interests exist.

wildlife. Here, we review the diversity and natural host range of β-CoVs in bats and examine the risk of humans inadvertently infecting free-ranging bats with SARS-CoV-2. Our review of the global distribution and host range of β-CoV evolutionary lineages suggests that 40+ species of temperate-zone North American bats could be immunologically naïve and susceptible to infection by SARS-CoV-2. We highlight an urgent need to proactively connect the wellbeing of human and wildlife health during the current pandemic and to implement new tools to continue wildlife research while avoiding potentially severe health and conservation impacts of SARS-CoV-2 "spilling back" into free-ranging bat populations.

Spillover of pandemic viruses

The threat of emerging infectious diseases (EIDs) to wildlife health and biodiversity conservation is recognized [1], but cross-species transmission of novel pathogens, or spillover, is typically viewed in the specific context of originating in a wildlife reservoir and transmitting to humans [2]. Research assessing EID risk has typically focused on identifying geographic regions [3, 4] and wildlife species [5–7] whereby spillover of zoonotic diseases into humans is most likely. Among recent pandemic zoonotic viruses, some have no evidence of transmission back to wildlife or domestic animal populations after establishment in people (e.g., human immunodeficiency virus, which causes acquired immunodeficiency syndrome), while others have repeatedly crossed species boundaries (e.g., pandemic H1N1 influenza A virus) [8, 9]. Evidence of "reverse zoonotic" transmission, sometime referred to as "spillback," from people to wildlife and domestic animals is widespread [9]; however, systematic surveys to determine the proportion of EIDs that spill back into novel wildlife hosts are lacking. Infection of bats by viruses of probable human origin has been recorded only twice [10, 11], and further transmission [12], or spread to a wider bat population, has not been recorded.

In December 2019, a novel coronavirus was detected from a cluster of 41 atypical pneumonia cases in Wuhan, China, and has since spread to cause a pandemic with significant global morbidity, mortality, and economic impact [13]. Phylogenetic evidence suggests that this virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the clade of SARS-related coronaviruses (SARSr-CoVs) that it belongs in evolved in Old-World bats of the family Rhinolophidae [14–16]. There is no epidemiological evidence of direct or indirect transmission of SARS-CoV-2 from bats to people, but a full genome of its closest known relative (with 96.2% sequence similarity) was reported from an Intermediate Horseshoe Bat (*Rhinolophus affinis*) sampled from Yunnan province, China, in 2013 [17]. The timing of SARS-CoV-2 spillover from bats and any involvement of intermediate host species remain undetermined [18, 19]. The United States currently has the highest number of confirmed human cases of COVID-19, the disease caused by SARS-CoV-2. The consequences of this pandemic are many and include the possibility of SARS-CoV-2 transmission from humans to free-ranging wildlife populations. Given the likely bat origin of SARS-CoV-2, free-ranging bats are a key group of concern for spillover from humans. Humans frequently handle and come into close contact with North American temperate-zone bats during the course of ecological research, wildlife rehabilitation, wildlife/pest control, and disease investigations. Anticipating the need for similar risk assessments across many potentially vulnerable species of wildlife and domesticated mammals globally, we here examine the possibility of humans inadvertently infecting free-ranging North American bats with SARS-CoV-2. We further discuss the possible public health and wildlife conservation consequences of SARS-CoV-2 becoming endemic in bats outside its natural host range.

Threats of SARS-CoV-2 to North American bats

The pandemic spread of SARS-CoV-2 may directly or indirectly threaten North American bat populations in at least three different ways. First, SARS-CoV-2 might infect any of the diverse and historically isolated 40+ endemic species of temperate-zone North American bats, with or without causing disease, morbidity, and mortality. Second, SARS-CoV-2 might infect and become established in one or more North American bat species, creating novel reservoirs capable of causing human infections (e.g., bat rabies lyssaviruses in the New World [20]). Third, if SARS-CoV-2 infection persists in North American bats of one or more species, it could potentially evolve or recombine with endemic viruses [19, 21] to become more pathogenic or infectious to humans or other animals. In addition to new public health challenges, the latter outcomes could quickly shift public perception of bats from mostly beneficial wildlife with associated disease risks that are manageable to bats posing unacceptable disease risks to human and animal health. Such a shift could increase the likelihood of negative human–bat interactions and conflicts, as well as undermine decades of concerted science, conservation, and education efforts aimed at conserving these valuable animals [22–24]. The potential threat of SARS-CoV-2 transmission from humans to other animals applies to many species of wildlife and domesticated mammals, but the likely bat origin of SARS-CoV-2 and the current threats to bat populations due to another disease in North America influenced us to focus this review on bats.

Lessons from an epizootic—Susceptibility of North American bats to an introduced pathogen

SARS-CoV-2 is not the first pathogen with the potential for inadvertent spread from people to North American bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that as early as 2006 began infecting hibernating bat populations in North America, spreading within and among species to alter the evolutionary trajectory of the continent's bats [25–28]. Genetic analyses indicate that *P. destructans* was introduced to North America [29], in our opinion likely by movement of humans or materials contaminated with fungal spores. White-nose syndrome (WNS), the disease caused by *P. destructans*, remains the only documented bat epizootic to cause multiyear, widespread mass mortality [30], although short-term bat die-offs have been also linked to Lloviu virus in Europe [31]. WNS has killed millions of North American bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the US and Canada (whitenosesyndrome.org, accessed 11 May 2020). Effective methods to mitigate WNS spread and impacts remain elusive despite substantial research effort, and targeted mitigation actions have had limited success against its impacts [32]. It took years of concerted international scientific effort to identify the cold-growing fungus, determine that it likely originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and pathogenicity, develop strategies to limit accidental translocation, and track its rapid spread through an immunologically naïve continental assemblage of hibernating bats [33–35].

The devastating impact of WNS on a diverse group of North American bats likely resulted from evolutionary isolation of the continent's bat fauna from other parts of the world for millions of years, despite other species of *Pseudogymnoascus* being present. Bats in both Europe and Asia can become infected by *P. destructans* but do not suffer mass mortality from WNS [36, 37]. The bat fauna spanning the higher latitudes of North America (in the US and Canada) is composed almost entirely of endemic species belonging to the family Vespertilionidae. Vespertilionid bats occur globally but likely originated and diversified in North America tens of millions of years ago before dispersing to other continents [38, 39]. No extant species of bat in

the Americas also occurs outside of the Americas [40, 41], and no bats migrate across the Pacific or Atlantic Oceans [42, 43]. The WNS epizootic demonstrates that a large proportion of these historically isolated bats can be vulnerable to a pathogen introduced from another continent during a single event. Additionally, bats already in a physiologically stressed condition due to WNS or other pressures may be more susceptible to viral infection, experience exacerbated disease outcomes, and/or experience increased viral shedding [44, 45]. The COVID-19 pandemic resembles WNS with respect to potential spread of a pathogen from another continent through interconnected, multispecies assemblages of North American bats that might be immunologically naïve and highlights deficits in our understanding of temperate-zone bat pathogens in North America.

Gaps in understanding global patterns of Bat–CoV diversity, evolution, and host range

Bats are among the world's most diverse mammals (comprising approximately 1,400 species [46]), and the global distribution and diversity of CoVs in bats proportionally reflects that of their hosts [47, 48]. Available evidence indicates that bats are natural reservoirs of CoVs, some of which have the potential to cause diseases in humans, domesticated animals, and wildlife [17, 47, 49–59]. Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events [47, 59–61]. Bats are the likely mammalian progenitor hosts of all alpha (α-) and beta (β-) CoVs [58, 59, 62, 63] and potentially all coronaviruses [60]. Alpha-CoVs of likely bat origin include the causative agent of swine acute diarrhea syndrome (SADS), which caused mass mortality of over 25,000 piglets on farms in Guangdong province, China [57], and a variant strain of porcine epidemic diarrhea virus (PEDV) that spread rapidly from China in recent decades and caused mass piglet mortality in multiple US states [64]. Human CoVs NL63 and 229E also likely had their evolutionary origins in bats [59, 65]. Two recent human disease epidemics (severe acute respiratory syndrome [SARS] and Middle East respiratory syndrome [MERS]) and now the current COVID-19 pandemic are caused by viruses that probably originated from β-CoVs circulating in bat populations in regions where outbreaks occurred [17, 19, 50–54, 58, 66–68].

The emergence of diseases like SADS, PEDV, SARS, MERS, and now COVID-19 strongly indicates a close association between CoVs that become pathogenic in humans and the wildlife reservoirs from which they originate [17, 50–54, 67]. The evolutionary relationships of CoVs within bats are consistent with geographically structured transmission cycles, with occasional transmission among related bat species [47, 58, 69]. These phylogeographic factors are also universal determinants of viral sharing among all mammals [70]. However, bat–virus association patterns can be particularly difficult to discern because bats often roost together in multispecies aggregations that can facilitate viral sharing, with each species capable of harboring multiple CoV lineages [47, 58, 68, 71]. Host shifts from bats to more divergent taxa are more difficult to predict—firstly, because the potential host breadth for many CoVs is broad [55, 56, 60, 72], and secondly, because host susceptibility and onward transmission involve complex, multistage processes [2, 12]. Bat–CoV associations likely remain substantially undersampled and understudied in temperate-zone North America [47, 71, 73, 74].

Are viruses like SARS-CoV-2 already present in North American bats?

