

Review

The Alleged Role of Bats in Successive Global Pandemics and Its Implications for Conservation

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Abstract

Bats (Chiroptera) account for approximately 25% of all known mammalian species and provide essential ecological services, including insect regulation, pollination, and seed dispersal. Despite their importance, they face significant conservation threats and persistently negative social perceptions. Owing to their innate immunity and tolerance, bats constitute a particularly efficient natural reservoir for a wide variety of potentially zoonotic viruses. Over the past two decades, bat-associated viruses have been central to multiple outbreaks of emerging infectious diseases. From severe acute respiratory syndromes to filoviral hemorrhagic fevers, bats have consistently acted as key reservoirs in pathogen emergence. This has further damaged the public perception of bats as dangerous animals and vectors of serious diseases, in some cases leading to increased persecution of their populations. However, spillover events should not be attributed to bats, but rather to human-driven environmental changes—including deforestation, land-use transformation, agricultural intensification, urban expansion, biodiversity loss, wildlife trade and research biosecurity—that amplify contact among humans, livestock, and wildlife or their potential zoonotic pathogens. Safeguarding bat populations, minimizing direct interactions with wildlife, and preserving intact ecosystems are critical not only for bat conservation but also for reducing zoonotic spillover risk. Furthermore, it is essential to strengthen social communication regarding the importance of bats, in order to counteract their negative reputation and promote greater public understanding of their ecological value. This article reviews health, sociological, and conservation dimensions of the issue, situating them within a broader context to provide an integrated, multidisciplinary understanding. Potential solutions and priority directions for future research are also discussed.

Keywords: bat conservation; bat stigma; viral reservoirs; ecological disruption; human–wildlife contact; zoonotic diseases



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1. Bats: A Group Facing Conservation Challenges and a Poor Reputation

Bats (Chiroptera) constitute approximately 25% of all known mammalian species worldwide, with more than 1450 species currently recognized [1]. They play essential ecological roles as insect controllers, pollinators, and seed dispersers [2]. With respect to their ecological importance, insectivorous bats consume large quantities of insects each night, thereby acting as natural biological controllers of agricultural pests [3] and constituting a key focus of functional conservation strategies, understood as the maintenance of such ecological roles [4]. Their economic contribution to the agricultural sector of the United

States has been estimated to exceed 3.7 billion US dollars per year, largely due to reduced pesticide use [5]. Meanwhile, frugivorous and nectarivorous bats play key roles in the pollination of tropical plants and seed dispersal, processes that are crucial for forest and ecosystem regeneration [6].

Despite their remarkable ecological importance, bats are among the most vulnerable mammalian groups to extinction, facing severe conservation threats while also suffering from a negative social perception rooted in myths and cultural superstitions [7–10]. According to IUCN assessments more than one-third of bat species are classified as threatened or data-deficient, while the majority show unknown or declining population trends [10]. Consequently, around 80% of assessed bat species require either conservation action or further research [10].

A substantial body of research indicates that the principal threats to bats arises from both anthropogenic and pathological factors, including habitat loss and fragmentation driven by urbanization, deforestation, and mining, as well as the widespread use of pesticides and agrochemicals, which reduce insect availability and promote the bioaccumulation of toxic substances [3,11]. In addition, bat populations in North America are severely affected by white-nose syndrome, a condition caused by the fungus *Pseudogymnoascus destructans* that has been responsible for the death of millions of individuals [12]. Bat mortality is also significantly increased by collisions with wind turbines, which are estimated to cause several hundred thousand deaths annually [13,14].

Direct persecution has historically been a major driver of bat mortality worldwide, particularly in the context of conflict-driven culling and disease control campaigns [9]. Conflict-driven culling has been particularly intense in fruit bats (flying foxes; *Pteropus* spp.), which are frequently perceived as agricultural pests due to the damage they can cause to commercial fruit crops [15]. A particularly well-documented example is provided by the Mauritian flying fox (*Pteropus niger*), where government-authorized mass culls contributed to an estimated population decline of approximately 50% and the subsequent uplisting of the species to *Endangered* on the IUCN Red List, without achieving its intended management objectives [16–18].

