

SARS-CoV-2: taxonomy, origin and constitution

SARS-CoV-2: taxonomia, origem e constituição

Omar Arafat Kdudsi Khalil¹, Sara da Silva Khalil²

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ABSTRACT: *Introduction:* SARS-CoV-2 is a new coronavirus, responsible for the current pandemic of COVID-19, which has already infected and caused the death of thousands of people around the world. *Objective:* To describe basic and fundamental aspects of SARS-CoV-2, such as its name, constitution, possible origins and classification. *Method:* Exploratory and descriptive bibliographic review, elaborated through researches on the Pubmed, Scopus, Google Scholar, and Scielo platforms. The terms used for the selection of materials were “SARS-CoV-2”, “COVID-19”, “spike-protein”, “classification”, “coronavirus” and their combinations. *Results:* Coronaviruses belong to the Coronaviridae family, which comprises two subfamilies, five genera, 26 subgenera and 46 virus species. SARS-CoV-2 belongs to the genus Betacoronavirus, subgenus Sarbecovirus, a coronavirus species related to the acute respiratory syndrome. Its classification, carried out by the International Committee on Taxonomy of Viruses (ICTV), was made in the light of mainly molecular and phylogenetic characteristics and not the actual disease it causes. This virus appeared in China, where people have the habit of consuming recently slaughtered domestic or wild animals. It is speculated that the horseshoe bat (*Rhinolophus sinicus*) is its primary host and that the Malayan pangolin (*Manis javanica*) is the secondary host. SARS-CoV-2 is an enveloped virus, approximately spherical and its virions have average diameters of 80-120 nm. It has a non-segmented RNA large size genome which encodes four main proteins spike (S), envelope (E), membrane (M) and nucleoprotein (N). Coronaviruses use S as the main target to neutralize antibodies and to bind to the angiotensin-converting enzyme 2. *Conclusion:* In-depth knowledge of the basic characteristics of SARS-CoV-2 is essential for better comprehension and understanding of epidemiological aspects, clinical, pathophysiological and treatment of COVID-19.

Keywords: SARS-CoV-2. Coronavirus. Classification. Viral structure. Origin.

RESUMO: *Introdução:* O SARS-CoV-2 é um novo coronavírus, responsável pela atual pandemia de COVID-19, o qual já infectou e causou a morte de milhares de pessoas em todo o mundo. *Objetivo:* Descrever aspectos básicos e fundamentais sobre o SARS-CoV-2, como nome, constituição, possíveis origens e classificação. *Método:* Revisão bibliográfica exploratória e descritiva, elaborada por meio de pesquisas nas plataformas PubMed, Scopus, Google Acadêmico, e SciELO. Os termos utilizados para a seleção dos materiais foram: “SARS-CoV-2”, “COVID-19”, “spike-protein”, “classification”, “coronavirus” e suas combinações. *Resultados:* Os coronavírus pertencem à família *Coronaviridae*, a qual abrange 2 subfamílias, 5 gêneros, 26 subgêneros e 46 espécies de vírus. O SARS-CoV-2 pertence ao gênero *Betacoronavirus*, subgênero *Sarbecovirus*, espécie *Severe acute respiratory syndrome-related coronavirus*, e está relacionado à síndrome respiratória aguda. Sua classificação foi realizada pelo *International Committee on Taxonomy of Viruses (ICTV)* levando-se em consideração principalmente características moleculares e filogenéticas e não a doença que causa. Este vírus surgiu na China, país em que há o hábito de consumir animais domésticos ou selvagens recentemente abatidos. Especula-se que o morcego-ferradura (*Rhinolophus sinicus*) seja o seu hospedeiro primário e que o pangolim malaio (*Manis javanica*) o hospedeiro intermediário. O SARS-CoV-2 é um vírus envelopado, aproximadamente esférico, e os seus vírions têm diâmetros médios de 80 a 120 nm. Possui genoma de RNA não segmentado, fita simples, codificando quatro proteínas principais: glicoproteína espicular (S), proteína do envelope (E), glicoproteína da membrana (M) e proteína do nucleocapsídeo (N). Os coronavírus utilizam a S como principal alvo para neutralizar anticorpos e para se ligar ao receptor enzima conversora de angiotensina 2. *Conclusão:* O conhecimento aprofundado sobre as características básicas do SARS-CoV-2 é fundamental para a melhor compreensão e entendimento dos aspectos epidemiológicos, clínicos, fisiopatológicos e para o tratamento da COVID-19.

Descritores: SARS-CoV-2; Coronavirus; Classificação; Estrutura viral; Origem.