Our examination of CoV evolutionary lineages and global distribution patterns of the diversity of bat species they infect suggests that temperate-zone North American bats could be

immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been detected in bats on most continents, sometimes with both types occurring in bats of the same species [58, 68]. However, an exception to this pattern is the lack of published evidence that β-CoVs infect bats of temperate-zone North America, despite several search efforts which used methods suitable to detect both α- and β-CoVs [59, 71, 74, 75]. Multiple novel α-CoVs have been detected and described in vespertilionid bats of the US and Canada, infecting species both living in close contact with humans and in remote wild areas [59, 71, 74–76]. However, SARSr-CoVs and β-CoVs of the viral subgenus *Sarbecovirus* have thus far been detected almost exclusively in species of the Old-World Chiropteran suborder Yinpterochiroptera (Fig 1A) [47, 58, 69]. The few exceptions to this pattern are the detection of novel Clade 3 and Clade 1 *Sarbecovirus* (*sensu* [53]) viruses in the wrinkle-lipped free-tailed bat (*Mops plicatus*, family Molossidae) in China [77] and the vespertilionid Leisler's noctule (*Nyctalus leisleri*) cohabiting a Bulgarian cave during autumn with several species of rhinolophids in which other SARSr β-CoVs were concurrently detected, suggesting cross-species infections (Fig 1A) [78]. Putative detections of a Clade 1 *Sarbecovirus* were also reported from guano samples of the

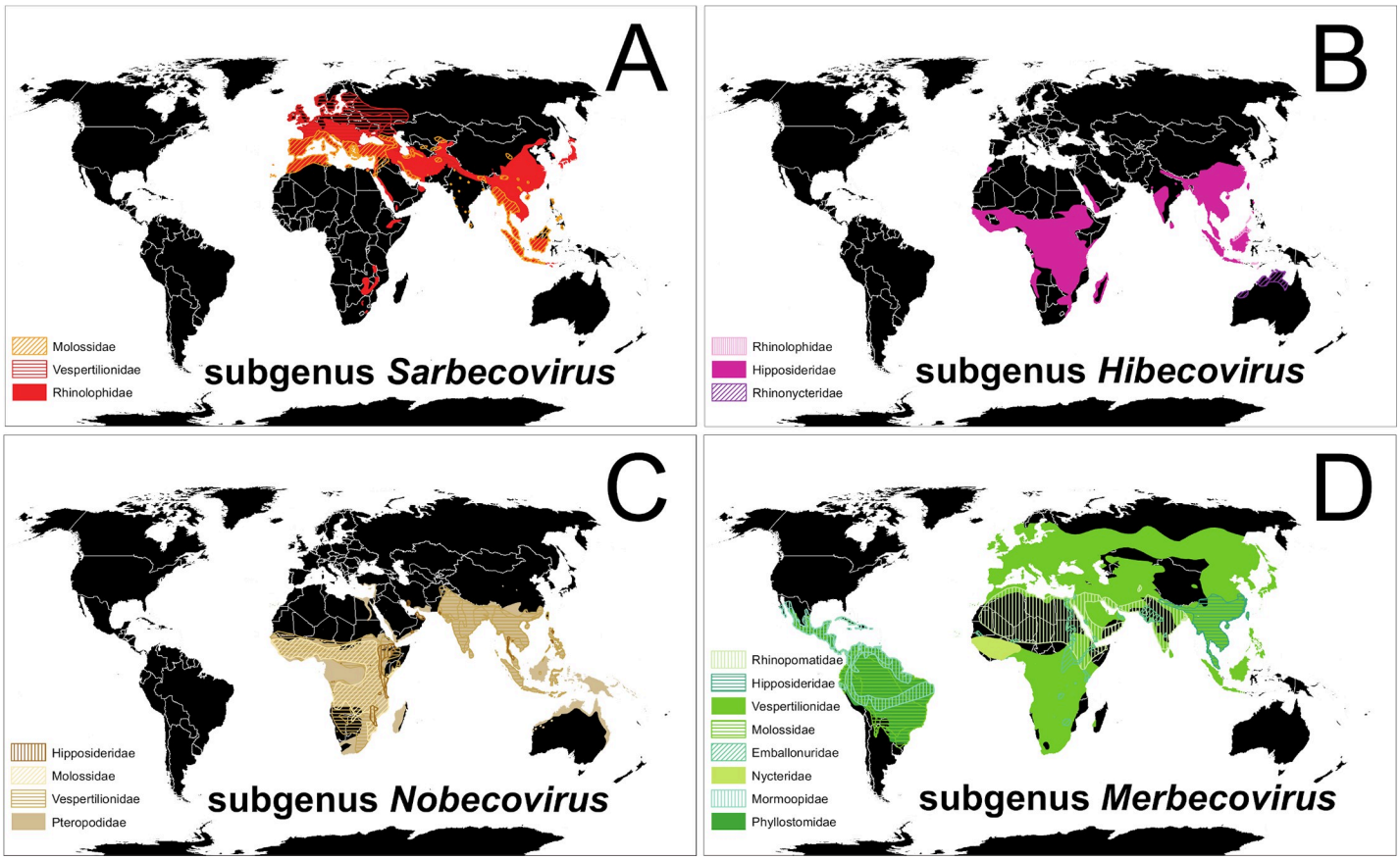

Fig 1. Global patterns of bats and associated β-CoVs. (A) Red-shaded distributions of bat species in which SARS-related β-CoVs of the subgenus *Sarbecovirus* have been detected; (B) pink-shaded distributions of bat species known to host β-CoVs of the subgenus *Hibecovirus*; (C) brown-shaded distributions of bats in which β-CoVs of the *Nobecovirus* lineage have been detected; and (D) green-shaded distributions of bats known to host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles within each panel represent different families of bats. A data table that includes all known bat species associations for each β-CoVs subgenus and peer-reviewed citations is available at US Geological Survey data release https://doi.org/10.5066/P9U461PJ. *Maps created using ArcMap (ESRI, Redlands, California, United States of America) and bat ranges derived from spatial data on terrestrial mammals from the International Union for the Conservation of Nature (IUCN 2020. The IUCN Red List of Threatened Species. January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020).* β-CoV, beta-coronavirus; MERS, Middle East respiratory syndrome; SARS, severe acute respiratory syndrome.

https://doi.org/10.1371/journal.ppat.1008758.g001

vespertilionid brown long-eared bat (*Plecotus auritus*) and the molossid European free-tailed bat (*Tadarida teniotis*) on Sardinia, where the same novel β-CoV was described in the greater horseshoe bat (*R. ferrumequinum*) [79].

Viruses in the β-CoV subgenera *Hibecovirus* and *Nobecovirus* also have been reported mostly from Old-World bat families Rhinolophidae, Hipposideridae, Rhinonycteridae, and Pteropodidae, except for novel viruses of the latter subgenus detected in four species of the vespertilionid genus *Scotophilus* in Asia and Africa (Fig 1B and 1C) [47, 58, 69].

Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineages) occur in a greater diversity of bat families and across more global regions than the other subgenera (Fig 1D) [47, 58, 69]. These widely distributed MERS-like viruses can cause disease in humans (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (Fig 1*D*) [47, 58, 69].

Lack of evidence for β-CoVs in temperate-zone North American bats

The several hundred species of extant bats spanning the Americas all belong to the suborder Yangochiroptera, which likely diverged from the Old-World suborder Yinpterochiroptera more than 50 million years ago (Fig 2) [80]. The only β-CoVs detected in the Americas to date

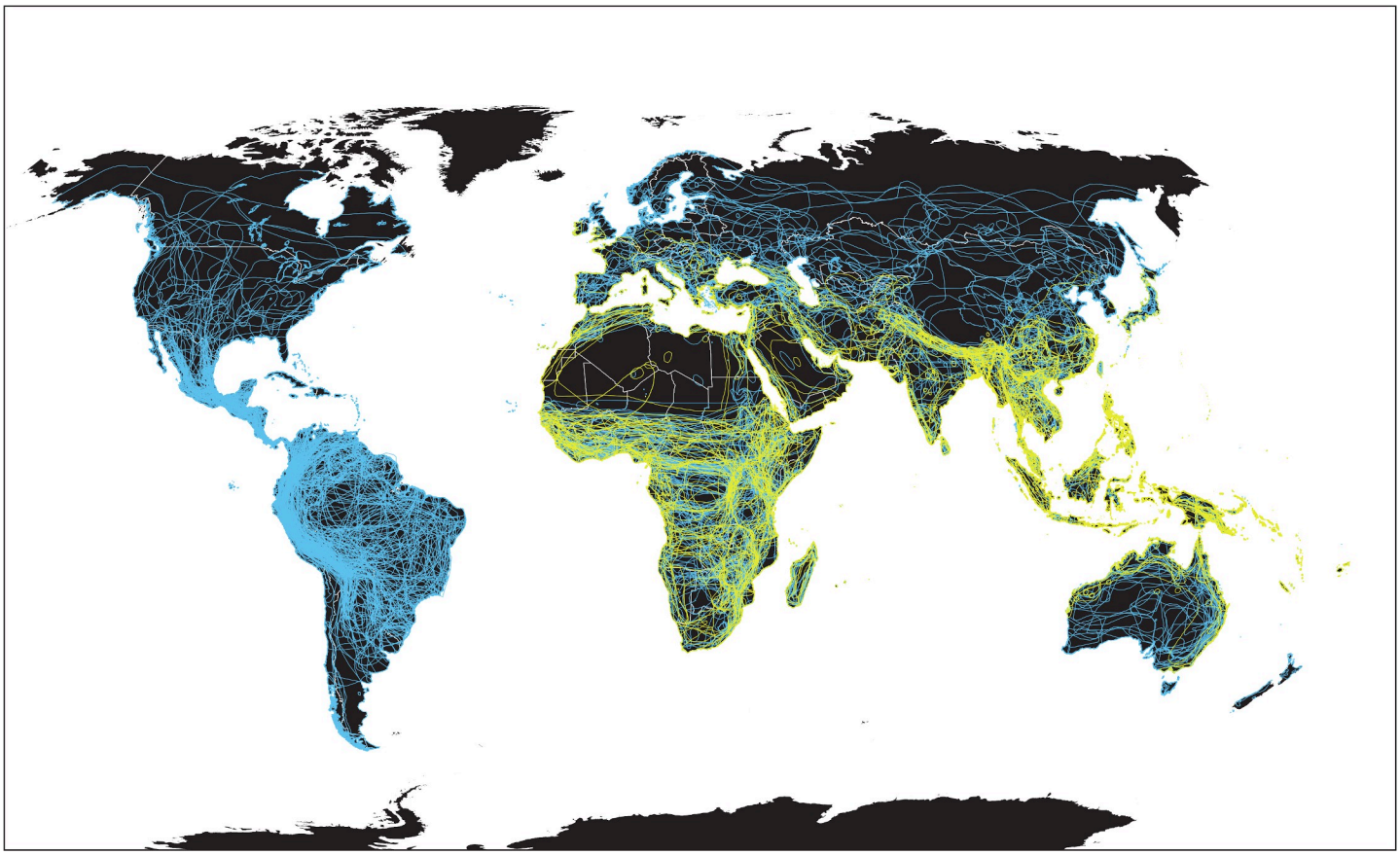

Fig 2. Old-World and New-World bats. Overlapping species distribution outlines of bats in the globally distributed suborder Yangochiroptera (blue) and Old-World Yinpterochiroptera (yellow). *Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the International Union for the Conservation of Nature Red List of Threatened Species, January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020.*