Since the Middle Ages, bats have symbolized darkness and death, being associated with demons, witches, and vampires—an image strengthened in the nineteenth-century literature and perpetuated in modern popular culture [19,20]. However, only three bat species worldwide feed on blood: *Desmodus rotundus*, *Diphylla ecaudata*, and *Diaemus youngi*. Even these vampire bat species also play an important ecological role, particularly in nutrient cycling within their respective ecosystems [21].

Bats have often been subjected to direct persecution due to misconceptions about their association with infectious diseases [10]. Intentional killing represented the primary source of documented mass mortality events in bats prior to 2000, occurring across multiple continents due to perceptions of bats as pests or disease reservoirs [9]. Large-scale elimination of bats, especially vampire bat control programs in Latin America, has been conducted for decades as a response to rabies transmission to livestock and humans, with tens of thousands of individuals removed in single interventions and substantial cumulative impacts over time [9,22]. However, evidence indicates that such management interventions have not reliably reduced disease incidence and may instead disrupt colony structure, promote dispersal, and potentially exacerbate pathogen prevalence and transmission dynamics, as observed in vampire bat–rabies and Egyptian fruit bat–Marburg virus systems [10,23–25].

Emerging zoonotic disease outbreaks have substantially influenced public perceptions of bats, often with negative consequences for their conservation [26]. During the COVID-19 pandemic, widespread media coverage linking bats to SARS-CoV-2 frequently lacked sufficient ecological and epidemiological context, contributing to public misconceptions

and increased hostility toward bats [27]. This misleading representation, which fails to reflect the complex pathways involved, has led to unjustified attacks on bat colonies, directly undermining conservation efforts [26,28,29].

A large-scale survey conducted in China revealed that 84% of respondents misunderstood the relationship between bats and COVID-19, and these misconceptions were associated with more negative perceptions of bats, despite educational interventions improving general knowledge [29]. Similar responses were documented during the Ebola outbreak in West Africa, when bats were widely portrayed as potential reservoirs of the virus, leading to fear-driven persecution, colony disturbance, eviction efforts, and localized culling campaigns in several African countries, including Cameroon and Nigeria [25].

Anthropogenic pressures such as habitat loss, hunting, and direct persecution not only threaten bat populations but may also facilitate zoonotic disease emergence. As a result, accurate science communication, responsible media reporting, and evidence-based management strategies are critical to prevent unjustified persecution of bats while promoting both biodiversity conservation and public health under the *One Health* principle [25,27,29].

2. Bats as Viral Reservoirs

Practically all zoonotic pandemics of the twenty-first century exhibit some link to a bat-related origin, including those responsible for major outbreaks such as Ebola, Marburg, Nipah, SARS-CoV, MERS-CoV, and SARS-CoV-2 [30]; however, as will be examined in this article, the matter is considerably more complex.

Reservoirs are best understood as ecological systems in which a pathogen can be maintained over time and from which infection may be transmitted to a target population, whereas reservoir hosts constitute only one component of this system [31,32]. In many zoonotic diseases, transmission to humans does not occur directly from reservoir hosts but rather through complex ecological and epidemiological networks involving intermediate or incidental hosts, environmental interfaces, and human activities that facilitate cross-species contact [33,34].

Bats have been identified as natural reservoirs for numerous viruses with zoonotic potential [35,36]. Comparative analyses have also suggested that bats harbor a higher number of zoonotic viruses per species than rodents [37]. Their highly social behavior and the frequent cohabitation of multiple species within shared roosts increase opportunities for interspecies transmission. Such ecological interactions can facilitate pathogen exchange and enhance the potential for viral genetic recombination [37].

Moreover, bats possess an innate immunity and tolerance that appear to permit persistent viral infections without triggering a strong inflammatory response [38,39]. Their immune system seems to tolerate chronic viral replication without causing severe disease in the host, thereby facilitating long-term maintenance and dissemination of viruses [30,38]. Additionally, some species migrate across vast distances, potentially spreading viruses silently [36,40–42].

