

BATS, VECTORS AND EMERGING DISEASES: A ONE HEALTH PERSPECTIVE

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ABSTRACT: This review explores the fundamental role of bats as reservoirs of infectious agents, emphasizing the One Health approach to understanding and mitigating the emergence of diseases. Bats harbor several zoonotic pathogens and facilitate their transmission between humans, domestic animals and wildlife. The study highlights the interconnectedness of ecosystems and the evolutionary dynamics of pathogens, highlighting factors such as habitat loss, climate change and human behavior that contribute to disease spread events. Bats, with their ancient evolutionary history and vast geographic distribution, serve as long-standing reservoirs for infectious agents around the world, posing risks when pathogens jump to new hosts. In addition, the review discusses the fundamental role of vectors associated with bats such as ticks, fleas and mosquitoes, and presents the main microorganisms detected in bats to date. Strategies to mitigate disease cycles without harming bat populations are crucial, considering their ecological importance and the complexity of wildlife-related disease dynamics. In conclusion, understanding the intricate relationships between bats and the emergence of diseases is essential for effective public health strategies. Preserving the habitat and life of bats, and at the same time monitoring the first signs of disease in these animals, can help prevent future outbreaks and protect human health.

Keywords: Spillover. wildlife reservoirs. Zoonoses. emerging diseases emergence.

1

RESUMO: Esta revisão explora o papel fundamental dos morcegos como reservatórios de agentes infecciosos, enfatizando a abordagem de Saúde Única para compreender e mitigar a emergência de doenças. Os morcegos abrigam diversos patógenos zoonóticos e podem facilitar sua transmissão entre seres humanos, animais domésticos e vida silvestre. O estudo destaca a interconexão dos ecossistemas e a dinâmica evolutiva dos patógenos, evidenciando fatores como perda de habitat, mudanças climáticas e comportamento humano que contribuem para eventos de disseminação de doenças. Os morcegos, com sua antiga história evolutiva e ampla distribuição geográfica, atuam como reservatórios de longa data para agentes infecciosos em todo o mundo, representando riscos quando esses patógenos transpassam a barreira interespecífica e infectam novos hospedeiros. Além disso, a revisão discute o papel fundamental dos vetores associados aos morcegos, como carrapatos, pulgas e mosquitos, e apresenta os principais microrganismos detectados nesses animais até o momento. Estratégias para mitigar os ciclos de transmissão de doenças sem prejudicar as populações de morcegos são essenciais, considerando sua importância ecológica e a complexidade da dinâmica das enfermidades relacionadas à fauna silvestre. Em conclusão, compreender as intrincadas relações entre os morcegos e a emergência de doenças é fundamental para o desenvolvimento de estratégias eficazes de saúde pública. A preservação dos habitats e das populações de morcegos, aliada ao monitoramento dos primeiros sinais de doenças nesses animais, pode contribuir para a prevenção de futuros surtos e para a proteção da saúde humana.

Palavras-chave: Spillover. reservatórios silvestres. Zoonoses. doenças emergentes.

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INTRODUCTION

Zoonoses are diseases that can be transmitted between animals and humans. Many diseases now known to be restricted to humans have already been studied and identified as having an animal origin. This is the case with AIDS, Ebola and numerous viral diseases that cause flu, such as influenza. Thinking of living beings as a large group reaffirms the Darwinian logic that humanity is a type of animal intrinsically linked to other animals, in its origin, in health and in disease (Quammen 2012).

With advances in the field of molecular biology, it has been possible to see through analysis of the genetic profile of microorganisms and the development of phylogenetic trees that infectious diseases have appeared and reappeared over periods of time, and such resurgences are motivated by a wide range of influences, such as: gene adaptation of the agent, polymicrobial diseases, susceptibility of the human host, demographic aspects and human behavior, cross-border trade and travel, wars and bioterrorism, occupational exposure, inappropriate use of antimicrobials, climate change, land use, poverty and social inequality, absence of public health services, animal populations, and famine. Around sixty to eighty percent of recent infections in humans have originated from animals, with a greater emphasis on rodents and bats (Morens and Fauci 2013).

