

**HOMEOPATHIC PROSPECTIVES AND THE ROLE OF ANIMAL IN TRANSMISSION
OF NOVEL CORONAVIRUS**

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ABSTRACT

Recently, a new viral-based infection has emerged as a respiratory disease caused by a novel (new) coronavirus that was first detected in Wuhan City, China. With any or many reasons, this newly emerged novel-Coronavirus (2019-nCoV) has now been recognized in more than 70 locations around the globe. The disease caused by 2019-nCoV has been named as “coronavirus disease 2019–COVID-19”. Viruses, a type of pathogen, can infect all types of living entities, from humans to plants and to even bacteria. The toxic agent replicates inside the living cells of organisms. Viruses can spread or transmit in a variety of ways, most of which we associate with vectors, or “living organisms that can transmit infectious pathogens between humans, or from animals to humans,” as explained by the World Health Organization (WHO). Mosquitoes are probably the most recognizable vector, responsible for spreading diseases like West Nile Virus, Malaria and Dengue Fever. Now scientists are racing to find the origin source of COVID-19, which is known as a zoonotic disease (or zoonoses). Zoonotic diseases are caused by the transmission of harmful germs (like viruses, bacterial, parasites and fungi) between humans and animals. Germs are spread between animals and humans. In our review include the information about homeopathic perspectives and the role animals in transmission of novel Coronavirus.

KEYWORDS: Homeopathic prospective, Animals, Viruses, humans, Bacteria, pathogens, WHO, Zoonotic disease, germs.**INTRODUCTION**

Coronaviruses are a group of enveloped viruses with nonsegmented, single-stranded, and positive-sense RNA genomes. Apart from infecting a variety of economically important vertebrates (such as pigs and chickens), six coronaviruses have been known to infect human hosts and cause respiratory diseases.^[1]

The global public health emergency of COVID-19 pandemic disease caused by severe acute respiratory syndrome coronavirus 2 (will be referred as SARS-CoV-2 here after) has been unfolding rapidly that emerged in Wuhan, China and has now spread to at least 180 countries. Detailed investigations found that SARS-CoV in 2003 was transmitted from civet cats to humans and MERS-CoV in 2012 from dromedary camels to humans. The genetic sequence of the SARS-CoV-2 enabled the rapid development of point of care real-time RT-PCR diagnostic tests specific for SARS-CoV-2 which is based on full genome sequence data on the Global Initiative on Sharing All Influenza Data [GISAID] platform.^[2]

The outbreak of emerging severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) disease (COVID-19) in China has been brought to global

attention and declared a pandemic by the World Health Organization (WHO) on March 11, 2020. Scientific advancements since the pandemic of severe acute respiratory syndrome (SARS) in 2002~2003 and Middle East respiratory syndrome (MERS) in 2012 have accelerated our understanding of the epidemiology and pathogenesis of SARS-CoV-2 and the development of therapeutics to treat viral infection. A zoonotic reservoir harkens back to the emergence of both SARS- and MERS-CoV.^[3,4] SARS-CoV, the first highly pathogenic human CoV, emerged in 2002 with transmission from animals to humans occurring in wet markets. Surveillance efforts found SARS-CoV viral RNA in both palm civets and raccoon dogs sold in these wet markets; however, SARS-CoV was not found in the wild, suggesting that those species served as intermediary reservoir as the virus adapted to more efficiently infect humans. Further surveillance efforts identified highly related CoVs in bat species. More recent work has demonstrated that several bat CoVs are capable of infecting human cells without a need for intermediate adaptation.^[5,6] Additionally, human serology data shows recognition of bat CoV proteins and indicates that low-level zoonotic transmission of SARS-like bat coronaviruses occurs outside of recognized

outbreaks. MERS-CoV is also a zoonotic virus with possible origins in bats, although camels are endemically infected and camel contact is frequently reported during primary MERS-CoV cases.^[7] For SARS-CoV, strict quarantine and the culling of live markets in Asia played a major role in ending the outbreak. With the cultural importance of camels, a similar approach for MERS-CoV was not an option and periodic outbreaks continue in the Middle East. These lessons from SARS and MERS highlight the importance of rapidly finding the source for 2019-nCoV in order to stem the ongoing outbreak.^[8]