https://doi.org/10.1371/journal.ppat.1008758.g002

belong to the subgenus *Merbecovirus* and appear restricted to two exclusively Neotropical bat families (Phyllostomidae and Mormoopidae) and one that is globally distributed (Molossidae). Distinct CoV lineages in the subgenus *Merbecovirus* were described from three species of *Pteronotus* (family Mormoopidae), four species of *Artibeus*, and Seba's short-tailed bat (*Carollia perspicillata*; family Phyllostomidae) from tropical regions of Mexico [47, 81]. Novel β-CoVs of the subgenus *Merbecovirus* were detected in two neotropical bat species of the family Molossidae: Wagner's bonneted bat (*Eumops glaucinus*) in southern Brazil and the broad-eared free-tailed bat (*Nyctinomops laticaudatus*) in southern Mexico [81, 82]. In vitro infections have shown that primary kidney cells from the Jamaican fruit-eating bat (*Artibeus jamaicensis*) can be infected with MERS-CoV, and virus replication and shedding was reported in experimentally infected bats of this species but without obvious clinical signs of disease [83]. Similar to the evidence for natural invasion of bat rabies viruses among New World bats [84], available evidence suggests β-CoVs may have arrived through South America and have long been evolving in Neotropical bats. Although some bat hosts of *Merbecoviruses* overlap geographically with species of temperate-zone North American bats, none occur outside of the Neotropics. Sampling has been limited, but we are not aware of any published detections of *Merbecoviruses* or any other β-CoVs in temperate-zone North American vespertilionid bats.

Our inference of true patterns of CoV occurrence and distribution in bat populations is limited by uneven global sampling. Yet SARSr-CoVs (*Sarbecovirus* spp.), a focus of many surveillance efforts, have been almost exclusively documented in Old-World Yinpterochiroptera. SARSr-CoVs were only found in the ultra-diverse and globally distributed bat suborder Yangochiroptera under conditions with plausible transmission from co-roosting *Rhinolophus* sp. bats [53, 85]. This absence of evidence for SARS-like β-CoVs in yangochiropteran bats in general, and in temperate-zone vespertilionid bats of North America in particular, likely represents a unique biogeographic pattern driven by underlying factors of host susceptibility or life history. These observations also point to the susceptibility of vespertilionid bats under circumstances of SARSr-CoV environmental exposure and that they may not be naturally immune to these viruses.

Bats rank among the most ecologically important mammals and play varied roles in most of Earth's ecosystems; bats pollinate and disperse seeds of numerous plants in tropical regions, and all over the world, bats are primary nocturnal predators of flying insects [23, 24]. Across the Holarctic, chiropteran species diversity is greatest among hibernating vespertilionid bats. At least 25 of the ecologically diverse vespertilionid species of bats in the US and Canada hibernate [86], which might influence their susceptibility to or interactions with viruses, as has been postulated for common vespertilionids infected with α-CoVs and rabies virus [44, 87–89]. Hibernation strategies vary among species of bats (e.g., degree of sociality, thermoregulatory behaviors, habitat selection) [90], but bat body temperatures during hibernation generally remain consistently below 10° C for periods lasting 7–9 months per year [91], providing a potential mechanism to limit viral replication and spread [92]. Experimental studies to assess the ability of SARS-CoV-2 or other β-CoVs to survive and replicate in bats (cell lines and individuals) at low temperatures [92, 93] would provide additional insight into risk of reverse zoonosis. However, appropriate tools for studying such possibilities are lacking, particularly immortalized cell lines from several hibernating, vespertilionid bats [59]. These tools would also enable interrogation of other physiological features of vespertilionids that may influence susceptibility, such as receptor-binding affinity and the expression of receptors across tissues. Scientists did not discover and isolate the obligately psychrophilic fungus that causes WNS until they collected samples in bat hibernation sites and moved culture dishes for incubation into laboratory refrigerators [25]. Similar innovative explorations outside the typical temperature conditions of laboratory experimentation could help assess the risk of SARS-CoV-2

infecting the more than two dozen species of bats in the US and Canada that hibernate to survive harsh temperate-zone winters.

Proactively connecting the wellbeing of human and bat populations

Scientists have long recognized the risk of pathogen spillover from humans to bats [94–96], but bat researchers in North America have not systematically addressed this risk prior to WNS. Outside of reservoir host studies, few bat researchers studied infectious diseases in bats before WNS emerged in 2007 [73] nor studied bat viruses (other than rabies) before bats were retrospectively connected to the SARS epidemic [15, 66, 97]. Fortunately, bat and wildlife disease researchers recently began addressing these knowledge gaps in more detail [7, 97, 98]. Possible explanations for why bats might host particularly pathogenic viruses include characteristics of their life history (e.g., long-lived, wide ranging, multispecies aggregations, daily and seasonal heterothermy) [97], unique physiology for repairing their damaged DNA [99], unique ability to suppress some of their innate immunity pathways [100–105], high species diversity [48], and unmatched metabolic range and high body temperatures during flight [106]. Bats also cryptically come into close contact with humans, increasingly in urban and periurban settings as a result of native habitat loss, often crossing human–wildlife interfaces [107–113].

Except for *Lyssavirus* infections, bats rarely show substantial signs of sickness from the same pathogens that cause virulent disease in humans. Bats cope with viral infections in ways that we do not yet fully comprehend, but learning how they do so may reveal important insights to develop therapeutics and ultimately to protect human health [103–105]. In vitro and laboratory studies demonstrate that bats can specifically regulate naïve immunity pathways to effectively cope with viral infection [114]. For example, dendritic cells generated from the bone marrow of the Egyptian rousette (*Rousettus aegyptiacus*) infected with Marburg virus down-regulate immune-stimulatory pathways and maturation of cells targeted by the virus while up-regulating pathogen-sensing pathways [115]. Unique bat immune regulation may occur with MERS-CoV infection, at least under experimental conditions [101]. Egyptian rousette bats experimentally challenged with SARS-CoV-2 by intranasal inoculation became transiently infected, shed virus, and one cohoused bat became infected but showed no clinical signs of disease other than rhinitis [116]. Our potential lack of understanding of clinical signs of illness in bats and the cryptic habits of many species also generally inhibit our ability to easily detect spillover of pathogens from human to bat populations. This may add to uncertainty about cross-species transmission and dispersal of CoVs among human and animal communities. Laboratory findings suggest human viruses that likely originated in bats, such as HCoV-NL63, are capable of infecting bat cells, at least in vitro [59]. SARS-CoV-2 and other CoVs have some of the longest genomes among all RNA viruses, and despite having specialized RNA proofreading machinery [117, 118], they are still prone to recombination and copy errors in hosts, sometimes resulting in functional adaptations (e.g., altered receptor binding capacity or temperature adaptation of enzymes) [119]. CoVs can even recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus [21]. Spillover of SARS-CoV-2 from infected humans to North American bats they handle or come in close contact with could lead to the virus becoming either less or more pathogenic to bats or other wildlife, domesticated animals, or humans through genetic mixing in one or more novel hosts. The public health and conservation consequences of a more virulent virus could be severe, whereas genetic mixing in a bat host that resulted in a less-virulent virus might go unnoticed.

Need for an interdisciplinary response

Effectively managing risks of human disease caused by emerging zoonotic pathogens and ensuring the health and conservation of wildlife species that are potential reservoirs of those disease agents can be synergistic goals under a One Health framework. Spillover risk (from or to wildlife) is often greatest in disturbed ecosystems where there is an elevated frequency of human–wildlife interactions or disruption of ecological patterns [3, 120–124]. Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities and ecological contexts that increase direct and indirect interactions with bats that could present health risks [2]. Furthermore, fear-based reactions to disease risk from wildlife, such as culling infected bat populations or indiscriminate killing, often have negative unintended consequences for the interconnected health of both humans and bats (e.g., culling of bats in a Uganda mine led to a more than doubling of Marburg virus prevalence in the bats living there) [30, 125–127]. Temperate-zone vespertilionid bats inhabiting human dwellings in the US and Canada represent a particularly relevant human–wildlife interface, in which conservation and management actions to proactively address the potential consequences for pathogen spillover are worth careful consideration [73].

