

## VIEWPOINTS

## Coronaviruses in Brazilian bats: A matter of concern?

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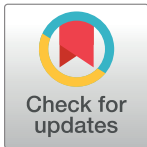
According to the United Nations Environment Programme (UNEP), Brazil is the most biologically diverse country in the world. It is estimated that Brazil hosts between 15% and 20% of the Earth's biological diversity, with the greatest number of endemic species on a global scale. Taking into account its wide natural diversity, Brazil suffers from serious environmental troubles. These problems, such as deforestation—leading to fragmentation and loss of habitats and overexploitation of plants, animals, and monoculture by agribusiness—are the main threats to Brazilian biodiversity [1]. Despite the plenteousness of legislation aiming protection and preservation of the natural environment, the continuing destruction of biomes is still an ongoing matter of concern [2].

The invasion of natural ecosystems facilitates the contact between people, domestic animals, and wildlife populations. Indigenous, isolated populations are at increasing risk of acquiring infectious agents to which they have not been previously exposed. The currently ongoing pandemic caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) plus the past outbreaks of Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) have once more highlighted (flipped the coin to reveal) how devastating and life threatening viral infections could be.

Multiple lines of evidence support an evolutionary origin for all human coronaviruses (CoV) from wild hosts, especially bats, which, due to its extraordinary adaptability to different niches, host a variety of microorganisms. Given the proper occasion, genetic diversity will play its part in evolution and eventually give rise to infectious agents, which could jump to a different animal species with unpredictable consequences. Bats are known to be reservoirs of a number of viruses with the potential to cause serious human diseases, including rabies, Ebola, Nipah, and the currently pandemic Coronavirus Disease 2019 (COVID-19), caused by SARS-CoV-2.

There is a consensus that the question is not “if” novel zoonotic viruses will rise but “when.” Currently, 2 to 3 novel RNA viruses are discovered every year; RNA viruses are the most common class of pathogens behind new human diseases [3]. Central and South America are considered world hotspots for the emergence of new mammalian viral zoonoses [4]. Brazil is a country of continental dimensions and home to an immense biodiversity and with more than 200 million inhabitants; with ecosystems constantly threatened by degradation, plus human and wildlife in close contact in several locations, these facilitate jumps of infectious agents between species.

Brazil is the country with the greatest diversity of mammals, with approximately 700 species, of which about 25% are bats [5]. At least 178 species of bats have been identified in



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different biomes, some of which definitely associated with the transmission of important zoonoses, such as rabies and histoplasmosis. Despite the large number of bat species, studies that explore the microbiomes of such species are scarce. Nevertheless, a few have revealed potential risks (e.g., pathogen spillover and/or transmission), such as CoV and representatives of other viral families in both synanthropic and sylvatic bats [6–9]. Members of the family Coronaviridae infect mammals, birds, and fish and are allocated into 4 genera: *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus*, and *Deltacoronavirus* (colloquially, alpha-, beta-, gamma-, and deltacoronaviruses). Due to the great diversity of alphacoronaviruses and betacoronaviruses reported in bats, it is believed that such species are reservoirs and progenitors of many members of these genera, whereas delta- and gammacoronaviruses seem to have originated from CoV of birds. The emergence of SARS-CoV-2 has thrust bat betacoronaviruses into the spotlight again. Most CoV recovered from Brazilian bats are alphacoronaviruses [6,7,10]. However, in 2016, 2 distinct betacoronaviruses that clustered within MERS-CoV were detected in bats with potential contact with humans from the Atlantic Forest biome [11]. Other betacoronaviruses were reported in Central and South America [8,9], highlighting the broad circulation of these viruses in neotropical bats. Furthermore, the diversified ecology, a high number of coexisting bat species and their local abundance in relation to other mammalian species could make neotropical bats major spreaders of viruses, as human population density increases in the ever growing occupation of neotropical ecosystems [9].

Should CoV in Brazilian bats be a matter of concern? A prudent answer to this question would certainly be positive. However, unfortunately, it is not possible to calculate the risk and/or the point in time where viral host switching events might occur; moreover, even more difficult would be to predict the emergence of an outbreak or epidemics. Nonetheless, it is possible to state categorically that this will happen, as we have seen with SARS-CoV-2 and many other emergent viruses that spilled over from wildlife with impact on human health in the last 20 years. Furthermore, the scarce but valuable data on viral detection in neotropical bats reinforce the need for expanded and continuing efforts to widen our knowledge on the viral communities of wild and synanthropic mammals. This will certainly contribute to contingency plans in the advent of potential viral threats to humans and/or other species.

How can we be prepared? Is there anything we can do to minimize the burden of such inevitable course? The answer, if it exists, is not simplistic. Improvements on the national health system (Sistema Único de Saúde (SUS))—to ensure sufficient and adequate access to health-care, allied to a strong focus on environmental education since the very early days of school attendance—would certainly have a positive effect on the formation of individuals concerned with environmental problems. Moreover, investments on research on the microbiome of wild and synanthropic animals may increase our degree of preparedness and contribute to contingency plans to reduce the potential risk of zoonotic diseases. However, the preventive measure that might have the most significant impact the emergence of new, potentially zoonotic viruses is the implementation of conservation policies to control the disturbance of biomes. Ensuring environmental interventions along with sustainable exploration of natural resources would minimize exposures to risk factors from emerging wildlife diseases, yet preserving wildlife in its natural “status quo,” thus contributing indirectly to accomplish the interrelated goals of health, environmental sustainability, and development.

Such achievement would require more profound interventions, where the One Health concept spanning human, animal, and environmental health would become part of a unified effort, stimulating inter- and multidisciplinary professional, disciplinary, and institutional bonds to work in a more integrated fashion [12]. A complex concern such as the emergence of infectious diseases, especially in low-income countries, needs to be addressed using this key concept, in which particular characteristics of human, environmental, and animal health are

considered in a unified way to more effectively detect, understand, prevent and, if necessary, to intervene aiming to solve related public health issues [2,13–16].

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