Structure

Coronaviruses are enveloped viruses with a positive-sense single

stranded RNA genome and a helical symmetry. The genomic size of coronaviruses ranges from

approximately 16 to 31 kilobases, extraordinarily large for an RNA virus. The name coronavirus is derived from the Greek (κορώνα, meaning crown) as the virus envelope appears under electron microscopy to be crowned by a characteristic ring of small bulbous structures.^[9] This morphology is actually formed by the viral spike proteins, which are proteins that populate the surface of the virus and determine host tropism. Coronaviruses are grouped in the order Nidovirales, named for the Latin (nidus, meaning nest) as all viruses in this order produce a 3' co-terminal nested set of subgenomic mRNAs during infection.^[10,11]

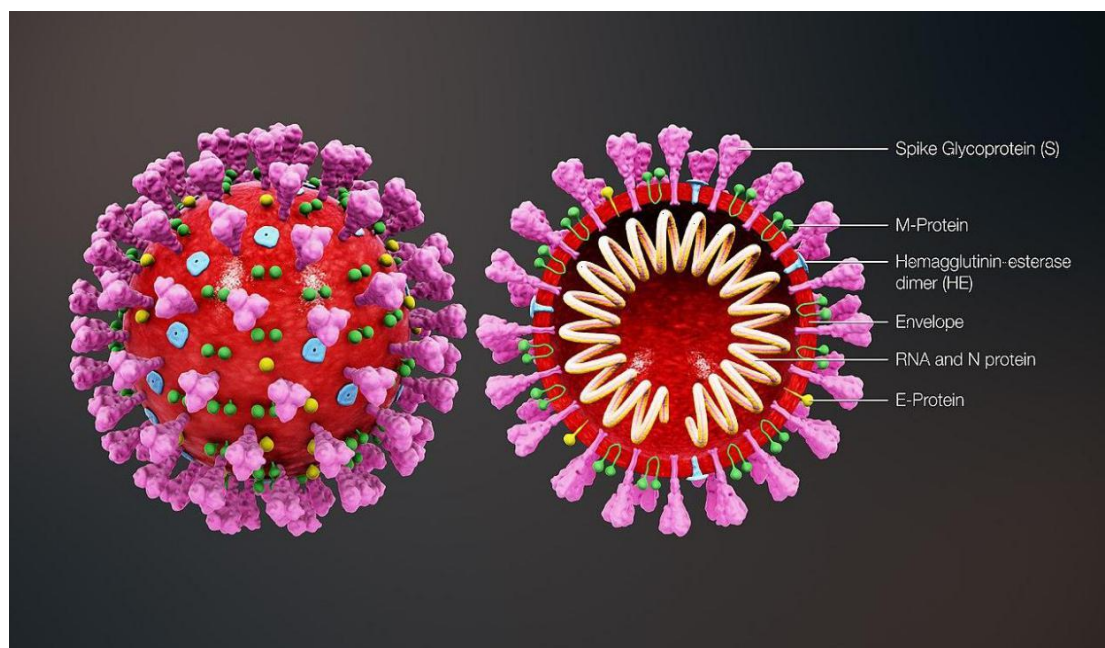


Fig. Structure of coronaviruses

Proteins that contribute to the overall structure of all coronaviruses are the spike envelope, membrane and nucleocapsid.^[12] In the specific case of SARS, a defined receptor-binding domain on S mediates the attachment of the virus to its cellular receptor, angiotensin-converting enzyme 2 (ACE2). Members of the group 2 coronaviruses also have a shorter spike-like protein called hemagglutinin esterase encoded in their genome, but for some reason this protein is not always brought to expression (produced) in the cell.^[13,14]

