

Studying bats using a One Health lens: bridging the gap between bat virology and disease ecology

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ABSTRACT Accumulating data suggest that some bat species host emerging viruses that are highly pathogenic in humans and agricultural animals. Laboratory-based studies have highlighted important adaptations in bat immune systems that allow them to better tolerate viral infections compared to humans. Simultaneously, ecological studies have discovered critical extrinsic factors, such as nutritional stress, that correlate with virus shedding in wild-caught bats. Despite some progress in independently understanding the role of bats as reservoirs of emerging viruses, there remains a significant gap in the molecular understanding of factors that drive virus spillover from bats. Driven by a collective goal of bridging the gap between the fields of bat virology, immunology, and disease ecology, we hosted a satellite symposium at the 2024 American Society for Virology meeting. Bringing together virologists, immunologists, and disease ecologists, we discussed the intrinsic and extrinsic factors such as virus receptor engagement, adaptive immunity, and virus ecology that influence spillover from bat hosts. This article summarizes the topics discussed during the symposium and emphasizes the need for interdisciplinary collaborations and resource sharing.

KEYWORDS bats, virology, disease ecology, immunity, ASV 2024, satellite symposium

Across the mammalian order, bats and rodents are the most diverse (1), with the bat order (Chiroptera) consisting of more than 1,470 species in over 20 families (2). Bats are keystone species of global ecosystems and perform essential ecological roles such as pollination, seed dispersal, and pest control. However, some bat species are also recognized as reservoir hosts of zoonotic viruses. These viruses include filoviruses [e.g., Ebola virus (EBOV) and Marburg virus (MARV)], henipaviruses (e.g., Hendra virus and Nipah virus), coronaviruses (CoVs) (e.g., SARS-CoV-like, SARS-CoV-2-like, and MERS-CoV-like viruses), and lyssaviruses (e.g., rabies virus) (Fig. 1A). Interestingly, bat species infected with MARV and Nipah virus (3, 4), or other closely related viruses, experience low levels of observable pathology and do not show clinical signs of disease, although some exceptions exist. Tacaribe virus causes a fatal infection in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*) (5), rabies virus can cause lethal infection in experimentally infected common vampire bats (*Desmodus rotundus*) (6), and Lloviu virus (LLOV) is speculated to cause lethal disease in infected Schreibers' long-fingered bats (*Miniopterus schreibersii*) (7). Thus, understanding the molecular factors that enable bats to better tolerate viral infections (Fig. 1B), along with determining extrinsic ecological factors that influence virus shedding in bats (Fig. 1C), will inform strategies to prevent virus spillover and future consequential outbreaks and pandemics.

Holistically studying factors that influence virus infection and shedding in bats will be best accomplished using a One Health approach. One Health is a concept that recognizes and emphasizes the interconnectedness of animal, human, and environment health. The

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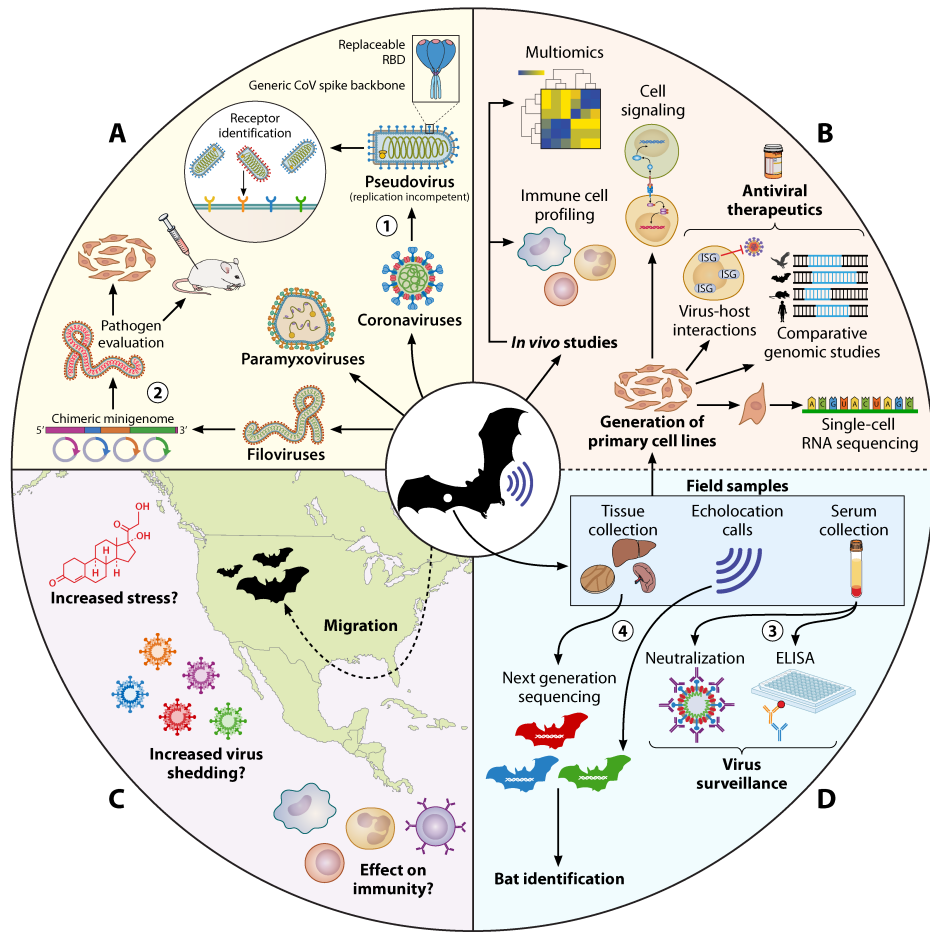


FIG 1 Studying bats using a One Health lens. (A) Some bat species are recognized as reservoir hosts of zoonotic viruses, including filoviruses, paramyxoviruses, and CoVs. The interaction of the CoV spike protein with cellular receptors is primarily mediated through the RBD. (1) Replication incompetent, vesicular stomatitis virus (VSV) pseudotyped viruses engineered with a generic CoV spike backbone and a replaceable RBD have been used to identify cellular receptors utilized by various sarbecoviruses and merbecoviruses. (2) Reverse genetics is an alternative approach to study the pathogenic potential of newly emergent viruses. Mühlberger et al. have developed this approach to generate infectious clones for LLOV, where a chimeric minigenome system complementing the missing genome ends of LLOV with the homologous regions from closely related filoviruses was used. LLOV isolates were used to evaluate virus replication in human and bat cell lines, along with the evaluation of pathogenicity in animal models. (B) Despite harboring viruses that are pathogenic in humans, infected bats do not show overt signs of disease. Research on bat immunity can help us understand the molecular factors that are involved in viral tolerance. One approach to studying bat immunity is the use of comparative genomic techniques and mechanistic characterization of cell signaling pathways and virus–host interactions. These approaches have demonstrated that some bat species have positively selected for genes within non-immune gene containing loci of their genomes to tolerate virus infections. The adaptation of new technologies to study bat immunology, such as scRNA-seq, has been critical for investigating immune cell populations without the need for cross-reactive reagents. (C) An important factor to prevent virus spillover from bats is understanding the intrinsic and extrinsic ecological factors that affect virus shedding in these mammals. Long-distance migration may function as a stressor for bats, as the energetic cost for undertaking such movements could weaken immune function. Migration occurs across bat families, and field studies that interrogate diverse metrics of glucocorticoid and immune activity across the annual cycle are needed to better understand how long-distance movements impact stress physiology, immune activity, and virus shedding in migratory bats. (D) Biosurveillance of bat populations is crucial for identifying and monitoring host species that may harbor pathogens. (3) Sero-surveillance, whether through detection of binding or neutralizing antibodies, can be a powerful tool for emerging zoonotic virus surveillance, circumventing challenges of detecting viral nucleic acid or virus isolates from sub-clinically infected wildlife hosts. Laing et al. have developed antigen-based multiplex serology assays to detect zoonotic viruses in bats, non-human animals, and humans (Continued on next page)

Fig 1 (Continued)

and are constructing sero-epidemiology models to elucidate spillover drivers. (4) Accurate identification of host species is essential for effective biosurveillance. DNA barcoding is a common molecular method for species identification, involving voucher specimen which can additionally be used for the generation of cell lines for *in vitro* work. The accuracy of DNA barcoding can be enhanced by ancillary ecological data, such as echolocation calls.

concept of One Health is particularly relevant for zoonotic pathogens, including viruses that originate in bats. For example, a recent study by Eby et al. (8) demonstrated that land-use change and climate change are altering bat residency, which is driving food shortages and clusters of virus spillover.

During the bat satellite symposium held at the 2024 American Society for Virology meeting, bat virologists, immunologists, and disease ecologists came together to share updates on their research, followed by a panel discussion on future directions for the fields. Here, we summarize key discussions from the satellite symposium (Table 1).

BATS AND THEIR VIRUSES

Since the emergence of SARS-CoV in 2002, MERS-CoV in 2012, and SARS-CoV-2 in 2019, thousands of related CoVs have been identified by genome sequencing of samples collected from diverse wildlife species and geographic locations (9–14). Unfortunately, due to the multitude of challenges with isolating viruses, many of the discovered viruses remain uncharacterized, leaving critical knowledge gaps about their potential to infect humans (15). To address this seemingly intractable problem, Letko et al. (15–18) developed a scalable approach to study CoV spike-mediated cell entry, which remains critical to understanding a virus' ability to jump cross-species molecular barriers (Fig. 1A). Since the interaction with cellular receptors is primarily mediated through the receptor-binding domain (RBD) within the CoV spike protein, a generic CoV spike backbone with a replaceable RBD was generated (17). Unlike the whole spike, the gene sequence for an RBD can be synthesized in 4–6 days for as little as US\$120. With this approachable and cost-effective tool, Letko et al. (17) tested almost a dozen RBDs for less than the cost of synthesizing one full CoV spike gene. In their proof-of-concept study with the *Sarbecovirus* subgenus, which includes SARS-CoV and SARS-CoV-2, they developed a panel of chimeric spikes with RBDs from 30 sarbecoviruses representative of every natural, unique RBD that has been published to date (17). This panel revealed large numbers of viruses with human cell compatibility—some with known receptors and some with completely unknown routes of entry. The approach was also rapid, allowing for the characterization

TABLE 1 2024 American Society for Virology bat satellite symposium program

Speaker	Session title
Elke Mühlberger	Assessing pathogenic potential and risk factors of newly discovered bat-derived filoviruses
Michael Letko Hannah Frank	Functional viromics of betacoronavirus entry Virus-driven selection and immunogenic evolution in bats
Eric Laing	Sero-surveillance as a tool to identify most probable bat hosts and population-level prevalence of zoonotic viruses
Kendra Phelps	Capturing ancillary ecological data during field biosurveillance – getting the most bat for your buck
Daniel Becker	Bat long-distance migration, immunity, and viral dynamics in the wild
Vincent Munster, Stephanie Seifert, Tony Schountz, and Arinjay Banerjee	Open discussion on where the bat virology and disease ecology fields are headed and how we may synergize our scientific efforts

of the SARS-CoV-2 receptor in the laboratory, without having to acquire a virus isolate or patient samples, just 12 days after the genome was published in January 2020 (17).

