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Review

Epidemiological research on SARS-CoV-2 in animals during the period 2020-2024

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Abstract: Coronaviruses are important pathogens responsible for respiratory and enteric diseases in mammals and birds. Among the identified coronaviruses, only six are known to infect humans: HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1, SARS-CoV, and MERS-CoV. This study provides a global perspective on SARS-CoV-2 infections in animals, highlighting the species that are receptive and susceptible to this virus in the context of a potential future pandemic. We analyzed epidemiological data on the evolution of infections in both domestic and wild animals, considering the limited number of similar studies conducted in Romania. To obtain a comprehensive overview of the impact of SARS-CoV-2, we correlated data on the first cases of COVID-19 in humans with information on animal infections between 2020 and 2024. So far, SARS-CoV-2 has been detected in 35 animal species across 10 families and 4 orders (*Carnivora, Artiodactyla, Primates*, and *Rodentia*). In Europe, the number of confirmed cases in animals has been significant, totaling 18 242 infections during the analyzed period. Our study confirms interspecies transmission events from humans to animals, from animals to animals, and from animals to humans emphasizing the need for continued epidemiological research.

Keywords: SARS-CoV-2, respiratory diseases, mammals, birds.

1. Introduction

The *Coronaviridae* family was established in 1975 by the International Committee on Taxonomy of Viruses [Patterson El et al., 2020]. In 2005, during the 10th International Nidovirus Symposium in Colorado, this family was divided into two subfamilies: *Coronavirinae* and *Torovirinae*.

The *Coronavirinae* subfamily (also known as *Orthocoronavirinae*) includes four main genera *Alphacoronavirus, Betacoronavirus, Gammacoronavirus,* and *Deltacoronavirus* as well as over 300 species and strains [Fernandez-Figueroa et al., 2024]. Among these, *Betacoronaviruses* predominantly affect bats but can also infect other mammals. In humans, two species (HCoV-HKU1 and HCoV-OC43) are responsible for mild rhinopharyngitis, while SARS-CoV and MERS-CoV have been associated with severe respiratory syndromes [McAloose et al., 2020, Perlman et Netland, 2009].

SARS-CoV-2 undergoes continuous mutations in its hosts, leading to the emergence of new variants, including Alpha, Beta, Gamma, Omicron, Lambda, and Mu GH [Kok et al., 2022].

The SARS-CoV-2 pandemic has had a significant impact, causing millions of infections and deaths in both humans and animals. Although the origin of the virus in humans remains uncertain, bats have been identified as the primary natural host [Perlman and Netland, 2009, Sharun et al., 2021].

SARS-CoV-2 has been identified in multiple animal species, including minks, raccoon dogs, cats, ferrets, hamsters, rodents, and white-tailed deer. The American mink is considered the most susceptible farmed species, with a high risk of interspecies transmission [Fernandez-Bellon et al., 2021].

Among pet animals, cats, ferrets, and hamsters are the most vulnerable, but their role in the circulation of the virus within the human population is considered limited. In wild animals and zoo populations, carnivores, great apes, and cervids have been reported as naturally infected [Yen et al., 2022].

The incubation period of the virus in animals is similar to that in humans, ranging from 2 to 14 days [Rivero et al., 2022].

The infection can be asymptomatic or cause mild respiratory and gastrointestinal symptoms, rarely progressing to severe pneumonia or death [Fang et al., 2023]. As with other respiratory viruses, SARS-CoV-2 appears to be transmitted among animals through direct contact, mainly via exposure to aerosols generated by coughing or sneezing, saliva droplets, and indirect contact through contaminated surfaces [Garigliany et al., 2020, Worobey et al., 2022]. The diagnosis of SARS-CoV-2 in animals relies on methods similar to those used in humans, including molecular and serological tests [Wang et al., 2020]. In addition to these routine testing methods, sequencing is commonly used to characterize strains involved in outbreaks [Medina-Enriquez et al., 2020]. Currently, there are no specific antiviral treatments for SARS-CoV-2 in animals, and disease management focuses on symptom relief and prevention of complications [Aguilo-Gisbert et al., 2021, Banerjee et al., 2021, Vanaart et al., 2022]. The isolation of infected animals is essential to limit the spread of the virus, while symptomatic treatments include the use of nonsteroidal anti-inflammatory drugs (NSAIDs) [Cohen., 2020, Petersen et al., 2022].

