

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 world,⁽²⁾ this made this species important in the ecosystems ecology.

When the COVID-19 pandemic was declared 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://gisaid.org) and [GenBank](https://genbank.org). 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 possibility 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.

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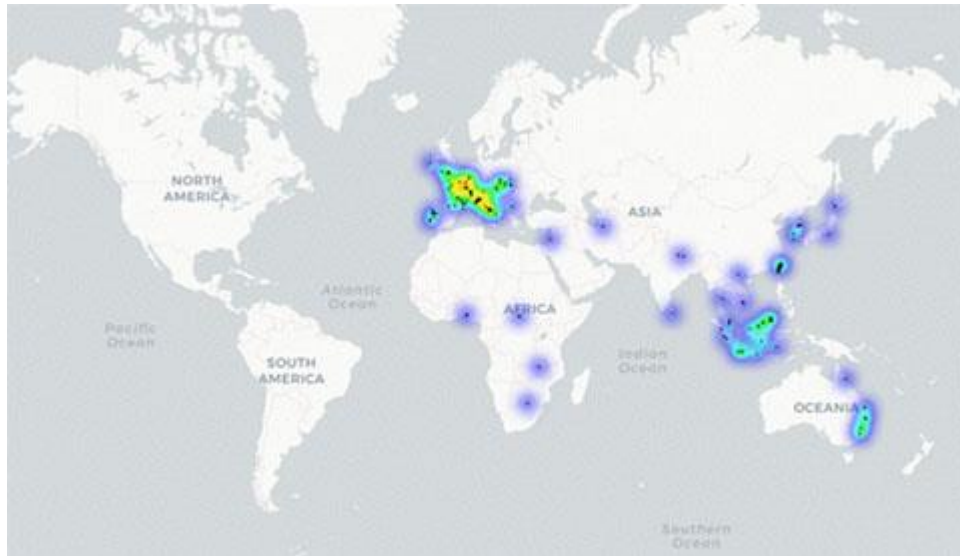
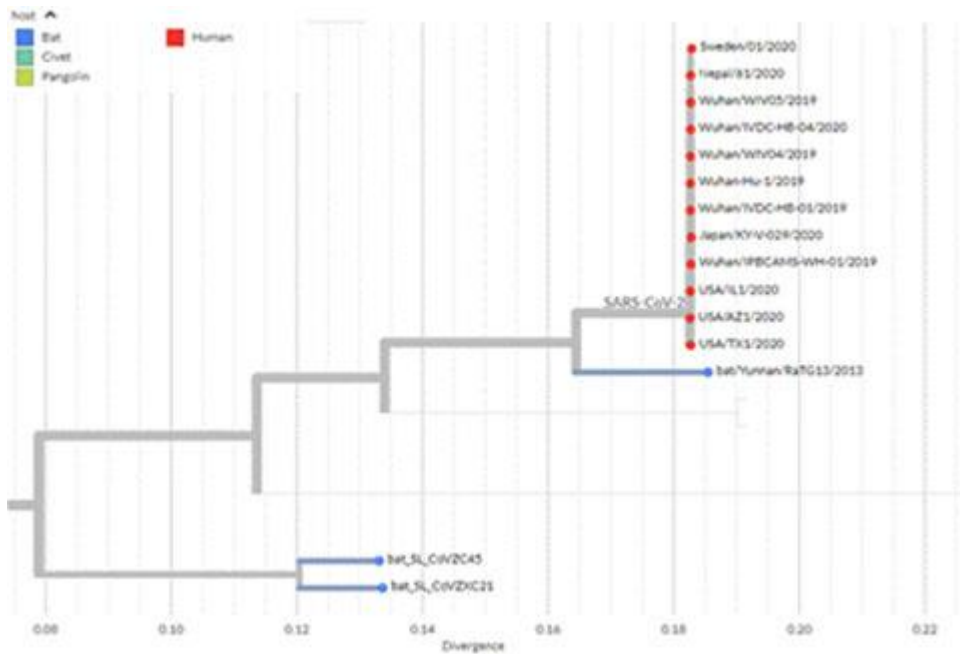


Fig. 1 - Distribution of species of the *Rhinolophidae* family in the world.



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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