

Original

Was SARS CoV-2 really of zoonotic origin?

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Knowing and deciphering the changes or mutations that viruses undergo over time is crucial to develop epidemiological surveillance strategies for SARS CoV 2. The virus has a single-stranded RNA and has evolutionary mechanisms called mutations, which give it biological efficacy to increase its transmissibility, modify its pathogenicity, thereby evading the host's immunity, thus modifying the antigenic response. Some time ago it was believed that changes in coronaviruses were slower than in most RNA viruses, but today relevant mutations in SARS CoV-2 have been observed today (1).

The spread of viruses in living ecosystems requires that microorganisms adapt to different hosts or that humans and animals respond immunologically to attack. This phenomenon generates a race for the evolutionary survival of pathogens that depend on the ability to infect new hosts and that can sometimes "jump" to other species. However, the immune system of the new host will try to eliminate these pathogens, which means that viruses and hosts are locked in an evolutionary game designed to find new strategies to defeat each other. During this process, RNA viruses gain biological efficacy and can evade host attacks (2).

There are more than 200 coronaviruses that live with bats without causing disease, and many of them also do not cause disease in humans or animals. Evidence indicates that recombination events occur within bats, particularly associated with the gene that codes for protein S (spike), which is responsible for the interaction and binding to the ACE2 receptor (3). For this reason, it is presumed that SARS CoV-2 came from bats and that there was an intermediate host in which mutants capable of interacting with receptors on human cells probably arose, as occurred with the SARS CoV epidemic in 2003 and MERS in 2013. But it is not yet clear whether the contact between bats and wild animals in the Wuhan market in China facilitated the entry of the virus into humans, thus initiating the COVID-19 pandemic (4).

The search for the intermediate host has erroneously targeted wild animals such as pangolins, snakes, turtles, and civets (5). However, the genetic sequences did not show a jump from these animals to humans (Figure 1).

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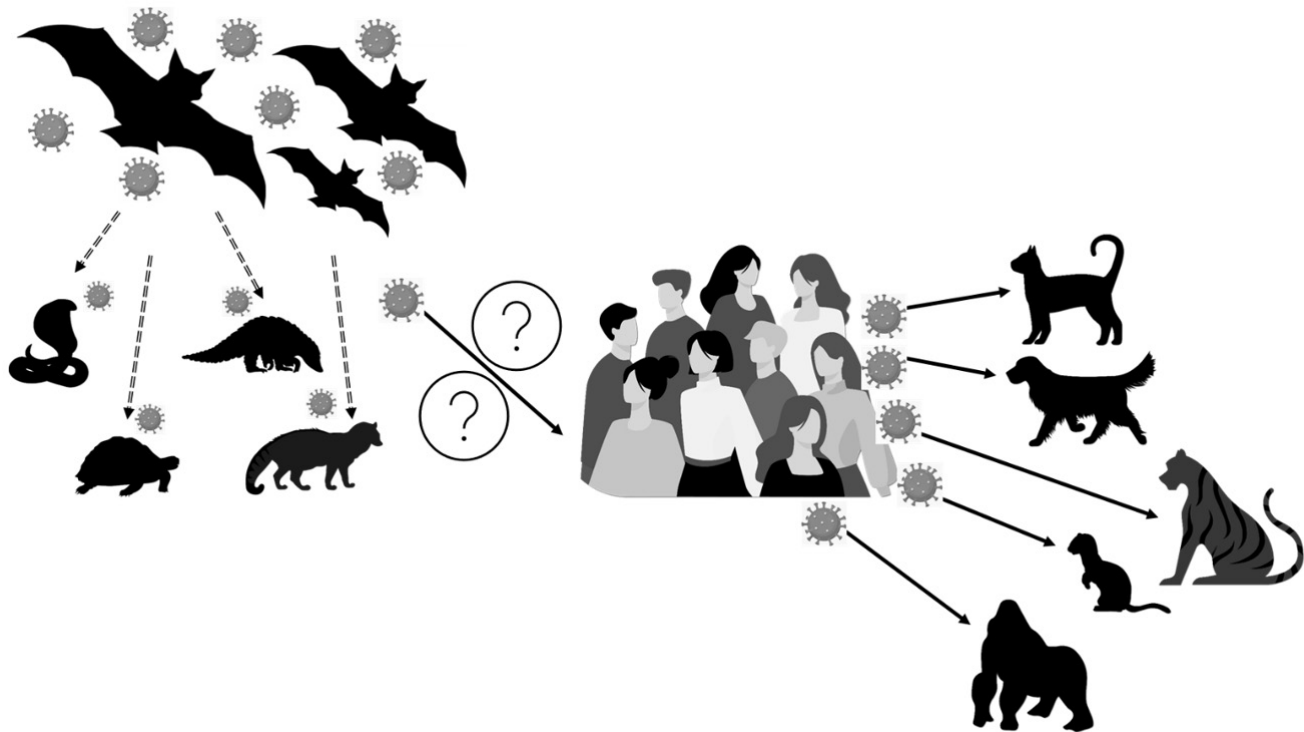


Figure 1. Spread of Coronavirus SARS CoV 2 between species.

Humans infected with SARS CoV-2 promote the spread of the virus to other species such as dogs, cats, captive animals such as big cats, gorillas (7), and animals raised for fur such as minks (8). With this outlook, it is important to carry out ecoepidemiological surveillance in animals that share the ACE2 cell receptor, the site where the SARS CoV-2 virus enters the host's cells. Mustelids (minks, otters, weasels, and ferrets) should be studied, as well as felines and different wild mammals such as deer and shrews (6).

During viral outbreaks other than SARS CoV-2 involving domestic animals, drastic measures such as mass elimination of herds of production animals such as pigs and poultry were applied to prevent viral shedding. However, when wildlife is involved, these extreme measures cannot be used due to the multiple ecological functions of economic importance, such as pest control, seed dispersal or pollination, among others. Therefore, it is crucial to conserve natural environments and educate the population for the care and protection of biodiversity. Wildlife is not a pet; it is not food, and you must learn to live with the precautionary measures promulgated by environmental and health authorities.

It is necessary that while animals are kept under human care, as occurs in zoos and breeding farms, the responsible human team must take care of the corresponding biosecurity measures (9).

To carry out timely epidemiological surveillance to identify mutations in the SARS CoV-2 virus, it is necessary to resort to sequencing and its analysis to characterize the genomic aspects of the virus. In addition, the information must be integrated and completed with the clinical and epidemiological data of the case.

The SARS CoV-2 pandemic has revealed the need to work together on human and animal health under the One health approach as previously proposed (10). We must pay close attention to the animals around us; they could be the bridge that leads us to an upcoming catastrophic zoonotic event.

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