Occasionally, drivers of genetic variation through mutation and recombination allow viruses to overcome species barriers [30,43–46]. Bats have been repeatedly implicated in the evolutionary origins and ecological maintenance of numerous zoonotic viruses with major public health consequences. Their unique immunological tolerance and ability to harbor highly pathogenic agents asymptotically have enabled several bat species to act as natural reservoirs or ancestral hosts in epidemic and pandemic events over recent decades [37,38,47,48].

3. The Role of Bats in Major Pandemics of the Twenty-First Century

During the end of the nineteenth and the first decades of the twenty-first centuries a succession of high-impact zoonotic outbreaks have occurred, many of which share a common denominator: probable or confirmed origins in bat reservoirs (Table 1). Each

episode has revealed, in its own way, the tightening ecological, agricultural and biomedical interdependencies that now define global susceptibility to emergent infectious diseases [49].

The Nipah virus (*Nipah henipavirus*, family *Paramyxoviridae*) constitutes one of the earliest and most illustrative examples of a bat-borne zoonosis, with fruit bats of the genus *Pteropus*—notably *P. giganteus*, *P. hypomelanus*, and *P. vampyrus*—acting as its natural reservoirs, and domestic pigs (*Sus scrofa domestica*) serving as amplifying hosts [50]. Human infection typically arises through direct contact with infected pigs or via consumption of fruit contaminated with bat saliva or urine [51]. The 1998–1999 outbreak in Malaysia and Singapore, which emerged at the intersection of tropical deforestation, expansion of intensive pig farming, and viral spillover from fruit bats, provided an early warning of the shifting global epidemiological landscape, while subsequent recurrent outbreaks in Bangladesh and India have underscored Nipah’s potential for sustained human-to-human transmission [51–55]. Nipah represented the first major ecological signal of the dangerous synergy between environmental degradation, industrialized livestock production, and the emergence of highly lethal zoonoses [56].

Barely three years after the Nipah outbreak, the emergence of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV-1) in Guangdong, China (2002–2003) exposed the pandemic potential of bat-derived coronaviruses [57–59]. Phylogenetic analyses and serological surveys identified horseshoe bats (*Rhinolophidae*)—notably *Rhinolophus pearsoni*, *R. pusillus*, *R. macrotis*, and *R. ferrumequinum*—as the primary natural reservoirs of SARS-related coronaviruses, while civet cats (*Paguma larvata*), sold in live-animal markets, served as key intermediate hosts enabling zoonotic spillover [58]. Sequencing work confirmed the viral zoonosis origin and consolidated the now-critical association between bats and emerging coronaviruses [58,60].

The emergence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Saudi Arabia in 2012 demonstrated, as previously shown by SARS-CoV-1, the capacity of a bat-derived coronavirus lineage to cross species barriers through intermediate hosts [61–63]. The pathogen, first isolated from dromedary camels (*Camelus dromedarius*), was found to be phylogenetically related to coronaviruses circulating in insectivorous bat species such as *Neoromicia capensis*, *Taphozous perforatus*, and *Vespertilio superans* [62,64–67].

Ebola virus disease (EVD), caused by *Zaire ebolavirus* of the *Filoviridae* family, has been epidemiologically associated with several species of African fruit bats (*Pteropodidae*), particularly *Hypsignathus monstrosus*, *Epomops franqueti*, and *Myonycteris torquata*. In these species, viral RNA and serological markers have been detected, suggesting their role as plausible natural reservoirs despite the absence of conclusive evidence for direct transmission to humans [47,68–71].