EPIDEMIOLOGY

So far, as on date 23 March 2020, 3,39,039 globally confirmed cases¹³ are reported and 81,093 confirmed cases from China but 3,270 deaths making China “Very High” under WHO risk assessment. Between lockdowns and quarantines, the COVID-19 epidemic in China peaked and plateaued by early February, to even decline

from there. Person-to-person transmission of SARS-CoV-2 in hospital and family settings may be suggested, as reports of infected travellers in other geographical regions surfaced. In India, 415 cases are reported till 23 March 2020, according to Ministry of Health & Family Welfare. Therefore, the Government of India has asked travellers from China to immediately report to nearest health facility in case they do not feel well.^[15,16,17]

DEFINITIONS

S.No.	Term	definition
1.	Suspect Case	<p>A patient with acute respiratory disorders {fever and at least one sign/symptom of respiratory disease (e.g. cough, shortness of breath or diarrhoea), AND If a person shows history of travel to or residence in a country/area or territory reporting transmission of COVID-19 disease during the 14 days prior to symptom onset.</p> <p>A patient/Health care worker with any acute respiratory illness AND If the person have been in contact with a confirmed COVID-19 in the last 14 days prior to onset of for signs of coronavirus.</p> <p>A patient with severe acute respiratory infection {fever and at least one sign/symptom of respiratory disease (e.g. cough, shortness breath)} AND requiring hospitalization AND with no other etiology that fully explains the clinical presentation.</p> <p>A case for whom testing for COVID-19 is inconclusive</p>
2.	Lab confirmed Case	A person with laboratory confirmation of COVID-19 infection, irrespective of clinical signs and symptoms
3.	Contact	<p>A contact is a person that is involved in any of the following:</p> <ul style="list-style-type: none"> • Providing direct care without proper personal protective equipment (PPE) for COVID-19 patient • Staying in the same close environment of a COVID-19 patient (including workplace, classroom, household, gatherings) • Travelling together in close proximity (within 1 m) with a symptomatic person who later tested positive for COVID-19
4.	High risk contact	<p>Contact with a confirmed case of COVID-19</p> <p>Travel to a province where COVID-19 LOCAL TRANSMISSION is being reported as per WHO daily situation report</p> <p>Touched body fluids of patients (respiratory tract secretions, blood, vomitus, saliva, urine, faeces)</p> <p>Touched or cleaned the linens, clothes or dishes of the patient</p> <p>Close contact, within 3 feet (1 metre) of the confirmed case</p> <p>Co-passengers in an airplane/vehicle seated in the same row, 3 rows in front and behind of a confirmed COVID-19 case</p> <p>Low risk Contact Shared the same space (same classroom/same room for work) or similar activity and not having high risk exposure to the confirmed/suspected case</p> <p>Travel in the same environment (bus/train/flight/any mode of transit) but not having high risk exposure as cited above</p> <p>Any traveller from abroad not satisfying high risk criteria</p>

PATHOPHYSIOLOGY

The pathological features of SARS-CoV-2 of family Coronaviridae measuring from 60 to 140 billionths of a metre across, having median R0 2.79 with early outbreak data following exponential growth have been shown to greatly resemble those seen in SARS and MERS coronavirus infection. First described in 1960s, the coronavirus gets its name from a distinctive corona or "crown" of sugary-proteins projecting from envelope surrounding the particle. Following the entry of coronavirus into the cell, the uncoated particle and the RNA genome is deposited into the cytoplasm. The coronavirus RNA genome has a 5' methylated cap and a 3' polyadenylated tail, which allows the RNA to attach to ribosomes for translation. Coronaviruses also have a protein known as a replicase encoded in its genome which allows the RNA viral genome to be transcribed into new RNA copies using the host cell's machinery. Coronaviruses have a non-structural protein – a protease – which can separate the proteins in the chain. The excess production of type 2 cytokines and an age dependant defect in T-cell and B-cell function could lead to a deficit in control of viral replication and more

prolonged proinflammatory responses, potentially leading to a poor outcome in patients of COVID-19.³¹ The main pathogenesis of SARS-CoV-2 as a respiratory system targeting virus is severe pneumonia, RNAemia and acute cardiac injury. In a first-hand data reported from Hospital of China, it was found that, by Jan 2, 2020, laboratory- confirmed SARS-CoV-2 infection admitted hospital patients had a higher plasma level of IL2, IL7, IL10, GSCF, IP10, MCP1, MIP1A.^[18]

