

## SARS-CoV-2 in domestic and wild animals: viral characteristics, genetics, epidemiology and transmission

### SARS-CoV-2 en animales domésticos y silvestres: características virales, genéticas, epidemiología y transmisión

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**Abstract:** COVID-19 is a global pandemic of zoonotic origin that has affected more than 620 million people and is caused by a new coronavirus called SARS-CoV-2. This is a compilation of recent literature on the characteristics, genome, epidemiology, transmission, interspecies transmission, interspecies barrier jumping, genetic characteristics and evolutionary potential of this virus. Some evidence suggests that the virus uses ACE2 to infect various wild animals such as bats, ferrets, pangolins, monkeys, mink, snakes, tigers and lions; and domestic animals such as cats, dogs, cows, buffaloes, goats, sheep and pigeons. However, they can jump the species barrier and infect humans. In addition, coronaviruses can adapt to any ecosystem, especially in wild environments, where they can be maintained through a transmission network in various wild and domestic animals, but they can break paradigms at any time. SARS-CoV-2 has caused a great impact on health systems and economies on all continents, but it is also causing radical damage, changes in habits and common lifestyles.

**Keywords:** SARS CoV-2, Zoonosis, Domestic and Wild Animals

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**Resumen:** COVID-19 es una pandemia global de origen zoonótico que ha afectado a más de 620 millones de personas, es causada por el nuevo coronavirus llamado SARS-CoV-2. El presente, se trata de una recopilación de información bibliográfica reciente sobre las características, genoma, epidemiología, transmisión, transmisión entre especies, salto de barrera entre especies, características genéticas y potencial evolutivo del mencionado virus. Algunas evidencias sugieren que el virus usa ACE2 para infectar a varios animales salvajes como: murciélagos, hurones, pangolines, monos, visones, serpientes, tigres y leones; y animales domésticos como: gatos, perros, vacas, búfalos, cabras, ovejas y palomas. Sin embargo, pueden saltar la barrera de las especies e infectar a los humanos. Además, los coronavirus pueden adaptarse a cualquier ecosistema, sobre todo en ambientes silvestres, donde pueden mantenerse a través de una red de transmisión, en diversos animales salvajes y domésticos, pero estos en cualquier momento pueden romper paradigmas. El SARS-CoV-2 a causado un gran impacto en los sistemas de salud y las economías de todos los continentes, pero también están provocando daños radicales, cambios en los hábitos y estilos de vida comunes.

**Palabras clave:** SARS CoV-2, Zoonosis, Animales domésticos y silvestres

## 1. Introduction

A new coronavirus (SARS-CoV-2) that causes severe acute respiratory syndrome in humans was determined for the first time in Wuhan in December 2019 (Sit et al., 2020); According to the World Health Organization (WHO) and the Pan American Health Organization (PAHO), in 2020, reported that COVID-19 is a pandemic and an international public health problem, with a mortality rate of up to 12% (given in the Wuhan epicenter) (Mizumoto & Chowell, 2020). So far, the dynamics of the new coronavirus are estimated at a transmission rate between  $R_0$  2.2 to 2.56; also, it is important to note that person-to-person transmission and fomite transmission have been linked to the spread of the disease (Sohrabi et al., 2020; Zhao et al., 2020).

As of October 14, 2022, more than 250 countries and territories have been affected by SARS-CoV-2 and 620,878,405 people infected with more than 6,543,143 deaths, with the European continent being the most affected with almost 258 million cases, followed by the Americas with 179 million cases. Countries such as the United States report 95,529,652 cases, Brazil 34,736,653 cases, Argentina 9,713,594 cases, Colombia 6,308,558 cases, Chile 4,674,373 cases and Peru 4,150,121 cases (WHO, 2022). In the world, the pandemic has caused an

unprecedented shock, where countries were forced to ban travel and create containment policies in order to mitigate the spread of the disease (Paul et al., 2020).

This pandemic virus can persist on surfaces such as plastic, glass or metal for up to nine days, but can be effectively inactivated by surface disinfection procedures using products such as 70% ethanol, 0.5% hydrogen peroxide and 0.1% sodium hypochlorite. However, SARS-CoV-2 can remain infective for 14 days at 4°C and 2 days at 20°C in wastewater (OIE, 2020).

Coronaviruses (CoV) mostly infect the respiratory tract, but can also affect the digestive tract, and few viruses can spread to the kidneys, liver or central nervous system. Some CoVs are endemic in domestic animals in different countries, but three are pandemic that have produced fatal cases in humans and they are: SARS-CoV-1, MERS-HCoV and the most recent SARS-CoV-2 (Abdel & Abdelwhab, 2020).