In their most recent work, Letko et al. (16) applied this concept of testing synthesized spike fragments from the *Merbecovirus* subgenus, which includes MERS-CoV. Merbecoviruses have been discovered in more bat species and over a wider geographic range compared to sarbecoviruses, potentially representing a greater zoonotic threat. The high sequence diversity among merbecoviruses is a significant challenge to the chimeric spike approach because there are few conserved amino acid stretches that flank the RBD in viruses of this subgenus. However, a pair of conserved glycine residues that delineated the exchangeable domain was identified, effectively allowing for the production and testing of 35 chimeric spikes representative of the published diversity for merbecoviruses (16). Screening of this panel against human and animal orthologues of known CoV receptors revealed known and new virus receptor interactions. *Merbecovirus* RBD clades were identified based on spike sequences and entry into Vero E6 and Huh-7.5 cell lines, resulting in four clades that can be applied to describe any merbecovirus. Clade 1 viruses use dipeptidyl peptidase IV (DPP4), clade 2 viruses use human and orthologous angiotensin-converting enzyme 2 (ACE2) in reservoir species, clade 3 viruses use only orthologous ACE2 in reservoir species, and several clade 4 RBDs use an unknown receptor to infect human cells (16). ACE2 was identified as the receptor for the entire HKU5 complex of merbecoviruses, which has been an elusive virus–host interaction in the field for almost 20 years (16). Importantly, this information provides a new framework for studying merbecoviruses and the evolution of their diverse receptor usage. This ongoing work will also identify merbecoviruses that carry the highest level of human cell compatibility, which is crucial for pandemic preparedness and broad-spectrum therapeutic design.

In addition to CoVs, some bat species are reservoir hosts of filoviruses, a group of negative-sense RNA viruses. Some members of the *Filoviridae* family, including EBOV, Sudan virus, and MARV, cause severe disease in humans with high case fatality rates (19). Due to recent advances in high-throughput sequencing technologies, genomic sequences of unknown filoviruses have been found in various vertebrate species, including bats, snakes, and fish (7, 20–25). This includes LLOV that was first detected in carcasses of Schreibers' bats in Spain in 2002 (7, 26), with recent isolation of the virus from Schreibers' bats in Hungary in 2022 (27, 28). The emergence of LLOV in Spain and Hungary correlated with unexplained increased mortality among Schreibers' bat colonies, including signs of respiratory distress, but it remains unclear if the fatalities were caused by LLOV infections (7, 29). The close relationship of LLOV to the highly pathogenic EBOV and MARV raises questions about its pathogenic potential for humans.

There are several challenges to studying the pathogenic potential of newly emergent viruses, such as LLOV. First, there might only be sequence information available but no isolates for infection studies. Second, while reverse genetics tools can be used to generate infectious clones based on published sequences, these sequences can be incomplete or erroneous. To address these issues, Mühlberger et al. (30) established a chimeric minigenome system for LLOV, where the missing genome ends for LLOV were complemented with the homologous regions from closely related filoviruses (Fig. 1A). Based on the minigenome results, recombinant infectious LLOV (rLLOV) clones were generated and used to evaluate pathogenicity (Fig. 1A). Studies with rLLOV also included assessment of host and cell tropism, replication efficiency, and innate immune signatures in critical target cells of filovirus infection, including Schreibers' long-fingered bat-derived kidney cells (SuBK12-08) and human-derived cell lines (31). Mühlberger et al. demonstrated that rLLOV can infect human cells, but it replicates slowly and fails to induce an inflammatory response in macrophages (31), in which the induction of an uncontrolled inflammatory response is a hallmark of fatal EBOV disease. These data were further supported by infection of interferon- α/β receptor knockout mice with authentic LLOV isolated from Schreibers' long-fingered bats in Hungary (27), which did not show signs of disease (32). Together, these data suggest that LLOV poses a low

risk to human health. Furthermore, these data suggest a tractable workflow to assess the pathogenic potential of newly emergent viruses and identify bottlenecks, such as missing or erroneous sequence information that hamper work on these viruses.

BAT IMMUNITY

Compared to humans and mice, understanding of bat immunology is limited in part because of species diversity and a lack of animal models, resources, and reagents (Table 2) (33). Much of the focus on bat immunology has been centered around the innate immune system (34–43). Additionally, a number of comparative genomic studies and functional characterizations have shown that bats have positively selected for genes within the non-immune loci of their genomes that are thought to help resist viruses (44–47). Although findings vary greatly between pathways and bat species, taken together, these studies suggest that bat immunity shares many of the fundamental signaling pathways that are found in humans, mice, and other mammals, with bat-specific adaptations that may aid in their resistance to or tolerance of viruses (48). However, even with these studies, much remains to be learnt about virus–host interactions in bats. Knowledge about the adaptive immune system of bats, especially B- and T-cell subsets and receptor repertoires is particularly limited when compared to knowledge of the bat innate immune system (48–50). Perhaps the biggest challenge in studying bat immunology is understanding the differences in immunity and pathogen response between the over 1,470 bat species. Bats vary widely in their ecology, geography, and viral flora (15, 51–53); all these factors have likely impacted the evolution of antiviral immunity. For example, straw-colored fruit bats (*Eidolon helvum*), found in the same geographic areas as EBOV, may have evolved to be refractory to EBOV infection (44). In addition, ACE2, DPP4, and other host proteins bound by CoVs are widely variable across bats (45). Due to constraints such as a paucity of captive colonies, traditional immunological reagents, and conservation concerns, most knowledge on bat immunity draws from a limited number of species (54).

Trends are changing as researchers adapt new technologies and existing tools to these non-model organisms (Fig. 1B). Next-generation sequencing techniques are often species-agnostic and have proven particularly useful for gaining insights into resistance of bats to infection. Transcriptomics has helped clarify bat responses to infections (61–64) and can be done from field samples (65). Long-read sequencing techniques have enabled the generation of reference bat genomes, along with insights into how gene loss and expansion may have impacted bat immunity and inflammation (66–69). Single-cell RNA sequencing (scRNA-seq) has been particularly useful for investigating immune cell populations without the need for antibodies specific to different cell types that are required in traditional flow cytometry analyses (61, 70, 71). Advances in the qualities of genomes and scRNA-seq have also yielded significant insights into bat B- and T-cell receptor repertoires (49), including the finding that bats in the Vespertilionidae family, the largest bat family, have two, independent, functional immunoglobulin heavy chain loci (72). Similarly, proteomics has provided additional insights into the bat immune phenotype in the wild and in response to viral infection (73–75). Additionally, as interest in bat immunology has increased, more institutions are establishing captive colonies for *in vivo* work, and researchers are creating primary cell cultures from a wider variety of species to test hypotheses *in vitro* (76, 77). These emerging methods will enhance knowledge not only of the fundamental components of bat immune systems, particularly the adaptive immune systems that are not well studied, but also of how conserved these mechanisms are across diverse bat species. Finally, a better understanding of how reservoir bat species better tolerate viral infections may one day pave the path for bat-inspired antiviral therapeutics for humans (54).

ECOLOGICAL PHYSIOLOGY

One of the central hypotheses to explain when and where bats actively shed viruses focuses on the role that physiological stress may play in disrupting tolerance of infection

TABLE 2 Resources available for bat-related research

Resource	Description
Bat1K Project	An initiative to generate and annotate genomes for all living bat species
Bat Conservation International	An organization committed to conserve the world's bats and their ecosystems through research
Bat Eco-Interactions	A platform for scientists to investigate bats and their role in our environment
Bat One Health	A forum for scientists interested in the connections between environmental change and health, where the goal is to understand pathogen emergence from bats
Batnames.org	A dynamic resource for the most up-to-date bat taxonomy, including number of bat species recognized
ChiroVox	The largest public library of bat calls currently available (55)
A Coalesced Mammal Database of Intrinsic and Extrinsic Traits	A comparative data set of ecological and life history traits among mammals (56)
Database of Bat-Associated Viruses	A comprehensive, up-to-date database of viruses detected in bats (57)
DarkCideS 1.0	A global database of bat caves and species, providing geographical location, ecological status, species traits, and parasites and hyperparasites (58)
EuroBaTrait 1.0	A species-level trait database of bats in Europe, including genetic composition, physiology, morphology, acoustic signature, roost type, diet, etc (59)
Global Union of Bat Diversity Networks	A community of bat researchers focused on enhancing research addressing bat diversification and sustainability
Global South Bats	A community of bat researchers in the Global South coming together to find solutions to common bat conservation challenges
The Global Virome in One Network data set	The largest open-access database on vertebrate–virus associations (60)
Latin American and Caribbean Bat Conservation Network	A network of 25 countries in Latin America and the Caribbean that promotes research and bat conservation
North American Society for Bat Research	A group that facilitates communication and collaboration among scientists, educators, and the public to promote the study and conservation of bats
WildTrax	An open data platform for environmental sensors, helping contribute data to the broader NABat program and international assessments
<i>Eptesicus fuscus</i> kidney cells (EFK3B)	Immortalized kidney cell line available through Kerafast (#CVCL_GZ34)
<i>R. aegyptiacus</i> fetal cells (R06E)	Immortalized fetal cell line available through BEI Resources (#NR-49168)
<i>Tadarida brasiliensis</i> lung cells (TbLu-1)	Primary lung-derived cell line available through ATCC (#CCL-88)

(78–80). Early work demonstrated links between stressors such as pregnancy and food scarcity with Hendra virus seropositivity in little red flying foxes (*Pteropus scapulatus*) (81), with more recent work showing food shortages interact with displacement of pteropid bats into novel habitats to predict seasonal pulses of Hendra virus shedding (82). Such patterns are likely explained by linkages among energetic demands, glucocorticoids, and immunity (Fig. 1C). Like any vertebrate, bats use glucocorticoids to increase energy mobilization and reallocation to meet immediate demands, but this can occur at the expense of physiological processes like the immune response (83, 84). However, the immune mechanisms linking stressors and viral shedding in bats remain poorly understood (85), and such work has focused predominantly on food scarcity with less attention to other energetic demands of bats in the wild (86, 87).