Conservation-compatible surveillance of bat viruses has demonstrated the potential for mutually beneficial collaboration between public health scientists and conservation stakeholders [94, 113, 125, 128, 129]. Disease-focused studies that integrate ecological principles into a rigorous study design provide the most informative context to interpret bat–virus associations and patterns of richness globally [130–132]. Assessing the risks of SARS-CoV-2 spillover into North American bats presents a timely opportunity to form multidisciplinary scientific teams that include experts on emerging infectious diseases and ecologists with expertise on North American bats [128]. Scientists researching emerging infectious diseases can benefit from sampling opportunities and methods that bat researchers have developed for observing, counting, and noninvasively sampling bats [73, 133]. Bat researchers can learn about human and animal health monitoring and supporting laboratory methods, including biosafety, secure handling/transport of CoV-positive samples, and training in the proper use of personal protective equipment (PPE) from professionals with expertise in veterinary and medical sciences [113, 131, 134, 135]. A shared goal of all stakeholders is to identify and implement simple, widely available diagnostic tests for detecting SARS-CoV-2 infection that are species-independent, practical for field and laboratory use, highly specific and sensitive, and that do not require strict biosafety containment [136]. All investigators can also work together to develop mutually beneficial goals, such as joint risk communications to the public with effective and balanced messaging about bat populations and higher risk activities for human–bat contact.

Adopting a precautionary approach in the face of global COVID-19 transmission among human populations, national and international wildlife organizations have advised limiting capturing and handling of bats in the field to minimize the risk of humans infecting wild bats with SARS-CoV-2 until further assessment can be made [137, 138]. The emergence of WNS in 2007 prompted a similar surge in interdisciplinary collaboration that enabled the rapid advances already mentioned and introduced changes to guidance for PPE use and disinfection practices for bat researchers and recreational cavers. Similarly, the emergence of SARS-CoV-2 and other viruses will likely alter the status quo of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases. For example, PPE, including respiratory protection, is a standard practice adopted by many bat virus researchers but by few others studying and regularly handling bats [134, 139]. The urgent research priority of a rapid, quantitative risk assessment and analysis of various mitigation options is currently underway [137, 140]. One key question is whether the proper use of

optimal PPE, including bidirectional N95 or equivalent masks, along with effective risk communication and adherence to other basic biosafety practices [134, 141, 142] during field work, can significantly reduce the transmission risk of SARS-CoV-2 from humans to bats. In the interim, until new guidelines are established for handling and for close-proximity work with bats, we have outlined gaps in our understanding of SARS-CoV-2 spillover risks at the interface between humans, domesticated animals, and free-ranging wildlife. Temporarily shifting to "hands-off" bat research methods also seems prudent, wherever possible, and could facilitate ongoing work with reduced risk.

Examples of "hands-off" research strategies

Multiple research strategies that do not involve close contact with free-ranging bats already exist for addressing critical gaps in understanding CoV diversity, distribution, evolution, and potential health effects in temperate-zone bats. For example, a combination of host-cell receptor analyses and in vitro and in vivo experimental infections across a diversity of bat and other mammalian species have helped inform potential host range expansion for SARS-CoV-2. The receptors that many CoVs use to gain access to host cells, such as angiotensin-converting enzyme 2 (ACE2) and dipeptidyl peptidase-4 (DPP4/CD26), have undergone positive selection in bats, resulting in diverse and recombinant CoV strains [72, 143]. These strains can likely bind to numerous variants of a host receptor protein and facilitate spillover into other animal species [72, 144]. SARS-CoV-2 targets and strongly binds to mammalian ACE2 cell receptors [72, 145, 146]. Beta-CoVs of the subgenus *Merbecovirus* (like those known to occur in the Americas) are not known to target ACE2 cell receptors, instead using as a receptor DPP4/CD26 or possibly other receptors [53, 144]. Current in silico predictions that bats will likely have low susceptibility to SARS-CoV-2 based on ACE2 structural analyses conflict with in vitro evidence and do not comprehensively account for ACE2 amino acid sequence variation (including intraspecific variation) that occurs within bats [17, 72, 145]. Assessing SARS-CoV-2 host range will require additional virus-host receptor binding assays in silico and in vitro [17, 53, 72, 144, 145], together with future experimental infection studies for confirmation of Koch's postulates. In addition, in vitro studies could evaluate species variability in innate immune responses. These investigations will help quantify the potential for North American bat infection and transmission among free-ranging populations.

Examples of other "hands-off" methods applicable to both bat disease and conservation research include the following: virus discovery and characterization focused on existing specimens archived in scientific museums or through partnerships and collaboration with established national bat disease monitoring or surveillance programs [147, 148]; monitoring echolocation calls to determine the occurrence, distributions, and seasonal or nightly activity patterns of bats [133, 149]; digital imaging methods for counting bats and studying physiology and behaviors in the context of disease [90, 108]; sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding [71, 150–152]; and mathematical modeling to predict susceptible host species, virus sharing among hosts, spread patterns, or to estimate mortality in affected populations [5, 70, 122, 135]. Promising areas for innovation include making technologies for bat research more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods [153, 154]. In addition to research, standardized field protocols and probabilistic sampling strategies are needed for monitoring bats and their viruses at continental scales (www.nabatmonitoring.org) [155, 156], as are longitudinal studies across multiple sites to better understand the ecological drivers of CoV dynamics and spillover [157].

Developing simple management tools and methods for rapidly assessing risks of virus spillover from humans to wildlife, while maintaining scientific rigor, could also help with future disease response. It might also be useful to prepare a suite of tools, protocols, and risk communication strategies for natural resource managers and public health officials to immediately deploy while risks are being assessed. Such prepared management resources could include public outreach material and guidelines for enhanced use of PPE for those in closest contact with potentially susceptible wildlife.

Conclusion

Many questions remain about the risk of SARS-CoV-2 to naïve wildlife populations, the influences of human behavior on those risks, and the potential for establishment of new CoV reservoirs. Cross-species virus transmission events are relatively rare, requiring an infectious reservoir host to be in contact with a recipient host when conditions concurrently favor susceptibility and onward transmission [12, 113, 114]. The currently unknown, but possible and potentially high-consequence, risk of SARS-CoV-2 transmission and establishment in North American bats (or other free-ranging mammals) warrants precaution [116, 140]. Strategically managing interactions between people and potentially susceptible or at risk species can decrease the probability of cross-species virus spillover [113]. Humans that frequently handle and come into close contact with North American temperate-zone bats, such as bat researchers, wildlife rehabilitators, wildlife/pest control workers, and disease investigators, can help decrease any chances of spillover by adopting basic PPE and biosafety practices and carefully evaluating how their actions might adversely affect bat populations. We are at a critical nexus of biosecurity and natural resource conservation that will require ingenuity and diligence to continue important research on bats whilst simultaneously evaluating the ecological future of SARS-CoV-2. Our actions during this current pandemic could profoundly influence and protect the health of both humans and wildlife in North America.

Supporting information

S1 Table. Global patterns of betacoronavirus (β-CoV) associations in bats. The table lists bat species in which betacoronaviruses (β-CoVs) were detected, organized by viral subgenera and clade (for Sarbecorviruses), bat family, bat suborder, and general global region where the species of bat occurs. Reference to the published literature sources of information for each row are listed in the last column. Provided in comma-separated value (.csv) format at https://doi.org/10.5066/P9U461PJ.
(XLSX)

Acknowledgments

We thank Thomas O'Shea, Brian Reichert, Michelle Verant, Richard "Chip" Clark III, Marcos Gorresen, Jill Baron, and Daniel Becker for helpful comments on earlier drafts of this manuscript.

The findings and conclusions in this report are those of the authors and do not necessarily represent the views of the Centers for Disease Control and Prevention or the Department of Health and Human Services, or the US Fish and Wildlife Service. The use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the US government.

