



Cross transmission species of SARS-COV-2 virus: Review

N. Benzerari ^{*},¹, I EL OUAR^{1,2}

¹ Pharmaceutical Sciences Research Center (CRSP)

² Faculty of Life and Natural Sciences, Frères Mentouri University,
Constantine 25000, Algeria
nedjmae@gmail.com

Abstract. COVID-19 (coronavirus disease 2019) is caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus, spreading rapidly around the world and causing an emerging pandemic. This article provides information about the probable natural reservoir of the virus and its possible intermediate host. Human-to-human transmission is the main cause of the spread of the virus, which is also transmitted to pets from humans. Research is needed to better understand the transmission mechanism of the virus.

Keywords: SARS-COV-2, Transmission, natural reservoir

1 Introduction

COVID-19 is a viral zoonosis caused by a virus of the coronaviridae family called SARS-CoV-2. The first cases of the disease appeared in December 2019 in Wuhan, China, and then rapidly spread to more than 200 countries, causing a pandemic and killing millions of people worldwide. Bats have been identified as a likely natural reservoir for the virus due to the high degree of similarity between SARS-CoV-2 and the virus stain Beta-CoV (RaTG-13) isolated from bats (Zhou et al., 2020; Shi et al., 2020).

The transmission of the virus to humans probably requires an intermediate host, several animal species are suggested such as pangolin, snake and turtle (Andersen et al., 2020; Zhang et al., 2020). Some studies have shown that there have also been cases of reverse zoonosis, transmission from humans to pets such as dogs and cats, and the role of the latter in spreading the disease (Zhang et al., 2020). In this review, we discuss the different modes of transmission to human via animals, from human to human but also from human to his domestic animals.

* Corresponding author

Received August 25, 2021; accepted October 20, 2021.

2 Virus structure

The SARS-Cov-2 belongs to the Coronaviridae family of Nidovirales order and Orthocoronavirinae subfamily, which is divided into four groups and that affect mammals and , specific to birds.. SARS- CoV-2 is the 7th virus in this family that affect human. The four virus genera HCoV-229E, HCoV-NL63, HCoVOC43 and HCoV-HKU1 cause a wide range of upper respiratory tract infections. Whereas SARS-CoV and MERS-CoV are responsible for atypical pneumonia (Lai et al., 2020) The genome alignment of coronavirus shows a 54% of identity between all coronaviruses, with the existence of conserved region regarding the non-structural proteins that present 58% identity among the different coronaviruses. The structural proteins have more diversity and represents 43% of whole genome (Chen et al, 2020).

Coronavirus SARS-CoV-2 is an enveloped virus of 60 to 160 nm with single stranded positive sense RNA genome of about 30kb. The genomic organization consisting of 5'—untranslated region (UTR), followed by ten open reading frames (ORF1a/b) encoding sixteen non-structural proteins (nsp1-nsp16), that form the viral replicase-transcriptase complexe, these sequences are shadowed by 4 genes encoding the structural proteins, nucleocapsid (N) spike (S), envelope (E), a membrane (M) and finally another untranslated region at 3'. The viral spike protein gives to the virus the crown-shaped appearance under the electron microscope (Ludwig et Zarbock., 2020). It is responsible for receptor binding and membrane attachment into host cells. The genomic organization consisting of 5'— untranslated region (UTR), followed by ten open reading frames (ORF1a/b) encoding sixteen non-structural proteins (nsp1-nsp16), that form the viral replicase-transcriptase complexe, these sequences are shadowed by 4 genes encoding the structural proteins, nucleocapsid (N) spike (S), envelope (E), a membrane (M) and finally another untranslated region at 3'(Yoshimoto., 2020; V'kovski et al., 2020).