Long-distance migration—defined as the seasonal, two-way movement of individuals between reproductive and wintering grounds (88)—has been established as a stressor in other taxa such as birds (89), where the energetic costs of preparing for or undertaking such movements can weaken immune function and allow chronic infections to reactivate (90, 91) (Fig. 1C). In contrast, such impacts of migration for bats have not been adequately explored. Migration occurs across bat families but is most common in the Vespertilionidae and Molossidae, where certain species seasonally migrate between 100 and 2,000 kilometers (92, 93). To date, studies of bats have shown that the energy

demands of migration can equal that of reproduction (94), where switching from the pre-migratory to migratory season occurs alongside adjusted allocations in different arms of the immune response (95), and that some measures of immunity differ between migratory and non-migratory individuals (96, 97). Field studies that interrogate diverse metrics of glucocorticoid and immune activity at fine time intervals across the annual cycle are needed to better understand if these long-distance movements function as a stressor in bats. Such work could be further advanced by adopting multi-omics approaches relevant to bats (65, 73) and by ultimately assessing biomarkers of enrichment in relation to viral positivity (74). These studies could then guide experimental approaches, such as by using glucocorticoid levels seen during migration in the field to inform *in vitro* or *in vivo* challenge studies that test effects on immunity and virus replication (33, 85). Methods used to study flying animal movement, including wind tunnels and the Motus Wildlife Tracking System (98), could also be used to quantify how migratory timing and duration affect bat stress physiology, immune activity, and viral shedding.

Animal migration has long been recognized as an important factor in shaping infectious diseases (99), and long-distance migration of bats in particular has the potential to affect where and when human exposure to zoonotic viruses is likely (100, 101). There remains an important need to understand how these seasonal, energetically costly movements affect immunology and the downstream implications for viral transmission and spatial spread (102). Robustly assessing when and how migration influences how bats tolerate zoonotic viruses is critical to better understand virus–host interactions and improve the ability to predict transmission risks.

BIOSURVEILLANCE AND BAT SPECIES IDENTIFICATION

In recent years, Nipah virus, EBOV, and MARV have been detected outside their historic ranges (103–107). While zoonotic transmission events leading to disease outbreaks are rare, these events highlight the challenges of rapid diagnostic confirmation and outbreak mitigation. In practice, there is a limited window of opportunity during which viruses are actively shed from a host. Evidence indicates that certain species of bats, such as *Pteropus* spp. and *Eidolon* spp. are hosts of henipaviruses, and *Rousettus* spp. and *Mops* spp. are hosts of filoviruses (4, 25, 108–117). However, many virus–host relationships remain less-defined, such as the case of EBOV (118, 119), which weakens early warning detection and global health security. Detection of viremia or virus shedding from bats is rare, especially for filoviruses, which are seldom identified via molecular analysis of non-lethally collected blood and mucosal samples. This makes it difficult to detect active infections without knowing *a priori* when they occur. In contrast, wildlife hosts may have detectable antibodies against specific pathogens for months or years following productive infection. Thus, measurement of virus-specific immunoglobulin G (IgG) antibodies provides indirect detection of previous infections and thus an alternate form of zoonotic virus surveillance (Fig. 1D), which can be leveraged to infer viral transmission dynamics in wildlife populations (120). Though it is important to note that in experimentally MARV-infected Egyptian fruit bats (*Rousettus aegyptiacus*), virus-specific IgG antibodies detected by enzyme-linked immunosorbent assay or microneutralization rapidly waned with bats losing detectable neutralizing antibodies in roughly 3 months, thus highlighting potential differences between field- and lab-based studies and perhaps also between bat species and virus types (121).

Most statistical approaches to interpreting serosurveillance data are limited to single-antigen analysis, which limits understanding of bat immunology and virus circulation within bat populations and communities. Furthermore, expected and unexpected antibody cross-reactivity frequently confounds conclusions from both single and multiple-antigen assays. For example, orthoebolavirus-positive antisera are highly cross-reactive with protein antigens from heterotypic EBOVs (122). Antigenic cartography permits visualization and an understanding of the relationship among viruses based on antigenicity instead of phylogenetics (123). Antigenic maps have been widely used

within influenza and SARS-CoV-2 studies to aid in guiding effectiveness of ancestral infection and vaccine-induced immunity against novel variants and strains (124–127). The development of antigenic maps for other priority zoonotic viruses, such as filoviruses and henipaviruses, could aid in establishing expectations of cross-reactivities between genetically characterized viruses (128) and assist in the rapid identification of antigenically novel viruses that are currently genetically undiscovered. Access to and serological testing of confirmed post-infection or post-immunization sera would be a first step toward understanding the serogroup relationships.

Laing et al. (129–131) have developed antigen-based multiplex serology assays to detect and identify zoonotic viruses and develop models that highlight underlying seasonal patterns of virus circulation and drivers of virus release in bat host populations, which are being used in active biosurveillance projects. New approaches such as phage immunoprecipitation sequencing (PhIP-seq) can facilitate a complete antibody profile of an individual's virome (132–134). However, cross-assay comparisons of peptide-based PhIP-seq and antigen-based multiplex tests will be necessary to validate epitope selection and interpretation of sero-surveillance. Ultimately, serosurveillance is useful for building sero-epidemiological models to elucidate the drivers and processes of virus transmission, estimating force-of-infection for zoonotic viruses, and providing valuable prevalence data to develop spatiotemporal spillover distributions and interfaces with sufficient resolution to inform mitigation strategies.

Biosurveillance of bat populations is crucial for identifying and monitoring host species that may harbor pathogens (135). Despite its importance, several gaps hinder the effectiveness of current biosurveillance efforts, particularly validation of the taxonomic assignment of bat species from which diagnostic samples were collected for pathogen screening, limited integration of ancillary ecological data to improve species identification and to provide context for interpreting bat-pathogen dynamics, and a lack of data sharing on publicly accessible databases.

Accurate identification of host species is essential for effective biosurveillance. DNA barcoding is the most commonly used molecular method for confirmation of species identification (136); however, conclusions about species identification based solely on a few hundred base pairs may lack the reliability needed to accurately differentiate closely related species (137). An example of this are two sibling bat species, the lesser mouse-eared bat (*Myotis blythii*) and the greater mouse-eared bat (*Myotis myotis*) (138), which are thought to undergo cryptic hybridization in areas where they coexist, such as Türkiye (139). To enhance the accuracy of species identification in bat biosurveillance, it is essential to complement host DNA barcoding with ancillary ecological data that can be easily collected in a field setting, such as echolocation calls (Fig. 1D). Echolocation calls are species-specific for most bat species and can provide an additional layer of confirmation for species identification (51), which can be particularly useful in areas where barcoding may fall short. Echolocation data can provide valuable insights into bat behavior, such as foraging patterns, roosting habits, and migration routes (51), which is informative for identifying high-risk areas for pathogen transmission. Furthermore, echolocation detectors are more affordable and compact, with some like the Echo Meter Touch (Wildlife Acoustics) costing as little as US\$179 and function using most smartphones and tablets, making detectors easily obtainable for bat biosurveillance studies.

A voucher specimen is a preserved whole-body organism and/or associated samples that serve as a verifiable and permanent record of a species occurrence from a specific location and at a specific time (140). The goal is for each voucher specimen to be a holistic specimen, where frozen tissues, as well as biological and diagnostic samples are collected in addition to dried skin and skeleton to maximize the amount of information collected from a single euthanized individual (141). Holistic voucher specimens preserved during field sampling and deposited for long-term storage in curated collections represent a pre-existing tool that can aid in pandemic preparedness, in addition to the identification of host species when zoonotic spillover events occur

(Fig. 1D) (142). If voucher specimens are preserved during field sampling, the origin of zoonotic diseases and viral spillover events could be more accurately and easily assessed. For infectious disease research, this ability to verify the host species identity coupled with ancillary ecological data is incredibly important in determining how pathogens can infect humans and the possible routes of transmission (143).

While the collection of diagnostic samples for molecular screening of viruses is often the primary focus of wildlife biosurveillance, taking a One Health approach by collecting ancillary ecological data can better inform virus-host dynamics. Combining host barcoding with echolocation and other ecological data types, such as holistic voucher specimens, with molecular screening for potential pathogens will create a more robust and comprehensive One Health approach to better inform transmission risk and develop intervention strategies (Fig. 1D). Moreover, sharing ecological ancillary data such as depositing voucher specimens in curated collections, publishing echolocation recordings, or uploading species occurrence records (e.g., ~4,300 individual occurrence records from the Western Asia Bat Research project published on the Global Biodiversity Information Facility) in publicly accessible databases benefits the scientific community including wildlife biosurveillance studies (144, 145).

FUTURE DIRECTIONS FOR THE FIELD

The fields of virology, immunology, and disease ecology have made steady progress to better understand disease tolerance and virus transmission in bats. However, during the symposium, it was evident that the lack of interdisciplinary collaborations between the three fields has left critical knowledge gaps that can only be addressed by larger multi-disciplinary studies. For example, studies have identified stressors in wild-caught bats that correlate with virus shedding, but the lack of molecular studies impedes our understanding of how and when infected bats shed viruses. Furthermore, biosurveillance studies have identified multiple novel viruses in bat species, but the lack of mechanistic studies has left gaps in our understanding of viral pathogenesis, transmission, and disease tolerance in these bats and other susceptible species. Indeed, for a holistic understanding of disease tolerance and viral shedding in bats, there is a need to develop large interdisciplinary, collaborative studies, for which we need to develop resource-sharing platforms and funding mechanisms (Table 2).