References

1. Daszak P, Cunningham AA, Hyatt A. Anthropogenic environmental change and the emergence of infectious diseases in wildlife. Acta Trop. 2001; 78(2):103–16. https://doi.org/10.1016/s0001-706x(00)00179-0 PMID: 11230820
2. Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, et al. Pathways to zoonotic spillover. Nat Rev Microbiol. 2017; 15(8):502–10. https://doi.org/10.1038/nrmicro.2017.45 PMID: 28555073
3. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, et al. Global hotspots and correlates of emerging zoonotic diseases. Nature Communications. 2016; 8:1124. https://doi.org/10.1038/s41467-017-00923-8.
4. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. Nature. 2008; 451:990–3. https://doi.org/10.1038/nature06536 PMID: 18288193
5. Han BA, Kramer AM, Drake JM. Global patterns of zoonotic disease in mammals. Trends Parasitol. 2016; 32(7):565–77. https://doi.org/10.1016/j.pt.2016.04.007 PMID: 27316904
6. Luis AD, O'Shea TJ, Hayman DTS, Wood JLN, Cunningham AA, Gilbert AT, et al. Network analysis of host–virus communities in bats and rodents reveals determinants of cross-species transmission. Ecol Lett. 2015; 18:1153–62. https://doi.org/10.1111/ele.12491 PMID: 26299267
7. Olival KJ, Hosseini PR, Zambrana-Torrelio C, Ross N, Bogich TL, Daszak P. Host and viral traits predict zoonotic spillover from mammals. Nature. 2017;646–650(546). https://doi.org/10.1038/nature22975.
8. Schrenzel MD, Tucker TA, Stalis IH, Kagan RA, Burns RP, Denison AM, et al. Pandemic (H1N1) 2009 virus in 3 wildlife species, San Diego, California, USA. Emerging Infectious Diseases. 2011; 17(4):747–9. https://doi.org/10.3201/eid1706.101355 PMID: 21470480
9. Messenger A, Barnes A, Gray GC. Reverse zoonotic disease transmission (Zooanthroponosis): a systematic review of seldom-documented human and biological threats to animals. PLoS ONE. 2014; 9(2):e89055. https://doi.org/10.1371/journal.pone.0089055 PMID: 24586500
10. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, et al. A strategy to estimate known viral diversity in mammals. mBio. 2013; 4(5):1–15. https://doi.org/10.1128/mBio.00598-13.
11. Esona MD, Mijatovic-Rustempasic S, Conrardy C, Tong S, Kuzmin IV, Agwanda B, et al. Reassortment group A rotavirus from straw-colored fruit bat (*Eidolon helvum*). Emerging Infectious Diseases. 2010; 16(12):1844–52. https://doi.org/10.3201/eid1612.101089 PMID: 21122212
12. Wasik BR, de Wit E, Munster V, Lloyd-Smith JO, Martinez-Sobrido L, Parrish CR. Onward transmission of viruses: how do viruses emerge to cause epidemics after spillover? Philosophical Transactions of the Royal Society B. 2019; 374(20190017). http://dx.doi.org/10.1098/rstb.2019.0017.
13. Huang C, Wang Y, Li X, Zhaou J, Hu Y, Zhang L, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. The Lancet. 2020; 395:497–506. https://doi.org/10.1016/S0140-6736(20)30183-5.
14. Ge X, Li J, Yang X, Chmura AA, Zhu G, Epstein JH, et al. Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature. 2013; 503:535–8. https://doi.org/10.1038/nature12711 PMID: 24172901
15. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, et al. Bats are natural reservoirs of SARS-like coronaviruses. Science. 2005; 310:676–9. https://doi.org/10.1126/science.1118391 PMID: 16195424
16. Guan Y, Zheng BJ, He YQ, Liu XL, Zhuang ZX, Cheung CL, et al. Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. Science. 2003; 302(5643):276–8. https://doi.org/10.1126/science.1087139 PMID: 12958366
17. Zhou P, Yang X, Wang X, Hu B, Zhang L, Zhang W, et al. A pnemonia outbreak associated with a new coronavirus of probable bat origin. Nature. 2020; 579:270–3. https://doi.org/10.1038/s41586-020-2012-7 PMID: 32015507
18. Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. Nat Med. 2020. https://doi.org/10.1038/s41591-020-0820-9.
19. Boni MF, Lemey P, Jiang X, Lam TT, Perry B, Castoe T, et al. Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. bioRxiv. 2020. https://doi.org/10.1101/2020.03.30.015008.
20. Banyard AC, Davis A, Gilbert AT, Markotter W. Bat rabies. In: Fooks AR, Jackson AC, editors. Rabies: scientific basis of the disease and its management: Academic Press; 2020. p. 231–76.

21. Huang C, Liu WJ, Xu W, Jin T, Zhao Y, Song J, et al. A bat-derived putative cross-family recombinant coronavirus with a reovirus gene. PLoS Pathog. 2016; 12(9):e1005883. https://doi.org/10.1371/journal.ppat.1005883 PMID: 27676249

22. Horan RD, Fenichel EP, Wolf CA, Graming BM. Managing infectious animal disease systems. Annual Review of Resource Economics. 2010; 2(1):101–24. https://doi.org/10.1146/annurev.resource.012809.103859.

23. Kunz TH, Braun de Torrez E, Bauer D, Lobova T, Fleming TH. Ecosystem services provided by bats. Ann N Y Acad Sci. 2011; 1223:1–38. https://doi.org/10.1111/j.1749-6632.2011.06004.x PMID: 21449963

24. Maine JJ, Boyles JG. Bats initiate vital agroecological interactions in corn. Proc Natl Acad Sci USA. 2015; 112(40):12438–43. https://doi.org/10.1073/pnas.1505413112 PMID: 26371304

25. Blehert DS, Hicks AC, Behr M, Meteyer CU, Berlowski-Zier BM, Buckles EL, et al. Bat white-nose syndrome: an emerging fungal pathogen? Science. 2009; 323:227. https://doi.org/10.1126/science.1163874 PMID: 18974316

26. Lorch JM, Meteyer CU, Behr MJ, Boyles JG, Cryan PM, Hicks AC, et al. Experimental infection of bats with *Geomyces destructans* causes white-nose syndrome. Nature. 2011; 480:376–8. https://doi.org/10.1038/nature10590 PMID: 22031324

27. Warnecke L, Turner JM, Bollinger TK, Lorch JM, Misra V, Cryan PM, et al. Inoculation of bats with European *Geomyces destructans* supports the novel pathogen hypothesis for the origin of white-nose syndrome. Proc Natl Acad Sci USA. 2012; 109:6999–7003. https://doi.org/10.1073/pnas.1200374109 PMID: 22493237

28. Frick WF, Puechmaille SJ, Hoyt JR, Nickel BA, Langwig KE, Foster JT, et al. Disease alters macroecological patterns of North American bats. Global Ecol Biogeogr. 2015; 24(7):741–479. https://doi.org/10.1111/geb.12290.

29. Drees KP, Lorch JM, Puechmaille SJ, Parise KL, Wibbelt G, Hoyt JR, et al. Phylogenetics of a fungal invasion: origins and widespread dispersal of white-nose syndrome. mBio. 2017; 8:e01941–17. https://doi.org/10.1128/mBio.01941-17 PMID: 29233897

30. O'Shea TJ, Cryan PM, Hayman DTS, Plowright RK, Streicker DG. Multiple mortality events in bats: a global review. Mamm Rev. 2016. https://doi.org/10.1111/mam.12064.

31. Kemenesi G, Kurucz K, Dallos B, Zana B, Földes F, Boldogh S, et al. Re-emergence of Lloviu virus in *Miniopterus schreibersii* bats, Hungary, 2016. Emerging Microbes & Infections. 2018; 7(66):1–4. https://doi.org/10.1038/s41426-018-0067-4.

32. Langwig KE, Voyles J, Wilber MQ, Frick WF, Murray KA, Bolker BM, et al. Context-dependent conservation responses to emerging wildlife diseases. Front Ecol Environ. 2015; 13(4):195–202. https://doi.org/10/f7bcq2.

33. Frick WF, Cheng TL, Langwig KE, Hoyt JR, Janicki AF, Parise KL, et al. Pathogen dynamics during invasion and establishment of white-nose syndrome explain mechanisms of host persistence. Ecology. 2017; 98(3):624–31. https://doi.org/10.1002/ecy.1706 PMID: 27992970

34. Frick WF, Puechmaille SJ, Willis CKR. White-nose syndrome in bats. In: Voigt CC, Kingston T, editors. Bats in the Anthropocene: Conservation of bats in a changing world: Springer; 2016. p. 245–62.

35. Cryan PM, Meteyer CU, Boyles JG, Blehert DS. White-nose syndrome in bats: illuminating the darkness. BMC Biology. 2013; 11:47. https://doi.org/10.1186/1741-7007-11-47 PMID: 23587401

36. Zukal J, Bandouchova H, Brichta J, Cmokova A, Jaron KS, Kolarik M, et al. White-nose syndrome without borders: *Pseudogymnoascus destructans* infection tolerated in Europe and Palearctic Asia but not in North America. Scientific Reports. 2016; 6:19829. https://doi.org/10.1038/srep19829 PMID: 26821755

37. Hoyt JR, Langwig KE, Sun K, Parise KL, Li A, Wang Y, et al. Environmental reservoir dynamics predict global infection patterns and population impacts for the fungal disease white-nose syndrome. Proceedings of the National Academy of Sciences. 2020; 117(13):7255. https://doi.org/10.1073/pnas.1914794117.

38. Arita HT, Vargas-Barón J, Villalobos F. Latitudinal gradients of genus richness and endemism and the diversification of New World bats. Ecography. 2014; 37:1024–33. https://doi.org/10.1111/ecog.00720

39. Peixoto FF, Braga PHP, Mendes P. A synthesis of ecological and evolutionary determinants of bat diversity across spatial scales. BMC Ecol. 2018; 18(18). https://doi.org/10.1186/s12898-018-0174-z.

40. Van Den Bussche RA, Hoofer SR. Phylogenetic releationships among recent Chiropteran families and importance of choosing appropriate out-group taxa. Journal of Mammalogy. 2004; 85(2):321–30. https://doi.org/10.1644/1545-1542(2004)085<0321:PRARCF>2.0.CO;2.

41. IUCN. The IUCN Red List of Threatened Species. 2020;(4 April 2020). Epub 2020–1.

42. Baker RR. The evolutionary ecology of animal migration. New York: Holmes & Meier Publishers; 1978. 1012 p.

43. Fleming TH, Eby P. Ecology of bat migration. In: Kunz TH, Fenton MB, editors. Bat ecology. Chicago: The University of Chicago Press; 2003. p. 156–208.

44. Davy CM, Donaldson ME, Subudhi S, Rapin N, Warnecke L, Turner JM, et al. White-nose syndrome is associated with increased replication of a naturally persisting coronaviruses in bats. Scientific Reports. 2018; 8(15508). https://doi.org/10.1002/ece3.3234.

45. Plowright RK, Field HE, Smith C, Divljan A, Palmer C, Tabor G, et al. Reproduction and nutritional stress are risk factors for Hendra virus infection in little red flying foxes (*Pteropus scapulatus*). Proceedings of the Royal Society B. 2008; 275:861–9. https://doi.org/10.1098/rspb.2007.1260 PMID: 18198149

46. Simmons NB, Cirranello AL. Bat Species of the World: A taxonomic and geographic database. 2020 [17 April 2020]. Available from: https://www.batnames.org/.

47. Anthony SJ, Johnson CK, Greig DJ, Kramer S, Che X, Wells H, et al. Global patterns in coronavirus diversity. Virus Evolution. 2017; 3(1):vex012. https://doi.org/10.1093/ve/vex012 PMID: 28630747

48. Mollentze N, Streicker DG. Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. Proc Natl Acad Sci USA. 2020. Epub 13 April 2020. www.pnas.org/cgi/doi/10.1073/pnas.1919176117.

