

Coronavirus-19 Disease (COVID-19) Overview, History, Classification, Structure, Hosts, Interaction with its Target Cell, Transmissions and Detection

Bahaa Kenawy Abuel-Hussien Abdel-Salam*

Department of Zoology, Faculty of Science, 61519 Minia University, El-Minia, Egypt

*Corresponding author: Bahaa Kenawy Abuel-Hussien Abdel-Salam, Department of Zoology, Faculty of Science, 61519 Minia University, El-Minia, Egypt, Tel: + 00201147075068, E-mail: bahaa.kenawy@mu.edu.eg

Received Date: June 10, 2022 Accepted Date: July 12, 2022 Published Date: July 16, 2022

Citation: Bahaa Kenawy Abuel-Hussien Abdel-Salam (2022) Coronavirus-19 Disease (COVID-19) Overview, History, Classification, Structure, Hosts, Interaction with its Target Cell, Transmissions and Detection. J Clin Trials Vaccine Res 1: 1-10.

Abstract

The COVID-19 was first officially recognized in Wuhan, China, in December 2019. Corona viruses are viruses belong to family Coronaviridae. SARS-CoV-2 is a spherical shaped and enveloped virus under beta-corona virus genus, which is 50-200 nm in diameter. SARS-CoV can infect animals such as cats, dogs and ferrets. The SARS-CoV-2 enters into the host cells by using the receptor-binding domain (RBD] of S protein that interacts with the cellular receptor angiotensin-converting enzyme 2 (ACE2]. Transmission of SARS CoV-2 to healthy individual occurs through respiratory droplets and aerosol from coughing and sneezing.

The thermal screening of visitors has become a normal response protocol since the SARS epidemic. It has been reported that the prevalence rates of co-infection of COVID-19 were above those previously reported in Wuhan, China. Disorders associated with COVID-19 include infection of neonates born to mothers with corona virus disease-2019, persisting olfactory dysfunction and exhibition of various gastrointestinal symptoms. It is incredibly important to address the potential responses of the human immune system during the SARS-CoV-2 infection. Humoral immune response, especially the production of neutralizing antibody, plays a protective role by limiting the infection at a later phase and prevents re-infection in the future. Until now, an efficient weapon against COVID-19 isn't gained by anybody. Despite the worsening trend of COVID-19, no drugs have been validated to exhibit significant efficacy in the clinical setting. The potential drugs, including remdesivir, hydroxychloroquine (HCQ], azithromycin, and immunomodulators, have not been subjected to large-scale studies or clinical trials. The aim of this paper is to make a sight on some points related to COVID-19.

Keywords: COVID-19; History; Classification; Structure; Hosts; Interaction; Transmissions; Detection; RBD; ACE2

^{©2022} The Authors. Published by the JScholar under the terms of the Creative Commons Attribution License http://creativecommons.org/licenses/ by/3.0/, which permits unrestricted use, provided the original author and source are credited.

Overview of Coronavirus-19 disease (COV-ID-19)

The COVID-19 was first officially recognized in Wuhan, China, in December 2019. It rapidly spread in China and became a global threat. By 7 May 2020, the causative pathogen, namely severe acute respiratory syndrome corona virus 2 (SARS-CoV-2] has infected 3,672,238 people and caused 254,045 deaths globally. A striking aspect of COVID-19 is that the disease became a pandemic in less than 3 months [1].