It is important to note that the evolutionary history of coronaviruses defines them as circulating viruses in mammals and birds; in the case, SARS-CoV-2 originally comes from bats, then spreads to intermediate hosts and then infects humans, who can then infect domestic animals, establishing a transmission network; therefore, the identity of the animal source of SARS-CoV-2 remains a key and urgent question to know. In addition, stopping future outbreaks of this type and preventing the transmission of zoonotic diseases to humans should be one of the main research priorities; therefore, it is necessary to consider appropriate eco-sanitary measures, to reduce viral transmission (Li X, 2020).

The objective of this article is to present a comprehensive review of the current literature on characteristics, genome, epidemiology, transmission, interspecies transmission, interspecies barrier jumping, genetic characteristics, and evolutionary potential of SARS-CoV-2.

## 2. Materials and methods

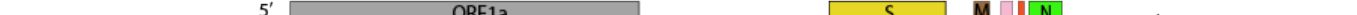
SARS-CoV-2 belongs to the order: *Nidovirales*, family: *Coronaviridae*, subfamily: *Coronavirinae*, genus: *Betacoronavirus*, subgenus: *Sarbecovirus*, lineage "B", originating from bats; it is an enveloped,

spherical virus, 120 nm in diameter, has a large single-stranded RNA genome of positive polarity, with a size of 30 Kb (Leroy et al., 2020) (Figure 1). The viral genome produces 16 non-structural proteins (nsp1 to nsp16) and four structural proteins, such as: spike (S), envelope (E), membrane (M) and nucleocapsid (N) (Figure 2) (Abdel & Abdelwhab, 2020; Chen, 2020).

The viral envelope consists of E and M proteins on which S is anchored. This new coronavirus enters host cells using the binding domain (RBD) of the S protein, which binds to the cellular receptor of angiotensin-converting enzyme 2 (ACE2). And of the co-receptor and TMPRSS2. The proportions of cells carrying ACE2 and TMPRSS2 are high in cats, low in pigs, very rare in dogs, and absent in chickens. Recurrent severe coronavirus infections for humans, originating from animals in the last two decades, this indicates that future outbreaks of related or unrelated Coronaviruses in humans are inevitable; for such a reason, there is an urgent need for improved universal and antiviral vaccines against CoVs (Abdel & Abdelwhab, 2020).

Currently, seven coronaviruses have been reported to infect humans, 3 of zoonotic origin associated with severe acute respiratory syndromes (SARS-CoV, MERS-CoV, and now SARS-CoV-2), and four are ubiquitous with seasonal circulation and mostly cause mild colds (HKU1, NL63, OC43, and 229E) (Leroy et al., 2020). Of these seven human coronaviruses, five are included within the genus beta-CoV, while the other two (NL63 and 229E) belong to the genus alpha-CoV. (Chen et al., 2020); in the case of canine respiratory coronavirus (CRCoV), responsible for respiratory diseases in dogs, it belongs to the genus beta-CoV and has 97% sequence similarity (of protein S) to that of human coronavirus (OC43), probably due to genetic recombination (Xu et al., 2020).

The most common CoV members infecting animals are infectious bronchitis virus (IBV;  $\gamma$ -CoV) in chickens; porcine transmissible gastroenteritis coronavirus (TGEV;  $\alpha$ -CoV), porcine hemagglutinating encephalomyelitis coronavirus (HEV;  $\beta$ -CoV) and porcine epidemic diarrhea coronavirus (PEDV;  $\beta$ -CoV) in pigs; bovine CoV (BCoV,  $\beta$ -CoV) in cattle; canine enteric coronavirus (CECoV;  $\alpha$ -CoV) and canine respiratory coronavirus (CRCoV;  $\beta$ -CoV) in dogs; feline coronavirus (FCoV;  $\alpha$ -CoV) in cats; and murine hepatitis virus (MHV;  $\beta$ -CoV) in mice. Interestingly, HCoV-OC43 and bovine BCoV share 95% genetic identity, indicating possible zoonotic transmission from cattle to humans 100 years ago. The transmission of HCoV-OC43 from bovine



### 3. Result

In a cohort study conducted after the emergence of COVID-19 between January and March 2020 in Wuhan, China, a seroprevalence of 14.70% was determined in cats; three cats with higher titers were owned by three patients, indicating possible direct human-to-cat transmission (Zhang et al., 2020). In Hong Kong between February 12 and March 25, SAR-COV-2 RNA was determined in 2 dogs, both canines contracted the infection in households with infected humans; the first dog was an old animal that appeared with symptoms associated with renal and cardiac failure problems, ultimately died; the second dog did not develop any clinical signs (Leroy et al., 2020).