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1. Professor at the Federal Institute of Education, Science and Technology of Paraná (IFPR), Londrina Campus, Londrina, PR, BR. Doctor in Biotechnology from Universidade Estadual Paulista (UNESP), Araraquara, SP, BR. ORCID ID: <https://orcid.org/0000-0002-4868-2026>. Email: gauarabe@yahoo.com.br.

2. Nursing, Master of Science in Nursing from University of Brasília (UnB). ORCID ID: <https://orcid.org/0000-0003-0072-2903>. E-mail: dasilva.saraa@gmail.com.

Correspondence: Omar A. K. Khalil. R. João XXIII, 600 - Judith, Londrina, PR. CEP: 86060-370. E-mail: gauarabe@yahoo.com.br.

INTRODUCTION

Viruses and viral diseases have been at the centers of science, agriculture, and medicine for millennia and some of our greatest challenges and triumphs have involved virology¹.

Infectious diseases afflict humanity since the beginning of civilization. The concern must be focused on the future and not on the past², however, the COVID-19 outbreak, caused by the zoonotic virus SARS-CoV-2 is, presently, the greatest global apprehension and one never seen before in the history of humanity.

Zoonoses are the diseases and infections that are naturally transmitted between vertebrate animals and humans, caused by exposure between them, and are usually limited to agents that can replicate in the animal host. This definition is valid even when the agent has the ability to, afterwards, spread within human populations without any animal exposure, as exemplified for the severe acute respiratory syndrome (SARS) coronavirus, MERS (Middle Eastern Respiratory Syndrome) coronavirus³, and SARS-CoV-2.

A significant number of the diseases currently affecting humans originated in sylvatic cycles, and have crossed over at one point or the other due to the ability of viruses to mutate rapidly and adapt to new species, especially in the case of RNA viruses. In zoonosis diseases, a spatial and physical association of feral and domesticated species creates the setting for viruses to cross the species barrier, resulting in emergent diseases. Humans have played a major part in such emerging zoonosis throughout the centuries, with activities such as farming, deforestation, and urbanization⁴. The study of how zoonotic viruses become human pathogens has already become a major focus of 21st century virology¹.

The 2003 outbreak of severe acute respiratory syndrome (SARS), a disease caused by a coronavirus identified as a etiological agent of severe acute respiratory syndrome, shocked the world as it spread swiftly from continent to continent, resulting in >8,000 infections, with approximately 10% mortality, and a devastating effect on local and regional economies, becoming the first pandemic of the 21st century⁵. Whereas COVID-19, declared a pandemic on March 11th of 2020 by the World Health Organization⁶, accounted for about 100.000 deaths after the announcement of this institution⁷. In fact, Covid-19 has already caused 10 times as many cases as SARS in a quarter of the time⁸.

The coronaviruses (CoVs) already identified might only be the tip of the iceberg, with potentially more novel and severe zoonotic events to be revealed⁹.

Even in the academic environment, there is still great difficulty to comprehend the basic aspects related to SARS-CoV-2, since the scientific production related

to this virus is recent and predominantly in a foreign language. Therefore, the objective of this article is to deal with the basic aspects related to the virus, such as its name, taxonomy, origin, and constitution.

METHOD

This is an exploratory and narrative review of basic aspects of SARS-CoV-2. The research was carried out in the Pubmed, Scopus, Google Scholar, and Scielo electronic databases, with a focus on obtaining and analyzing articles published in 2019 and 2020. The Health Sciences Descriptors (either alone or combined) used were: “SARS-CoV-2” along with terms “COVID-19”, “spike-protein”, “classification”, “coronavirus”. The terms were defined by the Medical Subject Headings (MeSH).

The materials were between April 1, 2020, and April 30, 2020. Original and review studies were obtained and analyzed, mainly in English, Spanish, and Portuguese in which the title, abstract, and topics were aligned with the terms of interest. The contents of interest were described according to their relevance in contributing to the objective of this study.

Origin: China

The two major outbreaks of infectious diseases caused by bat CoVs (SARS and COVID-19) emerged in China. The factors that contributed to the emergence of these diseases in this country were: (1) the vast homeland plus diverse climates that bring about a great biodiversity including that of bats and bat-borne viruses—the majority of CoVs can be found in China and more than 50% of the identified species (22/38) were named by Chinese scientists studying local bats or other mammals; (2) most of the bat hosts of these CoVs live near humans, potentially transmitting viruses to humans and livestock; (3) Chinese food culture maintains that live slaughtered animals are more nutritious, and this belief may enhance viral transmission¹⁰. This last factor had already been pointed out more than a decade ago as a strong alert: the presence of a large reservoir of SARS-CoV-like viruses in horseshoe bats, together with the culture of eating exotic mammals in southern China, is a time bomb for the possibility of the re-emergence of SARS and other novel viruses from animals or laboratories¹¹.