History of COVID-19

In 1960, the corona virus was characterized for the first time isolated from a child with upper respiratory tract infections [2]. Then, the HCoV-OC43 and HCoV-229E strains of corona viruses were identified from the persons suffering from colds [3, 4]. However, these two viruses and infectious bronchitis virus, mouse hepatitis virus, and swine transmissible gastroenteritis virus were morphologically similar under electron microscopy; therefore, this new group of viruses was named corona virus in the late 1960s [2]. The term coron used to mean crown-like structure surrounded by surface projection of the viruses under electron microscopy [2]. The HCoV-OC43 and HCoV-229E strains of corona virus cause common cold in human prevalent worldwide [2, 5]. In November 2002, corona virus (SARS-CoV] causing pandemic severe acute respiratory syndrome (SARS] was first identified in Foshan, Guangdong, China. Approximately 29 separate countries were affected by SARS-CoV and at least 831 people were 96 died worldwide among over 8000 infected cases [6]. The human corona virus NL63 (HCoV-NL63] was first identified in 2004 in Netherland from a seven-month-old child with bronchiolitis [7]. A novel strain of corona virus HKU1 (HCoV-HKU1] has been discovered in 2005 which was isolated and characterized from an adult human suffering from chronic pulmonary disease in Hong Kong [8]. The Middle East respiratory syndrome-related corona virus (MERS-CoV] is another species of corona virus; first reported in 2012 in Saudi Arabian patient suffering from pneumonia [9]. As of April, 2019, globally 2374 MERS-CoV confirmed cases have been reported with a total of 823 deaths from 27 countries worldwide [10]. The latest strain of a pandemic corona virus is SARS-CoV-2 which causes COVID-19; reported, 2019 in Wuhan of China on 31 December [11]. Due to extremely high contagiousness of SARS-CoV-2; as of May 20, 2020, more than 5000,000 cases of COVID-19 have been confirmed from 213 affected countries and territories with more than 334,000 deaths.

Classification of COVID-19

Structure of COVID-19

Corona viruses are viruses belong to family Coronaviridae. They can produce diseases in human and animal. Under this family, there are four genera; Alpha-corona virus, Beta-corona virus, Gamma-corona virus, and Delta-corona virus.

Mild illness in the upper respiratory tract can be produced by the human corona viruses while some strains are lethal and can cause severe acute respiratory syndrome (SARS], middle East respiratory syndrome (MERS] and corona virus disease 2019 (COVID-19] [6, 9, 12]. So, COVID-19 has been divided into four types: mild, moderate, severe, and critical cases [13].

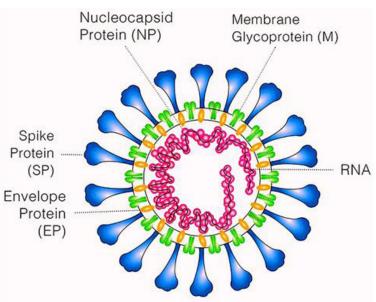


Figure 1: Structure of SARS-CoV-2

SARS-CoV-2 is a spherical shaped and enveloped virus under beta-corona virus genus, which is 50-200 nm in diameter. The viral genome is a ~30 kb sized single-stranded positive sense RNA materials from which four structural proteins and 16 non-structural proteins are produced. The structural proteins are spike (S], envelope (E], membrane (M] and nucleocapsid (N] [14]. Wu, *et al.*, 2020 indicated that the viral envelope consists of E and M proteins on which S is anchored15]] (Figure 1).

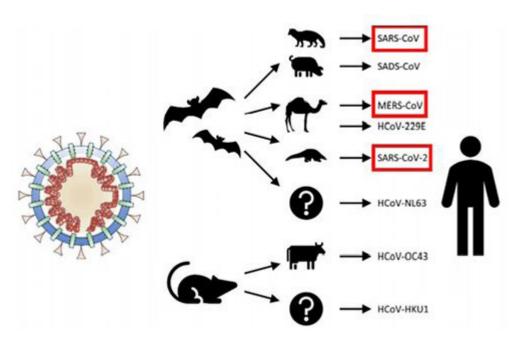


Figure 2: Animal origins of human corona viruses (SARS-CoV, MERS-CoV and SARS-CoV-2)

Hosts of COVID-19

Figure (2) show that the severe acute respiratory syndrome corona virus (SARS-CoV] and Middle East respiratory syndrome corona virus (MERS-CoV] were transmitted to humans from bats by civet cats and dromedary camels, respectively. The 2019 SARS-CoV-2 was likely transmitted to humans through pangolins that are illegally sold in Chinese markets [16, 17].