2

Infectious disease is a kind of natural mortar that connects one animal to another within the elaborate biophysical buildings we call ecosystems. Pathogens are like predators that eat their prey, being as natural as a lion attacking a zebra. Just as predators have their usual prey, their preferred targets, so do pathogens. And just as a lion can occasionally stray from its natural behavior and attack a cow that has invaded its habitat, a pathogen can also switch to a new target host. Circumstances change and, with them, so do the demands and opportunities. When a pathogen moves from a non-human animal to a person and manages to establish itself there, we have what we call *spillover* and the emergence of a zoonosis (Quammen 2012).

This process has occurred in the history of countless diseases, including some pandemics, such as the plague, Spanish flu, monkey pox, bovine tuberculosis, Nile fever, rabies, hantavirus, COVID-19, among others. Their animal origins were diverse, ranging from wild pigs and waterfowl to non-human primates and bats, as well as their territorial origins, passing through America and Eurasia as well as Africa and Oceania. This form of interspecies jumping is common, not rare. Around sixty percent of emerging infectious diseases affecting humans are zoonotic, originating in animals, and more than two thirds of them originate in wildlife.

According to the International Livestock Research Institute, two million people are killed each year by diseases that spread to humans from wild and domestic animals (Robbins 2012). Some diseases can be more complex to combat than others, such as yellow fever, which not only has non-human primates and humans involved in the epidemiological chain, but also mosquitoes, which can give rise to countless new types of new species that are sources of infection for the agent, since controlling mosquitoes is extremely more difficult than controlling wild or domestic outbreaks of disease (Morens and Fauci 2013).

Microorganisms often "hide" in what we call a reservoir host. A reservoir is a living organism that carries the pathogen, chronically harboring it while suffering little or no disease. In situations where infectious agents no longer seem to occur in certain territories, they may actually be residing in a place where biological diversity is high and the ecosystem is relatively undisturbed. When ecological disturbance occurs, these agents reveal themselves (Shaheen et al. 2022). Emerging diseases consist of pathogens present in a territory that have mutated, resulting in variants that behave differently in the new target. An example of this is influenza, which mutates regularly, leading to the need for annual vaccine updates (Morens and Fauci 2013).

This understanding of how zoonoses arise and how *spillover* occurs enables international agencies to make progress in combating new diseases with pandemic and epidemic potential, identifying them in places before they even reach humans and spread (Shaheen et al. 2022). While it has been feasible to eradicate some infectious diseases and effectively control many others in recent decades, it seems unlikely that we will be able to eliminate the vast majority of emerging infectious diseases in the near future. This is due to the fact that pathogenic microorganisms have the ability to undergo rapid genetic changes, resulting in new phenotypic characteristics that take advantage of changes in the host and the available environmental conditions (Robbins 2012).

The advantages conferred by microorganisms can only be tackled and overcome through rigorous surveillance, continuous and dedicated research, as well as the rapid development and implementation of countermeasures, such as monitoring tools, diagnostics, drugs and vaccines. Identifying, diagnosing, sequencing and typing new microorganisms in new locations are important tools in the fight against new outbreaks. The fight against emerging infectious diseases needs to be a constant effort (Morens and Fauci 2013).

THE IMPORTANCE OF WILDLIFE IN THE EMERGENCE OF INFECTIOUS DISEASES

Diseases have historically originated in forests and wildlife, before spreading to human communities. Two notable examples are plague and malária. Experts claim that in the last fifty years, the number of emerging diseases has increased fourfold, largely due to the constant expansion of areas inhabited by humans into animal habitats, especially in tropical regions identified as hotspots for the spread of disease around the world. In addition, with global mobility facilitated by modern air travel and the illicit wildlife trade, there is significant potential for serious outbreaks to occur in densely populated areas (Quammen 2012).

