

Zoonotic origin and transmission of Coronavirus

Research Article

Catarina Bubach Ribeiro Alves¹, Sara Evelin Penha Gonçalves Soares¹, Izabella Pedro da Rocha Langa¹, Gustavo José Rossoni Ronchi¹, Valmin Ramos-Silva, MD, PhD²

¹Graduating. Medicine course. Higher School of Sciences of Santa Casa de Misericórdia de Vitória (ES), Brazil

²Professor of the Master's Program in Public Policy and Local Development, EMESCAM

Abstract:

The Coronavirus pandemic has affected and killed thousands of people on all continents. The role of zoonotic transmission of the virus and which animals are associated as hosts of the Coronavirus are still discussed. A scope review was carried out following the methodological framework suggested by Arksey and O'Malley (2005). Search for articles in PUBMED, published from 2019 on, using the keywords "Coronavirus, Animal, Transmission". 92 articles were retrieved and submitted to the procedures for reading titles, abstracts and selected articles, which were read in full for the preparation of this scope review. 61 were excluded because they did not contain the abstract or because they did not meet the objectives of the study and 31 articles were part of this review or discussion of the results.

Keywords: COVID Coronavirus, Animal, Transmission

INTRODUCTION

The pandemic related to a new Coronavirus (SARS-CoV-2), originating in China, infected more than 75,000 individuals and spread to all continents, resulting in the death of more than 11,400 people. It is still discussed which animals act as hosts and in the spread of the virus¹.

Brazil records 1,891 cases of the disease and 34 deaths, all with human-to-human transmission from people infected abroad. It is estimated that poverty and social inequality will increase due to the spread of the disease². In early February 2020, the Ministry of Health declared a Public Health Emergency of National Importance due to human infection with the new Coronavirus (2019-nCoV), through Ordinance MS No. 188/2020³.

In this sense, this scope review aims to describe the current evidence about animals with the potential to

be hosts and disseminators of Coronavirus for humans.

METHODS

A scope review was carried out following the methodological framework suggested by Arksey and O'Malley (2005)⁴. We tried to answer the following question: which animals are associated as hosts of Coronavirus. The search for articles on PUBMED, published from 2019, was carried out on March 18, 2020, using the keywords "Coronavirus, Animal, Transmission". 92 articles were retrieved and submitted to the procedures for reading titles, abstracts and selected articles, which were read in full for the preparation of this scope review. Thus, the construction of this review was based on published information, as listed in the references.

RESULTS

All publications were in the English language. Of the 92 studies evaluated, 61 were excluded because they did not contain the abstract and did not meet the objectives of the study and 31 were part of this review or the discussion of results.

Coronavirus disease (COVID-19) is caused by SARS-CoV2 and current evidence indicates the zoonotic origin of the virus from animal trade in the city of Wuhan, China, with probable the zoonotic origin of COVID-19, which evolved with the person to person transmission⁵.

The zoonotic overflow corresponds to the transmission of pathogens by animals and represents a global burden on public health, but the phenomenon is still not well understood. Thus, coronaviruses and influenza viruses, circulate in nature in various animal species. Alpha-coronaviruses and beta-coronaviruses can infect mammals, while gamma-coronaviruses and delta-coronaviruses tend to infect birds, and some are transmitted to mammals. Literature suggests that bats are the most likely initial source of the current 2019 CoV (2019nCoV) outbreak in China. Transmission continued from human to human through close contact and through the handling of contaminated waste and respiratory secretions⁶⁻⁹.

The dromedary camel (*Camelus dromedarius*), a natural reservoir of coronavirus¹⁰ is the only animal identified as an amplifier of the coronavirus of the Middle East respiratory syndrome (MERS-CoV), secreting viruses in body fluids, especially in nasal and rectal discharges, infecting the epithelium of human airways. The role of an asymptomatic human carrier or, less likely, of an unknown animal host that has direct contact with infected camels and humans is suspected¹¹.

Coronaviruses are the well-known cause of severe respiratory, enteric and systemic infections in a wide variety of hosts, including man, mammals, fish and birds¹². Bats have been identified as a natural reservoir of a variety of coronaviruses (CoVs) and several of them have caused disease in humans and domestic animals through interspecies transmission. In view of the diversity of CoVs, it is expected to discover other bat CoVs¹³.