HISTOPATHOLOGY

From the histopathological data obtained on the lungs of two patients undergoing lung lobectomies for adenocarcinoma who were retrospectively found to have had SARS-CoV-2 infection at the time of surgery, the lungs of both 'accidental' cases showed oedema, exudates as large protein globules, vascular congestion combined with inflammatory clusters of fibrinoid material, multinucleated giant cells and hyperplasia of pneumocytes.^[19]

REPLICATION CYCLE OF CORONA VIRUS

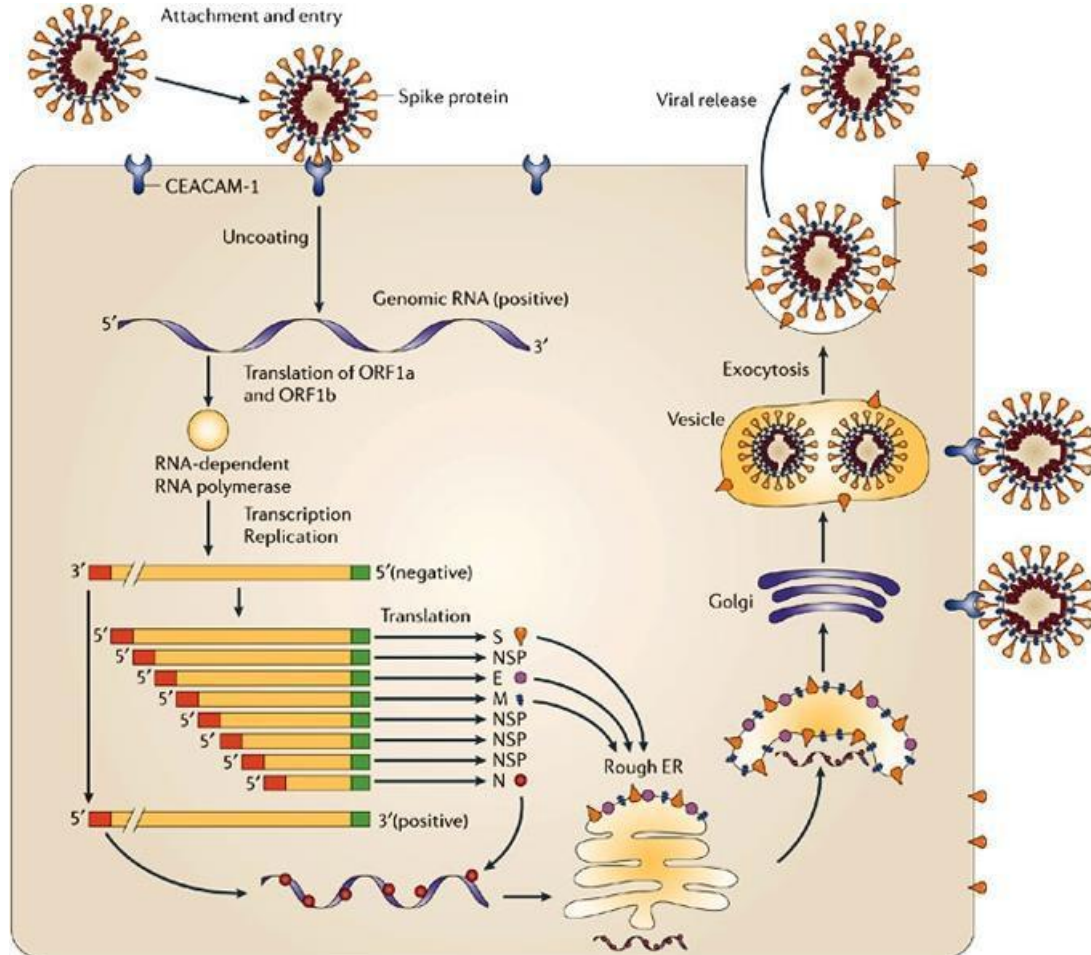


Fig. Replication cycle of Coronavirus.

