

# COVID-19 and threats to bats

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Bats are very diverse, including over 1400 species (Simmons and Cirranello 2020), meaning that one in every five living mammal species is a bat. These remarkable animals include species living on every continent except Antarctica. Many of them perform essential ecosystem services including consuming large quantities of insects, dispersing seeds, and pollinating flowers of numerous tropical and sub-tropical plants including many of economic importance (e.g., durian in southeast Asia, agaves used to make tequila in North America; Kunz et al. 2011). Lamentably, the International Union for the Conservation of Nature Red List (2020) identifies 77 species of bats as Endangered. Most bats are small mammals with low rates of reproduction (typically one or two young per year) and exceptionally long lifespans, with some individuals living over 40 years in the wild (Munshi-South and Wilkinson 2010).

In general, bats are remarkably tolerant of some viral infections (Brook et al. 2020). Bats have been said to harbor more zoonotic viruses than other mammals (Olival et al. 2017). Yet in a recent comprehensive data synthesis, Mollentze and Streicker (2020) demonstrated that the proportion of zoonotic viruses (DNA and RNA) varies little across orders of birds and mammals. The number of zoonotic viruses in an order is a simple function of the numbers of species in it. The richness of zoonotic viruses in rodents and bats reflects their diversity (number of species). Bats are indeed “special” (Brook and Dobson 2015), but it is because of their marvelous diversity.

Recently Professor Huabin Zhao (College of Life Sciences, Wuhan University) alerted us to the impact that COVID-19 could have on governmental and public perceptions of bats (Zhao 2020). Specifically, bats have played a role in the evolutionary history of the severe acute respiratory syndrome (SARS)-CoV-2 virus (Zhou et al. 2020). This could be another reason for people to fear these mammals, even in China where bats traditionally have been strong positive symbols (Sung 2002). We know what can happen when people fear bats and characterize them solely as disease reservoirs (e.g., O’Shea et al. 2016). Recently, in Peru, citizens fearful of bats as a source of COVID-19 burned bats in their cave roosts ([phys.org/news/2020-03-peru-blamed-coronavirus.html](https://phys.org/news/2020-03-peru-blamed-coronavirus.html)). Reactionary efforts against bats will exacerbate other threats to viability of bat populations that we know can decline very rapidly. Within 10 years of the 2006 introduction of white-nose syndrome (WNS) to the eastern United States, we lost millions of bats, and populations of some species were reduced by over 90% (Frick et al. 2010). The fungus that causes WNS, which had been introduced from Europe, kills bats by interfering with their rhythm of hibernation (Cryan et al. 2010). Because WNS is an ongoing threat to bats (Lorch et al. 2016), limiting negative perceptions of bats is particularly important in North America,

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but this also applies globally where various bat species are threatened by habitat destruction, hunting, and persecution (IUCN 2020).

Phylogenetically, the virus (SARS-CoV-2) responsible for the disease COVID-19 is most closely related to bat coronaviruses (Zhou et al. 2020; SARS-CoV). This suggests that the virus causing COVID-19 originated in bats (Andersen et al. 2020). But we do not know when or how the initial spillover from bats occurred. The SARS-CoV-2 virus is 96% similar to the virus found in horseshoe bats (Zhou et al. 2020). However, in evolutionary terms, a few percentage points of difference can mean a lot; consider that the genomes of humans and chimpanzees are ~95% similar (Britten 2002). Viruses can evolve quickly, but Boni et al. (2020) used phylogenetic reconstruction to estimate that the bat virus and the human virus SARS-CoV-2 diverged 40–70 years ago. Massive sampling gaps and the lack of preventative surveillance research means we do not know what other animals might have been intermediate hosts. Previous zoonotic viruses such as SARS-CoV and Middle East respiratory syndrome (MERS)-CoV apparently originated in bats but were transmitted to humans through other intermediate mammalian hosts such as civets and camels (Wang et al. 2005, 2006; Chu et al. 2014). How did the virus that causes COVID-19 get into the human population? Many people (“the public”) expect scientists to have answers to all of these questions. But we do not—at least not yet. Indeed, science is about unanswered (and even unasked) questions. We do know that anthropogenic land use and encroachment likely played a role in the spillover of many zoonotic viruses into humans (Jones et al. 2013). Furthermore, global travel played an even more important role in the spread of the COVID-19 pandemic (Chinazzi et al. 2020). On a positive note, the pandemic has generated unprecedented levels of collaboration among scientists and institutions, increasing our ability to rapidly acquire, analyze, and critically assess data.

We must recognize that in matters of zoonotic diseases such as COVID-19, we set the stage for our own fortune. Increasing human populations encroach more every year on wildlife and natural spaces. Our impact goes beyond habitat destruction and climate change. It extends to using wildlife as pets or harvesting them as bushmeat even when or where other protein sources are readily available (Fèvre et al. 2006; Wang et al. 2006; Golden et al. 2011). Now scientists that work on bats are struggling with other questions. Could humans transfer COVID-19 to bats? How can we protect both bats and people? We repeatedly see that we need more data to make informed decisions. Aside from bats and coronaviruses, how can we predict and avoid zoonotic spillover events such as that leading to the COVID-19 pandemic? A future pandemic may not involve bats and coronaviruses. Bats live very long lives and apparently do not get seriously ill from some of the pathogens that they host—perhaps they hold the key to treatments not yet discovered. Regardless, human activities that modify infection processes and contact between wildlife, domestic animals, and humans—not bats themselves—cause zoonotic spillover events.

As Walt Kelly’s (1972) cartoon character Pogo said, “we have met the enemy and he is us”.

## Author contributions

MBF, SM, SMT, NBS, and DJB conceived and designed the study. MBF, SM, SMT, NBS, and DJB drafted or revised the manuscript.

## Competing interests

Brock Fenton is an editorial board member.

## Data availability statement

All relevant data are within the paper.

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