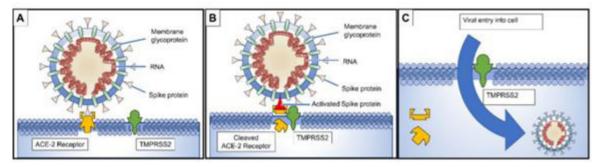
SARS-CoV can infect animals such as cats, dogs and ferrets [18, 19, 20]. However, there is very limited information regarding the investigations on SARS-CoV-2 in animals. A recent study found that SARS-CoV-2 could recognize the host cells receptor ACE2 of pigs, ferrets, cats, orangutans, monkeys, and humans with similar efficiencies [21]. Several cases of SARS-CoV-2, which causes COVID-19 in human; have been confirmed in animals. Laboratory studies also showed that cat and ferrets are highly susceptible to SARS CoV-2 that was isolated from human [22, 23]. To date, there is no published report so far on the investigation of SARS-CoV-2 in domestic pets, which were in contact with COVID-19 patients.

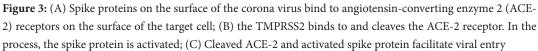
Corona viruses circulate in bats usually move through

an intermediate animal host until crossing the boundary between organisms to infect humans [24]. Different species of bats in China carry genetically diverse corona viruses, some of which are direct ancestors of SARS-CoV [24, 25, 26]. Indeed, the first SARS-CoV that caused a human outbreak derived from SARSlike CoV circulating in Chinese horseshoe Rhinolophus bats which apparently adapted to wild Himalayan palm-civet before spreading in humans [27]. The MERS-CoV originated from a Pipistrellus bat CoV and was probably transmitted to humans through contact with infected camels [28, 29, 30]. Soon after the first outbreak of SARS-CoV-2 in humans, it was reported that this new virus was related to a bat-borne corona virus (BatCoV RaTG13] present in the Rhinolophus affinis bat species [31]. The identification of an intermediate animal hosts has been the subject of intense research and it was claimed that a pangolin (Manis javanica] was the intermediate host for SARS-CoV-2 [32]. The SARS-CoV-2 receptor ACE2 from bat and pangolin and several other species were found to resemble that of human [33].

Interaction of COVID-19 with its target cell

In Figure 3 the SARS-CoV-2 enters into the host cells by using the receptor-binding domain (RBD] of S protein that interacts with the cellular receptor angiotensin-converting enzyme 2 (ACE2] [34]. The type II transmembrane serine protease (TMPRSS2] expression increases cellular uptake of the corona virus [35, 36, 37].





SARS-CoV-2 has recently been documented to able to bind the alveolar pneumocytes that express ACE2 at their surface [31, 38]. Yet, in humans, the ACE2 mRNAs were found expressed in virtually all organs including the heart, blood vessels, kidney and testis, opening the possibility for this virus to infect other tissues beside lung [39, 40]. ACE2 is a known peptidase that regulates the rennin angioten-aldosterone system (RAAS], thus controlling blood pressure. It is not surprising, therefore, that initials reports indicated that hypertension, diabetes and cardiovascular diseases were the most common co morbidity in COVID-19 disease [41].

ACE2 is also expressed by the small intestine enterocytes and expected to regulate the gut antimicrobial peptides expression [42]. Moreover, this peptidase is also present on the arterial and venous endothelial cells, and arterial smooth muscle [43]. In normal human lung, the ACE2 protein is found on type I and II alveolar epithelial lung cells [44]. High expression of ACE2 has also reported on oral mucosal epithelial cells of [45].

ACE2 plays an important glycemic protective function in the pancreas [46]. Low ACE2 expression in the kidney is also associated with progressive renal diseases including diabetic nephropathy [47]. Human ACE2 mRNA expression and human ACE2 protein polymorphism influence SARS-CoV-2 susceptibility and COVID-19 disease outcome.

A for the SARS-CoV, the S1 domain of the spike protein mediates ACE2 receptor binding whereas the S2 domain is a membrane-associated portion that likely undergoes post-binding transconformational modifications allowing membrane fusion. The viral receptor binding domain (RBD] located in S1 has been narrowed down to amino acid residues 318 to 510 [48]. A point mutation Leu584Ala in ACE2 markedly attenuated the shedding of the enzyme and facilitated SARS-CoV entry into target cells [49]. A soluble form of ACE2 lacking the cytoplasmic and transmembrane domain of the molecule was reported capable of blocking binding of SARS-CoV spike protein to ACE2 [50]. Expression of ACE2 was found down regulated in cells infected by SARS-CoV [34]. A recombinant SARS-CoV spike protein was found to down regulated ACE2 expression through release of sACE2 and thereby promotes lung injury [51]. Among other antiviral effects of Chloroquine on SARS-CoV *in vitro*, a glycosylation deficit of the ACE2 virus cell surface receptor could be attributed [52, 53].