ABOUT AN ROLE OF ANIMAL IN TRANSMISSION OF NOVEL CORONAVIRUS

Research shows that the SARS-CoV-2 coronavirus causing Covid-19 disease is most likely a zoonotic virus. Different varieties of this virus are found in some bat species in China. On certain materials, depending on the temperature, surface, humidity, chemical composition, the virus may persist for several hours. Therefore, it cannot be excluded that through other factors to which the virus does not work, it can be transmitted, such as certain animal species that do not get sick but can be carriers. Of course, what kind of objects or animals the SARS-CoV-2 Coronavirus can last for many hours depends on the specifics of specific environmental conditions, the specifics of the materials on which the virus is found. In addition, it cannot be ruled out that new mutations of Coronavirus will arise as a result of constant mutations that can be transmitted to specific animals to a greater extent. Therefore, the goal of reducing the risk of infection is to maintain high epidemiological and sanitary safety standards.

Somewhere in China, a bat flits across the sky, leaving a trace of coronavirus in its droppings, which fall to the forest floor. A wild animal, possibly a pangolin snuffing

for insects among the leaves, picks up the infection from the excrement.^[20]

The novel virus circulates in wildlife. Eventually an infected animal is captured, and a person somehow catches the disease, then passes it on to workers at a wildlife market. A global outbreak is born.^[21]

ECOLOGY

Coronavirus may be of zoonotic origin, and bats are most likely the natural hosts for all presently known Coronavirus. Between SARS pandemic in 2002 and 2003, the first hints pointed to a zoonotic origin of the SARS-CoV, with civets as the suspected natural source of human infection.^[23] Genetically diversified SARS-like coronaviruses were then found in Chinese Rhinolophid bats, and two novel bat coronaviruses from Chinese horseshoe bats in Yunnan Province, China are reported to be very closely related to SARS-CoV, implying that Chinese horseshoe bats are natural host of SARS-CoV. Regarding SARS-CoV-2, it showed a high sequence identity to some bat CoVs such as BatCoV RaTG13 (96% nt identity to SARS-CoV-2) previously detected in Rhinolophusaffinis from Yunnan Province, indicating a bat origin of SARS-CoV-2 Generally, bat habitats are far from human activity areas, and the virus was probably

transmitted to humans by another animal host. Bat SARS like-CoVs cannot directly infect humans unless they undergo mutation or recombination in animal hosts. For example, animal hosts of SARS-CoV and MERS-CoV are the civet and camel (Figure) before transmission to humans. Regarding the intermediate animal host of SARS-CoV-2, it has been reported that the sequence

identity between pangolin origin CoVs and SARS-CoV-2 is 99%, indicating that SARS-CoV-2 may be of pangolin origin. Many studies in China are tracking other potential animal hosts of SARS-CoV-2, which is of great significance for the prevention and control of COVID-19.^[24]