Vaccination of domestic animals could serve as a preventive strategy to prevent the transmission of the virus to wildlife.

2. Materials and Methods

For the development of this study, information was gathered from the official website of the OIE [World Organisation for Animal Health, 2024] and the FAO database [Food and Agriculture Organization of the United Nations, 2024], which provide global data on SARS-CoV-2 outbreaks in both domestic and wild animals. Given the wide range of hosts that the virus can infect, the potential for adaptation and large-scale transmission remains significantly high.

To obtain a comprehensive overview of this disease, data from the first reported cases of COVID-19 in humans were analyzed and correlated with SARS-CoV-2 infections in animals during the 2020-2024 period. To enhance accessibility of information, tables and figures were created to visually illustrate epidemiological data across different geographical regions and highlight animal species susceptible to SARS-CoV-2 infection. The close interactions between humans and animals suggest the occurrence of reverse zoonosis during the SARS-CoV-2 pandemic, emphasizing the role of behavioral transmission factors and the potential for virus spread among animals. These findings underscore the importance of continuous monitoring to detect and respond to potential resurgence.

Through this study, we aimed to track the evolution of confirmed SARS-CoV-2 cases, identify susceptible animal species, and analyze the geographical distribution of cases between 2020 and 2024.

3. Results

Worldwide, numerous cases of SARS-CoV-2 (18 740) have been reported in both domestic and wild animals during the period 2020-2024, as presented in Table 1.

Table 1. Overview of SARS-CoV-2 Cases in Animals (2020-2024).

No.	Continent	The total number of cases SARS-CoV-2
1.	Europe	18242
2.	North America	314
3.	South America	123
4.	Asia	56
5.	Africa	5
6.	**TOTAL**	**18740**

The highest number of confirmed SARS-CoV-2 cases in animals was recorded among mustelids. In this regard, the significant increase in confirmed cases in Europe can be attributed to the large number of mustelid farms present on the continent, as illustrated in the following figures [Zhou et al., 2020].

The number of SARS-CoV-2 cases in animals varied considerably by continent, as follows: Europe reported the highest number, with 18 242 cases, followed by North America with 314 cases, South America with 123 cases, Asia with 56 confirmed cases, and Africa with the lowest count, recording only 5 cases (Figure 1).

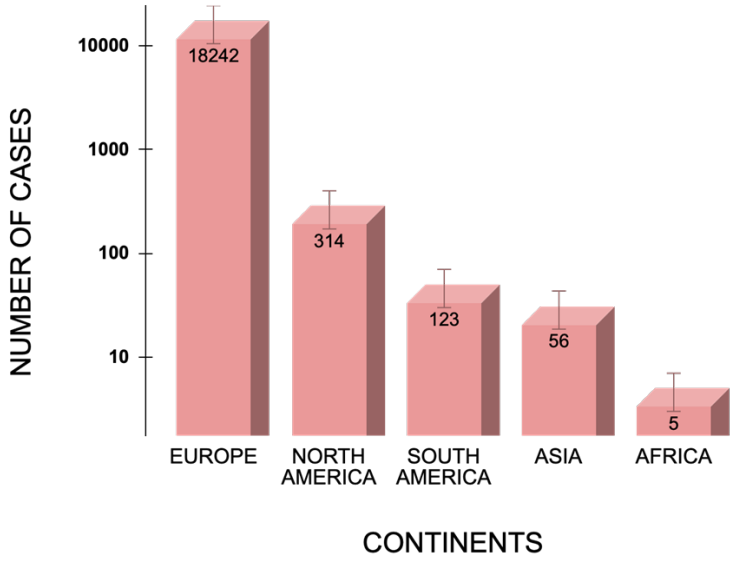

Figure 1: Dynamics of the Total Number of Confirmed SARS-CoV-2 Infection Cases in Animals During the 2020-2024 Period.

