



Bats and COVID-19: villains or victims?

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Abstract: Since the beginning of the COVID-19 pandemic, bats are being pointed as responsible for its origin, even without solid scientific evidence. In this opinion piece, we discuss the most updated information on bats and COVID-19 and argue that bats should not be blamed for a disease they are not responsible for. Bats should be seen not as dangerous animals but, instead, as sources of several scientific insights useful for human health.

Keywords: Chiroptera; spillovers; wildlife; zoonoses; zoonotic spillovers.

Morcegos e a COVID-19: vilões ou vítimas?

Resumo: Morcegos e COVID-19: vilões ou vítimas? Desde o início da epidemia de COVID-19, morcegos estão sendo apontados como os culpados por sua origem, mesmo sem evidências científicas sólidas que apontem para tal. Neste artigo de opinião trazemos informações atualizadas sobre morcegos e COVID-19 e discutimos porque morcegos não deveriam ser culpados por uma doença pela qual não foram responsáveis. Morcegos não deveriam ser vistos como animais perigosos, mas sim como fontes de várias ideias e abordagens científicas úteis para a saúde humana.

Palavras-chave: Chiroptera; doenças zoonóticas; transferência de patógenos; vida silvestre; zoonoses.

Since the beginning of the COVID-19 pandemic, we have been flooded by information pointing to bats as responsible for its origin. However, there is no consensual, categorical study to date showing a direct connection between bats and the SARS-CoV-2 virus, responsible for the COVID-19 pandemic. On the contrary, the available studies point to the existence of an intermediate host, whose identity is unknown at the moment. The search for this host began with the sequencing of the SARS-CoV-2 genome (Wu et al. 2020), the virus causing the disease in humans. The genome of a coronavirus (RaTG13) previously isolated from *Rhinolophus affinis* bats in China is about 96% similar to the SARS-CoV-2 genome (Zhou et al. 2020). Although the RaTG13 coronavirus has high genetic similarity to SARS-CoV-2, there are divergences in the viral receptor ligand domain (RBD) region, suggesting that this bat coronavirus cannot efficiently bind to human ECA2. On the other hand, a pangolin coronavirus has a strong resemblance to SARS-CoV-2 in the RBD region, which supports the hypothesis of an intermediate host.

This genetic distance suggests that SARS-CoV-2 and RaTG13 diverged about 40 to 70 years. In other words, decades have passed since these viruses shared a common ancestor, but since then those viruses differentiated (Zhou et al. 2020). Such divergence may also point to the existence of not just one, but multiple intermediate hosts.

Pangolins (*Manis javanica*) have been identified as this potential intermediate host, a hypothesis that has not yet been ruled out. However, coronaviruses isolated from pangolins also proved to be too distinct to represent the direct ancestors of SARS-CoV-2 (Lam et al. *in press*). Snakes had also been suggested as potential intermediate hosts, a possibility that also seems to have been refuted. There is consensus among scientists that SARS-CoV-2 originated from wildlife (Fam et al. 2020) but, in fact, this origin has not yet been found in nature.

Bats have received considerable attention in relation to coronaviruses, mainly because they carry a great variety of such viruses and are their natural and ancestral reservoirs (Ge et al. 2015). Moreover, since the SARS epidemic, in 2002, their mobility – acquired through flight – was identified as a characteristic that could enhance pathogen dispersion. In consequence of this attention, more viruses were found in this group. As would be expected, rodents and bats, the most diverse groups among mammals harbor viruses proportional to their diversity, but a recent study clearly shows that bats and rodents – usually the ‘villains’ pointed out in epidemics – are neither more nor less important as reservoirs of viruses with potential for contamination in humans than other animals. In fact, there is a relationship between greater potential for virus transmission among mammals with high abundance, such as those we raise and with whom we maintain greater contact, such as goats, pigs and cattle (Mollentze & Steicker 2020).

Our understanding of the complex viral transmission dynamics from wildlife to humans will remain limited until we have carefully searched for viruses circulating in a much more representative sample of all animal taxa.

Fam et al. (2020) suggest that SARS-CoV-2 has become a human specialist. This means high performance to infect *Homo sapiens* and less ability to have the same efficiency to infect other species unless new mutations and/or recombination create a derived coronavirus capable of breaking the species barriers again, fueling this never-ending arms race between hosts and pathogens. Such a scenario demonstrates the complexity of the process, and the complexity of the topic itself for non-specialists. Furthermore, unfortunately, the details of the intricate and intriguing network of relationships between pathogens, primary and intermediate hosts, their transmission mechanisms, and the possibilities of associated mutations are not always conveyed in a complete and correct manner to the general public, contributing to misguided and hasty interpretations. In doubt or in a hurry to point out a 'culprit' for COVID-19, bats ended up being held responsible for something they were not directly involved in. And the results have been extremely negative for a group that, unfortunately, already suffers from an unfair negative reputation among the public opinion.

Reports of increased cases of persecution, vandalism, and destruction of roosts and bat populations have boomed around the world since the beginning of the pandemic (Fenton et al. 2020, Zhao 2020). Such acts will negatively affect the conservation of the group and the irreplaceable ecosystem services provided by the 1421 species of bats described to date (Wilson & Mittermeier 2019). Such services include the pollination of hundreds of plant species, many of which are of economic interest, seed dispersal and habitat regeneration, the control of insect populations, including agricultural 'pests' and disease vectors for humans and commercial animals (Kunz et al. 2011; Ghanem & Voigt 2012).