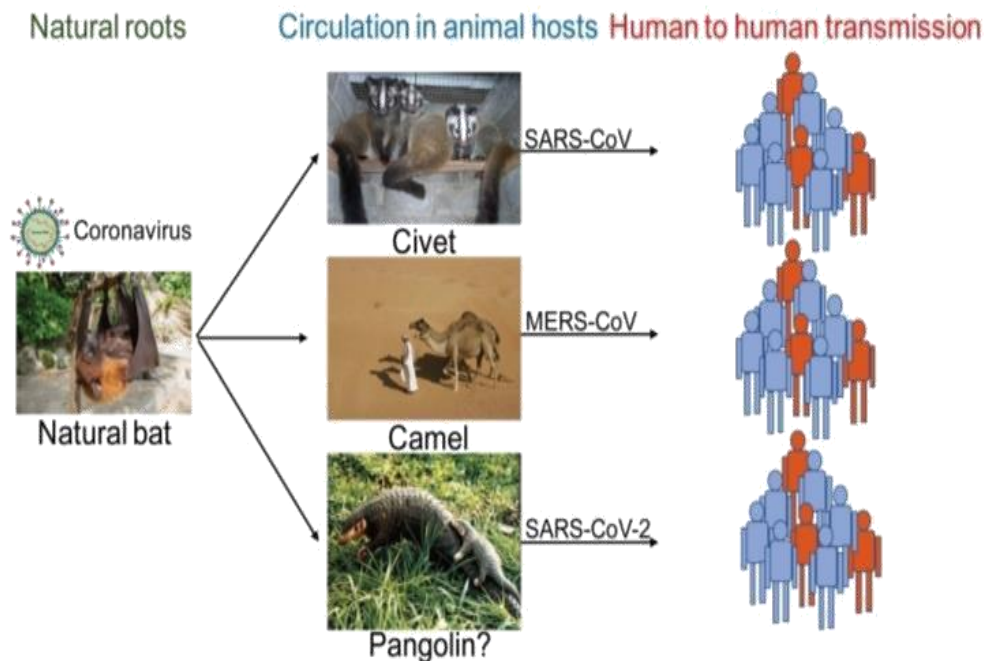


Figure: Ecology of emerging coronaviruses SARS-CoV, MERS-CoV, and SARS-CoV-2 are all bat origin coronaviruses, which cause human infections after circulation in animal hosts of civet, camel, and pangolin bats are hosts for viruses.

Bats are implicated in what seems to be more than their share [of zoonoses]. There are a lot of different species of bats. One-quarter of all mammal species are bats. But there are other things about them including aspects of their immune system. There have been some discoveries lately that bat immune systems are "downregulated" in a certain way that allows for the metabolic stresses of being a mammal that flies. And the downregulating of the immune system to avoid

overreaction to those stresses seems, perhaps, also to create an environment in which viruses are more tolerated in bats than in other mammals.^[25]

CONCLUSION

In our review including the information about homeopathic prospective and also A role of animals in transmission of novel coronaviruses. According to homeopathic approach, the homeopathic medication is beneficial for the prevention of this infection and for this purpose the medication is takes upto one month for relief from COVID -19 disease. And also animals play an Important role for the spreading of this infection as towards the human beings. In human beings, this virus undergoes replication inside the body and it spread with one person to another, hence it said to be pandemic.

REFERENCES

1. Unhale, Shrikrushna & Bilal, Quazi & Sanap, Shubham & Thakhre, Suraj & Wadatar, Shreya & Bairagi, Rohit & Sagrula, Prof & Biyani, Dr. (2020). A REVIEW ON CORONA VIRUS (COVID-19). International Journal of Pharmaceutical and Life Sciences, 6: 109-115.
2. Kan, B.; Wang, M.; Jing, H.; Xu, H.; Jiang, X.; Yan, M.; Liang, W.; Zheng, H.; Wan, K.; Liu, Q.; et al. Molecular evolution analysis and geographic investigation of severe acute respiratory syndrome coronavirus-like virus in palm civets at an animal market and on farms. J. Virol, 2005; 79: 11892–11900.
3. Lau, S.K.; Woo, P.C.; Li, K.S.; Huang, Y.; Tsoi, H.W.; Wong, B.H.; Wong, S.S.; Leung, S.Y.; Chan, K.H.; Yuen, K.Y. Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. Proc. Natl. Acad. Sci. USA, 2005; 102: 14040–14045.
4. Menachery, V.D.; Yount, B.L., Jr.; Debbink, K.; Agnihothram, S.; Gralinski, L.E.; Plante, J.A.; Graham, R.L.; Scobey, T.; Ge, X.Y.; Donaldson, E.F.; et al. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. Nat. Med, 2015; 21: 1508–1513.