There is also a need to study viruses and other microorganisms that are pathogenic in bats. Current research efforts are predominantly focused on bat-associated viruses with zoonotic potential. Thus, research on viruses that cause disease in bats, such as Tacaribe virus, is largely limited. In addition, non-viral microorganisms, such as bacteria, have not been extensively studied in bats, although microbiome profiling has been performed in some bat species, and some bacterial taxa (such as bartonellae and mycoplasmas) have been more robustly studied in bats (146–148). Furthermore, there is limited research on the ecological overlap of bat species and other animals. Studying the environment along with the animals and their microbes using a One Health lens will lead to a more holistic understanding of interactions that occur between various animal species, including bats and their microbes, and lead to the discovery of extrinsic factors that influence pathogen shedding in wildlife.

Bat research has been slow over the last two decades largely due to the lack of molecular tools and cross-reactive reagents that would enable researchers to comprehensively study immunity and infection in the over 1,470 bat species. Indeed, the need to develop a resource-sharing platform along with interdisciplinary funding opportunities was strongly highlighted during the closing panel discussion (Table 2). The concluding session once again highlighted the need to bridge the gap between field- and laboratory-based studies to better understand how bats tolerate virus infections, along with discovering and characterizing the intrinsic and extrinsic factors that lead to virus shedding in bats. In summary, the field of bat research is rapidly growing, and this area of research presents a unique opportunity for trainees to hone their skills in applying One Health solutions to zoonosis and wildlife conservation.

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REFERENCES

- Burgin CJ, Colella JP, Kahn PL, Upham NS. 2018. How many species of mammals are there? *J Mammal* 99:1–14. <https://doi.org/10.1093/jmammal/gyx147>
- Hao X, Lu Q, Zhao H. 2024. A molecular phylogeny for all 21 families within Chiroptera (bats). *Integr Zool* 19:989–998. <https://doi.org/10.1111/1749-4877.12772>
- Schuh AJ, Amman BR, Jones MEB, Sealy TK, Uebelhoefer LS, Spengler JR, Martin BE, Coleman-McCray JAD, Nichol ST, Towner JS. 2017. Modelling filovirus maintenance in nature by experimental transmission of Marburg virus between Egyptian roussette bats. *Nat Commun* 8:14446. <https://doi.org/10.1038/ncomms14446>
- Halpin K, Hyatt AD, Fogarty R, Middleton D, Bingham J, Epstein JH, Rahman SA, Hughes T, Smith C, Field HE, Daszak P, Henipavirus Ecology Research Group. 2011. Pteropid bats are confirmed as the reservoir hosts of henipaviruses: a comprehensive experimental study of virus transmission. *Am J Trop Med Hyg* 85:946–951. <https://doi.org/10.4269/ajtmh.2011.10-0567>
- Cogswell-Hawkinson A, Bowen R, James S, Gardiner D, Calisher CH, Adams R, Schountz T. 2012. Tacaribe virus causes fatal infection of an ostensible reservoir host, the Jamaican fruit bat. *J Virol* 86:5791–5799. <https://doi.org/10.1128/JVI.00201-12>
- Almeida MF, Martorelli LFA, Aires CC, Sallum PC, Durigon EL, Massad E. 2005. Experimental rabies infection in haematophagous bats *Desmodus rotundus*. *Epidemiol Infect* 133:523–527. <https://doi.org/10.1017/S0950268804003656>

7. Negredo A, Palacios G, Vázquez-Morón S, González F, Dopazo H, Molero F, Juste J, Quetglas J, Savji N, de la Cruz Martínez M, Herrera JE, Pizarro M, Hutchison SK, Echevarría JE, Lipkin WI, Tenorio A. 2011. Discovery of an ebolavirus-like filovirus in Europe. *PLoS Pathog* 7:e1002304. <https://doi.org/10.1371/journal.ppat.1002304>
8. Eby P, Peel AJ, Hoegh A, Madden W, Giles JR, Hudson PJ, Plowright RK. 2023. Pathogen spillover driven by rapid changes in bat ecology. *Nature* 613:340–344. <https://doi.org/10.1038/s41586-022-05506-2>
9. Cui J, Li F, Shi Z-L. 2019. Origin and evolution of pathogenic coronaviruses. *Nat Rev Microbiol* 17:181–192. <https://doi.org/10.1038/s41579-018-0118-9>
10. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, Daszak P, Eaton BT, Zhang S, Wang L-F. 2005. Bats are natural reservoirs of SARS-like coronaviruses. *Science* 310:676–679. <https://doi.org/10.1126/science.1118391>
11. Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Xie J-Z, Shen X-R, Zhang Y-Z, Wang N, Luo D-S, Zheng X-S, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L. 2017. Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLoS Pathog* 13:e1006698. <https://doi.org/10.1371/journal.ppat.1006698>
12. Li D, Gong X-Q, Xiao X, Han H-J, Yu H, Li Z-M, Yan L-N, Gu X-L, Duan S-H, Xue-jie Yu. 2021. MERS-related CoVs in hedgehogs from Hubei Province, China. *One Health* 13:100332. <https://doi.org/10.1016/j.onehlt.2021.100332>
13. Lam TT-Y, Jia N, Zhang Y-W, Shum MH-H, Jiang J-F, Zhu H-C, Tong Y-G, Shi Y-X, Ni X-B, Liao Y-S, et al. 2020. Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. *Nature* 583:282–285. <https://doi.org/10.1038/s41586-020-2169-0>
14. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Crameri G, Zhang S-Y, Wang L-F, Daszak P, Shi Z-L. 2013. Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature* 503:535–538. <https://doi.org/10.1038/nature12711>
15. Letko M, Seifert SN, Olival KJ, Plowright RK, Munster VJ. 2020. Bat-borne virus diversity, spillover and emergence. *Nat Rev Microbiol* 18:461–471. <https://doi.org/10.1038/s41579-020-0394-z>
16. Letko M. 2024. Functional assessment of cell entry and receptor use for merbecoviruses. *bioRxiv*. <https://doi.org/10.1101/2024.03.13.584892s>
17. Letko M, Marzi A, Munster V. 2020. Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. *Nat Microbiol* 5:562–569. <https://doi.org/10.1038/s41564-020-0688-y>
18. Seifert SN, Bai S, Fawcett S, Norton EB, Zvezdaryk KJ, Robinson J, Gunn B, Letko M. 2022. An ACE2-dependent Sarbecovirus in Russian bats is resistant to SARS-CoV-2 vaccines. *PLoS Pathog* 18:e1010828. <https://doi.org/10.1371/journal.ppat.1010828>
19. Rougeron V, Feldmann H, Grard G, Becker S, Leroy EM. 2015. Ebola and Marburg haemorrhagic fever. *J Clin Virol* 64:111–119. <https://doi.org/10.1016/j.jcv.2015.01.014>
20. Horie M. 2021. Identification of a novel filovirus in a common lancehead (*Bothrops atrox* (Linnaeus, 1758)). *J Vet Med Sci* 83:1485–1488. <https://doi.org/10.1292/jvms.21-0285>
21. Yang XL, Tan CW, Anderson DE, Jiang RD, Li B, Zhang W, Zhu Y, Lim XF, Zhou P, Liu XL, Guan W, Zhang L, Li SY, Zhang YZ, Wang LF, Shi ZL. 2019. Characterization of a filovirus (Mengla virus) from *Rousettus* bats in China. *Nat Microbiol* 4:390–395. <https://doi.org/10.1038/s41564-018-0328-y>
22. Shi M, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, Eden JS, Shen JJ, Liu L, Holmes EC, Zhang YZ. 2018. The evolutionary history of vertebrate RNA viruses. *Nature* 556:197–202. <https://doi.org/10.1038/s41586-018-0012-7>
23. Hierweger MM, Koch MC, Rupp M, Maes P, Di Paola N, Bruggmann R, Kuhn JH, Schmidt-Posthaus H, Seuberlich T. 2021. Novel filoviruses, hantavirus, and rhabdovirus in freshwater fish, Switzerland, 2017. *Emerg Infect Dis* 27:3082–3091. <https://doi.org/10.3201/eid2712.210491>
24. He B, Hu T, Yan X, Pa Y, Liu Y, Liu Y, Li N, Yu J, Zhang H, Liu Y, Chai J, Sun Y, Mi S, Liu Y, Yi L, Tu Z, Wang Y, Sun S, Feng Y, Zhang W, Zhao H, Duan B, Gong W, Zhang F, Tu C. 2024. Isolation, characterization, and circulation sphere of a filovirus in fruit bats. *Proc Natl Acad Sci U S A* 121:e2313789121. <https://doi.org/10.1073/pnas.2313789121>
25. Goldstein T, Anthony SJ, Gbakima A, Bird BH, Bangura J, Tremeau-Bravard A, Belaganahalli MN, Wells HL, Dhanota JK, Liang E, et al. 2018. The discovery of Bombali virus adds further support for bats as hosts of ebolaviruses. *Nat Microbiol* 3:1084–1089. <https://doi.org/10.1038/s41564-018-0227-2>
26. Ramírez de Arellano E, Sanchez-Lockhart M, Perteguer MJ, Bartlett M, Ortiz M, Campioli P, Hernández A, Gonzalez J, Garcia K, Ramos M, Jiménez-Clavero MÁ, Tenorio A, Sánchez-Seco MP, González F, Echevarría JE, Palacios G, Negredo A. 2019. First evidence of antibodies against Lloviu virus in Schreiber's bent-winged insectivorous bats demonstrate a wide circulation of the virus in Spain. *Viruses* 11:360. <https://doi.org/10.3390/v11040360>
27. Kemenesi G, Tóth GE, Mayora-Neto M, Scott S, Temperton N, Wright E, Mühlberger E, Hume AJ, Suder EL, Zana B, et al. 2022. Isolation of infectious Lloviu virus from Schreiber's bats in Hungary. *Nat Commun* 13:1706. <https://doi.org/10.1038/s41467-022-29298-1>
28. Tóth GE, Hume AJ, Suder EL, Zeghib S, Ábrahám Á, Lanszki Z, Varga Z, Tauber Z, Földes F, Zana B, Scaravelli D, Scicluna MT, Pereswiet-Soltan A, Görföi T, Terregino C, De Benedictis P, García-Dorival I, Alonso C, Jakab F, Mühlberger E, Leopardi S, Kemenesi G. 2023. Isolation and genome characterization of Lloviu virus from Italian Schreiber's bats. *Sci Rep* 13:11310. <https://doi.org/10.1038/s41598-023-38364-7>
29. Kemenesi G, Kurucz K, Dallos B, Zana B, Földes F, Boldogh S, Görföi T, Carroll MW, Jakab F. 2018. Re-emergence of Lloviu virus in *Miniopterus schreibersii* bats, Hungary, 2016. *Emerg Microbes Infect* 7:66. <https://doi.org/10.1038/s41426-018-0067-4>
30. Manhart WA, Pacheco JR, Hume AJ, Cressey TN, Deflub LR, Mühlberger E. 2018. A chimeric Lloviu virus minigenome system reveals that the bat-derived filovirus replicates more similarly to ebolaviruses than marburgviruses. *Cell Rep* 24:2573–2580. <https://doi.org/10.1016/j.celrep.2018.08.008>
31. Hume AJ, Heiden B, Olejnik J, Suder EL, Ross S, Scoon WA, Bullitt E, Ericsson M, White MR, Turcinovic J, Thao TTN, Hekman RM, Kaserman JE, Huang J, Alysandratos K-D, Toth GE, Jakab F, Kotton DN, Wilson AA, Emili A, Thiel V, Connor JH, Kemenesi G, Cifuentes D, Mühlberger E. 2022. Recombinant Lloviu virus as a tool to study viral replication and host responses. *PLoS Pathog* 18:e1010268. <https://doi.org/10.1371/journal.ppat.1010268>
32. Fletcher P, Feldmann F, Takada A, Crossland NA, Hume AJ, Albariño C, Kemenesi G, Feldmann H, Mühlberger E, Marzi A. 2023. Pathogenicity of Lloviu and Bombali viruses in type I interferon receptor knockout mice. *J Infect Dis* 228:S548–S553. <https://doi.org/10.1093/infdis/jiad226>
33. Banerjee A, Misra V, Schountz T, Baker ML. 2018. Tools to study pathogen-host interactions in bats. *Vir Res* 248:5–12. <https://doi.org/10.1016/j.virusres.2018.02.013>
34. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, Wang L-F, Shi Z-L, Zhou P. 2018. Dampened STING-dependent interferon activation in bats. *Cell Host Microbe* 23:297–301. <https://doi.org/10.1016/j.chom.2018.01.006>
35. Zhou P, Cowled C, Todd S, Crameri G, Virtue ER, Marsh GA, Klein R, Shi Z, Wang L-F, Baker ML. 2011. Type III IFNs in pteropid bats: differential expression patterns provide evidence for distinct roles in antiviral immunity. *J Immunol* 186:3138–3147. <https://doi.org/10.4049/jimmunol.1003115>
36. Cowled C, Baker ML, Zhou P, Tachedjian M, Wang L-F. 2012. Molecular characterisation of RIG-I-like helicases in the black flying fox, *Pteropus alecto*. *Dev Comp Immunol* 36:657–664. <https://doi.org/10.1016/j.dci.2011.11.008>
37. Zhou P, Cowled C, Mansell A, Monaghan P, Green D, Wu L, Shi Z, Wang L-F, Baker ML. 2014. IRF7 in the Australian black flying fox, *Pteropus alecto*: evidence for a unique expression pattern and functional conservation. *PLoS One* 9:e103875. <https://doi.org/10.1371/journal.pone.0103875>
38. Zhou P, Tachedjian M, Wynne JW, Boyd V, Cui J, Smith I, Cowled C, Ng JHJ, Mok L, Michalski WP, Mendenhall IH, Tachedjian G, Wang L-F, Baker ML. 2016. Contraction of the type I IFN locus and unusual constitutive expression of IFN- α in bats. *Proc Natl Acad Sci U S A* 113:2696–2701. <https://doi.org/10.1073/pnas.1518240113>
39. Ahn M, Anderson DE, Zhang Q, Tan CW, Lim BL, Luko K, Wen M, Chia WN, Mani S, Wang LC, Ng JHJ, Sobota RM, Dutertre C-A, Ginhoux F, Shi