Condemning bats is also a mistake from a scientific point of view. Several studies have shown that bats have high resistance to viral infections, not reacting with the typical inflammatory response that occurs in several animals, including humans (Hayman 2019; Huang et al. 2019). This inflammatory response is a way of fighting infection, but when it exceeds certain levels, it may cause pathological damage to organisms, contributing to aging and age-related diseases. Bats have a natural ability to mitigate inflammation caused by stress and infection, therefore being excellent models to understand how to deal with viral infections (Huang et al. 2019). Mechanisms of gene expression and self-repair in bat DNA – not seen in humans or other mammals – also seem to explain another unique characteristic of this group: its longevity, which is much higher than that expected for animals of their size (Teeling et al. 2018). This makes bats ideal models for finding solutions to slow the aging process, as well as finding treatments for age-related diseases in humans. Further, bats have low susceptibility to cancer (Huang et al. 2019), and the oral microflora of some species, for example, appears to decrease susceptibility to caries (Brändel et al. 2013). These should be reasons enough to look at these animals as potential reservoirs, not of diseases, but of extremely useful information for humans. But in the midst of a pandemic – and in the search for a 'culprit' – this importance seems irrelevant.

Dangerous are also the alarmist views pointing to the enormous risk we would be taking because we live with many species and, consequently, with the viruses, bacteria and other microorganisms that they host (e.g. Lapola 2020). Should we blame our rich biodiversity for spillovers caused not by the animals themselves, but by human action and the way we interact with the natural environment? Obviously not. All animals, including mammals – and we humans are no exception – are natural hosts for thousands of species of microorganisms, but only a small portion of this biota has lethal potential, and those with pandemic lethal potential are even fewer. Brazil is a megadiverse country, third in the world in terms of bat species richness (182 so far – Nogueira et al. 2018), first in the world in number of primate species, being among the top three of birds, amphibians and reptiles, among several other animal and plant groups. Attributing a direct causal relationship such as 'more species, more viruses, more danger' is not correct, simply because such a relationship does not necessarily exist. There are several other variables that need to be considered in a zoonotic contamination process.

Zoonotic spillovers are complex processes (Plowright et al. 2017; Ellwanger & Chies 2018), but the knowledge accumulated so far shows that their occurrence may not result from the direct presence of animals, and even less from high levels of biodiversity, but from human action and how we interact with the natural environment. Indeed, the reduction in the number of species and their habitats seems to be a much more direct cause for the spread of diseases of wildlife origin (Ezenwa et al. 2006; Keesing et al. 2010). In fact, several studies point to the existence of the so-called 'dilution effect', i.e., in the presence of several potential host species of the same virus (or its variants), the encounter rate between infected individuals and individuals likely to be infected decreases, transmission rates decrease, as well as decreases the density of infected individuals in populations of the different species present (Ostfeld & Keesing 2000; Schmidt & Ostfeld 2001; Swaddle & Calos 2008). Interestingly, it was recently proposed that the reduction in the dispersion of pathogens that followed the extinction of the mammalian megafauna at the end of the Quaternary might have led to an increase in the emergence of diseases of zoonotic origin in humans (Doughty et al. *in press*). The fact is that the development model that we insist on following is the cause of the environmental imbalances that we are witnessing, is at the origin of the COVID-19 pandemic, and will be the cause of others that will follow if we do not change our action on the planet. Simplistically associating bats, or any other animals, with zoonotic spillovers is clearly a disservice both to them and to humans. Service will be to take advantage of this moment to become aware that our depredatory actions on habitats and species also have consequences for our survival as individuals, perhaps as a species, and with that beginning to change the way we act on our planet. There is no lack of papers showing the link between environmental imbalances and emerging infectious diseases in the literature (e.g. Daszak et al. 2001, Weiss & McMichael 2004, Jones et al. 2008 Ellwanger et al. 2020). However, there is a lack of effective actions to avoid the environmental imbalances that are consequences of the predatory advance on natural areas by human activities such as urbanization (Rezende et al. 2018, Favoretto et al. 2019), agriculture (Fernandes et al. 2013, Andrade et al. 2016) and mining (Rotureau et al. 2006; Tuesdays-Trettel et al. 2019).

As we wrote this point of view, an article by Thomas Lovejoy, a renowned conservationist with several studies in the Neotropical region, was published in the National Geographic magazine (May 2020). We took the liberty of concluding by reproducing an excerpt of his words in that article: “*Nature sustains us. It’s where we originated. The lesson for humanity from this pandemic is not to be afraid of nature, but rather to restore it, embrace it, and understand how to live with and benefit from it. All that biodiversity is essentially a gigantic library of solutions, pretested by natural selection and evolution, to various biological challenges. The idiosyncratic biology of bats, for example—the fact that they are somehow immune to the coronavirus—might contribute to development of a treatment in humans. Humanity has huge respect for libraries of our own works; there is every reason to treat the living library of nature with the same respect and care.*”

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Author Contributions

Maria João Ramos Pereira: Contributed equally to manuscript preparation.

Enrico Bernard: Contributed equally to manuscript preparation.

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Conflict of interest

MJRP, EB and LMSA are, respectively, Vice-President, President and Founder and Coordinator of the Cerrado Secretariate of the Sociedade Brasileira para o Estudo de Quirópteros – SBEQ (Brazilian Bat Research Society).

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