The emergence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Wuhan, China, in late 2019 transformed longstanding warnings about zoonotic coronaviruses into a global crisis. Genomic analyses revealed that SARS-CoV-2 shares about 96% sequence identity with a horseshoe bat-associated coronavirus (*Rhinolophus affinis*) detected in 2013 by the Wuhan Institute of Virology, and shows additional similarities with strains found in *R. malayanus* and *R. sinicus* [72–75]. Although the Malayan pangolin (*Manis javanica*) was proposed as a potential intermediate host [76], the observed genetic divergence indicates an evolutionary separation spanning several decades [77].

The re-emergence of Marburg virus (*Marburg marburgvirus*) across Africa between 2021 and 2023 renewed global concern over the continent’s established filovirus hotspots [78–80]. Extensive virological and epidemiological investigations have identified the Egyptian fruit bat (*Rousettus aegyptiacus*) and Sundeval’s roundleaf bat (*Hipposideros caffer*) as the principal natural reservoirs in Africa, with the virus having been isolated from apparently healthy individuals of these species in Uganda [81–83]. These findings highlight the

zoonotic risk associated with human exposure to caves and mines inhabited by infected bat colonies [79,81].

Collectively, these cases underscore the pivotal role of diverse bat species as reservoirs or ancestral hosts of highly pathogenic viruses, which has contributed to their negative public perception and may promote their persecution, ultimately undermining bat conservation efforts. However, human activities that increase close contact with bats may play a more important role in zoonotic spillover events than the mere presence of bats themselves [84–87].

Table 1. Summary of bat-associated viruses: family, genetic material, host dynamics and scientific evidence regarding their evolutionary origin.

Outbreak/Disease	Viral Family (Genus)	Genetic Material	Proposed Reservoir (Long-Term Maintenance)	Proposed Host (Intermediate or Accidental)	Studies Supporting Zoonotic/Animal Origin	Studies Disputing Zoonotic Origins
Nipah Virus (NiV) Disease	Paramyxoviridae	-ssRNA	Fruit bats (<i>Pteropus</i> spp.)	Intermediate: Pigs Accidental: Humans.	[51,53,56,88]	-
SARS (SARS-CoV-1)	Coronaviridae (Betacoronavirus)	+ssRNA	Horseshoe bats (<i>Rhinolophus sinicus</i>).	Intermediate: Civets. Accidental: Humans.	[45,58,60]	-
MERS (MERS-CoV)	Coronaviridae (Betacoronavirus)	+ssRNA	Bats (<i>Vespertilio superans</i> and others).	Intermediate: Dromedary camels. Accidental: Humans.	[62,64–66,89]	-
Ebola (Ebola virus)	Filoviridae	-ssRNA	Fruit bats.	Intermediate: Non-human primates and forest antelopes. Accidental: Humans.	[47,68,70,90,91]	[92]
COVID-19 (SARS-CoV-2)	Coronaviridae (Betacoronavirus)	+ssRNA	Bats <i>Rhinolophus</i> sp.	Intermediate: Pangolins. Accidental: Humans.	[72,75,77,93–99]	[100–108]
Marburg (Marburg virus)	Filoviridae	-ssRNA	Egyptian fruit bat (<i>Rousettus aegyptiacus</i>).	Accidental: Humans.	[81–83]	-

4. Ecological and Socio-Economic Drivers of Pandemic Emergence

According to several authors, the primary drivers of epidemics and pandemics lie in the structure of modern human society rather than in wildlife itself [109,110]. Growing evidence indicates that anthropogenic environmental changes are key drivers of zoonotic emergence. Deforestation, habitat fragmentation, agricultural expansion, livestock intensification, urbanization, international trade, and increased human mobility have profoundly altered wildlife communities and ecological dynamics. These disruptions increase contact among humans, domestic animals, and wildlife reservoirs, thereby facilitating pathogen spillover and transmission [111,112]. These processes also reshape host community composition, often favoring generalist species that are more competent reservoirs for zoonotic pathogens [113,114]. As a result, ecological imbalances and habitat displacement induced by human activity can elevate pathogen prevalence within animal populations while simultaneously increasing the likelihood of cross-species transmission [40,115].