- Z-L, Irving AT, Wang L-F. 2019. Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. *Nat Microbiol* 4:789–799. <https://doi.org/10.1038/s41564-019-0371-3>
40. Banerjee A, Falzarano D, Rapin N, Lew J, Misra V. 2019. Interferon regulatory factor 3-mediated signaling limits Middle-East respiratory syndrome (MERS) coronavirus propagation in cells from an insectivorous bat. *Viruses* 11:152. <https://doi.org/10.3390/v11020152>
 41. Banerjee A, Rapin N, Bollinger T, Misra V. 2017. Lack of inflammatory gene expression in bats: a unique role for a transcription repressor. *Sci Rep* 7:2232. <https://doi.org/10.1038/s41598-017-01513-w>
 42. Banerjee A, Rapin N, Miller M, Griebel P, Zhou Y, Munster V, Misra V. 2016. Generation and characterization of *Eptesicus fuscus* (Big brown bat) kidney cell lines immortalized using the *Myotis polyomavirus* large T-antigen. *J Virol Methods* 237:166–173. <https://doi.org/10.1016/j.jviromet.2016.09.008>
 43. Banerjee A, Subudhi S, Rapin N, Lew J, Jain R, Falzarano D, Misra V. 2020. Selection of viral variants during persistent infection of insectivorous bat cells with Middle East respiratory syndrome coronavirus. *Sci Rep* 10:7257. <https://doi.org/10.1038/s41598-020-64264-1>
 44. Ng M, Ndungo E, Kaczmarek ME, Herbert AS, Binger T, Kuehne AI, Jangra RK, Hawkins JA, Gifford RJ, Biswas R, Demogines A, James RM, Yu M, Brummelkamp TR, Drosten C, Wang L-F, Kuhn JH, Müller MA, Dye JM, Sawyer SL, Chandran K. 2015. Filovirus receptor NPC1 contributes to species-specific patterns of ebolavirus susceptibility in bats. *Elife* 4:e11785. <https://doi.org/10.7554/eLife.11785>
 45. Frank HK, Enard D, Boyd SD. 2022. Exceptional diversity and selection pressure on coronavirus host receptors in bats compared to other mammals. *Proc Biol Sci* 289:20220193. <https://doi.org/10.1098/rspb.2022.0193>
 46. Cui J, Eden J-S, Holmes EC, Wang L-F. 2013. Adaptive evolution of bat dipeptidyl peptidase 4 (dpp4): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. *Virol J* 10:1–5. <https://doi.org/10.1186/1743-422X-10-304>
 47. Scheben A, Mendivil Ramos O, Kramer M, Goodwin S, Oppenheim S, Becker DJ, Schatz MC, Simmons NB, Siepel A, McCombie WR. 2021. Long-read sequencing reveals rapid evolution of immunity- and cancer-related genes in bats. *bioRxiv*. <https://doi.org/10.1101/2020.09.09.290502:2020.09.09.290502>
 48. Banerjee A, Baker ML, Kulcsar K, Misra V, Plowright R, Mossman K. 2020. Novel insights into immune systems of bats. *Front Immunol* 11:26. <https://doi.org/10.3389/fimmu.2020.00026>
 49. Zhou H, Li J, Zhou D, Wu Y, Wang X, Zhou J, Ma Q, Yao X, Ma L. 2023. New insights into the germline genes and CDR3 repertoire of the TCRβ chain in *Chiroptera*. *Front Immunol* 14:1147859. <https://doi.org/10.3389/fimmu.2023.1147859>
 50. Lu D, Liu K, Zhang D, Yue C, Lu Q, Cheng H, Wang L, Chai Y, Qi J, Wang L-F, Gao GF, Liu WJ. 2019. Peptide presentation by bat MHC class I provides new insight into the antiviral immunity of bats. *PLoS Biol* 17:e3000436. <https://doi.org/10.1371/journal.pbio.3000436>
 51. Kunz TH, Fenton MB. 2005. *Bat ecology*. University of Chicago Press.
 52. Luis AD, Hayman DTS, O'Shea TJ, Cryan PM, Gilbert AT, Pulliam JRC, Mills JN, Timonin ME, Willis CKR, Cunningham AA, Fooks AR, Rupprecht CE, Wood JLN, Webb CT. 2013. A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? *Proc Biol Sci* 280:20122753. <https://doi.org/10.1098/rspb.2012.2753>
 53. Luis AD, O'Shea TJ, Hayman DTS, Wood JLN, Cunningham AA, Gilbert AT, Mills JN, Webb CT. 2015. Network analysis of host–virus communities in bats and rodents reveals determinants of cross-species transmission. *Ecol Lett* 18:1153–1162. <https://doi.org/10.1111/ele.12491>
 54. Baid K, Irving AT, Jouvenet N, Banerjee A. 2024. The translational potential of studying bat immunity. *Trends Immunol* 45:188–197. <https://doi.org/10.1016/j.it.2024.01.007>
 55. Görföl T, Huang JC-C, Csorba G, Győrössy D, Estók P, Kingston T, Szabadi KL, McArthur E, Senawi J, Furey NM, et al. 2022. ChiroVox: a public library of bat calls. *PeerJ* 10:e12445. <https://doi.org/10.7717/peerj.12445>
 56. Soria CD, Pacifici M, Di Marco M, Stephen SM, Rondinini C. 2021. COMBINE: a coalesced mammal database of intrinsic and extrinsic traits. *Ecology* 102:e03344. <https://doi.org/10.1002/ecy.3344>
 57. Chen L, Liu B, Yang J, Jin Q. 2014. DBatVir: the database of bat-associated viruses. *Database (Oxf)* 2014:bau021. <https://doi.org/10.1093/database/bau021>
 58. Tanalgo KC, Tabora JAG, de Oliveira HFM, Haelewaters D, Beranek CT, Otálora-Ardila A, Bernard E, Gonçalves F, Eriksson A, Donnelly M, et al. 2022. DarkCideS 1.0, a global database for bats in karsts and caves. *Sci Data* 9:155. <https://doi.org/10.1038/s41597-022-01234-4>
 59. Froidevaux JSP, Toshkova N, Barbaro L, Benítez-López A, Kerbiriou C, Le Viol I, Pacifici M, Santini L, Stawski C, Russo D, et al. 2023. A species-level trait dataset of bats in Europe and beyond. *Sci Data* 10:253. <https://doi.org/10.1038/s41597-023-02157-4>
 60. Carlson CJ, Gibb RJ, Albery GF, Brierley L, Connor RP, Dallas TA, Eskew EA, Fagre AC, Farrell MJ, Frank HK, Muylaert RL, Poisot T, Rasmussen AL, Ryan SJ, Seifert SN. 2022. The global virome in one network (VIRION): an atlas of vertebrate-virus associations. *mBio* 13:e0298521. <https://doi.org/10.1128/mbio.02985-21>
 61. Gamage AM, Chan WOY, Zhu F, Lim YT, Long S, Ahn M, Tan CW, Hiang Foo RJ, Sia WR, Lim XF, He H, Zhai W, Anderson DE, Sobota RM, Dutertre C-A, Wang L-F. 2022. Single-cell transcriptome analysis of the *in vivo* response to viral infection in the cave nectar bat *Eonycteris spelaea*. *Immunity* 55:2187–2205. <https://doi.org/10.1016/j.immuni.2022.10.008>
 62. Irving AT, Zhang Q, Kong P-S, Luko K, Rozario P, Wen M, Zhu F, Zhou P, Ng JHJ, Sobota RM, Wang L-F. 2020. Interferon regulatory factors IRF1 and IRF7 directly regulate gene expression in bats in response to viral infection. *Cell Rep* 33:108345. <https://doi.org/10.1016/j.celrep.2020.108345>
 63. Gerrard DL, Hawkinson A, Sherman T, Modahl CM, Hume G, Campbell CL, Schountz T, Fietze S. 2017. Transcriptomic signatures of Tacaribe virus-infected Jamaican fruit bats. *mSphere* 2:e00245-17. <https://doi.org/10.1128/mSphere.00245-17>
 64. Kessler S, Burke B, Andrieux G, Schinköthe J, Hamberger L, Kacza J, Zhan S, Reasoner C, Dutt TS, Kaukab Osman M, Henao-Tamayo M, Staniek J, Villena Ossa JF, Frank DT, Ma W, Ulrich R, Cathomen T, Boerries M, Rizzi M, Beer M, Schwemmler M, Reuther P, Schountz T, Ciminski K. 2024. Deciphering bat influenza H18N11 infection dynamics in male Jamaican fruit bats on a single-cell level. *Nat Commun* 15:4500. <https://doi.org/10.1038/s41467-024-48934-6>
 65. Huang Z, Whelan CV, Foley NM, Jebb D, Touzalin F, Petit EJ, Puechmaillie SJ, Teeling EC. 2019. Longitudinal comparative transcriptomics reveals unique mechanisms underlying extended healthspan in bats. *Nat Ecol Evol* 3:1110–1120. <https://doi.org/10.1038/s41559-019-0913-3>
 66. Moreno Santillán DD, Lama TM, Gutierrez Guerrero YT, Brown AM, Donat P, Zhao H, Rossiter SJ, Yohe LR, Potter JH, Teeling EC, Vernes SC, Davies KTJ, Myers E, Hughes GM, Huang Z, Hoffmann F, Corthals AP, Ray DA, Dávalos LM. 2021. Large-scale genome sampling reveals unique immunity and metabolic adaptations in bats. *Mol Ecol* 30:6449–6467. <https://doi.org/10.1111/mec.16027>
 67. Jebb D, Huang Z, Pippel M, Hughes GM, Lavrichenko K, Devanna P, Winkler S, Jermini LS, Skirmuntt EC, Katzourakis A, et al. 2020. Six reference-quality genomes reveal evolution of bat adaptations. *Nature* 583:578–584. <https://doi.org/10.1038/s41586-020-2486-3>
 68. Ahn M, Cui J, Irving AT, Wang L-F. 2016. Unique loss of the PYHIN gene family in bats amongst mammals: implications for inflammasome sensing. *Sci Rep* 6:21722. <https://doi.org/10.1038/srep21722>
 69. Morales A, Dong Y, Brown T, Baid K, Kontopoulos D, Gonzalez V, Huang Z, Ahmed A, Hilgers L, Winkler S, et al. 2023. Reference-quality bat genomes illuminate adaptations to viral tolerance and disease resistance. *Res Square*. <https://doi.org/10.21203/rs.3.rs-2557682/v1>
 70. Aso H, Ito J, Ozaki H, Kashima Y, Suzuki Y, Koyanagi Y, Sato K. 2022. Single-cell transcriptome analysis illuminating the characteristics of species-specific innate immune responses against viral infections. *Gigascience* 12:giad086. <https://doi.org/10.1093/gigascience/giad086>
 71. Levinger R, Tussia-Cohen D, Friedman S, Lender Y, Nissan Y, Fraimovitch E, Gavriel Y, Tearle J, Kolodziejczyk AA, Gomes T, Kunowska N, Weinberg M, Donati G, James KR, Yovel Y, Hagai T. 2023. Spatial and single-cell transcriptomics illuminate bat immunity and barrier tissue evolution. *bioRxiv*. <https://doi.org/10.1101/2023.10.30.564705>
 72. Pursell T, Reers A, Mikelov A, Kotagiri P, Ellison JA, Hutson CL, Boyd SD, Frank HK. 2024. Genetically and functionally distinct immunoglobulin heavy chain locus duplication in bats. *bioRxiv*. <https://doi.org/10.1101/2024.08.09.606892>