Origin: horseshoe bat (*Rhinolophus sinicus*)

Overflow is the term derived from “Spillover” (“Host Transfer” or “Host switching”), which designates the process in which the passage of naturally infecting pathogen agent of an infected animal population occurs to a host species previously not affected by this agent, such as the human species. The persistence or not of the

infection, whether in an endemic or epidemic manner, will depend on the easiness for the inter-human transmission of the emerging pathogen to occur, greatly determined by the genetic and physiological characteristics of the emerging pathogen and the new host¹².

Coronaviruses (CoVs) are zoonotic viruses with the ability to infect a diversity of animals (domestic or not) and humans. These nonspecific properties that CoVs possess may be due to accessory CoV genes, which are already thought to play a role in host tropism and adaptation to a new host. S-Glycoprotein appears to be the main determinant for the success of initial events of infection between species¹³, while the angiotensin-converting enzyme 2 (ACE2) is known as a human receptor for this viral spike surface glycoprotein, which facilitates its transmission between species¹⁴.

Among animals, it is evident that bats are the group of mammals that harbor the largest number of CoVs and that many other animal CoVs recognize their ancestors in bat CoVs¹⁵.

Domestic animals may have important roles as intermediate hosts that enable virus transmission from natural hosts to humans. In relation to SARS-CoV, it is suggested that bats may be the natural hosts for SARS-CoV and that civets (*Paguma larvata*) were only intermediate hosts, whereas, for MERS-CoV, the dromedary camels were only intermediate hosts¹⁶. In both of these epidemics, these viruses have likely originated from horseshoe bats (*Rhinolophus sinicus*) and then jumped into another amplification mammalian host, the Himalayan palm civet (*Paguma larvata*) for SARS-CoV and the dromedary camel (*Camelus dromedarius*) for MERS-CoV before crossing species barriers to infect humans. Based on the 339 complete SARS-related coronavirus genomes analysis, it is suggested that the SARS-CoV-2 might also have originated from bats, however, it is not possible to determine whether another intermediate or amplification animal host infected by this virus would be related to COVID-19¹⁷.

It is possible that SARS-CoV-2 entered human populations through intermediate host(s). However, few SARS-CoV-2-related viruses have been described in mammals other than bats and humans.

The SARS-CoV-2-related viruses are still poorly sampled in mammals (even in bats) to reach a conclusion. The identification of two distinct viral clusters in pangolins indicates that SARS-CoV-2-related virus might be more widely distributed in wild mammals than expected¹⁸.

The high similarity between the Guangdong pangolin CoVs and SARS-CoV-2 in the RBD raises concern that these viruses might be readily transmitted to human populations. More work is necessary to explore the pathogenicity and diversity of CoVs in pangolins. Nevertheless, due to their status of being endangered, and the risk of causing future CoV outbreaks, the hunting, handling, and trafficking of pangolins should be strictly

prohibited. Further surveillance of SARS-CoV-2-related viruses in mammals might help to clarify the origin of SARS-CoV-2¹⁸.

There is evidence to point to the Malayan pangolin (*Manis javanica*) as the probable origin of SARS-CoV-2, responsible for the outbreak of COVID-19. Through the analysis from lung samples of two dead Malayan pangolins with a frothy liquid in their lungs and pulmonary fibrosis discovered close to when the COVID-19 outbreak occurred, a Pangolin-CoV was identified, with a potential kinship of SARS-CoV-2 (91.02% genomic similarity and 90.55% genomic similarity with BatCoV RATG13, a Cov of bats), being the coronavirus most closely related to SARS-CoV-2 already described. Considering the widespread of SARSr-CoVs in natural reservoirs, such as bats, camels, and pangolins, these findings are significant for attempts to block interspecies viral transmission¹⁹.

The close phylogenetic relationship to BatCoV RaTG13 provides evidence that SARS-CoV-2 may have originated in bats²⁰. This way, similar to what happened in 2002²¹, civets can be the intermediate hosts for the transmission of SARS-CoV to humans.

Virus name

The naming of a new virus is important not only for the virologists in long-term, but also for efficient communication to the public in general. In all the major emerging zoonotic viruses events over the past 25 years, the naming of the new virus has not been straightforward and most went through a renaming process²².