The emergence of global pandemics is increasingly understood as the result of complex interactions between ecological, evolutionary, and socio-economic factors rather than isolated zoonotic events (Figure 1). These processes disrupt the ecological “dilution effect”

of biodiversity and create conditions that facilitate pathogen circulation across species boundaries [114,116,117]. In biodiverse ecosystems, a higher number of less competent hosts can reduce transmission efficiency; however, anthropogenic pressures often erode this buffering capacity, leading to increased disease risk [111].

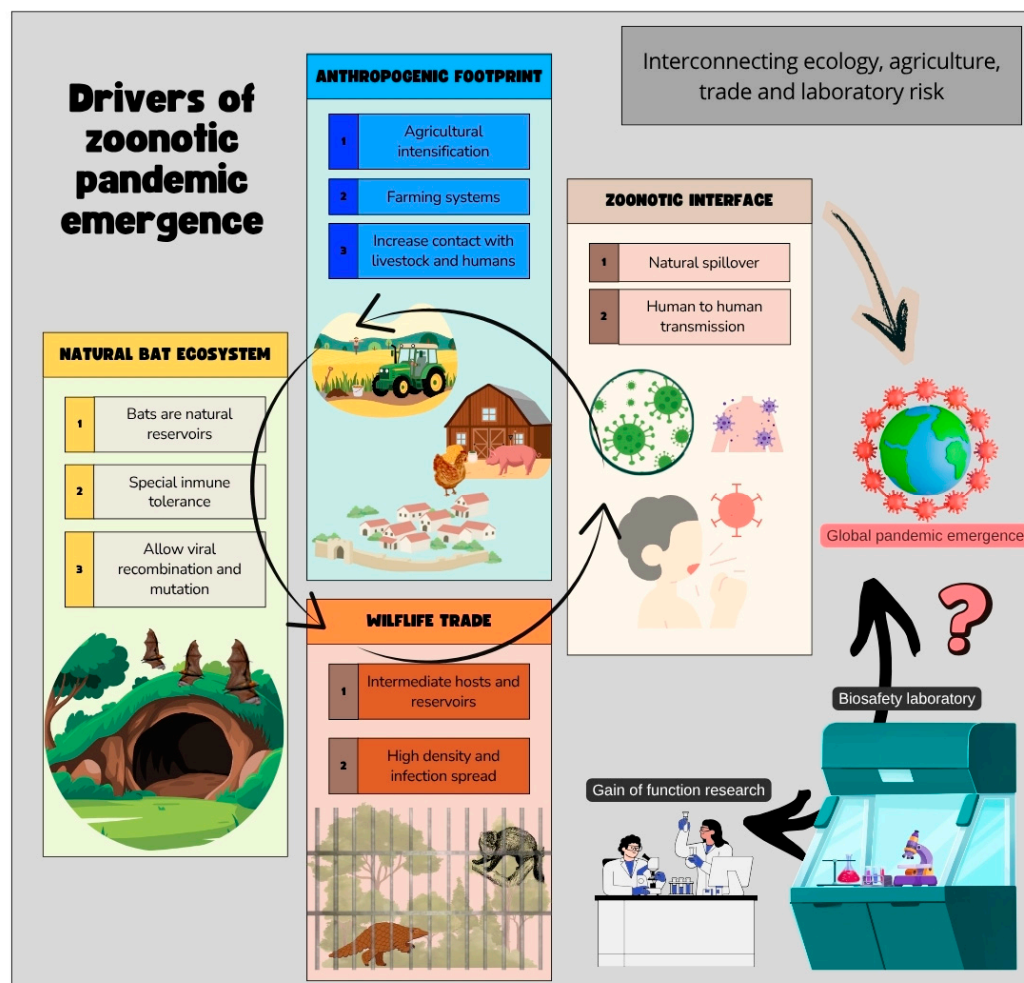


Figure 1. Drivers of zoonotic pandemic emergence, interconnecting ecology, agriculture, trade and spillover with a relationship loop and the current debate regarding the role of potential lab incidents or escapes.

