




LETTER TO THE EDITOR

Origins of SARS-CoV-2: navigating in genes

Orígenes del SARS-CoV-2: navegando en los genes

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Dear Editor:

SARS-CoV-2 causes COVID-19 pandemic;⁽¹⁾ COVID-19 is associated with high morbidity and mortality in patients with chronic diseases and the elderly.⁽²⁾ This is a coronavirus that has mutated for decades causing outbreaks in humans.⁽³⁾ Due to the promptness of declaration of the pandemic, its origins have been wrapped in the spotlight, that is why the objective of this letter is to shed light on the research that exists in this regard.

All coronaviruses share the same evolutionary ancestry, the new coronavirus is related to betacoronaviruses and within the Sarbecovirus lineage, specifically, those that infect bats.⁽⁴⁾ Other studies indicate that it is possibly due to a mutation of the coronavirus that infects pangolins⁽¹⁾ and snakes.⁽⁵⁾ Phylogenetic analyzes show recombination of bat coronaviruses that share the ORF1b site.⁽⁵⁾ To date, the closest described relative to the new coronavirus nCoV-



2019 in a non-human host is a bat SARSr-CoV RaTG13 (Genbank MN996532)⁽⁴⁾ sampled from a bat *Rhinolophus affinis* in Yunnan province in 2013 (Figure). These viruses have an amazingly fast mutation rate; recombination can occur within the viral Spike glycoprotein, which

recognizes a cell surface receptor.⁽⁵⁾ Coronaviruses should be kept under epidemiological surveillance since a new outbreak that could turn into a pandemic may exist very soon. More studies are still needed to pinpoint the origins of SARS-CoV-2.

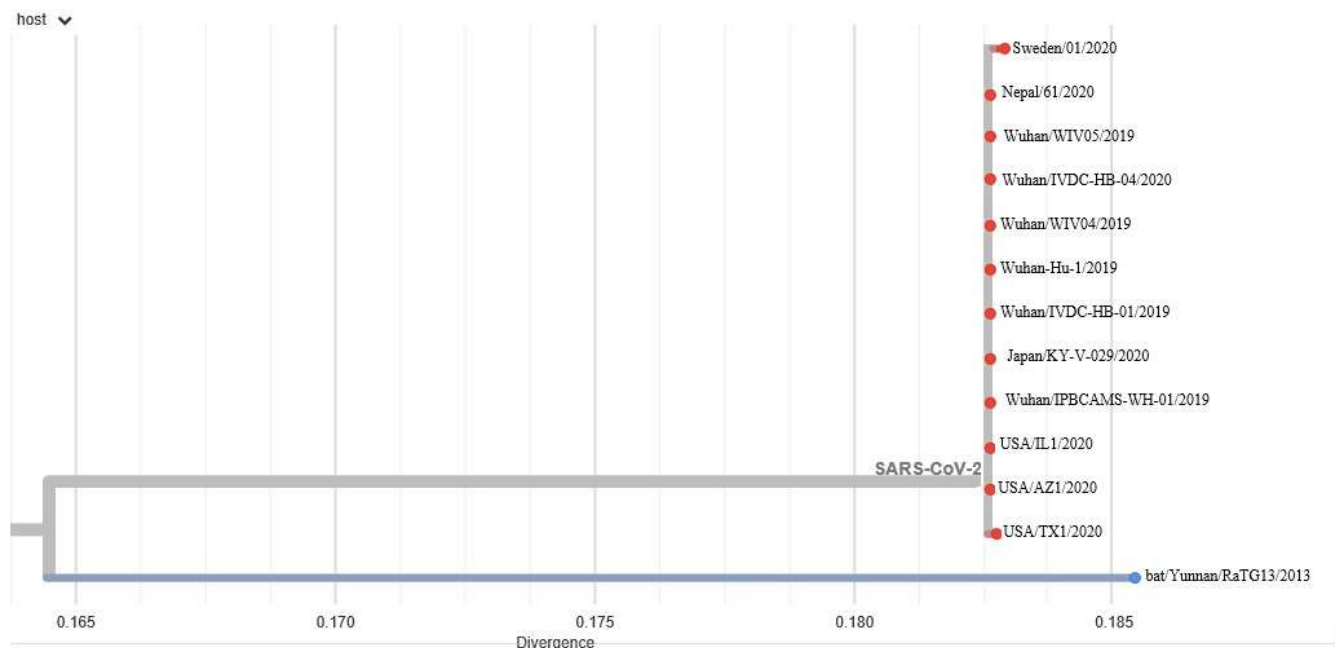


Figure. View of the phylogenetic clade of related betacoronaviruses from different hosts. Adapted from Nextstrain. 2020.

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Conflict of interests

The author has no conflicts of interests to declare.