Changes in ecosystems, such as deforestation, urbanization, climate change and environmental degradation, can lead to an increase in encounters between wildlife and humans. This can result in an increased risk of infectious disease transmission. Wildlife, due to its wide genetic diversity, can be a favorable environment for the mutation and evolution of pathogens, and these genetic changes can give rise to more virulent or more transmissible variants that pose a threat to global health. The detection of diseases in wild animals can serve as an early warning indicator of the presence of dangerous pathogens. This can provide valuable information for the prevention and control of infectious disease outbreaks in humans. Wildlife conservation is intrinsically linked to human health, and therefore maintaining healthy ecosystems and biodiversity can reduce the risk of these diseases emerging (Daszak et al. 2000).

The dynamics of wildlife populations and their seasonal migrations or long-distance movements can play an important role in the spread of pathogens (Shaheen et al. 2022). For example, the migration of birds can transport pathogens from one region to another, or the migration of marine mammals to coastal areas, contributing to the geographical dispersal of diseases. Habitat degradation and deforestation often lead to greater interaction between wildlife, domestic animals and humans, increasing the risk of infectious disease transmission. As humans expand into previously untouched areas, more frequent encounters with wildlife can occur, increasing the chances of exposure to pathogens. This same exposure can occur in recurring ecotourism habits or the migration of indigenous peoples. The illegal wildlife trade is also a significant concern, as it can introduce pathogens to new regions (Quammen 2012).

According to experts, the key to predicting and preventing the next pandemic lies in understanding the protective effects provided by untouched nature. An example of this is evidenced in the Amazon, where a study revealed that an increase of approximately four

percent in deforestation resulted in an increase of almost fifty percent in the incidence of malaria. This was due to the favorable environment for the development of mosquitoes, the transmitters of the disease, which thrive in newly deforested areas that offer the right combination of sunlight and water (Quammen 2012).

Ecological imbalance undoubtedly leads to the emergence of new infection conditions, where microorganisms encounter species that are not adapted to their pathogenicity mechanisms (Shaheen et al. 2022). Another example of this was the migration of the West Nile virus from Africa to North America, which found in its new habitat a new susceptible host, the American thrush, which became a source of infection and amplifier of the agent for mosquitoes and humans in the United States. Another example was the spread of Lyme disease, which evolved in the midst of deforestation responsible for decreasing the population of predators, increasing the population of rodents that amplify the disease. This spread was partly due to the loss of skunks and squirrels that fed on tick vectors in the forest environment (Quammen 2012).

Many of the pathogens that move between wildlife, domestic animals and humans have existed in wild animals for a long period of time (Daszak et al. 2000). Originally, these pathogens did not necessarily cause disease, they evolved together with their natural hosts over millions of years (Shaheen et al. 2022). Over this time, they have established a kind of equilibrium, replicating slowly and steadily, passing discreetly through the host population. This has allowed them to ensure long-term security by avoiding short-term success in the form of maximum replication in each host individual. This strategy has been successful, however, when humans disturb this balance, whether by invading host populations, hunting for meat, displacing or destroying ecosystems, their actions increase the risk, providing opportunities for these pathogens to jump from their natural hosts to new hosts. These new hosts can be any animal, but are often humans, due to their intrusive and abundant presence in environments, offering a rich place of opportunity for these pathogens (Quammen 2012).

The study of diseases in wild animals is fundamental to understanding and preventing the emergence of infectious diseases. Research into the ecology of pathogens and the dynamics of wildlife populations can lead to more effective prevention and control strategies. According to experts, the most effective approach to preventing future outbreaks in humans is the so-called One Health approach. This is a global program involving a community of more than six hundred scientists and other professionals, promoting the notion that human, animal and

environmental health are intrinsically linked and must be addressed and managed holistically (Quammen 2012).

THE ROLE OF BATS IN MAINTAINING INFECTIOUS AGENTS IN POPULATIONS

The order Chiroptera is the most diverse and geographically distributed mammal taxon. It has been proven that bats are part of our ancient native fauna. Fossil records from Queensland, Australia, show that small bats have existed there for at least 55 million years, while human presence is much more recent, dating back only tens of millennia (Quammen 2012).