Phylogenetic analysis suggests that bats are natural reservoirs of SARS-CoV14, and that a new

coronavirus (2019-nCoV) causes symptoms in humans similar to those caused by SARS-CoV. It is possible that an animal sold at the seafood market in Wuhan (China) or a hidden reservoir of wild animals from viruses may represent an intermediate host, which facilitated the emergence of the virus in humans^{12,15-17}.

Many patients were exposed to wild animals at the wholesale market in Wuhan, which also sold birds, snakes, bats and other farm animals. Research indicates that 2019-nCoV has genetic information similar to bat coronavirus. This may be the result of a recombinant virus between the bat coronavirus and a coronavirus of unknown origin suggesting that homologous recombination can occur and contribute to transmission between 2019-nCoV species¹⁸.

It has also been shown that the virus is associated with acute swine diarrhea syndrome (SADS-CoV), an acute and highly contagious enteric disease and very common among pigs in China, characterized by watery diarrhea and vomiting¹⁹. The disease has a wide tropism of species and is capable of infecting cell lines of several species, including bats, mice, rats, gerbils (with almost one hundred species, found in Africa and Asia, in deserts or arid regions), hamsters, pigs, chickens, non-human and human primates. The potential for transmissibility between species of SADS-CoV is highlighted, although additional surveillance in other animal populations is necessary to fully understand the ecology of this CoV of HKU2 origin from bat²⁰.

In addition to bats and camels, other transmitting animals are suspected. Transgenic hDPP4 mice infected with aerosols and instillation by MERS-CoV simulated the clinical symptoms of moderate diffuse interstitial pneumonia and transgenic mice exposed to the MERS-CoV aerosol developed progressions of lung diseases and pathologies that most resembled those seen in humans²¹. MERS-CoV, found in bats and hedgehogs (*Erinaceus amurensis*, Schrenk, 1858), an insectivorous animal considered an important viral reservoir, shows evidence of recombination with bat viruses²².

Coronaviruses (CoVs) cause infections, mainly in birds and mammals, but in the last few decades, they have been shown to infect humans as well, as in the outbreak of severe acute respiratory syndrome in

2003 and, more recently, the Middle East respiratory syndrome – MERS²³.

More than 60% of the main recent outbreaks of infectious diseases worldwide were of zoonotic origin and more than 70% are of wildlife, appearing to present non-random global patterns. They are probably motivated by socioeconomic, environmental and ecological factors and represent a significant burden for global economies and public health^{24,25,26}.

As human health and animal health are linked, an intersectoral interpretation of data from zoonotic disease information, surveillance and monitoring will improve disease prevention, prediction and control, to investigate how mammalian host distributions determine disease patterns and predict risks of future zoonotic diseases²⁷. However, this is made difficult in cases where the animal is only the host as with many viral diseases.

In this sense, four endemic human coronaviruses (HCoV-229E, -NL63, -OC43, HKU1) contribute to a considerable portion of infections of the upper and lower respiratory tract in adults and children, with clinical manifestations similar to many other agents of the common cold. Primordial associations for all four viruses may have existed with bats and rodents. HCoV-OC43 is thought to have emerged from ancestors in domestic animals, such as cattle or pigs, while HCoV-229E may actually be transferred from dromedary camels similar to the Middle Eastern respiratory syndrome coronavirus²⁸.

There is epidemiological and molecular analysis evidence of the association of bats, after passing into intermediate hosts, at the origin of the COVID-19 pandemic²⁹. The role of pigs and birds with zoonotic potential of coronaviruses is also suspected.

The animal coronavirus crossed the species barrier to infect humans, determined by the host virus³⁰. The zoonotic origin of COVID-19 subsequently resulted in the transmission of the disease from person to person³¹.

CONCLUSION

There is evidence of the zoonotic and phylogenetic origin of the virus by the animal trade and that bats, a natural reservoir of viruses, are the probable source of the current outbreak of COVID19, given

that coronavirus and influenza viruses circulate in nature in various animal species, including birds, pigs, bats, rodents, fish, with interspecies transmission. The camel is another animal considered to be a natural reservoir of the coronavirus and the only one identified as a virus secretor by infectious body fluids through nasal and rectal discharge, but the possibility of an asymptomatic human carrier in the transmission process is suspected.