The name of the virus is not necessarily connected to a disease, but to its characteristics, such as its phylogeny. There is a vast quantity of viruses with phenotypic characteristics that are not known, which makes the sequences of its genomes the only precise characteristic known for the great majority of virus [viruses] and that can be used to define specific ones. Based on this, Coronaviridae Study Group (CSG) of the International Committee of Taxonomy of Viruses (ICTV), responsible for the classification of viruses and the naming of taxa of the Coronaviridae family, designated the virus responsible for the outbreak of the COVID-19 diseases as SARS-CoV-2²³.

The term “corona” derives from the structural glycoprotein’s organization around the virus, which resembles a crown¹³.

Although the CGS claimed that they did not intend to make any reference to SARS disease, it is pointed out that the name of the virus as SARS-CoV-2 was not adequate, because SARS is a disease name, and to name the new virus SARS-CoV-2 actually implies that it causes SARS or similar, especially to scientists without much knowledge of virology and to citizens in the public domain. Furthermore, the new virus name is also not consistent with the disease name COVID-19. On the basis of special

clinical, virological, and epidemiological characteristics and the uncertainty of the novel coronavirus, to avoid the misleadingness and confusion, and to help scientists and the public with better communication, a group of virologists in China, suggest renaming SARS-CoV-2 as human coronavirus 2019 (HCoV-19). Such a name distinguishes the virus from SARS-CoV and keeps it consistent with the WHO name of the disease it causes, COVID-19²⁴. On the other hand, it is still possible to find the designation 2019-nCoV as a descriptor of this virus²⁵.

The WHO does not recommend the usage of the term SARS for the outbreak caused by the new coronavirus in 2020. Instead, in order to avoid unnecessary fear in some populations, especially in Asia, which was the most affected by the SARS outbreak in 2003²⁶, it is more appropriate to name it COVID-19.

Regarding the name of the disease, COVID-19 (short for “coronavirus disease 2019”) is the term of a viral disease that followed WHO best practices for the naming of new human infectious diseases, which were developed in consultation and collaboration with the World Organization for Animal Health (OIE) and the Food and Agriculture

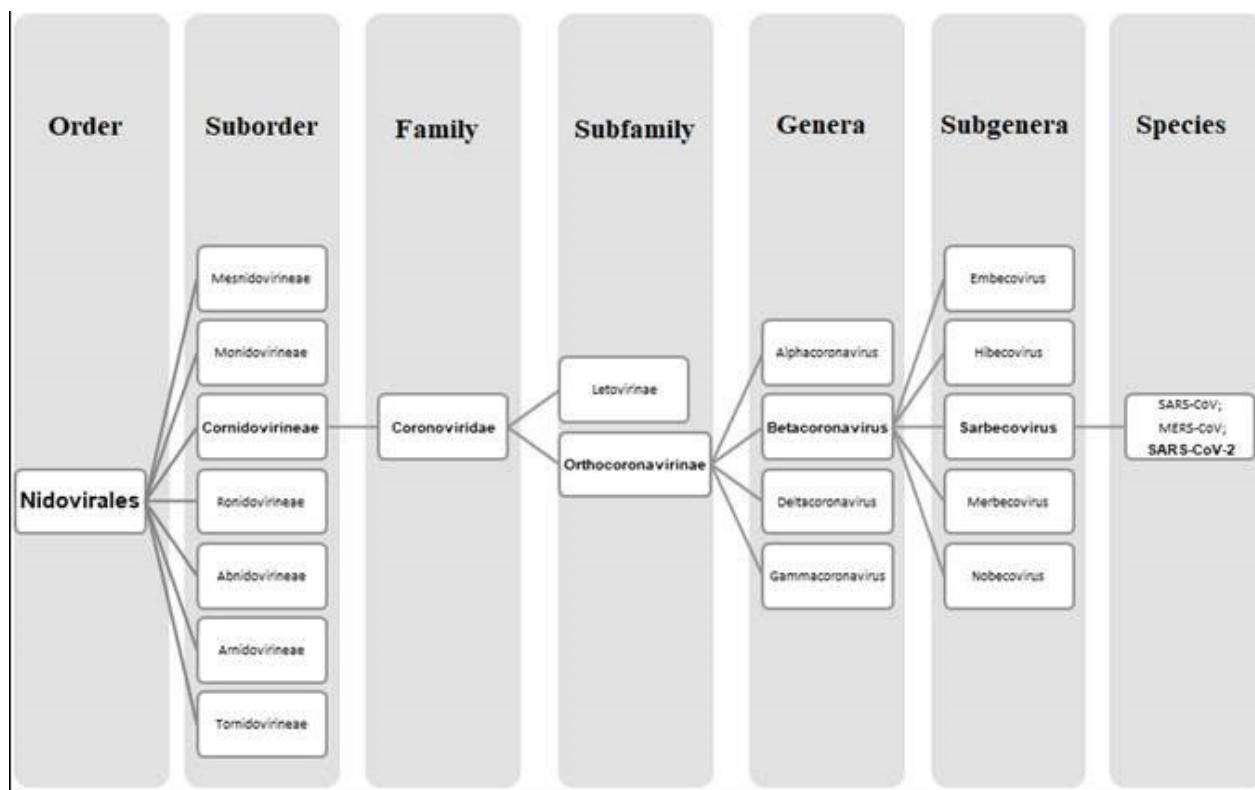
Organization of the United Nations (FAO)²⁷.