Bats are considered to be ancient reservoirs of infectious diseases. As animals with an evolutionary history spanning millions of years, they have undergone a process of coevolution with various microorganisms, making them resistant to most of the diseases they cause. This is different from what happens when these microorganisms reach species that did not evolve with them, humans for example, and the impact will undoubtedly be severe since this new host does not have specific immune defenses to fight them (Quammen 2012). An example of this negative impact was what happened in Malaysia with the emergence of the henipahvirus, which infected fruit bats, and at some point, due to the constant contact of domestic pigs with the saliva of bats present in fallen fruit from trees, the virus jumped to a new species, and then reached humans, causing 106 deaths from neurological and disabling disorders in the rural region of the country (Chua et al. 2003). Something similar happened with the hendravirus in Australia, but in an urban environment. With urbanization, bats changed their habitat in search of food, and began to transmit the virus to horses and humans, with a mortality rate of approximately 70% (Field et al. 2010).

SARS-CoV-2 is also believed to have arisen in this way, through interaction between humans, pigs and bats in China, however more studies are needed as SARS viruses are complex in their natural history. Two other epidemics, one in China and one in Saudi Arabia, were caused by coronaviruses that closely resemble SARS-CoV-2, SARS-CoV and MERS-CoV. SARS emerged in Guangdong province in southern China and was marked by fever, headache and the subsequent appearance of respiratory symptoms, including cough, dyspnea and pneumonia. The disease caused by this virus was highly transmissible between humans, spreading throughout China and to 28 other countries, causing 774 fatal cases of the disease. MERS emerged as a respiratory syndrome similar to that caused by SARS, and although less

transmissible, it had a 15% higher lethality. Discoveries about the nipah and hendra viruses led researchers to consider bats as possible reservoirs of these deadly viruses. In 2005, a breakthrough was made when two independent research groups reported, almost simultaneously, the discovery of novel SARS-CoV-related coronaviruses in horseshoe bats of the genus *Rhinolophus* in China, which were named SARS-like coronaviruses (SL-CoV). These bat SL-CoVs showed 88-90% genomic sequence identity with each other and 87-92% identity with human SARS-CoV isolates. Further studies with bats from other regions demonstrated this same similarity, and also showed that both viruses were able to use the same receptor for specific protein functions. There was indeed a close phylogenetic relationship between these two viruses, strongly suggesting that they both originated from bats. In the case of MERS-CoV, after the reported human cases, it was identified in different species of bats. More recent ancestry analysis has speculated that MERS-CoV may have jumped from bats to camels approximately 20 years ago in Africa, with camels then being imported to the Arabian Peninsula. Most, if not all, alphacoronaviruses and betacoronaviruses currently circulating in different mammals are believed to be evolutionarily linked to ancestral coronaviruses originating from bats (Hu et al. 2015).

The transmission of microorganisms from bats to humans and other animals requires the alignment of various factors, including the ecological, epidemiological and behavioral determinants of exposure to pathogens, and human factors that can affect susceptibility to infection. It is believed, for example, that urban bats have a greater potential to transmit diseases than other bats, because they tend to stay in the same place and experience a reduction in regular exposure to microorganisms that they used to acquire in the wild. This previous exposure helped keep infection to a minimum. As a result, more bats, due to factors such as poor nutrition, loss of habitat and other elements, end up being infected and consequently spread a greater amount of microorganisms in urban areas (França et al. 2024, França et al. 2025a, França et al. 2025b, França et al. 2025c, França et al. 2025d). Another example is feeding habits, as hematophagous bats are very likely to transmit viruses through their saliva, such as the rabies virus, while insectivorous bats are more likely to carry infectious agents transmitted by arthropods. In addition, the physiology of bats, evolved for flight conditions, allows for a compatible and favorable blood regulation for the development and maintenance of several families of pathogens (Altringham et al. 2011).