On March 27, in Belgium, virus was determined by PCR in a symptomatic cat with the presence of diarrhea, vomiting, and difficulty breathing; three days later, viral RNA was identified in samples collected from the oral, nasal, and rectal cavity of an asymptomatic cat from Hong Kong; both cats were infected in households with humans infected with the novel coronavirus (Leroy et al., 2020; Hossain et al., 2020).

In the United States, on April 21, 2020, the CDC and the National Veterinary Services Laboratories (NVSL) announced two cats with respiratory signs and confirmed with the virus in New York, one of the owners had COVID-19 and the other did not (Zhang et al., 2020). Between April and May, in northern Spain, one of eight cats tested positive for SARS-CoV-2 RNA in nasal swabs; the cat had contact with an infected patient with severe COVID-19 symptoms (Abdel & Abdelwhab, 2020). On the other hand, on May 2, in France, the first cat infected with the virus was described and presented clinical signs of respiratory and digestive problems; from which two samples were taken from the animal: one from a negative nasal swab and another from a rectal swab that curiously tested positive for viral RNA; the cat belonged to a person with the disease (Hossain et al., 2020).

Similarly, the U.S. National Veterinary Services Laboratories, announced on April 5, 2020, at a New York zoo, the first report of a tiger infected with SARS-CoV-2, showing signs of respiratory illness, such as dry cough and decreased appetite; however, the Wildlife

Conservation Society (WCS) announced on April 22 that all lions and tigers at the zoo tested positive for viral RNA in fecal samples by PCR. These animals were likely infected by a zookeeper who showed no symptoms of the disease, but was actively spreading the virus (AVMA, 2020).

On the other hand, at the end of April, Dutch authorities reported confirmed cases of SARS-CoV-2 in a dog owned by an owner with COVID-19; in addition, viral infection was reported in: 3 cats and mink living together on a farm (DeLong, 2020); in the Netherlands, on May 7, 2020, several cases of infections were reported, in mink from four different farms, with presence of gastrointestinal and respiratory disease; the mortality rate was 1.2% to 2.4% and deaths were mainly observed in pregnant females. In both cases, farm breeders tested positive for the new coronavirus and it is believed that they were sources of infection for mink and then mink-to-mink transmission occurred and then the virus spread to domestic cats (Abdel & Abdelwhab, 2020; Hossain et al., 2020).

Mattar & Gonzalez (2018) stated that, in Brazil, by RT-PCR, canine coronavirus strains, similar to those found in other countries and associated with pandemic severe acute respiratory syndrome were described in tissue samples from five puppies that died as a consequence of severe gastroenteritis.

In Ecuador Orlando (2021), out of 47 animals (dogs and cats) from 26 households, 13 animals (12 dogs and one cat) tested positive by PCR for SARS-CoV-2.

The virus is generally transmitted through respiratory droplets emitted by sneezing, coughing, talking or breathing, which can enter the body through the nose, mouth and conjunctiva. Indirect transmission can also occur through contamination of surfaces, fomites or feces, and asymptomatic hosts can spread the virus through respiratory droplets (Leroy et al., 2020). Also, kissing and licking pets are presumed to be additional risk factors that facilitate virus transmission (Hossain et al., 2020).

The structural and biochemical properties of the SARS-CoV-2 S antigen allow it not only to have affinity for the human ACE2 receptor but also for that of several species of domestic animals (dogs, cats, and



ferrets) and farm animals (cows, sheep, pigs, orangutans, monkeys, and horses) (Sun et al., 2020; Hossain et al., 2020; Andersen et al., 2020).

Consequently, many animals could become infected with this new coronavirus and then act as intermediate hosts in the spread of the virus. In the context of the COVID-19 pandemic to the present, the possibility of cats and dogs becoming infected but not participating in the spread of the virus must be addressed (Hossain et al., 2020).

Although there is no evidence that domestic animals can transmit the virus to humans, Shi and collaborators (2020) describe through experiments carried out in cats and ferrets infected with SARS-CoV-2 strains, the presence of: virus detection, specific respiratory symptoms and viral transmission from infected cats to healthy cats through respiratory droplets and respiratory tract. In addition, similar experiments in dogs showed that they are less susceptible to the new coronavirus (Fig. 3). However, pigs, chickens and ducks were not susceptible to the virus; therefore, no viral RNA was detected and these animals were seronegative (Shi et al., 2020; McNamara et al., 2020).

It is important to note that SARS-CoV-1 and SARS-CoV-2 coronaviruses are two closely related viruses of zoonotic origin with a high capacity to cross species barriers. Studies of viral sequences related to this new coronavirus in various species of *Rhinolophus* bats and Malayan pangolins (*Manis javanica*), have led to the conclusion that the zoonotic origin of SARS-CoV-2 is from the bat and used the pangolin as an intermediate host (Zhou et al, 2020; Li X. et al., 2020). Furthermore, it is of notable relevance to describe that there is a significant difference in the binding domain of the bat virus to the human receptor; so that, the S protein of the RaTG13 coronavirus from the bat *Rhinolophus affinis* does not bind well to the human receptor (Andersen et al.2020), whereas the S protein of the intermediate virus binds well to ACE2 from humans, ferrets, cats and other species that have high receptor homology (Wan et al., 2020).