In particular, as we have seen, bats constitute important reservoirs for numerous coronaviruses due to evolutionary adaptations in their metabolism and immune systems that allow them to harbor viruses with limited pathogenic effects [112]. This reservoir capacity should not be interpreted as an intrinsic threat but rather as part of long-standing ecological equilibria that become problematic only under conditions of intensified human–wildlife interaction [112]. The convergence of high host density, environmental stress, and poor biosecurity conditions in such settings creates ideal conditions for viral recombination and adaptation to new hosts [118]. Furthermore, spillover risk is unevenly distributed across phylogenetic groups and geographic regions, being closely associated with areas undergoing rapid environmental and socio-economic change [110,119].

Recently, Gippet et al. [120] examined the role of the wildlife trade as a major driver of pathogen transmission between animals and humans. This trade, which affects approximately one quarter of all mammal species, involves multiple stages—including harvesting, breeding, transport, market distribution, and end use—that increase opportunities for cross-species contact and, consequently, pathogen spillover. Using a comparative analysis of more than 2000 mammal species, the authors show that traded species are significantly more likely to

share pathogens with humans than non-traded species, even after accounting for phylogenetic relationships, geographic distribution, and sampling effort. The study further demonstrates that live-animal trade and illegal trade substantially amplify this risk, and that the cumulative duration a species spends in trade is a strong predictor of its zoonotic pathogen richness. Overall, the findings highlight wildlife trade as a structural driver of emerging infectious diseases and underscore the need to integrate zoonotic risk assessment into trade regulation and strengthen biosurveillance to help prevent future pandemics [120].

Consequently, contemporary research emphasizes that pandemics should not be attributed solely to wildlife reservoirs but rather to the broader socio-ecological systems created by human activities that intensify pathogen circulation and transmission opportunities [87,103,110,112,118] in both directions [121]. This viewpoint underscores the importance of interdisciplinary approaches integrating ecology, epidemiology, economics, and public health to improve the understanding and mitigation of emerging infectious diseases. It also highlights the need for preventive strategies centered on sustainable land-use, biodiversity conservation, and the regulation of high-risk interfaces, rather than reactive measures targeting wildlife species.

5. Biosafety Risks and the Origins of COVID-19 Competing Scientific Theories

When discussing the relationship between bats and recent pandemics, we are addressing the core of modern viral evolution: natural reservoirs, ecosystem disruptions, and, in some cases, high-risk laboratory research that collected bat-derived viruses (Figure 1). Although laboratory-acquired infections and accidental pathogen escape events are uncommon, documented cases involving diverse biological agents, predominantly bacterial pathogens, underscore the ongoing challenges associated with biosafety and biosecurity management [92].

At the same time, the global expansion of high-containment laboratories—comprising thousands of BSL-3 laboratories and more than one hundred BSL-4 facilities, predominantly located in high-income countries—has outpaced the development of harmonized regulatory frameworks, particularly with regard to dual-use research of concern (DURC) [122]. In this context, DURC refers to legitimate scientific research involving high-risk pathogens that can improve public health and disease prevention, but whose findings or materials could also be accidentally released or deliberately misused in ways that pose significant risks to public health or security.

These trends intersect with ongoing debates over gain-of-function (GOF) research, which seeks to enhance pathogen traits to better understand transmissibility and virulence [123]. Ethical and policy responses have emphasized the need for proportional risk–benefit assessment, robust oversight, and international coordination [123]. Overall, current evidence points to a complex system in which ecological change, scientific research, and biosafety governance jointly influence the emergence, amplification, and management of infectious disease threats, requiring integrated and globally coordinated approaches [124,125].