The flight abilities of this mammal influence the occurrence of new diseases not only physiologically, but also geographically, as they are able to fly long distances in search of food, depending on the relief conditions of the region, and consequently act as a migratory agent. Bats are known for their exceptional flying abilities, and their flight capacity can vary depending on the species. On average, most bat species can fly distances ranging from 20 to 50 kilometers in a single night. Some migratory bat species can fly much further in their seasonal migrations. A notable example is the free-tailed bat, *Tadarida brasiliensis*, which is widely found in the Americas. This species is known for its long migrations and can fly hundreds of kilometers in a single night during its spring and autumn migrations. In some regions, these bats have been recorded flying up to 1,600 kilometers in seasonal migrations (Altringham et al. 2011). Some bats, such as *Desmodus rotundus*, are known to be hematophagous and transmit rabies to livestock and river-dwelling populations. Because they feed exceptionally on blood, they are much less resistant to fasting, due to the absence of pancreatic β -cells that is characteristic of these types of bat. This absence prevents the bat's liver from producing glycogen reserves and means that it has to search for food every day, making its contact with other animals even greater, and also increasing the chances of interaction between animals and new pathogens. The potential to fly long distances, migratory habits, gregarious habits and longevity make them a vehicle with more potential for transmitting zoonotic viruses than other animals (Di Tosto et al. 2006).

The relationship between bats and the maintenance of infectious diseases in populations is a complex topic that requires a comprehensive One Health approach (Quammen 2012). Bats play several roles in this context, because in addition to acting as reservoirs and amplifiers of infectious diseases, they play a fundamental role for the ecosystem of the places they inhabit. One of the most important roles of bats is in seed dispersal, contributing to biodiversity and the restoration of ecosystems. Two other fundamental roles are in the biological control of insects and small birds and in pollination, where these types of animals are needed in certain places to prevent pests from appearing and green areas from shrinking (Altringham et al. 2011).

Environmental disturbances such as deforestation, climate change, dam construction and urbanization of forest areas can lead to bat migration and closer interaction with humans and domestic animals, increasing the risk of disease transmission and genetic mutation processes. Natural changes in the environment, as well as those produced by human activities,

promote new interactions between microorganisms, vectors and mammalian hosts (Daszak et al. 2000).

The field of research into bats and infectious diseases involves several disciplines, such as ecology, epidemiology, veterinary medicine and public health. A One Health approach promotes collaboration between these disciplines, enabling the understanding and management of the risks of zoonotic diseases associated with bats and recognizing the need to think about these associated factors in order to achieve human health. This approach is crucial to preventing disease outbreaks and promoting sustainable coexistence between bats and society (Quammen 2012).

THE ROLE OF VECTORS IN CONTACT WITH BATS

The importance of bat vectors in disease transmission is a topic of great relevance in public health research and epidemiology. Vectors, such as ticks, fleas and mosquitoes, play a key role in spreading pathogens from bats to other animals, including humans. Vectors can transport bat pathogens to distant areas, extending the geography of diseases. This can be particularly relevant in contexts of climate change, which can expand the distribution areas of vectors.

Ticks (Ixodoidea)

Ticks are arthropods that necessarily feed on blood. They are found all over the world and comprise more than nine hundred species known to parasitize terrestrial vertebrates. The evolutionary history of this group dates back around a hundred million years, when there was widespread genetic diversification and dispersal across territories. Ticks are divided into two main categories: hard ticks, represented by the Ixodidae family, which is the most numerous, and soft ticks, belonging to the Argasidae family (Sándor et al. 2021).

Bats, on the other hand, have a wide geographical distribution, a great diversity of species and also show various evolutionary adaptations, making them ideal hosts for the parasitism of these arthropods. Soft ticks, although a minority, have a worldwide distribution with a greater focus on tropical regions, and are related to most human diseases. In addition, they are highly resistant to extreme fasting and are easier to transfer pathogens to other animals, making them great potential vectors. Some other points favor this parasitism, such as morphological adaptations for flight, making it difficult for the bat to eliminate ticks; resting

in caves and various shelters, places with large numbers of ticks; and sociability, increasing the proximity of ectoparasite-free animals to other infested animals (Sándor et al. 2021).