REFERENCES

- [1.] Shen Z, Xiao Y, Kang L, et al. Genomic diversity of SARS-CoV-2 in Coronavirus Disease 2019 patients. *Clin Infect Dis*. 2020;ciaa203. doi:10.1093/cid/ciaa203
- [2.] BRASIL. Ministério da Saúde. Disponível em <https://www.google.com/search?q=atualiza%C3%A7%C3%A3o+dados+coronavirus+minist%C3%A9rio+da+saude&oq=atualiza%C3%A7%C3%A3o+dados+coronavirus+minist%C3%A9rio+da+saude&aqs=chrome..69i57j12041j0j7&sourceid=chrome&ie=UTF-8> Acesso 22/03/2020.
- [3.] BRASIL. Ministério da saúde. Portaria nº 188, de 3 de fevereiro de 2020. Declara Emergência em Saúde Pública de importância Nacional em decorrência da Infecção Humana pelo novo Coronavírus (2019-nCoV). Disponível em <http://www.in.gov.br/en/web/dou/-/portaria-n-188-de-3-de-fevereiro-de-2020-241408388> Acesso em 21/03/2020
- [4.] Shen Z, Xiao Y, Kang L, et al. Genomic diversity of SARS-CoV-2 in Coronavirus Disease 2019 patients. *Clin Infect Dis*. 2020;ciaa203. doi:10.1093/cid/ciaa203
- [5.] H. Arksey, L.O'Malley, "Scoping studies: towards a methodological framework," *International Journal of Social Research Methodology*. 2005;8: 19–32.
- [6.] Rothan HA, Byrareddy SN. The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak. *J Autoimmun*. 2020;102433. doi:10.1016/j.jaut.2020.102433

- [7.] Widagdo W, Sooksawasdi Na Ayudhya S, Hundie GB, Haagmans BL. Host Determinants of MERS-CoV Transmission and Pathogenesis. *Viruses*. 2019;11(3):280. Published 2019 Mar 19. doi:10.3390/v11030280
- [8.] Hemida MG. Middle East Respiratory Syndrome Coronavirus and the One Health concept. *PeerJ*. 2019;7:e7556. doi:10.7717/peerj.7556
- [9.] Rodriguez-Morales AJ, Bonilla-Aldana DK, Balbin-Ramon GJ, et al. History is repeating itself: Probable zoonotic spillover as the cause of the 2019 novel Coronavirus Epidemic. *Infez Med*. 2020;28(1):3–5;
- [10.] Nishiura H, Linton NM, Akhmetzhanov AR. Initial Cluster of Novel Coronavirus (2019-nCoV) Infections in Wuhan, China Is Consistent with Substantial Human-to-Human Transmission. *J Clin Med*. 2020;9(2):E488. Published 2020 Feb 11. doi:10.3390/jcm9020488
- [11.] Kandeil A, Gomaa M, Nageh A, et al. Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Dromedary Camels in Africa and Middle East. *Viruses*. 2019;11(8):717. doi:10.3390/v11080717
- [12.] Al-Ahmadi K, Alahmadi M, Al-Zahrani A. Spatial association between primary Middle East respiratory syndrome coronavirus infection and exposure to dromedary camels in Saudi Arabia. *Zoonoses Public Health*. 2020;10.1111/zph.12697. doi:10.1111/zph.12697.
- [13.] Malik YS, Sircar S, Bhat S, et al. Emerging novel coronavirus (2019-nCoV)-current scenario, evolutionary perspective based on genome analysis and recent developments. *Vet Q*. 2020;40(1):68–76. doi:10.1080/01652176.2020.1727993
- [14.] Wang N, Luo C, Liu H, et al. Characterization of a New Member of Alphacoronavirus with Unique Genomic Features in Rhinolophus Bats. *Viruses*. 2019;11(4):379. doi:10.3390/v11040379
- [15.] Chen YN, Hsu HC, Wang SW, Lien HC, Lu HT, Peng SK. Entry of *Scotophilus* Bat Coronavirus-512 and Severe Acute Respiratory Syndrome Coronavirus in Human and Multiple Animal Cells. *Pathogens*. 2019;8(4):259. doi:10.3390/pathogens8040259
- [16.] Yu P, Hu B, Shi ZL, Cui J. Geographical structure of bat SARS-related coronaviruses. *Infect Genet Evol*. 2019;69:224–229. doi:10.1016/j.meegid.2019.02.001.
- [17.] Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet*. 2020;395(10224):565–574. doi:10.1016/S0140-6736(20)30251-8.
- [18.] Wan Y, Shang J, Graham R, Baric RS, Li F. Receptor Recognition by the Novel Coronavirus from Wuhan: an Analysis Based on Decade-Long Structural Studies of SARS Coronavirus. *J Virol*. 2020;94(7):e00127-20. doi:10.1128/JVI.00127-20
- [19.] Ji W, Wang W, Zhao X, Zai J, Li X. Cross-species transmission of the newly identified coronavirus 2019-nCoV. *J Med Virol*. 2020;92(4):433–440. doi:10.1002/jmv.25682
- [20.] Chen X, Zhang XX, Li C, et al. Epidemiology of porcine epidemic diarrhea virus among Chinese pig populations: A meta-analysis. *Microb Pathog*. 2019;129:43–49. doi:10.1016/j.micpath.2019.01.017
- [21.] Yang YL, Qin P, Wang B, et al. Broad Cross-Species Infection of Cultured Cells by Bat HKU2-Related Swine Acute Diarrhea Syndrome Coronavirus and Identification of Its Replication in Murine Dendritic Cells *In Vivo* Highlight Its Potential for Diverse Interspecies Transmission. *J Virol*. 2019;93(24):e01448-19. doi:10.1128/JVI.01448-19.
- [22.] Hao XY, Lv Q, Li FD, Xu YF, Gao H. The characteristics of hDPP4 transgenic mice subjected to aerosol MERS coronavirus infection via an animal nose-only exposure device. *Animal Model Exp Med*. 2019;2(4):269–281. doi:10.1002/ame2.12088
- [23.] Lau SKP, Luk HKH, Wong ACP, et al. Identification of a Novel Betacoronavirus (*Merbecovirus*) in Amur Hedgehogs from