49. Hu D, Zhu C, Wang Y, Ai L, Yang LQ, Ye F, et al. Virome analysis for identification of novel mammalian viruses in bats from southeast China. Scientific Reports. 2017; 7:10917. https://doi.org/10.1038/s41598-017-11384-w PMID: 28883450

50. Cheng VCC, Lau SKP, Woo PCY, Yuen KY. Severe acute respiratory syndrome coronavirus as an agent of emerging and reemerging infection. Clinical Microbiology Reviews. 2007; 20(4):660–94. https://doi.org/10.1128/CMR.00023-07 PMID: 17934078

51. Cui J, Li F, Shi Z. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019; 17:181–92. https://doi.org/10.1038/s41579-018-0118-9 PMID: 30531947

52. Fan Y, Zhao K, Shi Z, Zhou P. Bat coronaviruses in China. Viruses. 2019; 11(210):1–11. https://doi.org/10.3390/v11030210.

53. Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. The Lancet. 2020. Epub January 29, 2020. https://doi.org/10.1016/S0140-6736(20)30251-8.

54. Zhao G. SARS molecular epidemiology: a Chinese fairy tale of controlling an emerging zoonotic disease in the genomics era. Royal Society Philosophical Transactions Biological Sciences. 2007; 362 (1482):1063–81. https://doi.org/10.1098/rstb.2007.2034.

55. Dong BQ, Liu W, Fan XH, Vijaykrishna D, Tang XC, Gao F, et al. Detection of a novel and highly divergent coronavirus from Asian leopard cats and Chinese ferret badgers in southern China. Journal of Virology. 2007; 81(13):6920–6. https://doi.org/10.1128/JVI.00299-07 PMID: 17459938

56. Shi J, Wen Z, Zhong G, Yang H, Wang C, Liu R, et al. Susceptibility of ferrets, cats, dogs, and different domestic animals to SARS-coronavirus-2. Science. 2020:1–23. https://doi.org/10.1126/science.abb7015.

57. Zhou P, Fan H, Lan T, Yang X, Shi W, Zhang W, et al. Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. Nature. 2018; 5556:255–8. https://doi.org/10.1038/s41586-018-0010-9.

58. Drexler JF, Corman VM, Drosten C. Ecology, evolution and classification of bat coronaviruses in the aftermath of SARS. Antiviral Res. 2014; 101:45–56. https://doi.org/10.1016/j.antiviral.2013.10.013 PMID: 24184128

59. Huynh J, Li S, Yount B, Smith A, Sturges L, Olsen JC, et al. Evidence supporting a zoonotic origin of human coronavirus strain NL63. Journal of Virology. 2012; 86(23):12818–25. https://doi.org/10.1128/JVI.00906-12.

60. Vijaykrishna D, Smith GJD, Zhang JX, Peiris JSM, Chen H, Guan Y. Evolutionary insights into the ecology of coronaviruses. Journal of Virology. 2007; 81(8):4012–20. https://doi.org/10.1128/JVI.02605-06 PMID: 17267506

61. Hall RJ, Wang J, Peacey M, Moore NE, McInnes K, Tompkins DM. New alphacoronavirus in *Mystacina tuberculata* bats, New Zealand. Emerging Infectious Diseases. 2014; 20(4):697–700. https://doi.org/10.3201/eid2004.131441 PMID: 24656060

62. Woo PCY, Lau SKP, Huang Y, Yuen K-Y. Coronavirus diversity, phylogeny and interspecies jumping. Exp Biol Med. 2009; 234(10):1117–27. https://doi.org/10.3181/0903-MR-94.

63. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, et al. Bats are natural reservoirs of SARS-like coronaviruses. Science. 2005; 310(5748):676–9. https://doi.org/10.1126/science.1118391 PMID: 16195424

64. Huang Y, Dickerman AW, Piñeyro P, Li L, Fang L, Kiehne R, et al. Origin, evolution, and genotyping of emergent porcine epidemic diarrhea virus strains in the United States. mBio. 2013; 4(5):e00737–13. https://doi.org/10.1128/mBio.00737-13 PMID: 24129257

65. Corman VM, Baldwin HJ, Tateno AF, Zerbinati RM, Annan A, Owusu M, et al. Evidence for an ancestral association of human coronavirus 229E with bats. Journal of Virology. 2015; 89(23):11858–70. https://doi.org/10.1128/JVI.01755-15 PMID: 26378164

66. Lau SKP, Woo PCY, Li KSM, Huang Y, Tsoi H, Wong BHL, et al. Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. Proc Natl Acad Sci USA. 2005; 102(39):14040–5. https://doi.org/10.1073/pnas.0506735102 PMID: 16169905

67. Yip CW, Hon CC, Shi M, lam TT, Chow KY, Zeng F, et al. Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. Infect, Genet Evol. 2009; 9:1185–96. https://doi.org/10.1016/j.meegid.2009.09.015.

68. Wong S, Lau S, Woo P, Yuen KY. Bats as a continuing source of emerging infections in humans. Rev Med Virol. 2007; 17(2):67–91. https://doi.org/10.1002/rmv.520 PMID: 17042030

69. Wong ACP, Li X, Lau SKP, Woo PCY. Global epidemiology of bat coronaviruses. Viruses. 2019; 11 (174). https://doi.org/10.3390/v11020174.

70. Albery GF, Eskew EA, Ross N, Olival KJ. Predicting the global mammalian viral sharing network using phylogeography. Nature Communications. 2020; 11(2260). https://doi.org/10.1038/s41467-020-16153-4.

71. Osborne C, Cryan P, O'Shea TJ, Oko LM, Ndaluka C, Calisher CH, et al. Alphacoronaviruses in New World bats: prevalence, persistence, phylogeny, and potential for interaction with humans. PLoS ONE. 2011; 6(5):e19156. https://doi.org/10.1371/journal.pone.0019156 PMID: 21589915

72. Damas J, Hughes GM, Keough KC, Painter CA, Persky NS, Corbo M, et al. Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. bioRxiv. 2020. https://doi.org/10.1101/2020.04.16.045302.

73. Weller TJ, Cryan PM, O'Shea TJ. Broadening the focus of bat conservation and research in the USA for the 21st century. Endangered Species Research. 2009; 8:129–45. https://doi.org/10.3354/esr00149.

74. Misra V, Dumonceaux T, Dubois J, Willis C, Nadin-Davis S, Severini A, et al. Detection of polyoma and corona viruses in bats of Canada. J Gen Virol. 2009; 90:2015–22. https://doi.org/10.1099/vir.0.010694-0 PMID: 19357225

75. Donaldson EF, Haskew AN, Gates JE, Huynh J, Moore CJ, Frieman MB. Metagenomic analysis of the viromes of three North American bat species: viral diversity among different bat species that share a common habitat. Journal of Virology. 2010; 84(24):13004–18. https://doi.org/10.1128/JVI.01255-10 PMID: 20926577

76. Dominguez SR, O'Shea TJ, Oko LM, Holmes KV. Detection of group 1 coronaviruses in bats in North America. Emerging Infectious Diseases. 2007; 13(9):1295–300. https://doi.org/10.3201/eid1309.070491 PMID: 18252098

77. Yang L, Wu Z, Ren X, Yang F, He G, Zhang JX, et al. Novel SARS-like betacoronaviruses in bats, China, 2011. Emerging Infectious Diseases. 2013; 19(6):989–91. https://doi.org/10.3201/eid1906.121648 PMID: 23739658

78. Drexler JF, Gloza-Rausch F, Glende J, Corman VM, Muth D, Goettsche M, et al. Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences. Journal of Virology. 2010; 84(21):11336–49. https://doi.org/10.1128/JVI.00650-10 PMID: 20686038

79. Lecis R, Mucedda M, Pidinchedda E, Pittau M, Alberti A. Molecular identification of Betacoronavirus in bats from Sardinia (Italy): first detection and phylogeny. Virus Genes. 2019; 55(1):60–7. https://doi.org/10.1007/s11262-018-1614-8 PMID: 30426315

80. Teeling EC, Springer MS, Madsen O, Bates P, O'Brien SJ, Murphy WJ. A molecular phylogeny for bats illuminates biogeography and the fossil record. Science. 2005; 307:580–4. https://doi.org/10.1126/science.1105113 PMID: 15681385

81. Anthony SJ, Ojeda-Flores R, Rico-Chávez O, Navarrete-Macias I, Zambrana-Torrelio C, Rostal MK, et al. Coronaviruses in bats from Mexico. J Gen Virol. 2013; 94:1028–38. https://doi.org/10.1099/vir.0.049759-0 PMID: 23364191

82. Góes LGB, Campos ACA, de Carvalho C, Ambar G, Quieroz LH, Cruz-Neto AP, et al. Genetic diversity of bats coronaviruses in the Atlantic forest hotspot biome, Brazil. Infect, Genet Evol. 2016; 4:510–3. http://dx.doi.org/10.1016/j.meegid.2016.07.034.