3 Virus transmission

3.1 Natural reservoiry

Phylogenetic analysis showed that the virus is approximately 89.1% similar to the viruses isolated from bats bat-SL-CoVZC45 and bat-SL-CoVZXC21 (Ludwig and Zarbock., 2020).The reason why researchers speculate that the virus originates from bats but has undergone genetic mutations that allow it to cross the species barrier and affect humans. Importantly, the virus isolated from pangolins shows 85.5 to 92.4% similarity with CoV2, which suggests that this animal may be an intermediate host between bats and humans (Davenne et al., 2020). The new coronavirus could be a mutated version of CoV-RaTG13 isolated from *Rhinolophus affinis* species from Yunnan province in China (Andersen et al., 2020; Zhou et al., 2020). Indeed, bats are the only mammals capable of flying, which allows them to migrate freely and therefore to be confronted to a number of pathogen that transmit to human and other animals (Yi et al., 2019). Analysis

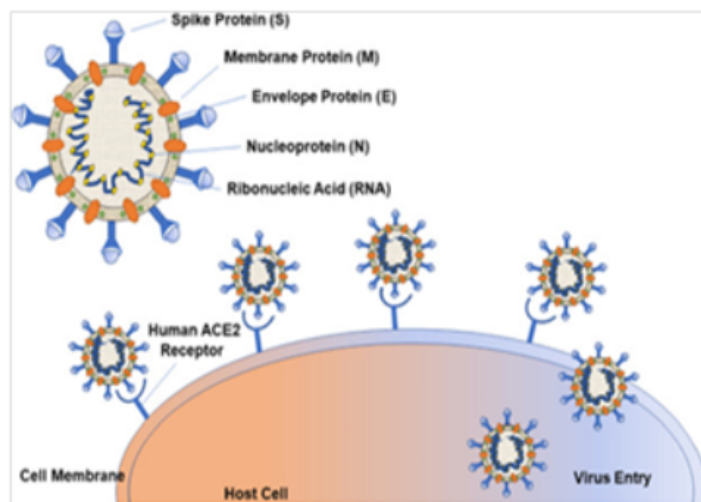


Fig. 1. Structure du sars-cov-2 (Naqvi et al., 2020)

of host-virus relationships, in different mammals, has shown that bats harbour a higher proportion of zoonotic viruses than other mammals (Olival et al., 2017). Importantly, different studies suggest that several bat species produce high levels of interferon making them better prepared to control viruses (Subudhi et al., 2019).

3.2 Intermindiate host

Although bats are the likely natural reservoir of SARS-CoV-2, the virus requires an intermediate host for transmission to humans. As in the SARS and MERS cases, the virus was transmitted to humans by exposure to the Himalayan palm civet (*Pagumalarvata*) and camel dromedary (*Camelusdromedarius*) respectively (Ahn et al., 2020; Rabi et al., 2020), various animal species, such as snakes, turtles and pangolins have been suggested as intermediate hosts for SARS-COV2 (Andersen et al., 2020; Zhang et al., 2020). At a press conference on 7 February 2020, Shen Yongyi and Xiao Lihua identified the pangolin as a potential source of the virus, their research was based on the genetic comparison of coronavirus collected from pangolins of the species *Manis javanica* and infected human. The researcher analysed more than 1000 samples and their study conclude that the -CoV level in pangolins was 70%. The genomic sequence of the isolated virus s was similar to that of SARS-CoV-2 by 99% (Li et al., 2020). The Malayan pangolins are nocturnal insectivorous mammals found in Southeast Asia but not in China, where the outbreak was first reported (Wong et al., 2020; Zhou et al., 2020). These animals were illegally introduced from their natural habitats to China by wildlife traffickers (Wong et al., 2020; Volpato et al., 2020) they are used as a food source and their scales are used in Chinese traditional medicine (Tommy

et al., 2020). Nevertheless, if these animals are considered as intermediate host, further investigation are needed to confirm this hypothesis.

3.3 Interhumaine transmission

Transmission of the virus can occur through direct contact with infected persons or indirectly

Direct transmission:

Transmission from aerosols of an infected individual appears to be the main mode of human-to-human transmission (Karia et al., 2020). Exhalation could emit the virus when coughed or sneezed up to 1 metres away (Bourouiba., 2020). Many infected patients with no clinical symptoms can excrete the virus through their respiratory droplets (Han and Yang., 2020).

Indirect transmission:

Indirect transmission can occur from contaminated surfaces or faeces (Hindson., 2020; Wu et al., 2020). SARS-CoV-2 RNA has been detected in the faeces of several patients (Yeo et al., 2020). Indeed, the study of Kampf et al., 2020 demonstrated that the virus can remain infectious on smooth substrates but no vertical transmission has been observed in pregnant women (Chen et al., 2020). Human coronaviruses are primarily respiratory and, to a lesser extent, digestive (Davenne et al., 2020). Infection with SARS-CoV-2 leads to ciliary dysfunction of epithelial cells and triggers an immune response, through the release of pro-inflammatory cytokines and activation of alveolar macrophages (Fu et al., 2020).