Recently, research into SARS-CoV-2 cell entry via ACE2 binding showed substantial commonalities between SARS-CoV and SARS-CoV-2 infection, including similar entry receptor selection [54]. SARS-CoV and SARS-CoV-2 share about 260 76% amino acids identity and most amino acid residues essential for ACE2 binding were conserved in the SARS-CoV-2 spike S1 domain. Another recent paper published reported the structural basis of SARS-CoV2 interaction with ACE2 [55]. The role of these isoforms in SARS-CoV-2 infection and COVID-19 outcome remains speculative.

ACE2 protein at the surface of lung alveolar epithelial cells enables SARS-CoV-2 to infect the respiratory tract. It can be hypothesized that the ACE2 levels correlate with susceptibility to SARS-CoV-2 infection. Apparently, men have a higher ACE2 expression in lung than women and Asian people express ACE2 higher than Caucasian and African American populations [44]. This is in agreement with the finding that conversion of Ang II to Ang (1-7] by ACE2 was higher in males than female 100, suggesting an over-expression of ACE2 in men. Because ACE2 is encoded by a gene located on the X chromosome and men express more ACE2 than women it could be speculated that depending the allele expressed by women, they could be considered of lower sensitivity against the most severe adverse effects of the infection57,56]]. All clinical reports published to date indicate that men represent between 66% and 75% of the most severe cases of COVID-19. During early SARS-CoV-2 infection and viral spread within body tissues, the ACE2 function is likely impaired either by steric hindrance of the peptidase domain of ACE2 following virus binding or by down regulation of ACE2 mRNA expression and ACE2 protein. In severe COVID-19 disease, the presence of the viral receptor on other tissues than lung may explain the multi-organ failure sometimes observed in clinic. Therefore we recommend incorporating quantification of ACE2 and AngII be added to the COVID-19 patients biological monitoring. The mechanism f or acute myocardial injury caused by SARS-CoV-2 during serious COVD-19 disease may be linked to catalytic activity inhibition of ACE2 [58].

Transmissions of COVID-19

Transmission of SARS CoV-2 to healthy individual occurs through respiratory droplets and aerosol from coughing and sneezing [59]. Surface or feces contaminations may also involve in indirect transmission with it [15, 60, 61]. It is already reported that many of the infected patients do not show any clinical symptoms but may shed the virus through their respiratory droplets [62]. On the other hand, the infected person may shed virus before onset of the symptoms, therefore, SARS CoV-2 can be transmitted to the healthy individuals in three possible ways; symptomatically, pre-symptomatically, and asymptomatically [63]. Moreover, SARS CoV-2 might be transmitted as airborne and closed environments contribute to the secondary transmission of the virus thereby promote the super-spreading phenomenon [64, 65].

Detection of COVID-19

The thermal screening of visitors has become a normal response protocol since the SARS epidemic [66]. Fever was a common symptom, 47.4% - 100%, among patients with pneumonia caused by severe acute respiratory syndrome corona virus 2 (SARS-CoV-2], [67]. Body temperature measurements once daily for healthcare workers and twice daily for people in isolation or quarantine are important measures to reduce the risk of cross infections. The HEAR Thermo, a watch-like wearable device, can measure body surface temperature and heart rate every 10 s with good reliability for testing and adequate validity of the criterion [68].

In the history of medicine, autopsies and tissue sampling have played a fundamental role in order to understand the pathogenesis of emerging diseases, including infectious ones; compared to the past, histopathology can be now expanded by innovative techniques and modern technologies. For the first time in worldwide literature, we provide a detailed postmortem and biopsy report on the marked increase, up to1 order of magnitude, of naked megakaryocyte nuclei in the bone marrow and lungs from serious COVID-19 patients. Most likely related to high interleukin-6 serum levels stimulating megakaryocytopoiesis, this phenomenon concurs to explain well the pulmonary abnormal immunothrombosis in these critically ill patients, all without molecular or electron microscopy signs of megakaryocyte infection [69].