83. Munster VJ, Adney DR, van Doremalen N, Brown VR, Miazgowicz KL, Milne-Price S, et al. Replication and shedding of MERS-CoV in Jamaican fruit bats (*Artibeus jamaicensis*). Scientific Reports. 2016; 6:21878. https://doi.org/10.1038/srep21878 PMID: 26899616

84. Hayman DTS, Fooks AR, Marston DA, Garcia-R JC. The global phylogeography of lyssaviruses—challenging the 'out of Africa' hypothesis. PLoS Negl Trop Dis. 2016; 10(12):e0005266. https://doi.org/10.1371/journal.pntd.0005266 PMID: 28036390

85. Tao Y, Tong S. Complete genome sequence of a severe acute respiratory syndrome-related coronavirus from Kenyan bats. Microbiology Resource Announcements. 2019; 8:e00548–19. https://doi.org/10.1128/MRA.00548-19 PMID: 31296683

86. Barbour RW, Davis WH. Bats of America. Lexington: The University Press of Kentucky; 1969. 286 p.

87. George DB, Webb CT, Farnsworth ML, O'Shea TJ, Bowen RA, Smith DL, et al. Host and viral ecology determine bat rabies seasonality and maintenance. Proc Natl Acad Sci USA. 2011; 108(25):10208–13. https://doi.org/10.1073/pnas.1010875108 PMID: 21646516

88. Davis AD, Morgan SM, Dupuis M, Poulliott CE, Jarvis JA, Franchini R, et al. Overwintering of rabies virus in silver haired bats (*Lasionycteris noctivagans*). PLoS ONE. 2016; 11(5):e0155542. https://doi.org/10.1371/journal.pone.0155542 PMID: 27195489

89. Subudhi S, Rapin N, Bollinger TK, Hill JE, Donaldson ME, Davy CM, et al. A persistently infecting coronavirus in hibernating *Myotis lucifugus*, the North American little brown bat. J Gen Virol. 2017; 98:2297–309. https://doi.org/10.1099/jgv.0.000898 PMID: 28840816

90. Hayman DTS, Cryan PM, Fricker PD, Dannemiller NG. Long-term video surveillance and automated analyses reveal arousal patterns in groups of hibernating bats. Methods in Ecology and Evolution. 2017; 8(12):1813–21. https://doi.org/10.1111/2041-210X.12823.

91. Speakman JR, Thomas DW. Physiological ecology and energetics of bats. In: Kunz TH, Fenton MB, editors. Bat ecology. Chicago: University of Chicago Press; 2003. p. 430–90.

92. Mollentze N, Streicker DG, Murcia PM, Hampson K, Biek R. Dynamics of viral index infections in novel hosts. bioRxiv. 2020. https://doi.org/10.1101/2020.04.09.033928.

93. Morimoto K, Patel M, Corisdeo S, Hooper DC, Fu ZF, Rupprecht CE, et al. Characterization of a unique variant of bat rabies virus responsible for newly emerging human cases in North America. Proceedings of the National Academy of Science. 1996; 93:5653–8. https://doi.org/10.1073/pnas.93.11.5653.

94. Epstein JH, Price JT. The significant but understudied impact of pathogen transmission from humans to animals. Mount Sinai Journal of Medicine. 2009; 76:448–55. https://doi.org/10.1002/msj.20140 PMID: 19787650

95. Constantine DG. Disease exchange between bats and researchers: problems and precautions. Aust Mammal. 1985; 8(325–329).

96. Sulkin SE, Allen R. Virus infections in bats. Monographs in Virology. 1974; 8:1–103. PMID: 4367453

97. Calisher CH, Childs JE, Field HE, Holmes KV, Schountz T. Bats: an important reservoir host of emerging viruses. Clinical Microbiology Reviews. 2006; 19(3):531–45. https://doi.org/10.1128/CMR.00017-06 PMID: 16847084

98. Luis AD, Hayman DTS, O'Shea TJ, Cryan PM, Gilbert AT, Pulliam JRC, et al. A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? Proceedings of the Royal Society B. 2013; 280(1756):20122753. https://doi.org/10.1098/rspb.2012.2753 PMID: 23378666

99. Zhang G, Cowled C, Shi Z, Huang Z, Bishop-Lilly KA, Fang X, et al. Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. Science. 2013; 339(6118):456–60. https://doi.org/10.1126/science.1230835 PMID: 23258410

100. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, et al. Dampened STING-dependent interferon activation in bats. Cell Host & Microbe. 2018; 23:1–5. https://doi.org/10.1016/j.chom.2018.01.006.

101. Ahn M, Anderson DE, Zhang Q, Tan CW, Lim BL, Luko K, et al. Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. Nature Microbiology. 2019. https://doi.org/10.1038/s41564-019-0371-3.

102. Zhou P, Tachedjian M, Wynne JW, Boyd V, Cui J, Smith I, et al. Contraction of the type I IFN locus and unusual constitutive expression of IFN-α in bats. Proc Natl Acad Sci USA. 2016; 113(10):2696–701. https://doi.org/10.1073/pnas.1518240113 PMID: 26903655

103. Banerjee A, Baker ML, Kulcsar K, Misra V, Plowright R, Mossman K. Novel insights into immune systems of bats. Frontiers in Immunology. 2020; 11(26). https://doi.org/10.3389/fimmu.2020.00026.

104. Mandl JN, Schneider C, Schneider DS, Baker ML. Going to bat(s) for studies of disease tolerance. Frontiers in Immunology. 2018; 9(2112). https://doi.org/10.3389/fimmu.2018.02112.

105. Subudhi S, Rapin N, Misra V. Immune system modulation and viral persistence in bats: understanding viral spillover. Viruses 2019 11(192). https://doi.org/10.3390/v11020192.

106. O'Shea TJ, Cryan PM, Cunningham AA, Fooks AR, Hayman DTS, Luis AD, et al. Bat flight and zoonotic viruses. Emerging Infectious Diseases. 2014; 20(5):741–5. https://doi.org/10.3201/eid2005.130539 PMID: 24750692

107. O'Shea TJ, Neubaum DJ, Neubaum MA, Cryan PM, Ellison LE, Stanley TR, et al. Bat ecology and public health surveillance for rabies in an urbanizing region of Colorado. Urban Ecosystems. 2011; 14:665–97. https://doi.org/10.1007/s11252-011-0182-7.

108. Salah Uddin Kahn M, Hossain J, Gurley ES, Nahar N, Sultana R, Luby SP. Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. EcoHealth. 2011; 7:517–25. https://doi.org/10.1007/s10393-010-0366-2.

109. Gilbert AT, Petersen BW, Recuenco S, Niezgoda M, Gómez J, Laguna-Torres VA, et al. Evidence of rabies virus exposure among humans in the Peruvian Amazon. The American Journal of Tropical Medicine and Hygiene. 2012; 87(2):206–15. https://doi.org/10.4269/ajtmh.2012.11-0689 PMID: 22855749

110. Kuzmin IV, Shi M, Orciari LA, Yager PA, Velasco-Villa A, Kuzmina NA, et al. Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001–2009. PLoS Pathog. 2012; 8(6). https://doi.org/10.1371/journal.ppat.1002786.

111. Messenger SL, Smith JS, Rupprecht CE. Emerging epidemiology of bat-associated cryptic cases of rabies in humans in the United States. Clin Infect Dis. 2002; 35(6):738–47. https://doi.org/10.1086/342387 PMID: 12203172

112. Moran D, Juliao P, Alvarez D, Lindblade KA, Ellison JA, Gilbert AT, et al. Knowledge, attitudes and practices regarding rabies and exposure to bats in two rural communities in Guatemala. BMC Research Notes. 2015; 8(1):955. https://doi.org/10.1186/s13104-014-0955-1.

113. Plowright RK, Eby P, Hudson PJ, Smith IL, Westcott D, Bryden WL, et al. Ecological dynamics of emerging bat virus spillover. Proceedings of the Royal Society B. 2015; 282:20142124. https://doi.org/10.1098/rspb.2014.2124 PMID: 25392474

114. Brook CE, Boots M, Chandran K, Dobson AP, Drosten C, Graham AL, et al. Accelerated viral dynamics in bat cell lines, with implications for zoonotic emergence. eLife. 2020; 9(e48401). https://doi.org/10.7554/eLife.48401.

115. Prescott J, Guito JC, Spengler JR, Arnold CE, Schuh AJ, Amman BR, et al. Rousette bat dendritic cells overcome Marburg virus-mediated antiviral responses by upregulation of interferon-related genes while downregulating proinflammatory disease mediators. mSphere. 2019; 4(6):e00728–19. https://doi.org/10.1128/mSphere.00728-19 PMID: 31801842

116. Schlottau K, Rissmann M, Graaf A, Schön J, Sehl J, Wylezich C, et al. Experimental transmission studies of SARS-CoV-2 in fruit bats, ferrets, pigs and chickens. The Lancet. 2020. https://dx.doi.org/10.2139/ssrn.3578792.

117. Denison MR, Graham RL, Donaldson EF, Eckerle LD, Baric RS. Coronaviruses: an RNA proofreading machine regulates replication fidelity and diversity. RNA Biology. 2011; 8(2):270–9. https://doi.org/10.4161/rna.8.2.15013 PMID: 21593585

118. Gorbalenya AE, Enjuanes L, Ziebuhr J, Snijder EJ. Nidovirales: evolving the largest RNA virus genome. Virus Research. 2006; 117:17–37. https://doi.org/10.1016/j.virusres.2006.01.017 PMID: 16503362

119. Menachery VD, Graham RL, Baric RS. Jumping species-a mechanism for coronavirus persistence and survival. Current Opinion in Virology. 2017; 23:1–7. https://doi.org/10.1016/j.coviro.2017.01.002 PMID: 28214731

120. Johnson CK, Hitchens PL, Pandit PS, Rushmore J, Evans TS, Young CCW, et al. Global shifts in mammalian population trends reveal key predictors of virus spillover risk. Proceedings of the Royal Society B. 2020; 287(20192736). https://doi.org/10.1098/rspb.2019.2736.

121. Murray KA, Daszak P. Human ecology in pathogenic landscapes: two hypotheses on how land use change drives viral emergence. Current Opinion in Virology. 2013; 3(1):79–83. https://doi.org/10.1016/j.coviro.2013.01.006 PMID: 23415415

122. Becker DJ, Czirják GÁ, Volokhov DV, Bentz AB, Carrera JE, Camus MS, et al. Livestock abundance predicts vampire bat demography, immune profiles and bacterial infection risk. Philosophical Transactions of the Royal Society B: Biological Sciences. 2018; 373(1745): 20170089. http://dx.doi.org/10.1098/rstb.2017.0089.