- China. *Viruses*. 2019;11(11):980. doi:10.3390/v11110980.
- [24.] Schoeman D, Fielding BC. Coronavirus envelope protein: current knowledge. *Virology*. 2019;16(1):69. Published 2019 May 27. doi:10.1186/s12985-019-1182-0
- [25.] Jones KE, Patel NG, Levy MA, et al. Global trends in emerging infectious diseases. *Nature*. 2008;451(7181):990–993. doi:10.1038/nature06536.
- [26.] Han BA, Kramer AM, Drake JM. Global Patterns of Zoonotic Disease in Mammals. *Trends Parasitol.* 2016;32(7):565–577. doi:10.1016/j.pt.2016.04.007.
- [27.] Nii-Trebi NI. Emerging and Neglected Infectious Diseases: Insights, Advances, and Challenges. *Biomed Res Int.* 2017;2017:5245021. doi:10.1155/2017/5245021.
- [28.] Wendt A, Kreienbrock L, Campe A. Zoonotic disease surveillance--inventory of systems integrating human and animal disease information. *Zoonoses Public Health.* 2015;62(1):61–74. doi:10.1111/zph.12120
- [29.] Corman VM, Muth D, Niemeyer D, Drosten C. Hosts and Sources of Endemic Human Coronaviruses. *Adv Virus Res.* 2018;100:163–188. doi:10.1016/bs.aivir.2018.01.001.
- [30.] Salata C, Calistri A, Parolin C, Palù G. Coronaviruses: a paradigm of new emerging zoonotic diseases. *Pathog Dis.* 2019;77(9):ftaa006. doi:10.1093/femspd/ftaa006.
- [31.] Fung SY, Yuen KS, Ye ZW, Chan CP, Jin DY. A tug-of-war between severe acute respiratory syndrome coronavirus 2 and host antiviral defence: lessons from other pathogenic viruses. *Emerg Microbes Infect.* 2020;9(1):558–570. Published 2020 Mar 14. doi:10.1080/22221751.2020.1736644
- [32.] Rothan HA, Byrareddy SN. The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak. *J Autoimmun.* 2020;102433. doi:10.1016/j.jaut.2020.102433].