The origin of SARS-CoV-2 remains a subject of scientific debate, and the precise pathways of emergence remain unresolved, primarily centered on two competing yet not mutually exclusive hypotheses: a natural zoonotic spillover from animals to humans and an accidental laboratory leak [72,100–102,104–108]. While some researchers express uncertainty but tentatively favor a zoonotic pathway [93,96], accumulating evidence continues to support multiple plausible routes of emergence [102,106,107]. Multiple studies have identified bats as the most likely natural reservoir of the ancestral virus, while wildlife species associated with the Huanan Seafood Market and other wildlife trade networks have been proposed as potential intermediates in cross-species transmission [126]. The predominant natural-origin hypothesis identifies bats as the primary reservoir, with pangolins proposed

as potential intermediate hosts facilitating cross-species transmission [95], a view further reinforced by genomic and ecological analyses [97–99].

At the same time, in the years preceding and following the SARS-CoV-2 outbreak, Chinese research laboratories conducted extensive sampling on bat coronaviruses from caves in Yunnan Province. Among these viruses, WIV1, characterized and studied at the Wuhan Institute of Virology, has been shown to be a closely related SARS-like coronavirus within the sarbecovirus clade, which includes efficient utilization of human ACE2 for cell entry [127]. The identification of distinctive genomic characteristics, especially the furin cleavage site, has generated scientific discussion regarding their evolutionary origin, including explanations based on natural evolutionary processes as well as alternative scenarios [93,128]. In this context, some authors highlight molecular and epidemiological characteristics they consider consistent with possible laboratory involvement [106,107], while ongoing discussions also examine the possibility that laboratory-based recombination or gain-of-function research may have contributed to the virus's emergence [101,102,107]. Current evidence indicates that such features can arise through natural evolutionary mechanisms, including recombination and selection processes commonly observed among coronaviruses [93,126]. Overall, while some questions remain unresolved, the preponderance of available evidence favors a zoonotic origin, and continued transparent, rigorous, and evidence-based research is necessary to further clarify the events surrounding the emergence of SARS-CoV-2 [126,129]. Regardless of the exact origins of SARS-CoV-2, greater consistency in biosecurity protocols at the international level should be implemented to mitigate potential laboratory escapes in the future.

6. Conclusions and Future Directions

As discussed throughout this work, bats should not be viewed as the primary drivers of zoonotic emergence. Although bats have been identified as natural reservoirs for numerous viruses with zoonotic potential [35,36,84], attributing recent pandemics primarily to bats oversimplifies the multifactorial processes underlying disease emergence. Current evidence indicates that spillover events are typically driven by interactions among wildlife reservoirs, domestic animals, environmental change, and anthropogenic factors that increase opportunities for pathogen transmission to human populations [34,87,94,109,110].

Economic analyses further indicate that habitat loss and ecosystem degradation systematically raise the risk of infectious disease outbreaks by increasing contact rates and altering host community structures [130]. Climate change and environmental stressors likewise reshape species distributions and pathogen dynamics, amplifying zoonotic risk under conditions of rapid urbanization and environmental transformation [131]. Epidemiological assessments also emphasize that zoonotic disease patterns are closely linked to anthropogenic pressures and structural weaknesses in public health governance [132]. From this perspective, outbreaks—often interpreted as stochastic events—may instead reflect the convergence of ecological disruption, agricultural expansion, rapid urban development, and limitations in global health governance [87,94,130–132].

Importantly, numerous vertebrate groups, including rodents, non-human primates, and birds, are recognized reservoirs of pathogens with zoonotic potential [133,134]. For instance, although passerine birds can harbor a wide range of viral, bacterial, and parasitic agents, they continue to be traded internationally as pets, with limited public concern regarding disease transmission [135,136]. Likewise, rodents and primates host a substantial diversity of zoonotic pathogens, with rodents serving as natural reservoirs of hantaviruses, which have recently attracted considerable attention [87,133,137,138]. Yet, despite their epidemiological relevance, these taxa have not attracted the same level of public scrutiny as bats. This disparity suggests that public attitudes toward wildlife are shaped not only

by objective assessments of disease risk but also by cultural perceptions, media narratives, and pre-existing human–animal relationships, often resulting in disproportionate negative responses toward bats [19,86].