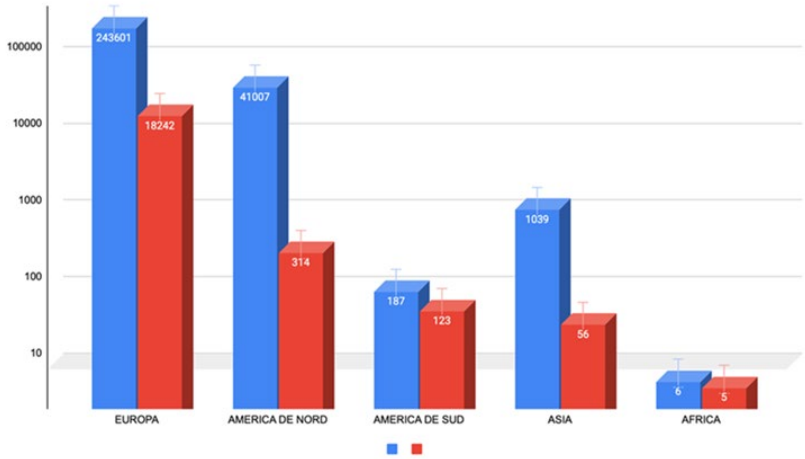

Figure 2: Dynamics of the Total Number of Confirmed Cases and Susceptible Animals to SARS-CoV-2 Infection During the 2020-2024 Period.

The data presented in Figure 2 highlight a significant difference between susceptible animals and the total number of confirmed SARS-CoV-2 cases, as well as variations between continents during the analyzed period.

In Europe, 243 601 susceptible animals were reported, of which only 18 242 were confirmed positive for SARS-CoV-2 infection.

In North America, 41 007 susceptible animals were notified, with only 314 confirmed cases.

In South America, a significant decrease in the number of cases was observed compared to Europe and North America. Out of 187 susceptible animals, only 123 were confirmed as positive cases.

Asia reported more susceptible animals to SARS-CoV-2 infection than South America, with 1,039 animals recorded, of which only 56 were diagnosed as positive.

A considerable difference was observed in Africa compared to other continents, where out of 6 susceptible animals, 5 were confirmed positive for SARS-CoV-2 infection.

Table 2. Annual distribution of confirmed SARS-CoV-2 infection cases in animals from 2020 to 2024.

Continet /year	2020	2021	2022	2023	2024	TOTAL
EUROPE	16189	304	1620	128	1	**18242**
ASIA	31	12	13	0	0	**56**
NORTH AMERICA	312	0	2	0	0	**314**
SOUTH AMERICA	122	1	0	0	0	**123**
AFRICA	1	4	0	0	0	**5**

