Letter to the Editor

**Bat reservoirs related to SARS-CoV-2**

Reservorios de murciélagos relacionados con el SARS-CoV-2

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Dear Editor,

Bats are mammals documented to be infected by coronavirus SARS-like related to SARS-CoV-2 which cause COVID-19.(1) Bats represent about 20% of all classified mammal species, over 1,200 species. They are largely fruit-eating, seed dispersers and pollinators around the wold,(2) this made this species important in the ecosystems ecology.

When the COVID-19 pandemic was declarated in december 2019, the search for origins was found in sequencing of coronavirus related to bats. This suggests that these animals may be long-term reservoir host for the coronavirus SARS-like betacoronaviruses and may recombine between species of bats.(1) The species of bats related to the coronavirus SARS-like are *Rhinolophus affinis* and *Rhinolophus sinicus* and are distributed principally in China, Europe and Africa (Fig. 1).(3) The sequences of new coronavirus has been submitted to [GISAID](https://www.gisaid.org/) and [GenBank](https://www.ncbi.nlm.nih.gov/genbank/). The most emparented coronavirus SARS-like is BetaCoV/bat/Yunnan/RaTG13/2013 found in *Rhinolophus affinis* with 96.2% (accession MN996532) similarity with WH-Human\_1 (SARS-CoV-2) (accession MN908947) (Fig. 2) the first sequencing sample in humans, although the SARS-CoV-2 was closer to the bat\_SL\_CoVZC45 (accession MG772933) and the bat\_SL\_CoVZXC21 (accession MG772934) both found in *Rhinolophus sinicus.*(3) The genus Rhinolophus (horseshoe bats) in the family Rhinolophidae demonstrated a high posibility to be the host of SARS-like betacoronaviruses(4) and could cause a future disease outbreak. We have to focus on possible mutations and hosts that may cause pandemics in the future and their zoonotic role.



**Fig. 1 -** Distribution of species of the *Rhinolophidae* family in the world.



Source: https://nextstrain.org/groups/blab/sars-like-cov

**Fig. 2 -** Phylogeny of SARS-like betacoronaviruses including novel coronavirus SARS-CoV-2.

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