Virus taxonomy

To ignore the adequate taxonomy is to ignore history; it is also to ignore the similarities and differences between living beings, as well as the evolutionist ideas of classification²⁸.

Phylogenetically, Coronaviridae belongs to Nidovirales in group IV, with a single genomic RNA fragment, oriented in a positive direction¹³ and comprises two subfamilies, five genera, 26 subgenera, and 46 virus species²⁹.

SARSr-CoVs belong to the subgenus Sarbecovirus (previously lineage B) of genus Betacoronavirus and occupy a unique phylogenetic position. SARS-CoV-2 is the name of the virus that belongs to the coronavirus species related to the acute respiratory syndrome, abbreviated as SARS-rCoV²⁹. The seventh human coronavirus, SARS-CoV-2, belongs to the genus Betacoronavirus, which also contains SARS-CoV and MERS-CoV³⁰. Figure 1 demonstrates the taxonomy of this virus.



Source: prepared by the authors (2020).

Figure 1. Taxonomy of SARS-CoV-2

The CoVs of the α and β genera generally infect mammals and humans, while the CoVs of the γ and δ genera mainly infect birds, but some of them can also infect mammals³¹.

The amino acid sequences of the seven conserved replicase domains in ORF1ab that were used for CoV species classification were 94.4% identical between SARS-CoV-2 and SARS-CoV, suggesting that the two viruses

belong to the same species, SARSr-CoV²⁰.

Phylogenetic studies on SARS-CoV-2 genomic sequences revealed that it clustered closely with sequences originating from SARS-like sequences from bats, within lineage B of the Betacoronavirus genus. HCoV-HKU1 and HCoV-OC43 are grouped in lineage A. MERS-CoV is found within lineage C, along with related camel derived MERS-CoV. Lineage C also groups viruses from bats and other mammals such as hedgehogs. Lineage D contains viral species infecting bats³².

SARS-CoV-2 constitution

Coronaviruses are roughly spherical and moderately pleomorphic and enveloped viruses. Virions have typically been reported to have average diameters of 80–120 nm³³. The CoVs have a positive-sense, non-segmented, single-stranded RNA, 5'-capped, 3'-polyadenylated, and astoundingly large size ranging from 27 to 32 kilobases³⁴.

The virus genome consists of six major open-reading frames (ORFs) that are common to coronaviruses and several other accessory genes²⁰. CoVs are characterized by the property of transcribing code mRNAs for each protein. This property allows the virus to control the rate of protein synthesis according to its state requirements and that of the host cell¹³. The coronavirus replication cycle is divided into several steps: attachment and entry, translation of viral replicase, genome transcription and replication, translation of structural proteins, and virion assembly and release³⁴.

CoVs encode membrane-associated proteins that are incorporated into virions: spike (S), envelope (E), membrane (M), and nucleoprotein (N)¹³. Virus infectivity studies using HeLa cells that expressed or did not express ACE2 proteins from humans were conducted to determine whether SARS-CoV-2 also uses ACE2 as a cellular entry receptor. Chinese horseshoe bats, civets, pigs, and mice] SARS-CoV-2 is able to use all ACE2 proteins, but not with aminopeptidase N (APN) and dipeptidyl peptidase 4 (DPP4), indicating that ACE2 is probably the cell receptor through which 2019-nCoV enters cells²⁰.

CoV uses its spike glycoprotein (S), the main target for neutralization antibody, to bind its receptor, and mediate membrane fusion and virus entry. The S protein contains two subunits, S1 and S2, mediating attachment and membrane fusion, respectively³⁵.

The type I glycoprotein S protrudes from the surface of the virus and attracted great attention because of its function in receptor binding cell³⁶. S-glycoprotein appears

to be the main determinant for the success of initial events of infection between species¹³.