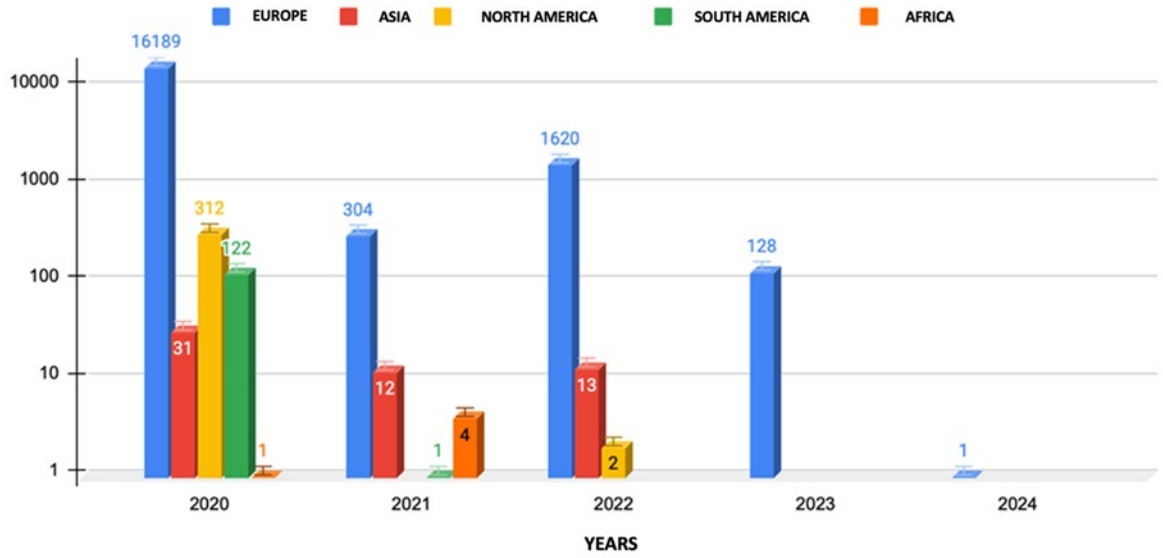

Figure 3: Dynamics of confirmed SARS-CoV-2 infection cases in animals from 2020 to 2024

Based on the data presented in Table 2 and Figure 3, we can observe the differences in confirmed cases by continent during the analyzed time period.

In Europe, the dynamics of confirmed cases were highly variable.

In 2020, the highest number of confirmed animal cases of SARS-CoV-2 infection was recorded, with 16 189 cases.

In 2021, there was a significant decrease in the number of animals testing positive for SARS-CoV-2, with only 304 cases. In the following year, 2022, the number of cases started to rise alarmingly, with 1 620 animals testing positive for SARS-CoV-2.

This was followed by another considerable decrease in confirmed cases, with only 128 cases in 2023, and so far, just one case has been confirmed in 2024.

In North America, the situation regarding SARS-CoV-2 infection in animals was not as dramatic as in Europe. In 2020, 312 cases were recorded, while in 2022, only two cases were confirmed, and no cases were confirmed in 2021, 2023, and 2024.

In South America, SARS-CoV-2 positive animals were reported only in 2020 and 2021, with 122 confirmed cases in 2020 and just one case in 2021.

Asia reported a significantly lower number of SARS-CoV-2 positive animals compared to Europe, with 31 confirmed cases in 2020, 12 cases in 2021, and 13 animals diagnosed as positive for SARS-CoV-2 in 2022.

Compared to the other continents, Africa recorded the fewest cases, with only five positive cases of SARS-CoV-2 infection between 2020 and 2024. In 2020, there was just one positive case (a puma), and in 2021, there were four confirmed cases (african lions).

Another aspect explored in this study was the influence of seasons on the number of confirmed SARS-CoV-2 cases. Table 3 illustrates the distribution of confirmed SARS-CoV-2 infections in domestic and wild animals across different seasons winter, autumn, summer, and spring during the period analyzed, 2020-2024.

Table 3. Distribution of the number of confirmed SARS-CoV-2 infection cases in animals during the years 2020-2024, by season.

SEASON	WINTER	AUTUMN	SUMMER	SPRING	TOTAL
Number of confirmed cases	15835	2761	144	130	18740

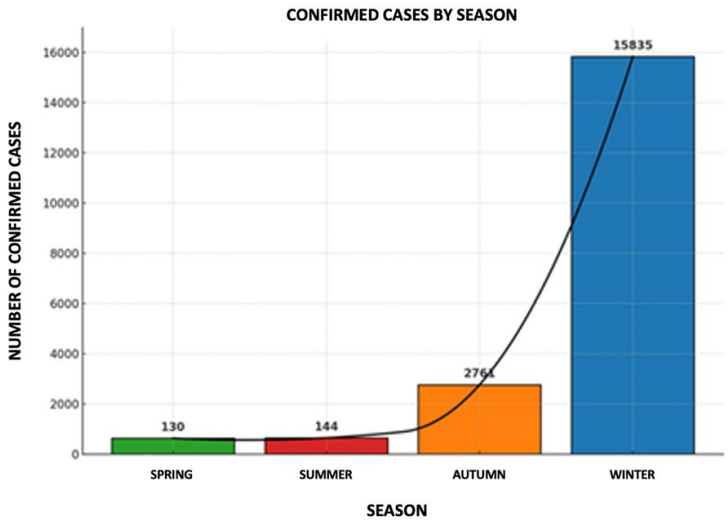

Figure 4: Dynamics of the total number of confirmed SARS-CoV-2 cases in animals during the years 2020-2024, by season.