SARS-COV-2 has arisen as a new pathogen frequently inducing sepsis-like manifestations in the host. Indeed, based on actual evidence showing hyperinflammation as well as T cell deficiencies and coagulation abnormalities, associated with life-threatening organ dysfunction, severe COVID-19 may be well consistent with a clinical diagnosis of viral sepsis, rather than with a mere hyperinflammatory disease. This conceptual framing may help to improve clinical management of severe COVID-19 patients, by providing a rationale for the development of novel balanced immunomodulatory approaches, combining both suppressive and activating immunotherapies [70].

The main focus of Coronavirus disease 2019 (COVID-19) infection is pulmonary complications through virus-related neurological manifestations, ranging from mild to severe, such as encephalitis, cerebral thrombosis, neurocognitive (dementia-like) syndrome, and delirium. The hospital screening procedures for quickly recognizing neurological manifestations of COVID-19 are often complicated by other coexisting symptoms and can be obscured by the deep sedation procedures required for critically ill patients. Here, we present two different case-reports of COVID-19 patients, describing neurological complications, diagnostic imaging such as olfactory bulb damage (a mild and unclear underestimated complication) and a severe and sudden thrombotic stroke complicated with hemorrhage with a low-level cytokine storm and respiratory symptom resolution. We discuss the possible mechanisms of virus entrance, together with the causes of COVID-19-related encephalitis, olfactory bulb damage, ischemic stroke, and intracranial hemorrhage [71].

References

1. Chih CL, Cheng YW, Po RH (2020) Co-infections among patients with COVID-19: The need for combination therapy with non-anti-SARS-CoV-2 agents? Journal of Microbiology, Immunology and Infection 53: 505-12.

2. Kahn JS, McIntosh K (2005) History and Recent Advances in Corona virus 338 Discovery. Pediatr Infect Dis J 24: S223-27.

3. Hamre D, Procknow JJ (1966) A new virus isolated from the human respiratory tract. Proc Soc Exp Biol Med 121: 190-3.

4. McIntosh K, Dees JH, Becker WB, Kapikian AZ, Chanock RM (1967) Recovery in tracheal organ cultures of novel viruses from patients with respiratory disease. Proc Natl Acad Sci 57: 933-40.

5. Zhang SF, Tuo JL, Huang XB, Zhu X, Zhang DM, et al. (2018) Epidemiology characteristics of human corona viruses in patients with respiratory infection symptoms and phylogenetic analysis of HCoV-OC43 during 2010-2015 in Guangzhou. PLoS One 13: e0191789.

6. Zhong NS, Zheng BJ, Li YM, Poon LLM, Xie ZH, Chan KH, et al. (2003) Epidemiology and cause of severe acute respiratory syndrome (SARS] in Guangdong, People's Republic of China, in February, 2013. Lancet 362: 1353-8.

7. Van der Hoek L, Pyrc K, Jebbink MF, Vermeulen-Oost W, Berkhout RJ, Wolthers KC, et al. (2004) Identification of a new human corona virus. Nat Med 10: 368-73.

8. Pyrc K, Berkhout B, van der Hoek L (2007) The novel human corona viruses NL63 and HKU1. J Virol 81: 3051-7.

9. Abdel-Moneim AS (2014) Middle East respiratory syndrome corona virus (MERS-CoV]: evidence and speculations. Arch Virol 159: 1575-84.

10. Ahmadzadeh J, Mobaraki K (2019) Epidemiological status of the Middle East respiratory syndrome corona virus in 2019: an update from January 1 to March 31, 2019. Int J Gen Med 12: 305-11.

11. Chan JFW, Yuan S, Kok KH, To, KKW, Chu H, Yang J, et al. (2020) A familial cluster of pneumonia associated with the 2019 novel corona virus indicating person-to-person transmission: a study of a family cluster. Lancet 395: 514-23.

12. Hui DS, Azhar EI, Madani TA, Ntoumi F, Kock R, Dar O, et al. (2020) The continuing 2019-nCoV epidemic threat of novel corona viruses to global health - The latest 2019 novel co-rona virus outbreak in Wuhan, China. Int J Infect Dis 91: 264-6.