The data available in the literature from a study that evaluated bats and their ticks in Europe and North Africa show that: there are 44 bat species currently infected by soft ticks; 76% of bat species live in rock and tree crevices; the majority are considered secondary hosts; the most infective stages are the larval stages in 93% of records; the pathogens most commonly detected in these bats were *Bartonella* spp., *Borrelia* spp., *Coxiella burnetii* and *Rickettsia* spp. (Sándor et al. 2021).

In Brazil, studies point to this intrinsic relationship in the Pantanal region, where 1,028 bats collected had infestations by different species of ticks, and in the Caatinga region, where 409 bats collected had infestations. The most frequent ticks were *Ornithodoros hasei* in both studies (Muñoz-Leal et al. 2016). In this tick species, a large study in French Guiana, which neighbors Brazil, found 29% (31/354) positivity for species of the *Rickettsia* genus. There were no detections of *Bartonella*, *Borrelia* and *C. burnetii*. However, although these agents have not been described in ticks in Brazil, this interaction is not excluded, since there are almost no studies with this focus of investigation and since bats have been shown to harbor these agents in their blood and organs (Tahir et al. 2016).

Fleas (Siphonaptera)

Fleas are obligate hematophagous parasites, most abundant and diverse in small and medium-sized mammals, with more than two thousand species currently known. Most flea species parasitize rodents, but they are not host-specific and generally exploit other groups of mammals, digesting the blood of bats very well. On the other hand, bats are often parasitized by fleas from the *Ischnopsyllidae* family, which do not exploit hosts other than bats. Thus, bats are seen as potential targets for fleas in general. This means that, although there are no reports of bats infested by cat fleas, this is possible, especially in urban environments (Krasnov et al. 2007).

In Madagascar and Algeria, bats were infested by *Thaumapsylla* and *Ischnopsyllus intermedius* fleas, respectively. In the United States, *Sternopsylla texanus* infest bats, and a genotype of *Bartonella* has already been described (Stuckey et al. 2017). A large-scale investigation on the territory of Russia identified several species of the *Ischnopsyllidae* family in bats (Orlova et al. 2022). Flea parasitism of prevalent bat species, as well as the presence of

infectious agents in these parasites, have been described worldwide, and in the Americas it has been well documented. A study in Canada observed that parasitism tends to occur in perches and other resting places, especially in breeding females that spend most of their time in these places (Krasnov et al. 2007).

Although not as common as the transmission of pathogens by other vectors, such as mosquitoes or ticks, there have been reports of cases in which fleas were involved in the transmission of diseases from bats to other animals. One notable example is the transmission of *Yersinia pestis*, the bacterium responsible for plague, from bats to other hosts via fleas. The vector relationship between fleas and bats is an ongoing field of research, and scientists are investigating the species of fleas associated with bats, the pathogens that can be transmitted and the mechanisms of transmission (Korine et al. 2012).

Mosquitoes (Culicidae)

Mosquitoes are hematophagous insects that are widely recognized for their importance in both natural ecosystems and human health. When a mosquito feeds on an infected bat, it can acquire the microorganism and subsequently transmit it to other animals or humans. There are thousands of species around the world, each with specific adaptations to its environment and life cycle. Tropical regions tend to have a greater diversity of this type of insect (Lampo et al. 2000).

Studies have reviewed cases in the literature in which it is possible to identify mosquitoes that have fed on bat blood. However, there is still little information on the primary mosquito vectors that feed on bats. Some flaviviruses, such as dengue virus (DENV), Koyose virus (YOKV), Tamana virus (TABV), Rio Bravo virus (RBV), Japanese encephalitis virus (JEV) and West Nile virus (WNV), have already been detected in bats, but viremia rates and their role in pathogen transmission are still poorly defined. These infections are believed to have occurred due to transmission by mosquito vectors, which play an important role in spreading these viruses among bats and potentially to other species. In relation to phlebotomines, the vectors of Leishmaniasis, bats prove to be a natural source of food for them, and this is because they share the same habitats in caves and shelters, in addition to bats being seen as excellent reservoirs of trypanosomatid (Lampo et al. 2000).

