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Letter to the Editor

Misconceptions and misinformation about bats and viruses



To the Editor,

In recent decades, the role of bats, order Chiroptera, as potential reservoirs for several zoonotic viruses has received considerable attention. This has dramatically increased since the emergence of the SARS-CoV-2 virus causing COVID-19, resulting in numerous recent reviews. Unfortunately, some of these contain outdated or false statements and incomplete treatments and/or misinterpretations of the published literature, such as Bonilla-Aldana et al. (2021). We herein report the main problems with their paper and illustrate our point with examples; a complete enumeration would be too extensive.

First, we submitted two independent Correspondences to the Journal, on 28/09/2020 and 30/09/2020, asking for a retraction of the accepted and “in Press, Pre-proof” paper published online on 20/08/2020. That paper contained multiple critical errors and misrepresentations related to bat taxonomy, ecology, and physiology, and the linkages between bats and specific viruses. Around 25/11/2020, the “In press” paper was substantially amended and expanded, however, these changes only fixed a minority of the reported problems and even added new ones, including several baffling sentences (e.g., “Bats are mammals, bone marrow and B cells”).

Second, Bonilla-Aldana et al. wrote a confusing/misleading section about bat nomenclature. As clearly expressed via a disclaimer on the NCBI-NIH website, the system used in their Taxonomy Browser is “not an authoritative source for nomenclature or classification”, and the NCBI-NIH advise to “consult the relevant scientific literature for the most reliable information”. Twenty years ago, molecular data clearly rejected the subdivision of the Order Chiroptera into ‘Megachiroptera’ (for which the authors created a new term in Table 2 and Fig. 1: the ‘Macrochiroptera’) and ‘Microchiroptera’ (Jebb et al., 2020; Teeling et al., 2000). The 1432 currently known bat species are subdivided into Yinpterochiroptera and Yangochiroptera; several species formerly grouped with ‘Microchiroptera’ are more closely related to ‘megabats’ than to other ‘microbats’. Using this established classification is critical to understanding bat evolution, including bats’ association with viruses (Foley et al., 2015; Teeling et al., 2018). Also, Bonilla-Aldana et al. include several misspelled or outdated genera/species names (e.g., *Sturmina* instead of *Sturnira*, *Dhiphylla* instead of *Diphylla*, *Hipposideros commersoni* instead of *Macronycteris commersonii*, *Hemiderma* instead of *Carollia*, *Artibeus turpis* instead of *Artibeus/Dermanura phaeotis*). Also, the species *Epomophorus gambianus* occurs in Africa and not in Asia, as reported in their Figure 1.

Third, Bonilla-Aldana et al. pack vague, incompatible, inaccurate, and incorrect statements in their overview of the biology and ecology of bats. For example, contrary to what they wrote, hematophagous (=feeding on blood) bats do not “capture birds and mammals” that are tens to several thousands of times heavier than them. They feed on these target animals by drinking blood from an incision on their skin. ‘Megabats’ do not weigh on average 1 kg; only the largest ones exceed 1 kg (Altringham, 2011). In our previous Correspondence, we wrote that “‘Microbats’, formerly representing ‘Microchiroptera,’ do not eat mainly flowers and fruit but insects”, a sentence that has been pasted in the paper, but without deleting the original sentence saying: “Their size ranges from 4 to 16 cm and feed mostly on flowers and fruit”, which is both confusing and contradictory. Also, it is unclear if the authors are referring to the wingspan size range, as they did before for the ‘Megabats’; if so, the statement is clearly wrong.

Fourth and most importantly, we found many problems with their review of the viruses listed as transmitted from bats to other mammals, including humans. It is concerning that despite affirming that they conducted a comprehensive review (as the authors claim in the online “highlights” of the paper), the bulk of their data (summarized in Tables 1, 2, and 3) are lacking any references, making it impossible to understand how the authors came up with an identified reservoir/host, their modes of transmission and related factors. For several of these viruses, transmission chains remain unknown (e.g., Ebola, Influenza A, togaviruses). Bonilla-Aldana et al. should have noted that some of the claims they made have been rejected by others (Dengue; Vicente-Santos et al., 2017). The authors also make incorrect claims, such as “Rabies transmission primarily occurs via direct bites or scratches from infected bats; secondary transmissions in humans take place through contact with infected pets”. According to the WHO, 99% of human cases of rabies are transmitted by domestic dogs.

In short, this tendentious review is far from comprehensive or accurate. The authors appear to have consulted a random subset of publications. The selection includes contradictory statements. The assignment of hosts and viruses is not consistent (e.g., for Ebola, several fruit bats in Table 1, and *Myotis* in the text; for Coronaviruses, *Dobsonia moluccensis* in Table 2, 12 different bat species in Table 1 [including *Dobsonia moluccensis*], bats and rodents in the text).

Anyone presenting a review of a taxonomic group and its diseases should include experts in the taxonomic group’s biology and ecology, as well as experts in the diseases reviewed. Otherwise, the review will only create confusion and misconceptions.

Conflict of interest

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