13. Zhiru G, Yinghui X, Chao S, Xu W, Ye G, Shi Q, Kewei M (2020) A Systematic Review of Asymptomatic Infections with COVID-19. Journal of microbiology, immunology, and infection.

14. Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, et al. (2020) Epidemiological and clinical characteristics of 99 cases of 2019 novel corona virus pneumonia in Wuhan, China: a descriptive study. Lancet 395: 507-13.

15. Wu Y, Guo C, Tang L, Hong Z, Zhou J, Dong X, et al. (2020) Prolonged 289 presence of SARSCoV-2 viral RNA in faecal samples. Lancet Gastroenterol Hepatol 5: 434-5.

16. Fan Y, Zhao K, Shi ZL, Zhou P (2019) Bat Corona viruses in China. Viruses 11: 210.

17. Cyranoski D (2020) Did pangolins spread the China corona virus to people? Nature 2020.

18. Enserink M (2003) Clues to the Animal Origins of SARS. Science 300: 1351.

 Guan Y, Zheng BJ, He YQ, Liu XL, Zhuang ZX, et al.
(2003) Isolation and characterization of viruses related to the SARS corona virus from animals in southern China. Science 302: 276-8.

20. Martina BE, Haagmans BL, Kuiken T, Fouchier RA, Rimmelzwaan GF. Van Amerongen G, et al. Virology: SARS virus infection of cats and ferrets. Nature 425: 915.

21. Wan Y, Shang J, Graham R, Baric RS, Li F (2020) Receptor Recognition by the Novel Corona virus from Wuhan: an Analysis Based on Decade-Long Structural Studies of SARS Corona virus. J Virol 94: e00127-00120. 22. Kim D, Quinn J, Pinsky B, Shah NH, Brown I (2020) Rates of co infection between SARS-CoV-2 and other respiratory pathogens. J Am Med Assoc 2020: 15.

23. Shi J, Wen Z, Zhong G, Yang H, Wang C, Huang B, et al. (2020) Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS-corona virus 2. Science 2020.

24. Afelt A, Frutos R, Devaux C (2018) Bats, Corona viruses, and Deforestation: Toward the Emergence of Novel Infectious Diseases? Front Microbiol 9: 702.

25. Hu B, Ge X, Wang LF, Shi Z. Bat origin of human corona viruses. Virol J 12: 221.

26. Forni D, Cagliani R, Clerici M, Sironi M (2017) Molecular Evolution of 512 Human Corona virus Genomes Trend Microbiol 25: 35-48.

27. Song HD, Tu CC, Zhang GW (2005) Cross-host evolution of severe acute respiratory syndrome corona virus in palm civet and human. Proc Natl Acad Sci USA 102: 2430-5.

28. Wang Q, Qi J, Yuan Y (2014) Bat origins of MERS-CoV supported by bat corona virus HKU4 usage of human receptor CD26. Cell Host & Microbe 16: 328-37.

29. Sabir JSM, Lam TTY, Ahmed MMM (2016) Co-circulation of three camel corona virus species and recombination of MERS-CoVs in Saudi Arabia. Science 351: 81-4.

30. Anthony SJ, Gilardi K, Menachery VD (2017) Further evidence for bats as the evolutionary source of Middle East respiratory syndrome corona virus. MBio 8: e00373-17.

31. Zhao Y, Zhao Z, Wang Y, Zhou Y, Ma Y, Zuo W (2019) Single-cell RNA expression profiling of ACE2, the putative receptor of Wuhan 2019-nCov. bioRxiv 2020.

32. Liu P, Chen W, Chen JP (2019) Viral metagenomics revealed Sendai virus and corona virus infection of Malayan pangolins (Manis javanica]. Viruses 11: 979.

33. Luan J, Lu Y, Jin X, Zhang L (2020) Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection. Biochem Biophys Res Com.

34. Xu X, Chen P, Wang J, Feng J, Zhou H, Li X, et al. (2020) Evolution of the novel corona virus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Sci China Life Sci 63: 457-60.

35. Kuba K, Imai Y, Rao S, Gao H, Guo F, Guan B, Huan Y, Yang P. Zhang Y. Deng W. et al. (2005) A crucial role of angiotensin converting enzyme 2 (ACE2] in SARS corona virus–induced lung injury. Nat Med 2005;11, 875–9.