73. Neely BA, Janech MG, Fenton MB, Simmons NB, Bland AM, Becker DJ. 2021. Surveying the vampire bat (*Desmodus rotundus*) serum proteome: a resource for identifying immunological proteins and detecting pathogens. *J Proteome Res* 20:2547–2559. <https://doi.org/10.1021/acs.jproteome.0c00995>
74. Becker DJ, Lei G-S, Janech MG, Bland AM, Fenton MB, Simmons NB, Relich RF, Neely BA. 2022. Serum proteomics identifies immune pathways and candidate biomarkers of coronavirus infection in wild vampire bats. *Front Virol* 2:862961. <https://doi.org/10.3389/fviro.2022.862961>
75. Hashimi M, Sebrell TA, Hedges JF, Snyder D, Lyon KN, Byrum SD, Mackintosh SG, Crowley D, Cherne MD, Skwarchuk D, Robison A, Sidar B, Kunze A, Loveday EK, Taylor MP, Chang CB, Wilking JN, Walk ST, Schountz T, Jutila MA, Bimczok D. 2023. Antiviral responses in a Jamaican fruit bat intestinal organoid model of SARS-CoV-2 infection. *Nat Commun* 14:6882. <https://doi.org/10.1038/s41467-023-42610-x>
76. Zhou P, Chionh YT, Irac SE, Ahn M, Jia Ng JH, Fossum E, Bogen B, Ginhoux F, Irving AT, Dutertre C-A, Wang L-F. 2016. Unlocking bat immunology: establishment of *Pteropus alecto* bone marrow-derived dendritic cells and macrophages. *Sci Rep* 6:38597. <https://doi.org/10.1038/srep38597>
77. Harazim M, Perrot J, Varet H, Bourhy H, Lannoy J, Pikula J, Seidlová V, Dacheux L, Martinková N. 2023. Transcriptomic responses of bat cells to European bat lyssavirus 1 infection under conditions simulating euthermia and hibernation. *BMC Immunol* 24:7. <https://doi.org/10.1186/s12865-023-00542-7>
78. Plowright RK, Peel AJ, Streicker DG, Gilbert AT, McCallum H, Wood J, Baker ML, Restif O. 2016. Transmission or within-host dynamics driving pulses of zoonotic viruses in reservoir–host populations. *PLoS Negl Trop Dis* 10:e0004796. <https://doi.org/10.1371/journal.pntd.0004796>
79. Subudhi S, Rapin N, Misra V. 2019. Immune system modulation and viral persistence in bats: understanding viral spillover. *Viruses* 11:192. <https://doi.org/10.3390/v11020192>
80. Gonzalez V, Banerjee A. 2022. Molecular, ecological, and behavioral drivers of the bat-virus relationship. *iScience* 25:104779. <https://doi.org/10.1016/j.isci.2022.104779>
81. Plowright RK, Field HE, Smith C, Divljan A, Palmer C, Tabor G, Daszak P, Foley JE. 2008. Reproduction and nutritional stress are risk factors for Hendra virus infection in little red flying foxes (*Pteropus scapulatus*). *Proc Biol Sci* 275:861–869. <https://doi.org/10.1098/rspb.2007.1260>
82. Becker DJ, Eby P, Madden W, Peel AJ, Plowright RK. 2023. Ecological conditions predict the intensity of Hendra virus excretion over space and time from bat reservoir hosts. *Ecol Lett* 26:23–36. <https://doi.org/10.1111/ele.14007>
83. Reeder DM, Kosteczko NS, Kunz TH, Widmaier EP. 2004. Changes in baseline and stress-induced glucocorticoid levels during the active period in free-ranging male and female little brown myotis, *Myotis lucifugus* (Chiroptera: Vespertilionidae). *Gen Comp Endocrinol* 136:260–269. <https://doi.org/10.1016/j.ygcen.2003.12.020>
84. Michael Romero L. 2002. Seasonal changes in plasma glucocorticoid concentrations in free-living vertebrates. *Gen Comp Endocrinol* 128:1–24. [https://doi.org/10.1016/S0016-6480\(02\)00064-3](https://doi.org/10.1016/S0016-6480(02)00064-3)
85. Becker DJ, Banerjee A. 2023. Coupling field and laboratory studies of immunity and infection in zoonotic hosts. *Lancet Microbe* 4:e285–e287. [https://doi.org/10.1016/S2666-5247\(23\)00032-0](https://doi.org/10.1016/S2666-5247(23)00032-0)
86. Gerow CM, Rapin N, Voordouw MJ, Elliot M, Misra V, Subudhi S. 2019. Arousal from hibernation and reactivation of *Eptesicus fuscus* gammaherpesvirus (EhV) in big brown bats. *Transbound Emerg Dis* 66:1054–1062. <https://doi.org/10.1111/tbed.13102>
87. Sandoval-Herrera NI, Mastromonaco GF, Becker DJ, Simmons NB, Welch KC Jr. 2021. Inter- and intra-specific variation in hair cortisol concentrations of Neotropical bats. *Conserv Physiol* 9:coab053. <https://doi.org/10.1093/conphys/coab053>
88. Dingle H. 2014. Migration: the biology of life on the move. Oxford University Press, USA.
89. Wikelski M, Tarlow EM, Raim A, Diehl RH, Larkin RP, Visser GH. 2003. Costs of migration in free-flying songbirds. *Nature* 423:704–704. <https://doi.org/10.1038/423704a>
90. Owen JC, Moore FR. 2008. Swainson's thrushes in migratory disposition exhibit reduced immune function. *J Ethol* 26:383–388. <https://doi.org/10.1007/s10164-008-0092-1>
91. Gylfe Å, Bergström S, Lundström J, Olsen B. 2000. Reactivation of *Borrelia* infection in birds. *Nature* 403:724–725. <https://doi.org/10.1038/35001663>
92. Fleming TH, Eby P, Kunz T, Fenton M. 2003. Ecology of bat migration, p 164–165. In *Bat ecology*. Vol. 156.
93. Bisson I-A, Safi K, Holland RA. 2009. Evidence for repeated independent evolution of migration in the largest family of bats. *PLoS One* 4:e7504. <https://doi.org/10.1371/journal.pone.0007504>
94. Sommers AS, Rogers EJ, McGuire LP. 2019. Migration and reproduction are associated with similar degrees of phenotypic flexibility in an insectivorous bat. *Oecologia* 190:747–755. <https://doi.org/10.1007/s00442-019-04449-2>
95. Voigt CC, Fritze M, Lindecke O, Costantini D, Pētersons G, Czirják GÁ. 2020. The immune response of bats differs between pre-migration and migration seasons. *Sci Rep* 10:17384. <https://doi.org/10.1038/s41598-020-74473-3>
96. Rogers EJ, McGuire L, Longstaffe FJ, Clerc J, Kunkel E, Fraser E. 2022. Relating wing morphology and immune function to patterns of partial and differential bat migration using stable isotopes. *J Anim Ecol* 91:858–869. <https://doi.org/10.1111/1365-2656.13681>
97. Rivera-Ruiz DA, Flores-Martínez JJ, Rosales C, Herrera Montalvo LG. 2023. Constitutive innate immunity of migrant and resident long-nosed bats (*Leptonycteris yerbabuena*) in the drylands of Mexico. *Diversity (Basel)* 15:530. <https://doi.org/10.3390/d15040530>
98. Taylor PD, Crewe TL, Mackenzie SA, Lepage D, Aubry Y, Crysler Z, Finney G, Francis CM, Guglielmo CG, Hamilton DJ, Holberton RL, Loring PH, Mitchell GW, Norris DR, Paquet J, Ronconi RA, Smetzer JR, Smith PA, Welch LJ, Woodworth BK. 2017. The Motus wildlife tracking system: a collaborative research network to enhance the understanding of wildlife movement. *Avian Conserv Ecol* 12. <https://doi.org/10.5751/ACE-00953-120108>
99. Altizer S, Bartel R, Han BA. 2011. Animal migration and infectious disease risk. *Science* 331:296–302. <https://doi.org/10.1126/science.1194694>
100. O'Shea TJ, Cryan PM, Cunningham AA, Fooks AR, Hayman DTS, Luis AD, Peel AJ, Plowright RK, Wood JLN. 2014. Bat flight and zoonotic viruses. *Emerg Infect Dis* 20:741–745. <https://doi.org/10.3201/eid2005.130539>
101. Peel AJ, Sargan DR, Baker KS, Hayman DTS, Barr JA, Cramer G, Suu-Ire R, Broder CC, Lembo T, Wang L-F, Fooks AR, Rossiter SJ, Wood JLN, Cunningham AA. 2013. Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. *Nat Commun* 4:2770. <https://doi.org/10.1038/ncomms3770>
102. Becker DJ, Ketterson ED, Hall RJ. 2020. Reactivation of latent infections with migration shapes population-level disease dynamics. *Proc Biol Sci* 287:20201829. <https://doi.org/10.1098/rspb.2020.1829>
103. Baden LR, Kanopathipillai R, Campion EW, Morrissey S, Rubin EJ, Drazen JM. 2014. Ebola—an ongoing crisis. *N Engl J Med* 371:1458–1459. <https://doi.org/10.1056/NEJMe1411378>
104. Arunkumar G, Chandni R, Mourya DT, Singh SK, Sadanandan R, Sudan P, Bhargava B, Gangakhedkar RR, Gupta N, Bhargava B. 2019. Outbreak investigation of Nipah virus disease in Kerala, India, 2018. *J Infect Dis* 219:1867–1878. <https://doi.org/10.1093/infdis/jiy612>
105. Yadav PD, Shete AM, Kumar GA, Sarkale P, Sahay RR, Radhakrishnan C, Lakra R, Pardeshi P, Gupta N, Gangakhedkar RR, Rajendran VR, Sadanandan R, Mourya DT. 2019. Nipah virus sequences from humans and bats during Nipah outbreak, Kerala, India, 2018. *Emerg Infect Dis* 25:1003–1006. <https://doi.org/10.3201/eid2505.181076>
106. Bonney JK, Adu B, Sanders T, Pratt D, Adams P, Asante IA, Bonney EY, Agbodji B, Kumordjie S, Faye M, et al. 2023. Marburg virus disease in Ghana. *N Engl J Med* 388:2393–2394. <https://doi.org/10.1056/NEJMc2300867>
107. Fontana L, Ondo Avomo CO, Ngomo Mikue LE, Fuga Eyemam DÑ, Nguere MA, Mometolo IE, Bibang Nzang RN, Nguema Maye DM, Giuliani R, Jacqueroiz F, Lang H-J, Kojan R, Chaillon A, Ngai S, le Polain de Waroux O, Silenzi A, Di Marco M, Negrón ME, Klena JD, Choi MJ, Mayer O, Scholte FEM, Welch SR, Zielinski-Gutierrez E, Diaz J. 2024. Case series of patients with Marburg virus disease, equatorial Guinea, 2023. *N Engl J Med* 391:283–285. <https://doi.org/10.1056/NEJMc2313181>
108. Halpin K, Young PL, Field HE, Mackenzie JS. 2000. Isolation of Hendra virus from pteropid bats: a natural reservoir of Hendra virus. *J Gen Virol* 81:1927–1932. <https://doi.org/10.1099/0022-1317-81-8-1927>