123. Wilkinson DA, Marshall JC, French NP, Hayman DTS. Habitat fragmentation, biodiversity loss and the risk of novel infectious disease emergence. Journal of the Royal Society Interface. 2018; 15 (20180403). http://dx.doi.org/10.1098/rsif.2018.0403.

124. Rulli MC, Santini M, Hayman DTS, D'Odorico P. The nexus between forest fragmentation in Africa and Ebola virus disease outbreaks. Scientific Reports. 2017; 7(41613). https://doi.org/10.1038/srep41613.

125. Sleeman JM, Richgels KLD, White CL, Stephen C. Integration of wildlife and environmental health into a One Health approach. Scientific and Technical Review of the Office International des Epizooties. 2019; 28(1):91–102. https://doi.org/10.20506/rst.38.1.2944.

126. Olival KJ. To cull, or not to cull, bat is the question. EcoHealth. 2015; 13(1):6–8. https://doi.org/10.1007/s10393-015-1075-7 PMID: 26631385

127. Amman BR, Luke Nyakarahuka, McElroy Anita K., Dodd Kimberly A., Sealy Tara K., Schuh Amy J., Shoemaker Trevor R., et al. Marburgvirus resurgence in Kitaka Mine bat population after extermination attempts, Uganda. Emerging Infectious Diseases. 2014; 20(10):1761–4. https://doi.org/10.3201/eid2010.140696 PMID: 25272104

128. Phelps KL, Hamel L, Alhmoud N, Ali S, Bilgin R, Sidamonidze K, et al. Bat research networks and viral surveillance: gaps and opportunities in western Asia. Viruses. 2019; 11(3):240. https://doi.org/10.3390/v11030240.

129. Peel AJ, Sargan DR, Baker KS, Hayman DTS, Barr JA, Crameri G, et al. Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. Nature Communications. 2013; 4(2770). https://doi.org/10.1038/ncomms3770.

130. Restif O, Hayman DTS, Pulliam JRC, Plowright RK, George DB, Luis AD, et al. Model-guided fieldwork: practical guidelines for multidisciplinary research on wildlife ecological and epidemiological dynamics. Ecol Lett. 2012; 15(10):1083–94. https://doi.org/10.1111/j.1461-0248.2012.01836.x PMID: 22809422

131. Wood JLN, Leach M, Waldman L, MacGregor H, Fooks AR, Jones KE, et al. A framework for the study of zoonotic disease emergence and its drivers: spillover of bat pathogens as a case study. Philosophical Transactions of the Royal Society B. 2012; 367:2881–92. https://doi.org/10.1098/rstb.2012.0228.

132. Plowright RK, Becker DJ, McCallum H, Manlove KR. Sampling to elucidate the dynamics of infections in reservoir hosts. Philosophical Transactions of the Royal Society B. 2019; 374:20180336. http://dx.doi.org/10.1098/rstb.2018.0336.

133. Kunz TH, Parsons S, editors. Ecological and behavioral methods for the study of bats. 2nd ed. Baltimore, MD: The Johns Hopkins University Press; 2009.

134. Amman BR, Schuh AJ, Towner JS. Ebola virus field sample collection. Methods in Molecular Biology. 2017; 1628:373–93. https://doi.org/10.1007/978-1-4939-7116-9_30 PMID: 28573636

135. Streicker DG, Winternitz JC, Satterfield DA, Condori-Condori RE, Broos A, Tello C, et al. Host–pathogen evolutionary signatures reveal dynamics and future invasions of vampire bat rabies. Proc Natl Acad Sci USA. 2016; 113(39):10926–31. https://doi.org/10.1073/pnas.1606587113 PMID: 27621441

136. Tan CW, Chia WN, Chen MI-C, Hu Z, Young BE, Tan Y-J, et al. A SARS-CoV-2 surrogate virus neutralization test (sVNT) based on antibody-mediated blockage of ACE2-spike (RBD) protein-protein interaction. Nature Research. In Review. https://doi.org/10.21203/rs.3.rs-24574/v1.

137. USGS. NWHC operations during the COVID-19 pandemic and information about coronaviruses in wildlife. USGS National Wildlife Health Center—Wildlife Health Bulletin. 2020;2020–03. Epub 1 April 2020.

138. IUCN. International Union for the Conservation of Nature statement on the COVID-19 pandemic. 2020.

139. FAO. Investigating the role of bats in emerging zoonoses: Balancing ecology, conservation and public health interests. Rome: Food and Agriculture Organisation of the United Nations.; 2011.

140. Runge MC, Grant EHC, Coleman JTH, Reichard JD, Gibbs SEJ, Cryan PM, et al. Assessing the risks posed by SARS-CoV-2 in and via North American bats—Decision framing and rapid risk assessment. US Geological Survey Open-File Report. 2020;2020–1060:43. https://doi.org/10.3133/ofr20201060.

141. Leung NHL, Chu DKW, Shiu EYC, Chan H, McDevitt JJ, Hau BJP, et al. Respiratory virus shedding in exhaled breath and efficacy of face masks. Nat Med. 2020. https://doi.org/10.1038/s41591-020-0843-2.

142. Institute of Medicine. Reusability of Facemasks During an Influenza Pandemic: Facing the Flu. Washington, DC: 2006.

143. Cui J, Eden J-S, Holmes EC, Wang LF. Adaptive evolution of bat dipeptidyl peptidase 4 (dpp4): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. Virology Journal. 2013; 10(304). https://doi.org/10.1186/1743-422X-10-304.

144. Letko M, Miazgowicz K, McMinn R, Seifert SN, Sola I, Enjuanes L, et al. Adaptive evolution of MERS-CoV to species variation in DPP4. Cell Reports. 2018; 24:1730–7. https://doi.org/10.1016/j.celrep.2018.07.045 PMID: 30110630

145. Luan J, Jin X, Lu Y, Zhang L. SARS-CoV-2 spike potein favors ACE2 from *Bovidae* and *Cricetidae*. J Med Virol. 2020. Epub 30 March 2020. https://doi.org/10.1002/jmv.25817.

146. Zhang H, Penninger JM, Li Y, Zhong N, Slutsky AS. Angiotensin-converting enzyme 2 (ACE2) as a SARS-CoV-2 receptor: molecular mechanisms and potential therapeutic target. Intensive Care Medicine. 2020; 46:586–90. https://doi.org/10.1007/s00134-020-05985-9 PMID: 32125455

147. Pieracci EG, Brown J.A., Bergman D.L., Gilbert A., Wallace R.M., Blanton J.D., Velasco-Villa A., Morgan C.N., Lindquist S. and Chipman R.B.,. Evaluation of species identification and rabies virus characterization among bat rabies cases in the United States. J Am Vet Med Assoc. 2020; 256(1):77–84. https://doi.org/10.2460/javma.256.1.77 PMID: 31841089

148. Dunnam JL, Yanagihara R, Johnson KM, Armien B, Batsaikhan N, Morgan L, et al. Biospecimen repositories and integrated databases as critical infrastructure for pathogen discovery and pathobiology research. PLoS Negl Trop Dis. 2018; 11(1):e0005133. https://doi.org/10.1371/journal.pntd.0005133.

149. Walters CL, Freeman R, Collen A, Dietz C, Fenton MB, Jones G, et al. A continental-scale tool for acoustic identification of European bats. Journal of Applied Ecology. 2012; 49(5):1064–74. https://doi.org/10.1111/j.1365-2664.2012.02182.x.

150. Drexler JF, Corman VM, Wegner T, Tateno AF, Zerbinati RM, Gloza-Rausch F, et al. Amplification of emerging viruses in a bat colony. Emerging Infectious Diseases. 2011; 17(3):449–56. https://doi.org/10.3201/eid1703.100526 PMID: 21392436

151. Walker FM, Williamson CHD, Sanchez DE, Sobek CJ, Chambers CL. Species from feces: order-wide identification of Chiroptera from guano and other non-invasive genetic samples. PLoS ONE. 2016; 11(9):e0162342. https://doi.org/10.1371/journal.pone.0162342 PMID: 27654850

152. Oyler-McCance SJ, Fike JA, Lukacs PM, Sparks DW, O'Shea TJ, Whitaker JO Jr. Genetic mark-recapture improves estimates of maternity colony size for Indiana bats. Journal of Fish and Wildlife Management. 2018; 9(1):25–35. https://doi.org/10.3996/122016-JFWM-093.

153. Hill AP, Davies A, Prince P, Snaddon JL, Doncaster CP, Rogers A. Leveraging conservation action with open-source hardware. Conservation Letters. 2019; 12(5):e12661. https://doi.org/10.1111/conl.12661.

154. Mac Aodha O, Gibb R, Barlow KE, Browning E, Firman M, Freeman R, et al. Bat detective—deep learning tools for bat acoustic signal detection. PLoS Comput Biol. 2018; 14(3):e1005995. https://doi.org/10.1371/journal.pcbi.1005995 PMID: 29518076

155. Mosher BA, Bernard RF, Lorch JM, Miller DAW, Richgels KLD, White CL, et al. Successful molecular detection studies require clear communication among diverse research partners. Front Ecol Environ. 2020; 18(1):43–51. https://doi.org/10.1002/fee.2141.

156. Carroll D, Daszak P, Wolfe ND, Gao GF, Morel CM, Morzaria S, et al. The Global Virome Project. Science. 2018; 359(6378):872–4. https://doi.org/10.1126/science.aap7463 PMID: 29472471

157. Plowright RK, Becker DJ, McCallum H, Manlove KR. Sampling to elucidate the dynamics of infections in reservoir hosts. Philosophical Transactions of the Royal Society B. 2019; 374:20180336. http://dx.doi.org/10.1098/rstb.2018.0336.