36. Glowacka, I, Bertram S, Muller, M.A.; Allen, P.; Soilleux, E.; Pfe_erle, S.; Ste_en, I.; Tsegaye, T.S.; He, Y.; Gnirss, K.; et al. Evidence that TMPRSS2 Activates the Severe Acute Respiratory Syndrome Corona virus Spike Protein for Membrane Fusion and Reduces Viral Control by the Humoral Immune Response. J. Virol 85: 4122-34.

37. Heurich A, Hofmann-Winkler H, Gierer S, Liepold T, Jahn O, Pohlmann S. TMPRSS2 and ADAM17 Cleave ACE2 Di_ erentially and Only Proteolysis by TMPRSS2 Augments Entry Driven by the Severe Acute Respiratory Syndrome Corona virus Spike Protein. J. Virol 88: 1293-307.

38. Wang PH, Cheng Y (2020) Increasing host cellular receptor—angiotensinconverting enzyme 2 (ACE2] expression by corona virus may facilitate 2019-nCoV infection. bioRxiv2020.

39. Donoghue M, Hsieh F, Baronas E (2000) A novel angiotensin-converting enzyme-related carboxypeptidase. (ACE2] converts angiotensin I to angiotensin 1–9. Circ Res 87: E1-9.

40. Tipnis SR, Hooper NM, Hyde R, Karran E, Christie G, Turner AJ (2000) A Human homolog of angiotensin-converting enzyme. Cloning and functional expression as a captopril-insensitive carboxypeptidase. J Biol Chem 275: 33238-43.

41. Bavishi C, Maddox TM, Messerli FH (2019) Corona virus Disease 2019 (COVID-19] Infection and Renin Angiotensin System Blockers. JAMA Cardiol.

42. Hashimoto T, Perlot T, Rehman A (2012) ACE2 links amino acid malnutrition to microbial ecology and intestinal inflammation. Zurich Open Repository and Archive 2012;(University of Zurich. 43. Hamming I, Timens W, Bulthuis M, Lely T, Navis G, et al. (2004) Tissue distribution of ACE2 protein, the functional receptor for SARS Corona virus. J Pathol 203: 631-37.

44. Sun P, Lu X, Xu C, Sun W, Pan B. Understanding of COVID-19 based on current evidence.J Med Virol.

45. Xu H, Zhong L, Deng J, Peng J, Dan H, Zeng X, Li T, Chen Q (2020) High expression of ACE2 receptor of 2019-nCoV on the epithelial cells of oral mucosa. Int J Oral Sci 12: 8.

46. Pedersen KB, Chhabra KH, Nguyen VK, Xia H, Lazartigues E. The transcription factor HNF1α induces expression of angiotensin-converting enzyme 2 (ACE2] in pancreatic islets from evolutionarily conserved promoter motifs. Biochim Biophys Acta 2013: 1829.

47. Reich HN, Oudit GY, Penninger JM, Scholey JW, Herzenberg AM (2008) Decreased glomerular and tubular expression of ACE2 in patients with type 2 diabetes and kidney disease. Kidney International 74: 1610-6.

48. Babcock GJ, Esshaki DJ, Thomas WD, Ambrosino DM (2004) Amino acids 270 to 510 of the severe acute respiratory syndrome corona virus spike protein are required for interaction with receptor. J Virol 78: 4552-4560.

49. Xiao F, Zimpelmann J, Agaybi S, Gurley SB, Puente L, Burns KD (2014) Characterization of Angiotensin-Converting Enzyme 2 Ectodomain Shedding from Mouse Proximal Tubular Cells. PLoS One 9: e85958.

50. Lambert D, Yarski M, Warner FJ (2005) Tumor Necrosis Factor- Convertase (ADAM17] Mediates Regulated Ectodomain Shedding of the Severe-acute Respiratory Syndrome- Corona virus (SARS-CoV] Receptor, Angiotensin-converting Enzyme-2 (ACE2]. J Biol Chem 280: 30113-9.

51. Glowacka I, Bertram S, Herzog P, Pfefferle S, Steffen I, et al. (2010) Differential Down regulation of ACE2 by the Spike Proteins of Severe Acute Respiratory Syndrome Corona virus and Human Corona virus NL63. J Virol 84: 1198-205.