Understanding the main structural and molecular components of SARS-CoV-2 is a fundamental way to reach COVID-19 therapy. As there is currently no pharmacological treatment available for this disease and due to its severity, there is an urgent need to find therapeutic options in support of the current protocols to assist in the prevention, treatment, control of symptomatology, and decrease the severity of SARS-CoV infections³⁷. Although vaccines under development are in advanced clinical stages, currently there are no licensed vaccines for any coronavirus yet. Despite efforts in fast-tracking vaccine development, completion dates for early clinical trials are estimated to be late 2020 to mid-2021 and it may still take longer before a vaccine is licensed for use globally, which emphasizes the need for proven public health strategies such as physical distancing, early detection, and self-isolation as important mitigation tools³⁸.

CONCLUSION

The new coronavirus SARS-CoV-2 is the etiological agent of COVID-19, a highly infectious disease that affects mainly the lower respiratory tract which the first cases were reported in China in 2019. Since then, the virus has spread all over the world, causing a pandemic that results in catastrophic consequences for global health and economy: besides the millions of deaths and permanent sequels in many survivors, it created or aggravated an economic crisis, especially in developing countries like Brazil.

Although there were initial discussions related to its name, ICTV officially designated it as SARS-CoV-2 and the WHO designated the name of the diseases as COVID-19. Both took into consideration technical and even ethical aspects, avoiding to stigmatize and deepen the prejudice and xenophobia that surround this theme.

Because it is a zoonotic virus with a spillover that is related to the horseshoe bat as a primary host and as a possible domesticated or commercialized secondary host for human food, SARS-CoV-2 raises the permanent challenge related to the human-animal relation, whose analysis of its interactions should predominate on the individual perspectives of one another if we wish to settle or avoid the emergence of new viral lineages or species in humans.

Finally, in-depth knowledge about the receptors and its targets on the basis of viral replication would be a great step forward to find a remedy for the SARS-CoV-2 infection³⁹.