The large size of the coronavirus RNA genome favors the occurrence of point mutations, deletions or insertions, which can sometimes lead to the appearance of different phenotypic characteristics of new viral variants. Mutations that occur in the coronavirus genome are drift or natural selection of mutations and by the exchange of genetic sequences of recombinations, which can be autologous, when the exchange occurs between viruses affecting one host species, or heterologous when the



exchange is between viruses affecting different host species (Decaro, 2010; Cui, 2019).

Coronaviruses are characterized by exceptional genetic plasticity and evolve rapidly, changing their antigenic profile, tissue tropism or host range through different mechanisms (Decaro & Lorusso, 2020); these, including SARS-CoV2, encoding a viral RNA polymerase (RdRp-nsp12) that is of low fidelity; i.e., it allows the occurrence of spontaneous mutations (incorporates incorrect nucleotides) during virus replication, as it has a low proofreading mechanism compared to other RNA viruses, leading to enhanced virulence and resistance to some antiviral drugs (Lung et al., 2020; Smith & Denison, 2013).

Recombination is an alternative mechanism that allows coronaviruses to acquire new biological properties in terms of virulence, host range and tissue tropism, so that CoV strains, which are non-pathogenic or low pathogenic in the original host, can increase their pathogenicity in the same species, or adapt to different species that disseminate in the new host exceptionally rapidly (Decaro & Lorusso, 2020), therefore, there is the uncertainty of the emergence of a new coronavirus with unpredictable phenotypic characteristics in terms of transmissibility and virulence, due to recombination of canine coronavirus and SARS-CoV-2 infections; However, the likelihood of such a scenario is difficult to assess (Decaro, 2013).

In a study described by Qui et al. (2020) on phylogenetic clustering and sequence alignment, it established that the new coronavirus could use ACE2 from various domestic animals such as cats, dogs, cows, buffaloes, goats, sheep and pigeons. Regarding the phylogenetic tree results, they showed that SARS-CoV-2 isolates from a cat in Wuhan are closely related to bat and pangolin isolates from the same region; but isolates from dogs, cats and tigers from France, the United States and Hong Kong have been combined with human isolates. Also, Hossain et al. (2020) describe that humans, cats, ferrets and different types of monkeys are at high risk of contracting the virus, while dogs, cows and goats, etc., are at moderate risk.

Birds represent the reservoir of Coronaviruses belonging to the genera *Gammacoronavirus* and *Deltacoronavirus*, bats are the natural reservoir of alpha and betacoronaviruses. However, several betacoronaviruses belonging to the subgenus *Embecovirus* have been

discovered in rodents, which could represent an important source of zoonotic disease.

There is growing evidence that all currently known HCoV recognize an animal origin, with bat or rodent CoVs being the most likely ancestors. In addition, HCoV-OC43 may be neuroinvasive, and likely, crossed species barriers to infect dogs and became established as canine Coronavirus (Decaro & Lorusso, 2020).

Finally, the origin of the virus is described to be from bats, as demonstrated by the evolutionary sequence of the genome; but, then it is likely to have passed to an intermediate animal host (dogs, pangolins and snakes are the main unknown suspects) to finally infect humans; however, natural transmission from infected humans to domestic animals such as: dogs, cats and mink; and wild animals such as: monkeys, tigers and lions has been documented (Hossain et al., 2020) (Figure 3).

#### **4. Conclusions**

SARS-CoV-2 has the proven ability to easily cross species barriers; likewise, viral transmission from sick owners to their pets is evident; furthermore, experimental transmission in unnatural conditions, in cats and ferrets, has been determined. This new virus can infect several species and different pets; therefore, further studies are needed to establish the interaction between the virus, the environment and various hosts.

Until now, ferrets, hamsters, cats and, to a lesser extent, bats, have been used to assess animal-to-animal transmission. However, given the prevalence and high genetic diversity of bat rCoV-SARS, coupled with human habits in modern agricultural practices, urbanization, decreasing wildlife living space, and environmental changes, could lead to the emergence of new viral variants in the future.

Therefore, it is recommended to take measures regarding human-wildlife contacts, also, massive genomic surveillance in wild animals should be implemented. Mass sequencing of SARS-CoV-2 strains detected in humans and wildlife CoV will help to further assess the origin of this new human pandemic and plan future measures capable of reducing the risk of occurrence of new CoV outbreak events.

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