109. Lebarbenchon C, Goodman SM, Hoarau AOG, Le Minter G, Dos Santos A, Schoeman MC, Léculier C, Raoul H, Gudo ES, Mavingui P. 2022. Bombali ebolavirus in *Mops condylurus* bats (Molossidae), Mozambique. *Emerg Infect Dis* 28:2583–2585. <https://doi.org/10.3201/eid2812.220853>
110. Kareinen L, Ogola J, Kivistö I, Smura T, Aaltonen K, Jääskeläinen AJ, Kibiwoot S, Masika MM, Nyaga P, Mwaengo D, Anzala O, Vapalahti O, Webala PW, Forbes KM, Sironen T. 2020. Range expansion of Bombali virus in *Mops condylurus* bats, Kenya, 2019. *Emerg Infect Dis* 26:3007–3010. <https://doi.org/10.3201/eid2612.202925>
111. Forbes KM, Webala PW, Jääskeläinen AJ, Abdurahman S, Ogola J, Masika MM, Kivistö I, Alburkat H, Plysunin I, Levanov L, Korhonen EM, Huhtamo E, Mwaengo D, Smura T, Mirazimi A, Anzala O, Vapalahti O, Sironen T. 2019. Bombali virus in *Mops condylurus* bat, Kenya. *Emerg Infect Dis* 25:955–957. <https://doi.org/10.3201/eid2505.181666>
112. Karan LS, Makenov MT, Korneev MG, Sacko N, Boumbaly S, Yakovlev SA, Kourouma K, Bayandin RB, Gladysheva AV, Shipovalov AV, Yurganova IA, Grigorieva YE, Fedorova MV, Scherbakova SA, Kuttyrev VV, Agafonov AP, Maksyutov RA, Shipulin GA, Maleev VV, Boiro M, Akimkin VG, Popova AY. 2019. Bombali virus in *Mops condylurus* bats, Guinea. *Emerg Infect Dis* 25:1774–1775. <https://doi.org/10.3201/eid2509.190581>
113. Pawęska JT, Jansen van Vuren P, Kemp A, Storm N, Grobbelaar AA, Wiley MR, Palacios G, Markotter W. 2018. Marburg virus infection in Egyptian rousette bats, South Africa, 2013–2014. *Emerg Infect Dis* 24:1134–1137. <https://doi.org/10.3201/eid2406.172165>
114. Amman BR, Jones MEB, Sealy TK, Uebelhoefer LS, Schuh AJ, Bird BH, Coleman-McCray JD, Martin BE, Nichol ST, Towner JS. 2015. Oral shedding of Marburg virus in experimentally infected Egyptian fruit bats (*Rousettus aegyptiacus*). *J Wildl Dis* 51:113–124. <https://doi.org/10.7589/2014-08-198>
115. Towner JS, Amman BR, Sealy TK, Carroll SAR, Comer JA, Kemp A, Swanepoel R, Paddock CD, Balinandi S, Khristova ML, et al. 2009. Isolation of genetically diverse Marburg viruses from Egyptian fruit bats. *PLoS Pathog* 5:e1000536. <https://doi.org/10.1371/journal.ppat.1000536>
116. Madera S, Kistler A, Ranaivoson HC, Ahyong V, Andrianiana A, Andry S, Raharinosy V, Randriambolamanantsoa TH, Ravelomanantsoa NAF, Tato CM, DeRisi JL, Aguilar HC, Lacoste V, Dussart P, Heraud J-M, Brook CE. 2022. Discovery and genomic characterization of a novel Henipavirus, Angavokely virus, from fruit bats in Madagascar. *J Virol* 96:e0092122. <https://doi.org/10.1128/jvi.00921-22>
117. Drexler JF, Corman VM, Gloza-Rausch F, Seebens A, Annan A, Ipsen A, Kruppa T, Müller MA, Kalko EK, Adu-Sarkodie Y, Oppong S, Drosten C. 2009. Henipavirus RNA in African bats. *PLoS One* 4:e6367. <https://doi.org/10.1371/journal.pone.0006367>
118. Plowright RK, Becker DJ, Crowley DE, Washburne AD, Huang T, Nameer PO, Gurley ES, Han BA. 2019. Prioritizing surveillance of Nipah virus in India. *PLoS Negl Trop Dis* 13:e0007393. <https://doi.org/10.1371/journal.pntd.0007393>
119. Han BA, Schmidt JP, Alexander LW, Bowden SE, Hayman DTS, Drake JM. 2016. Undiscovered bat hosts of filoviruses. *PLoS Negl Trop Dis* 10:e0004815. <https://doi.org/10.1371/journal.pntd.0004815>
120. Clancey E, Nuismier SL, Seifert SN. 2024. Using serosurveys to optimize surveillance for zoonotic pathogens. *bioRxiv:2024.02.22.581274*. <https://doi.org/10.1101/2024.02.22.581274>
121. Schuh AJ, Amman BR, Sealy TK, Spengler JR, Nichol ST, Towner JS. 2017. Egyptian rousette bats maintain long-term protective immunity against Marburg virus infection despite diminished antibody levels. *Sci Rep* 7:8763. <https://doi.org/10.1038/s41598-017-07824-2>
122. Macneil A, Reed Z, Rollin PE. 2011. Serologic cross-reactivity of human IgM and IgG antibodies to five species of Ebola virus. *PLoS Negl Trop Dis* 5:e1175. <https://doi.org/10.1371/journal.pntd.0001175>
123. Sitaras I. 2020. Antigenic cartography: overview and current developments, p 61–68. In *Animal influenza virus: methods and protocols*
124. Cai Z, Zhang T, Wan X-F. 2012. Antigenic distance measurements for seasonal influenza vaccine selection. *Vaccine (Auckl)* 30:448–453. <https://doi.org/10.1016/j.vaccine.2011.10.051>
125. Wilks SH, Mühlemann B, Shen X, Türel S, LeGresley EB, Netzl A, Caniza MA, Chacaltana-Huarcaya JN, Corman VM, Daniell X, et al. 2023. Mapping SARS-CoV-2 antigenic relationships and serological responses. *Science* 382:ead0070. <https://doi.org/10.1126/science.adj0070>
126. Rössler A, Netzl A, Knabl L, Bante D, Wilks SH, Borena W, von Laer D, Smith DJ, Kimpel J. 2023. Characterizing SARS-CoV-2 neutralization profiles after bivalent boosting using antigenic cartography. *Nat Commun* 14:5224. <https://doi.org/10.1038/s41467-023-41049-4>
127. Wang Y, Tang CY, Wan X-F. 2022. Antigenic characterization of influenza and SARS-CoV-2 viruses. *Anal Bioanal Chem* 414:2841–2881. <https://doi.org/10.1007/s00216-021-03806-6>
128. Natesan M, Jensen SM, Keasey SL, Kamata T, Kuehne AI, Stonier SW, Lutwama JJ, Lobel L, Dye JM, Ulrich RG. 2016. Human survivors of disease outbreaks caused by Ebola or Marburg virus exhibit cross-reactive and long-lived antibody responses. *Clin Vaccine Immunol* 23:717–724. <https://doi.org/10.1128/CI.00107-16>
129. Laing ED, Mendenhall IH, Linster M, Low DHW, Chen Y, Yan L, Sterling SL, Borthwick S, Neves ES, Lim JSL, Skiles M, Lee BPY-H, Wang L-F, Broder CC, Smith GJD. 2018. Serologic evidence of fruit bat exposure to filoviruses, Singapore, 2011–2016. *Emerg Infect Dis* 24:114–117. <https://doi.org/10.3201/eid2401.170401>
130. Schulz JE, Seifert SN, Thompson JT, Avanzato V, Sterling SL, Yan L, Letko MC, Matson MJ, Fischer RJ, Tremeau-Bravard A, Seetahal JFR, Ramkissoon V, Foster J, Goldstein T, Anthony SJ, Epstein JH, Laing ED, Broder CC, Carrington CVF, Schountz T, Munster VJ. 2020. Serological evidence for Henipa-like and filo-like viruses in Trinidad bats. *J Infect Dis* 221:S375–S382. <https://doi.org/10.1093/infdis/jiz648>
131. Dovih P, Laing ED, Chen Y, Low DHW, Ansil BR, Yang X, Shi Z, Broder CC, Smith GJD, Linster M, Ramakrishnan U, Mendenhall IH. 2019. Filovirus-reactive antibodies in humans and bats in Northeast India imply zoonotic spillover. *PLoS Negl Trop Dis* 13:e0007733. <https://doi.org/10.1371/journal.pntd.0007733>
132. Shrock EL, Shrock CL, Elledge SJ. 2022. VirScan: high-throughput profiling of antiviral antibody epitopes. *Bio Protoc* 12:e4464–e4464. <https://doi.org/10.21769/BioProtoc.4464>
133. Ruhs EC, Chia WN, Foo R, Peel AJ, Li Y, Larman HB, Irving AT, Wang L, Brook CE. 2023. Applications of VirScan to broad serological profiling of bat reservoirs for emerging zoonoses. *Front Public Health* 11:1212018. <https://doi.org/10.3389/fpubh.2023.1212018>
134. Tiu CK, Zhu F, Wang L-F, de Alwis R. 2022. Phage ImmunoPrecipitation Sequencing (PhiP-Seq): the promise of high throughput serology. *Pathogens* 11:568. <https://doi.org/10.3390/pathogens11050568>
135. Phelps KL, Hamel M, Alhmoud N, Ali S, Bilgin R, Sidamonidze K, Urushadze L, Karesh W, Olival KJ. 2019. Bat research networks and viral surveillance: gaps and opportunities in Western Asia. *Viruses* 11:240. <https://doi.org/10.3390/v11030240>
136. von Cräutlein M, Korpelainen H, Pietiläinen M, Rikkinen J. 2011. DNA barcoding: a tool for improved taxon identification and detection of species diversity. *Biodivers Conserv* 20:373–389. <https://doi.org/10.1007/s10531-010-9964-0>
137. Ruedi M, Manzinalli J, Dietrich A, Vinciguerra L. 2023. Shortcomings of DNA barcodes: a perspective from the mammal fauna of Switzerland. *Hystrix Ital J Mammal* 34:54–61. <https://doi.org/10.4404/hystrix-00628-2023>
138. Furman A, Çoraman E, Nagy ZL, Postawa T, Bilgin R, Gajewska M, Bogdanowicz W. 2013. Phylogeography of the large *Myotis* bats (Chiroptera: Vespertilionidae) in Europe, Asia Minor, and Transcaucasia. *Biol J Linn Soc Lond* 108:189–209. <https://doi.org/10.1111/j.1095-8312.2012.01994.x>
139. Berthier P, Excoffier L, Ruedi M. 2006. Recurrent replacement of mtDNA and cryptic hybridization between two sibling bat species *Myotis myotis* and *Myotis blythii*. *Proc Biol Sci* 273:3101–3109. <https://doi.org/10.1098/rspb.2006.3680>
140. Simmons NB, Voss RS. 2009. Collection, preparation, and fixation of specimens and tissues, p 849–867. In *Ecological and behavioral methods for the study of bats*. Johns Hopkins University Press Baltimore, Maryland.
141. Lendemer J, Thiers B, Monfils AK, Zaspel J, Ellwood ER, Bentley A, LeVan K, Bates J, Jennings D, Contreras D, Lagomarsino L, Mabee P, Ford LS, Guralnick R, Gropp RE, Revelez M, Cobb N, Seltmann K, Aime MC. 2020. Corrigendum: the extended specimen network: a strategy to enhance US biodiversity collections, promote research and education. *Bioscience* 70:195–195. <https://doi.org/10.1093/biosci/biz165>
142. Yates TL, MillsJN, ParmenterCA, Ksiazek TG, ParmenterRR, Vande Castle JR, CalisherCH, NicholST, AbbottKD, YoungJC. 2002. The ecology and evolutionary history of an emergent disease: hantavirus pulmonary syndrome: evidence from two El Niño episodes in the American southwest suggests that El Niño-driven precipitation, the initial catalyst of a trophic cascade that results in a delayed density-dependent rodent response, is sufficient to predict heightened risk for