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REFERENCES

1. Enquist LW. Virology in the 21st century. *J Virol.* 2009;83(11):5296-308. doi: <https://doi.org/10.1128/JVI.00151-09>.
2. Santos NSO. Novos desafios no ensino da virologia. *Rev Pan-Amaz Saude.* 2018;9(1):7-8. doi: <https://doi.org/10.5123/S2176-62232018000100001>.
3. Chomel BB. Zoonoses. *Ref Mod Biomed Sci.* 2014. doi: <https://doi.org/10.1016/B978-0-12-801238-3.02426-0>.
4. Foster JE. Viruses as pathogens: animal viruses affecting wild and domesticated species. In: Tennant P, Fermin G, Foster J, editors. *Viruses. Molecular biology, host interactions, and applications to biotechnology.* London: Academic Press; 2018. Chap. 8, p.189-216. doi: <https://doi.org/10.1016/B978-0-12-811257-1.00008-5>.
5. Leduc JW, Barry MA. SARS, the first pandemic of the 21st century. *Emerging Infect Dis.* 2004;10(11):e26. doi: https://doi.org/10.3201/eid1011.040797_02.
6. World Health Organization (WHO). Coronavirus disease 2019 (COVID-19) Situation Report – 51. Data as reported by national authorities by 10 AM CET 11 March 2020. Available from: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200311-sitrep-51-covid-19.pdf?sfvrsn=1ba62e57_10.
7. World Health Organization (WHO). Coronavirus disease 2019 (COVID-19) Situation Report – 82. Data as received by WHO from national authorities by 10:00 CET, 11 April 2020. Available from: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200411-sitrep-82-covid-19.pdf?sfvrsn=74a5d15_2.
8. Gates B. Responding to Covid-19 - a once-in-a-century pandemic? *N Engl J Med.* 2020;382:1677-9. doi: <https://doi.org/10.1056/NEJMp2003762>.
9. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X, Cheng Z, Yu T, Xia J, Wei Y, Wu W, Xie X, Yin W, Li H, Liu M, Xiao Y, Gao H, Guo L, Xie J, Wang G, Jiang R, Gao Z, Jin Q, Wang J, Cao B. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet.* 2020;395:497-506. doi: [https://doi.org/10.1016/S0140-6736\(20\)30183-5](https://doi.org/10.1016/S0140-6736(20)30183-5).
10. Fan Y, Zhao K, Shi Z-L, Zhou P. Bat coronaviruses in china. *Viruses.* 2019;11(210):14. doi: <https://doi.org/10.3390/v11030210>.
11. Cheng VCC, Lau SKP, Woo PCY, Yuen KY. Severe acute respiratory syndrome coronavirus as an agent of emerging and reemerging infection. *Clin Microbiol Rev.* 2007;20(4):660-94. doi: <https://doi.org/10.1128/CMR.00023-07>.
12. Confalonieri UEC. Emergência de doenças infecciosas humanas: processos ecológicos e abordagens preditivas. *Oecol Aust.* 2010;14(3):591-602. doi: <https://doi.org/10.4257/oeco.2010.1403.01>.
13. Kasmi Y, Khataby K, Souiri A, Ennaji MM. Coronaviridae: 100,000 years of emergence and reemergence. In: Ennaji MM, editor. *Emerging and reemerging viral pathogens. Vol. I. Fundamental and Basic Virology Aspects of Human, Animal and Plant Pathogens.* London: Elsevier Academic Press; 2020. v.1, p.127-49. doi: <https://doi.org/10.1016/B978-0-12-819400-3.00007-7>.
14. Wu A, Peng Y, Huang B, Ding X, Wang X, Niu P, Meng J, Zhu Z, Zhang Z, Wang J, Sheng J, Quan L, Xia Z, Tan W, Cheng G, Jiang T. Genome composition and divergence of the novel coronavirus (2019-nCoV) originating in china. *Cell Host Microbe.* 2020;27(311):325-8. doi: <https://doi.org/10.1016/j.chom.2020.02.001>.
15. Decaro N, Lorusso A. Novel human coronavirus (SARS-CoV-2): a lesson from animal coronaviruses. *Vet Microbiol.* 2020;244:108693. doi: <https://doi.org/10.1016/j.vetmic.2020.108693>.
16. Cui J, Li F, Shi Z-L. Origin and evolution of pathogenic coronaviruses. *Nat Rev Microbiol.* 2019;17(3):181-192. doi: <https://doi.org/10.1038/s41579-018-0118-9>.
17. Chan JF-W, Kok K-H, Zhu Z, Chu H, Kai-Wang K, To KK-W, Yuan S, Yuen K-Y. Genomic characterization of the 2019 novel human pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. *Emerg Microbes Infect.* 2020;9(1):221-36. doi: <https://doi.org/10.1080/22221751.2020.1719902>.
18. Han G-Z. Pangolins harbor SARS-CoV-2-related coronaviruses. *Trends Microbiol.* 2020;28(7):515-7. doi: <https://doi.org/10.1016/j.tim.2020.04.001>.
19. Zhang T, Wu Q, Zhang Z. Probable pangolin origin of SARS-CoV-2 associated with the COVID-19 outbreak. *Curr Biol.* 2020;30(76):1346-51.e2. doi: <https://doi.org/10.1016/j.cub.2020.03.022>.
20. Zhou P, Yang XL, Wang X-G, Hu B, Zhang L, Zhang W, Si H-R, Zhu Y, Li B, Huang C-L, Chen H-D, Chen J, Luo Y, Guo H, Jiang R-D, Liu M-Q, Chen Y, Shen X-R, Wang X, Zheng X-S, Zhao K, Chen Q-J, Deng F, Liu L-L, Yan B, Zhan F-X, Wang Y-Y, Xiao G-F, Shi Z-L. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature.* 2020;579:270-86. doi: <https://doi.org/10.1038/s41586-020-2012-7>.
21. Organização Pan-Americana de Saúde (OPAS). COVID-19 (doença causada pelo novo coronavírus). *Folha Informativa,* 2020. Atual. 17 abr. 2020. Disponível em: https://www.paho.org/bra/index.php?option=com_content&view=article&id=6101:covid19&Itemid=875.
22. Wang L-F, Anderson DE, Mackenzie JS, Merson MH. From Hendra to Wuhan: what has been learned in responding to emerging zoonotic viroses. *Lancet.* 2020;395(1022422-28):e33-e34. doi: [https://doi.org/10.1016/S0140-6736\(20\)30350-0](https://doi.org/10.1016/S0140-6736(20)30350-0).
23. Gorbalenya AE, Baker SC, Baric RS, De Groot RJ, Drosten C, Gulyaeva AA, Haagmans BL, Lauber C, Leontovich AM, Neuman BW, Penzar D, Perlman S, Poon LLM, Samborskiy DV, Sidorov IA, Sola I, Ziebuhr J. The species severe acute respiratory syndrome related coronavirus: classifying 2019-