4. Discussion

Between 2020 and 2024, a total of 18,740 confirmed cases of SARS-CoV-2 infection were reported globally in both domestic and wild animals. Among all affected taxonomic groups, mustelids recorded the highest number of cases. This high prevalence can be particularly attributed to the large number of mink farms in Europe, which facilitated virus transmission within animal populations.

The geographical distribution of confirmed SARS-CoV-2 cases in animals showed significant variation across continents. Europe reported the highest number of cases (18,242), followed by North America (314), South America (123), Asia (56), and Africa, which recorded the fewest cases (5). These differences reflect not only the distribution of susceptible animal populations but also the intensity of epidemiological surveillance and testing in each region.

Moreover, a notable disparity was observed between the total number of susceptible animals and the number of confirmed cases. This may suggest the existence of protective factors, underreporting, or limitations in testing capacity. Analysis of the temporal evolution of confirmed cases over the five-year period revealed variable dynamics, particularly in Europe. A peak was recorded in 2020, with 16,189 confirmed cases, followed by a sharp decline in 2021 (304 cases). In 2022, the number of cases increased again significantly (1,620 cases), followed by another drop in 2023 (128 cases), and only one case reported in 2024.

Another aspect investigated was the influence of seasonality on the number of confirmed cases. The data illustrate the distribution of SARS-CoV-2 infections in domestic and wild animals according to season (winter, spring, summer, and

autumn) during the analyzed period. These seasonal variations may suggest a role for climatic conditions or seasonal behavioral patterns of animals and their interactions with humans in the transmission of the virus.

5. Conclusions

Our study highlights the impact of SARS-CoV-2 infection on animals globally between 2020 and 2024, with a significant number of cases reported in both domestic and wild species.

Although the overall trend showed a decrease in the number of infections during this period, Europe recorded the highest number of confirmed animal cases (18 242), followed at a considerable distance by North America and other continents.

The identification of SARS-CoV-2 in 35 species across ten families and four animal orders underscores the epidemiological complexity of the virus and its potential for transmission. In this context, Greece stood out with a high percentage of confirmed cases in animals.

Given these findings, it is essential to continue epidemiological studies to better understand the transmission mechanisms and the virus's adaptability across different species.

The development of effective prevention and control measures is crucial, not only for the protection of animal health but also to reduce the risk of zoonotic transmission, thus contributing to a better management of future pandemic threats.