- human contraction of hantavirus pulmonary syndrome. *Bioscience* 52:989–998. [https://doi.org/10.1641/0006-3568\(2002\)052\[0989:TEAEHO\]2.0.CO;2](https://doi.org/10.1641/0006-3568(2002)052[0989:TEAEHO]2.0.CO;2)
143. Thompson CW, Phelps KL, Allard MW, Cook JA, Dunnum JL, Ferguson AW, Gelang M, Khan FAA, Paul DL, Reeder DM, Simmons NB, Vanhove MPM, Webala PW, Weksler M, Kilpatrick CW. 2021. Preserve a voucher specimen! The critical need for integrating natural history collections in infectious disease studies. *mBio* 12:e02698-20. <https://doi.org/10.1128/mBio.02698-20>
144. Phelps K, Al Abdulasalam Z, Al-Hmoud N, Ali S, Alrwashdeh M, Bilgin R, Ghazaryan A, Hamel L, Hasanov N, Natradze I, Papov G, Sidamonidze K, Spalton A, Urushadze L, Olival KJ, Attaullah. 2024. Distribution of bat species in Western Asia: occurrence records from the Western Asia Bat Research Network (WAB-Net) project. *Biodivers Data J* 12:e132199. <https://doi.org/10.3897/BDJ.12.e132199>
145. Phelps K, Abdulasalam Z, Al-Hmoud N, Ali S, Alrwashdeh M, Bilgin R, Ghazaryan A, Hamel L, Hasanov N, Natradze I, Papov G, Sidamonidze K, Spalton A, Urushadze L, Olival KJ, Attaullah. 2024. The Western Asia Bat Research Network (WAB-Net) project. Version 1.4. EcoHealth Alliance. <https://doi.org/10.15468/ezy5th>
146. Szentivanyi T, McKee C, Jones G, Foster JT. 2023. Trends in bacterial pathogens of bats: global distribution and knowledge gaps. *Transbound Emerg Dis* 2023:1–17. <https://doi.org/10.1155/2023/9285855>
147. Volokhov DV, Lock LR, Dyer KE, DeAnglis IK, Andrews BR, Simonis MC, Stockmaier S, Carter GG, Downs CJ, Fenton MB, Simmons NB, Becker DJ. 2023. Expanded diversity of novel hemoplasmas in rare and undersampled Neotropical bats. *One Health* 17:100633. <https://doi.org/10.1016/j.onehlt.2023.100633>
148. Frank HK, Boyd SD, Hadly EA. 2018. Global fingerprint of humans on the distribution of *Bartonella* bacteria in mammals. *PLoS Negl Trop Dis* 12:e0006865. <https://doi.org/10.1371/journal.pntd.0006865>