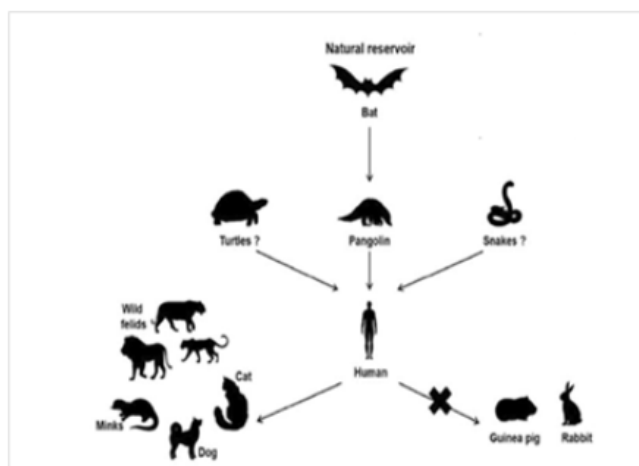


Fig. 2. Eventuelle transmission entre différentes espèces (Do Vale et al., 2021)

3.4 Human-animal transmission

The close relationship between pets and their owners has raised concerns among researchers about the risk of transmission of SARS-CoV-2 from humans to animals and the role of animals in spreading the disease (Hernández et al., 2020; Newman et al., 2020). The first report of 'reverse zoonosis' was reported in Hong Kong, where a dog of a COVID-19 patient was noticed positive after several PCR tests but no clinical signs were identified (THC et al., 2020). Later, other pets became infected through contact with sick humans, including another dog in Hong Kong and a cat in Belgium, this latter had diarrhoea, vomiting and breathing difficulties as symptoms (with COVID-19). A study was conducted on the seroprevalence of the virus in Wuhan cats by indirect enzyme-linked immunosorbent assay (ELISA) and neutralization test showed that three cats were positive for SARS-CoV-2, they were infected during the epidemic after their owners (Zhang et al., 2020). Another investigation indicated notable detection of neutralizing antibodies in 13 dogs (3.4%) and 6 cats (3.9%) (Patterson et al., 2020).

Other experimental studies have shown that cats are susceptible to SARS-CoV-2 infection and are able to transmit it to other cats through direct contact (Halfmann et al., 2020; Shi et al., 2020), with some degree of interstitial pneumonia, loss of cilia, epithelial necrosis, inflammation of the trachea and nasal turbinates in the epithelial cells (Shi et al, 2020). In addition, to necrotic debris in the tonsil, submucosal glands of the trachea and enterocytes of the small intestine (Segalés et al., 2020).

According to a study carried out in a veterinary hospital in south-east England, cats and dogs can acquire the English variant of the B.1.1.7 lineage from infected owners. The clinical manifestations are atypical, with severe cardiac abnormalities secondary to myocarditis and impairment of the patient's general health but without any primary respiratory signs (Ferasin et al., 2021). However, it is unclear whether pets are able to transmit the virus to humans (Hernandez et al., 2020.)

4 Conclusion

According to studies carried out by several researchers, SARS-CoV-2 probably has the bat as a natural reservoir, due to its ability to adapt to viral infections, and requires an intermediate host to be transmitted to humans, most likely the pangolin. The virus could be transmitted to pets from their owners, according to recent research. The spread of the virus is mainly due to human-to-human transmission. Nonetheless, further studies are needed to confirm whether the virus has been transmitted to human as a result of natural mutation.

References

1. Ahn DG, Shin HJ, Kim MH, Lee S, Kim HS, Myoung J, Kim BT, Kim SJ (2020) Current status of epidemiology, diagnosis, therapeutics, and vaccines for novel coronavirus disease 2019 (COVID-19). *J Microbiol Biotechnol* 30:313-324.

2. Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF (2020) The proximal origin of SARS-CoV-2. *Nat Med* 26:450–452.
3. Andersen, K.G., Rambaut, A., Lipkin, W.I., Holmes, E.C., and Garry, R.F. (2020). The proximal origin of SARS-CoV-2. *Nature Medicine*. 26(4): p. 450-452.
4. Chen, H. Guo, J. et al. (2020). "Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records." *The Lancet* 395(10226): 809-815.
5. Davenne, E., Giot, J-B., Huynen, P. (2020). Coronavirus et CoviD-19 : le point sur une pandémie galopante. *Rev Med Liege*, 75 : 4 : 218-225.
6. do Vale, B., A. P. Lopes, et al. (2021). "Bats, pangolins, minks and other animals - villains or victims of SARS-CoV-2?" *Veterinary Research Communications* 45 (1): 1-19.
7. Drexler, J. F., Corman, V. M., Drosten, C. (2014). Ecology, evolution and classification of bat coronaviruses in the aftermath of SARS. *Antiviral Res*, 101, 45-56.
8. Ferasin, L. Fritz, M et al. (2021). "Myocarditis in naturally infected pets with the British variant of COVID-19." *bioRxiv*: 2021.2003.2018.435945.
9. Fu, Y. Cheng, Y. Wu, Y. (2020). Understanding SARS-CoV-2-mediated inflammatory responses : from mechanisms to potential therapeutic tools. *Virology* Sin.
10. Halfmann, P.J. Hatta, M. Chiba, S. Maemura, T. Fan, S. Takeda, M. et al. (2020) Transmission of SARS-CoV-2 in Domestic Cats. *New England Journal of Medicine*. 383(6):592-4.
11. Han, Y. and H. Yang (2020). "The transmission and diagnosis of 2019 novel coronavirus infection disease (COVID-19): A Chinese perspective. *Journal of Medical Virology* 92(6): 639-644.
12. Hernandez M, Abad D, Eiros JM, Rodriguez-Lazaro D. (2020). Are Animals a Neglected Transmission Route of SARS-CoV-2? *Pathogens* ;9 (6).
13. Hindson, J. (2020). COVID-19 : faecal-oral transmission?. *Nature Reviews Gastroenterology Hepatology*.
14. Kampf, G. Todt, D. Pfaender, S. Steinmann, E. (2020) Persistence of coronaviruses on inanimate surfaces and its inactivation with biocidal agents. *Journal of Hospital Infection* ; Vol.104, no 3, Pages 246–251.
15. L. Bourouiba (2020) Turbulent Gas Clouds and Respiratory Pathogen Emissions: Potential Implications for Reducing Transmission of COVID-19 , *JAMA*, 26 mars 2020.
16. Lai, C.-C., Shih, T.-P., Ko, W.-C., Tang, H.-J., Hsueh, P.-R. (2020). Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and corona virus disease-2019 (COVID-19): the epidemic and the challenges. *International Journal of Antimicrobial Agents*, 105924
17. Li, X., J. Zai, et al. (2020). "Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2." *Journal of Medical Virology* 92(6): 602-611.
18. Ludwig S, Zarbock A (2020) Coronaviruses and SARS-CoV-2: a brief overview. *Anesth Analg* 131:93–96.
19. Naqvi, A. A. T., Fatima, K., Mohammad, T., Fatima, U., Singh, I. K., Singh, A., ... Hassan, M. I. (2020). Insights into SARS-CoV-2 genome, structure, evolution, pathogenesis and therapies: Structural genomics approach. *Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease*, 165878.
20. Newman A, Smith D, Ghai RR, Wallace RM, Torchetti MK, Loiacono C, et al. (2020) First Reported Cases of SARS-CoV-2 Infection in Companion Animals - New York, March-April 2020. *MMWR Morb Mortal Wkly Rep* ; 69(23):710-713.