In fact, the relationship between bats and mosquitoes may be bidirectional, since many bats have a diet that includes insects, insectivores. For example, in the southeastern United

States, it has been observed that mosquitoes *Culex quinquefasciatus*, *Culex coronator*, *Culiseta melanura*, *Culex salinarius*, *Culex erraticus* and *Coquillettidia perturbans* were consumed between 12% and 50% by bats sampled. This variation in mosquito ingestion can be explained by several variables, such as the larval prevalence of mosquitoes in the area, the size and species of the bats, the temperature and the various stress conditions present. Bats also play an important role in controlling the mosquito population, proving that contact with infectious agents transmitted by them can also be acquired by other routes (Hughes et al. 2022).

ONE HEALTH APPROACH TO MITIGATE THE RISKS OF PATHOGEN SPOILOVER

The One Health approach requires integrated strategies that consider human, animal and environmental health in an interconnected way. Innovative solutions can combine technological advances, real-time monitoring and community engagement to prevent future outbreaks.

A central proposal is the use of monitoring systems based on artificial intelligence and machine learning to detect emerging patterns of interaction between bats, their pathogens and the environment. Ecological sensors placed in bat habitats could collect data on movement, population density and the general health of the animals, while algorithms analyze this data in real time to predict areas at high risk of overflow. This technology could be integrated into national surveillance programs, providing early warnings about ecological changes that favor the emergence of diseases (Davenport and Kalakota 2019).

Another solution is to develop ecological buffer zones in areas at high risk of contact between humans and bats, such as degraded forests and peri-urban regions. These zones, planned on the basis of epidemiological risk maps, could include planting fruit tree species that attract bats to locations far from human populations, reducing the likelihood of direct contact. At the same time, these areas could serve as controlled spaces for studying the dynamics of pathogens in bats, with systematic collection of biological samples (Davenport and Kalakota 2019).

In addition, community-based educational interventions can be powerful tools for reducing risky interactions. Environmental education programs involving local communities can help deconstruct myths about bats and foster safe behaviors, such as avoiding the consumption of bushmeat or contact with bat colonies. These actions could be strengthened by

interactive digital campaigns and educational games that increase engagement, especially among young people (Newman et al. 2012).

In the field of biotechnology, research into preventive zoonotic vaccines aimed at pathogens with pandemic potential found in bats, such as the Nipah virus or coronavirus, should be expanded. Such vaccines could be applied selectively to populations of animals at risk, reducing their viral load and limiting the likelihood of spillover. This approach requires international and ethical collaboration, respecting biodiversity and avoiding negative impacts on ecosystems (Anthony et al. 2013).

One promising strategy involves the creation of regional biobanks of biological samples from bats and their associated ecosystems. These biobanks would allow for the systematic storage of samples of bats' blood, tissues and ectoparasites, as well as environmental samples such as soil and water from their habitats. In parallel, microbiome studies could identify microbial patterns that indicate the state of health of bat populations and possible changes associated with the emergence of zoonotic pathogens. This approach would allow continuous monitoring of microbial diversity and early identification of imbalances that could favor spillover. In addition, biobanks would be crucial resources for future investigations of outbreaks and the development of countermeasures, such as vaccines and therapies (Anthony et al. 2013).

13

Engaging local communities in participatory surveillance efforts can be a powerful tool for mitigating risks. Through the use of mobile apps and digital platforms, residents of areas close to bat habitats could report observations of colonies, behavioral changes, bat mortality or the emergence of new urban shelters. These tools could be gamified to encourage continued use, offering virtual or educational rewards for the most engaged users. The data collected would be analyzed by systems based on artificial intelligence, allowing for dynamic and collaborative risk mapping. This approach not only increases vigilance, but also raises awareness and empowers communities as active agents in disease prevention (Newman et al. 2012).