52. Vincent MJ, Bergeron E, Benjannet S, (2005) Chloroquine is a potent inhibitor of SARS corona virus infection and spread. Virol 2: 69. 53. Devaux CA, Rolain JM, Colson P, Raoult D (2020) New insights on the antiviral effects of chloroquine against corona virus: what to expect for COVID-19? Int J Antimicrob Agents.

54. Hoffmann M, Kleine-Weber H, Schroeder S (2020) SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. Cell 181: 1-10.

55. Yan R, Zhang Y, Li Y, Xia L, Guo Y, Zhou Q (2020) Structural basis for the recognition of the SARS-CoV-2 by fulllength human ACE2. Science 2020;367: 1444-8.

56. Burrell LM, Harrap SB, Velkoska E, Patel SK (2013) The ACE2 Gene: It's Potential as a Functional Candidate for Cardiovascular Disease. Clin Sci 124: 65-76.

57. White MC, Fleeman, Arnold AC (2019) Sex differences in the metabolic effects of the rennin angiotensin system. Biol Sex Differ 10: 31.

58. Zheng YY, Ma YT, Zhang JY, Xie X (2020) COVID-19 and the cardiovascular system. Nat Rev Cardiol 17: 259-260.

59. Guarner J (2020) Three Emerging Corona viruses in Two Decades: The Story of SARS, MERS, and Now COVID-19. Am J Clin Pathol 153: 420-1.

60. Hindson J (2020) COVID-19: faecal-oral transmission? Nat Rev Gastroenterol Hepatol 17: 259.

61. Van Doremalen N, Bushmaker T, Morris DH, Holbrook MG, Gamble A, et al. (2020) Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1. N Engl J Med 382: 1564-7.

62. Yu X, Yang R (2020) COVID-19 transmission through asymptomatic carriers is a challenge to containment. Influenza Other Respir Viruses 2020.

63. Hossain MG, Javed A, Akter S, Saha S (2020) SARS-CoV-2 host diversity: An update of natural infections and experimental evidence. J Microbiol Immunol Infect.

64. Morawska L, Cao J (2020) Airborne transmission of SARS-CoV-2: The world should face the reality. Environ Int 139: 105730.

65. Nishiura H, Oshitani H, Kobayashi T, Saito T, Sunagawa T, et al. (2019) Closed environments facilitate secondary transmission of corona virus disease 2019 (COVID-19]. medRxiv 28: 20029272.

66. McDonald LC, Simor AE, Su IJ, Maloney S, Ofner M, Chen KT, et al. (2004) SARS in healthcare facilities, Toronto and Taiwan. Emerg Infect Dis 10: 777–81.

67. Chih CL, Shih TP, Ko WC, Tang HJ, Hsueh PR (2019) Severe acute respiratory syndrome corona virus 2 (SARS-CoV-2] and corona virus disease-2019 (COVID-19]: the epidemic and the challenges. Int J Antimicrob Agents 55: 105924.

68. Yeh CY (2019) Development and validation of wearable devices used for continuous monitoring of body surface temperature. Tainan. Taiwan. National Cheng Kung University

69. Luca R, Giulia L, Vincenzo N, Beatrice L, William G, et al. (2020) A proof of evidence supporting abnormal immunothrombosis in severe COVID-19: naked megakaryocyte nuclei increase in the bone marrow and lungs of critically ill patients. Platelets 31: 1085–89.

70. Giovanni R, Vincenzo N, Enrico T, Tommaso T, Patrizia C, Mario L (2020) COVID-19: more than a cytokine storm. Riva et al. Critical Care 24: 549.

Gabriele M, Veronica R, Gabriele Z, Vincenzo N, Elena
D, Alessandra M, Claudia B, Michele Z, Stefano M, Alberto B.
Mild to Severe Neurological Manifestations of COVID-19: Cases
Reports. Int. J. Environ. Res. Public Health 18: 3673.

Submit your manuscript to a JScholar journal and benefit from:

- Convenient online submission
- Rigorous peer review
- Timmediate publication on acceptance
- Open access: articles freely available online
- High visibility within the field

Better discount for your subsequent articles

Submit your manuscript at http://www.jscholaronline.org/submit-manuscript.php