- nCoV and naming it SARS-CoV-2. Coronaviridae Study Group of the International Committee on Taxonomy of Viruses. *Nat Microbiol.* 2020;5(536):536-44. doi: <https://doi.org/10.1038/s41564-020-0695-z>.
24. Jiang S, Shi Z, Shu Y, Song J, Gao GF, Tan W, Guo D. A distinct name is needed for the new coronavirus. *Lancet.* 2020;395(1022821-27):949. doi: [https://doi.org/10.1016/S0140-6736\(20\)30419-0](https://doi.org/10.1016/S0140-6736(20)30419-0).
 25. Jiang S, Hillyer C, Du L. Neutralizing antibodies against SARS-CoV-2 and other human coronaviruses. *Trends Immunol.* 2020;41(5):355-359. doi: <https://doi.org/10.1016/j.it.2020.03.007>.
 26. World Health Organization (WHO). Naming the coronavirus disease (COVID-19) and the virus that causes it. Geneva; 2020 [cited 2020 April 12]. Available from: [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-\(covid-2019\)-and-the-virus-that-causes-it](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it).
 27. World Health Organization (WHO). Novel coronavirus (2019-nCoV) situation report – 22. Geneva; 2020. Available from: <https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200211-sitrep-22-ncov.pdf>.
 28. Calisher CH. Qual é a diferença entre uma espécie de vírus e um vírus? A mesma diferença existente entre Homo sapiens e você. *Rev Pan-Amaz Saude.* 2010;1(3):137-9. doi: <https://doi.org/10.5123/S2176-62232010000300019>.
 29. International Committee on Taxonomy of Viruses (ICTV). Virus taxonomy: 2018b release. EC 50, Washington, DC; July 2018. Email ratification February 2019 (MSL #34). Available from: <https://talk.ictvonline.org/taxonomy/>.
 30. Ko W-C, Rolain J-M, Lee N-Y, Chen P-L, Huang CT, Lee P-I, Hsueh P-R. Arguments in favour of remdesivir for treating SARS-CoV-2 infections. *Int J Antimicrob Agents.* 2020;55(4):article 105933. doi: <https://doi.org/10.1016/j.ijantimicag.2020.105933>.
 31. Woo PC, Lau SKP, Lam CSF, Lau Ccy, Tsang AKL, Lau JHN, Bai R, Teng JLL, Tsang CCC, Wang M, Zheng, B-J, Chan K-H, Yuena K-Y. Discovery of seven novel Mammalian and avian coronaviruses in the genus deltacoronavirus supports bat coronaviruses as the gene source of alphacoronavirus and betacoronavirus and avian coronaviruses as the gene source of gammacoronavirus and deltacoronavirus. *J Virol.* 2012;86(7):3995-4008. doi: <https://doi.org/10.1128/JVI.06540-11>.
 32. Jaimes JA, André NM, Chappie JS, Millet JK, Whittaker GR. Phylogenetic analysis and structural modeling of SARS-CoV-2 spike protein reveals an evolutionary distinct and proteolytically sensitive activation loop. *J Mol Biol.* 2020;432(10):3309-25. doi: <https://doi.org/10.1016/j.jmb.2020.04.009>.
 33. Masters PS. The molecular biology of coronaviruses. *Adv Virus Res.* 2006;66:193-292. doi: [https://doi.org/10.1016/S0065-3527\(06\)66005-3](https://doi.org/10.1016/S0065-3527(06)66005-3).
 34. Fung S, Liu DX. Human coronavirus: host-pathogen interaction. *Annu Rev Microbiol.* 2019;73:529-57. doi: <https://doi.org/10.1146/annurev-micro-020518-115759>.
 35. Ou X, Liu Y, Lei X, Li P, Mi D, Ren L, Guo L, Guo R, Chen T, Hu J, Xiang Z, Mu Z, Chen X, Chen J, Hu K, Jin Q, Wang J, Qian Z. Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS-CoV. *Nat Commun.* 2020;11(1620):1-12. doi: <https://doi.org/10.1038/s41467-020-15562-9>.
 36. Luan J, Lu Y, Jin X, Zhang L. Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection. *Biochem Biophys Res Commun.* 2020;526(121):165-9. doi: <https://doi.org/10.1016/j.bbrc.2020.03.047>.
 37. Fuzimoto AD, Isidoro C. The antiviral and coronavirus-host protein pathways inhibiting properties of herbs and natural compounds – Additional weapons in the fight against the COVID-19 pandemic? *J Tradit Complement Med.* 2020;10(40):405-19. doi: <https://doi.org/10.1016/j.jtcme.2020.05.003>.
 38. Koirala, A, Joo JY, Khatami A, Chiu C, Britton, PN. Vaccines for COVID-19: the current state of play. *Paediatr Respir Rev.* 2020;35:43-9. doi: <https://doi.org/10.1016/j.prrv.2020.06.010>.
 39. Vellingiri B, Jayaramayya K, Iyer M, Narayanasamy A, Govindasamy V, Giridharan B, Ganesan S, Venugopal A, Venkatesan D, Ganesan H, Rajagopalan K, Rahman PKSM, CHO S-G, Kumar NS, Subramaniamk MD. COVID-19: a promising cure for the global panic. *Sci Total Environ.* 2020;725:138227. doi: <https://doi.org/10.1016/j.scitotenv.2020.138277>.

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