Finally, it is essential to implement integrated and collaborative governance, connecting researchers, health professionals, environmental agencies and local communities. Global One Health programs could benefit from the creation of specialized regional hubs, where data and solutions can be shared in an agile and effective manner, aligned with global zoonosis surveillance and response strategies (Newman et al. 2012).

ERADICATE NO KILLING: ETHICAL STRATEGIES TO MITIGATE THE DISEASES

It is important to note that most bat species do not pose a significant threat to public health and play an important role in balancing the ecosystem. In general, they have a remarkable diversity of feeding habits and play important ecological roles (Mikich and Bianconi 2005).

Some families and species specialize in different types of food. Some families, such as Vespertilionidae and Molossidae, consist of bats that feed exclusively on insects, playing a crucial role in controlling insect populations and contributing to pest regulation. Bats of the Phyllostomidae family exhibit a wide diversity in their diets, some are frugivorous, while others are nectarivorous,. These bats play an essential role in seed dispersal and pollination of various plant species, contributing to the regeneration of forested areas (Reis 2007).

There are only three species of hematophagous bats, and all of them are found in neotropical regions, including Brazil. They feed on the blood of vertebrates and act to control the populations of their prey, a role that is also important for ecological balance. Some bats hunt small vertebrates, such as rodents, birds, amphibians, reptiles and even other bats, and are therefore recognized as carnivorous bats. An example of a carnivorous bat is the *Chrotopterus auritus*, which plays the same population control role as hematophagous bats. Bats from the Noctilionidae family, such as the fishing bat *Noctilio leporinus*, are piscivores and have a diet consisting mainly of fish and other marine animals. They play an important role in the ecology of aquatic environments (Reis 2007).

Popular myths make people see bats as dangerous pests to our health, and this has led to the death of several important species. Much of this is due to the alarming period that the world experienced with rabies in the 1990s and the impact that bats still have on the occurrence of human cases described in recent years. In Brazil, for example, there are currently around 178 species of bat and only three feed on blood, and yet the idea still prevails that all bats are vampires and capable of transmitting rabies, even though most hematophagous bats live in rural environments near livestock farms and are a minority among bats. University outreach and scientific discussion about the role of bats in the occurrence of infectious diseases should be done with caution and responsibility. In addition to bat hunting, forest destruction has also had an impact on the decline of bat populations and their migration to urban areas. Of course, most species adapted to the urban environment migrate for food and favorable conditions for

survival, but deforestation has influenced this migration and the death of many species (Jacobi 2003).

Non-destructive strategies for managing bat populations are essential to mitigate zoonotic disease risks while preserving their ecological roles. These approaches can be adapted to various contexts, including urban and rural environments. One effective strategy is physical exclusion, which involves identifying entry and exit points in buildings and using barriers such as nets or exclusion devices to prevent bats from accessing these spaces. Modifying habitats by removing nearby food sources, such as fruit trees, and dense vegetation can discourage bats from settling in urban areas. Similarly, increasing lighting in roosting areas can deter bats, as they prefer darker environments (Kotait 2003).

Providing alternative shelters, such as installing nest boxes in appropriate locations, offers a humane solution by redirecting bats to safer areas. Collaboration with wildlife experts or environmental agencies is vital to ensure best practices and compliance with region-specific regulations. Additionally, sealing cracks and openings in buildings, once bats have vacated, can prevent their return. In some cases, sound and visual repellents, such as high-frequency devices or flashing lights, can be used to discourage bats, although these methods may vary in effectiveness depending on the species. Public education plays a critical role in fostering coexistence, raising awareness about bats' ecological importance, and promoting non-lethal management practices. Continuous monitoring of implemented measures is necessary to adapt strategies as required, ensuring long-term success in managing bat populations ethically and sustainably (Kotait 2003).

15

Population control must be carried out with sensitivity and respect for the role of these animals in the ecosystem. Seeking guidance from qualified professionals is essential to ensure that the practices adopted comply with laws and ethical standards.

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