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Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Aguilo-Gisbert J, Padilla-Blanco M, Lizana V, et al. First description of SARS-CoV-2 infection in two feral American mink (Neovison vison) caught in the wild. Animals (Basel). 2021;11(5):1422. doi: 10.3390/ani11051422.
2. Banerjee A, Mossman K, Baker ML. Zooanthroponotic potential of SARS-CoV-2 and implications of reintroduction into human populations. Cell Host Microbe. 2021;29(2):160–164. doi: 10.1016/j.chom.2021.01.004.
3. Cohen J. From mice to monkeys, animals studied for coronavirus answers. Science. 2020;368(6488):221–222. doi: 10.1126/science.368.6488.221.
4. Fang R, Yang X, Guo Y, et al. SARS-CoV 2 infection in animals: Patterns, transmission routes, and drivers. Eco Environ Health. 2023;3(1):45–54. https://doi.org/10.1016/j.eehl.2023.09.004.
5. Fernandez-Bellon H, Rodon J, Fernandez-Bastit L, et al. Monitoring natural SARS-CoV-2 infection in lions (Panthera leo) at the Barcelona Zoo: Viral dynamics and host responses. Viruses. 2021;13(9):1683. doi: 10.3390/v13091683.
6. Fernández-Figueroa AE, Espinosa-Martínez DV, Miranda-Ortiz H, et al. Evidence of SARS-CoV-2 infection in companion animals from owners who tested positive for COVID-19 in the Valley of Mexico. Mol Biol Rep. 2024;51(1):186. doi: 10.1007/s11033-023-09099-5.
7. Garigliany M, Van Laere AS, Clercx C, et al. SARS-CoV-2 natural transmission from human to cat, Belgium, March 2020. Emerg Infect Dis. 2020;26(12):3069–3071. doi: 10.3201/eid2612.202223.
8. Kok KH, Wong SC, Chan WM, et al. Co circulation of two SARS-CoV-2 variant strains within imported pet hamsters in Hong Kong. Emerg Microbes Infect. 2022;11(1):689–698. doi: 10.1080/22221751.2022.2040922.
9. McAloose D, Laverack M, Wang L, et al. From people to Panthera: Natural SARS-CoV-2 infection in tigers and lions at the Bronx Zoo. mBio. 2020;11(5):e02220-20. doi: 10.1128/mBio.02220-20.
10. Medina-Enriquez MM, Lopez-Leon S, Carlos-Escalante JA, et al. ACE2: The molecular doorway to SARS-CoV-2. Cell Biosci. 2020;10(1):148. doi: 10.1186/s13578-020-00519-8.
11. Patterson EI, Elia G, Grassi A, et al. Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. Nat Commun. 2020;11(1):6231. doi: 10.1038/s41467-020-20097-0.
12. Perlman S, Netland J. Coronaviruses post-SARS: update on replication and pathogenesis. Nat Rev Microbiol. 2009;7(6):439–450. doi: 10.1038/nrmicro2147.
13. Petersen E, Ntoumi F, Hui DS, et al. Emergence of new SARS-CoV-2 variant of concern Omicron (B.1.1.529)–highlights Africa's research capabilities, but exposes major knowledge gaps, inequities of vaccine distribution, inadequacies in global COVID-19 response and control efforts. Int J Infect Dis. 2022;114(2):268–272. doi: 10.1016/j.ijid.2021.11.040.

14. Rivero R, Garay E, Botero Y, et al. Human-to-dog transmission of SARS-CoV-2, Colombia. Sci Rep. 2022;12(1):7880. doi: 10.1038/s41598-022-11847-9.
15. Sharun K, Tiwari R, Saied ARA, Dhama K. SARS-CoV-2 vaccine for domestic and captive animals: an effort to counter COVID-19 pandemic at the human animal interface. Vaccine. 2021;39(49):7119–7122. oi: 10.1016/j.vaccine.2021.10.053.
16. Vanaart AE, Velkers FC, Fischer EAJ, et al. SARS-CoV-2 infection in cats and dogs in infected mink farms. Transbound Emerg Dis. 2022;69(1):3001–3007. doi: 10.1111/tbed.14173.
17. Wang Z, Shan Z, Qing C, Jun L. The Coronavirus Prevention Manual. Skyhorse Publishing: New York, USA, 2020; pp. 1–244.
18. Worobey M, Levy JI, Serrano LM, et al. The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic. Science. 2022;377(6609):951–959. doi: 10.1126/science.abp8715.
19. Yen HL, Sit THC, Brackman CJ, et al. Transmission of SARS-CoV-2 delta variant (AY.127) from pet hamsters to humans, leading to onward human-to-human transmission: A case study. Lancet. 2022;399(10329):1070–1078. doi: 10.1016/S0140-6736(22)00326-9.
20. Zhou P, Yang XL, Wang GX, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature. 2020;579(7798):270-273. doi:10.1038/s41586-020-2012-7.
21. FAO. SARS-CoV-2 in animals – Situation updates. https://www.fao.org/animal-health/situation-updates/sars-cov-2-in-animals/en (accessed on 11 April 2024).
22. World Organisation for Animal Health. Available online: https://www.woah.org/en/home/ (accessed on 23 February 2024).

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