21. Olival, K.J.; Hosseini, P.R.; Zambrana-Torrel, C.; Ross, N.; Bogich, T.L.; Daszak, P. (2017) Host and viral traits predict zoonotic spillover from mammals. *Nature*, 546, 646–650.
22. Patterson, EI. Smith, SL. Anderson, ER. Patterson, GT. Lucente, MS. Basano, FS. et al. (2020) Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. *BioRxiv*.
23. R. Karia, I. Gupta, H. Khandait, A. Yandav et A. Yandav (2020). COVID-19 and its Modes of Transmission , *SN Compr Clin Med.*, vol. 2, no 10, p. 1798–1801.
24. Rabi FA, Al Zoubi MS, Al-Nasser AD, Kasasbeh GA, Salameh DM (2020) SARS-CoV-2 and coronavirus disease 2019: what we know so far. *Pathogens*. 9:1–14.
25. Segalés, J., M. Puig, et al. (2020). "Detection of SARS-CoV-2 in a cat owned by a COVID-19affected patient in Spain." *Proceedings of the National Academy of Sciences* 117 (40): 24790-24793.
26. Shi J, Wen Z, Zhong G, Yang H, Wang C, Huang B, Liu R, He X, Shuai L, Sun Z, Zhao Y, Liu P, Liang L, Cui P, Wang J, Zhang X, Guan Y, Tan W, Wu G, Chen H, Bu Z (2020) Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS-coronavirus 2. *Science* 368:1016–1020.
27. Subudhi, S., N. Rapin, et al. (2019). "Immune System Modulation and Viral Persistence in Bats: Understanding Viral Spillover." *Viruses* 11(2): 192.
28. T. H. C. Sit et al., (2020) Infection of dogs with SARS-CoV-2. *Nature*, 10.1038/s41586-020-2334-5.
29. Tommy Tsan-Yuk Lam, Na Jia, Ya-Wei Zhang, Marcus Ho-Hin Shum, Jia-Fu Jiang, Hua-Chen Zhu, Yi-Gang Tong, Yong-Xia Shi, Xue-Bing Ni, Yun-Shi Liao, Wen-Juan Li, Bao-Gui Jiang, Wei Wei, Ting-Ting Yuan, Kui Zheng, Xiao-Ming Cui, Jie Li, Guang-Qian Pei, Xin Qiang, William Yiu-Man Cheung, Lian-Feng Li, Fang-Fang Sun, Si Qin, Ji-Cheng Huang, Gabriel M. Leung, Edward C. Holmes, Yan-Ling Hu, Yi Guan et Wu-Chun Cao, Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins , *Nature*, vol. 583, no 7815, 9 juillet 2020, p. 282–285.
30. V'kovski, P., Kratzel, A., Steiner, S., Stalder, H., Thiel, V. (2020). Coronavirus biology and replication: implications for SARS-CoV-2. *Nature Reviews Microbiology*.
31. Volpato G, Fontefrancesco MF, Gruppuso P, Zocchi DM, Pieroni A (2020) Baby pangolins on my plate: possible lessons to learn from the COVID-19 pandemic. *J Ethnobiol Ethnomed* 16:1–12.
32. Wong G, Bi YH, Wang QH, Chen XW, Zhang ZG, Yao YG (2020) Zoonotic origins of human coronavirus 2019 (HCoV-19 / SARSCoV-2): Why is this work important? *Zool Res* 41:213–219.
33. Wu, F. Zhao, S. Yu, B. et al. (2020) A new coronavirus associated with human respiratory disease in China. *Nature* 579, 265–269.
34. Ye ZW, Yuan S, Yuen KS, Fung SY, Chan CP, Jin DY (2020) Zoonotic origins of human coronaviruses. *Int J Biol Sci* 16:1686–1697.
35. Yeo, C., S. Kaushal, et al. (2020). "Enteric involvement of coronaviruses: is faecal–oral transmission of SARS-CoV-2 possible?" *The Lancet Gastroenterology Hepatology* 5(4): 335-337.
36. Yi Fan, Kai Zhao, Zheng-Li Shi, Peng Zhou (2019) Bat Coronaviruses in China. *Viruses* 2019, 11, 210.
37. Yoshimoto, F. K. (2020). "The Proteins of Severe Acute Respiratory Syndrome Coronavirus-2 (SARS CoV-2 or n-COV19), the Cause of COVID-19." *The Protein Journal* 39 (3): 198-216.
38. Zhang, T., Wu, Q., and Zhang, Z. (2020). Probable pangolin origin of SARS-CoV-2 associated with the COVID-19 outbreak. *Current Biology*. 30(8): p. 1346-1351.e2.

39. Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W et al (2020) A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 579:270–273.