Future research should place greater emphasis on systematically evaluating the relationship between anthropogenic environmental changes, such as intensive pig farming, and zoonotic spillover into human populations through robust surveillance under the *One Health* principle. In particular, further investigation is needed into the effects of land-use change, urban expansion, deforestation, and agricultural intensification, all of which have been increasingly associated with altered patterns of contact among wildlife, livestock, and humans. Comparative and correlative studies could provide valuable insights by examining differences in estimated spillover risk across regions characterized by varying degrees of human environmental disturbance, thereby identifying recurring spatial and ecological patterns linked to zoonotic emergence. At the same time, more controlled and longitudinal research designs are necessary to clarify causal mechanisms and assess how specific anthropogenic pressures influence pathogen transmission dynamics over time. Such studies should integrate ecological, epidemiological, and socio-economic variables in order to develop predictive models of spillover risk and to support evidence-based public health and environmental policy interventions.

In addition, several authors have called for increased caution regarding gain-of-function research because of the potential risks associated with the manipulation of highly pathogenic viruses [125,139]. Beyond technical and regulatory measures, fostering more informed public attitudes toward wildlife and infectious disease ecology is also essential, as emphasized by MacFarlane and Rocha [28].

In the face of these challenges, we argue that it is imperative to promote integrated conservation initiatives that encompass several complementary dimensions. These should include the legal protection of natural roosts and habitats, ensuring that critical breeding, foraging, and hibernation sites are effectively safeguarded while avoiding pathogen transmission [140]; and targeted environmental education programs aimed at demystifying negative perceptions, reducing unfounded fears, and preventing persecution.

From a practical management perspective, conservation actions should prioritize the maintenance and restoration of habitat connectivity, the installation of artificial roosts where natural structures have been lost, and the implementation of operational curtailment protocols in wind farms during periods of high bat activity [13,14]. At the policy level, these measures must be embedded within robust regulatory frameworks that integrate biodiversity conservation into land-use planning and energy development, ensuring that environmental impact assessments adequately consider bat populations. Strategies to mitigate human–bat conflict should further include the development of non-invasive exclusion techniques for buildings, as well as rapid-response protocols to address public health concerns without resorting to lethal control.

Several successful conservation initiatives demonstrate the feasibility and effectiveness of these management approaches. Notably, Bat Conservation International (BCI) has developed a range of evidence-based programs focused on both roost protection and the mitigation of anthropogenic mortality. Through its global conservation efforts, BCI has promoted the identification, legal protection, restoration, and long-term management of critical bat roosts, including caves, mines, forests, and other habitats essential for breeding, hibernation, and migration. In parallel, the organization has become a leading actor in addressing bat fatalities associated with wind energy development, promoting acoustic deterrent technologies and the implementation of smart curtailment strategies that temporarily restrict turbine operation during periods of elevated bat activity. The success of these initiatives highlights the importance of collaborative approaches involving researchers, industry stakeholders, governmental agencies,

and conservation organizations in developing scalable solutions to emerging threats facing bat populations [141–143]. These experiences illustrate how conservation interventions grounded in scientific evidence can effectively reduce human-induced threats while supporting broader sustainability objectives.

In summary, bats embody a paradox: they are often feared and misunderstood and are recognized as natural reservoirs for the emergence of zoonotic pathogens, including coronaviruses linked to recent pandemics, yet they play critical ecological roles [94,131]. More broadly, bats illustrate how unawareness, combined with the amplification of disease risk through human-driven habitat alteration and urbanization, can threaten both biodiversity and public health [130,132], thereby further exacerbating their negative reputation among the general population. Transparent, evidence-based messaging that emphasizes both the low-risk bats pose to humans under normal conditions and their substantial ecological and economic benefits, particularly as natural pest controllers will reduce persecution and foster coexistence. Engaging local communities, stakeholders, and the media in responsible communication practices can help reshape public attitudes and counteract misinformation. Ultimately, education and responsible public communication constitute fundamental pillars for improving the relationship between humans and bats, highlighting their role as key components of ecosystems and valuable allies in sustainable agriculture.

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