5. Menachery, V.D.; Yount, B.L., Jr.; Sims, A.C.; Debbink, K.; Agnihothram, S.S.; Gralinski, L.E.; Graham, R.L.; Scobey, T.; Plante, J.A.; Royal, S.R.; et al. SARS-like WIV1-CoV poised for human emergence. *Proc. Natl. Acad. Sci. USA*, 2016; 113: 3048–3053. [CrossRef]
6. Wang, N.; Li, S.Y.; Yang, X.L.; Huang, H.M.; Zhang, Y.J.; Guo, H.; Luo, C.M.; Miller, M.; Zhu, G.; Chmura, A.A.; et al. Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Viol. Sin*, 2018; 33: 104–107.
7. Anthony, S.J.; Gilardi, K.; Menachery, V.D.; Goldstein, T.; Ssebide, B.; Mbabazi, R.; Navarrete-Macias, I.; Liang, E.; Wells, H.; Hicks, A.; et al. Further Evidence for Bats as the Evolutionary Source of Middle East Respiratory Syndrome Coronavirus. *mBio*, 2017; 8.
8. Mizumoto K, Chowell G. Estimating risk for death from 2019 novel coronavirus disease, China, January–February 2020. *Emerg Infect Dis*. 2020 Jun. Available from: <https://doi.org/10.3201/eid2606.200233>. Accessed on: 18 March 2020.
10. World Health Organisation. Novel Coronavirus (2019-nCoV). Available from: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>. Accessed on: 29 January 2020.
11. Zhang S, Diao MY, Yu W, Pei L, Lin Z, Chen D. Estimation of reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on Diamond Princess cruise ship: A data-driven analysis. *International Journal of Infectious Diseases*, 2020; 93: 201-204.
12. NBC News. Coronavirus map: The COVID-19 virus is spreading across the world. Here's where cases have been confirmed. Available from: <https://www.nbcnews.com/health/health-news/coronavirus-map-confirmed-cases-2020-n1120686>. Accessed on 19 March 2020.
13. Aljazeera News. Italy reports 475 new coronavirus deaths in a day- Live updates. Available from: <https://www.aljazeera.com/news/2020/03/europe-closes-borders-curb-coronavirus-spread-live-updates-200318000201088.html>. Accessed on: 19 March 2020.
14. BBC News. Coronavirus: Trump puts US on war footing to combat outbreak. Available from: <https://www.bbc.com/news/world-us-canada-51955450>. Accessed on: 19 March 2020.
15. CNA News. Spain's Coronavirus tally climbs to 13716. Available from: <https://www.channelnewsasia.com/news/world/coronavirus-covid19-spain-tally-climbs-mar-18-12552488>. Accessed on: 19 March 2020.
16. Italy coronavirus deaths rise in Spain. Available from: <https://www.bbc.com/news/world-europe-51952712>. Accessed on 11 March 2020.
17. China. COVID-19 Coronavirus outbreaks. Worldometers.info.com Available from: Worldometers.info/coronavirus/ Accessed on 18 March 2020.
18. World Health Organisation. Novel Coronavirus (2019-nCoV). Available from: <https://www.who.int/news-room/detail/28-01>.
19. 2020-who-china-leadersdiscuss-next-steps-in-battle-against-coronavirus-outbreak. Accessed on: 29 January 2020.
20. Vijaykrishna, D.; Smith, G.J.; Zhang, J.X.; Peiris, J.S.; Chen, H.; Guan, Y. Evolutionary insights into the ecology of coronaviruses. *J. Virol*, 2007; 81: 4012–4020.
21. Corman, V.M.; Muth, D.; Niemeyer, D.; Drosten, C. Hosts and Sources of Endemic Human Coronaviruses. *Adv. Virus Res.* 2018; 100: 163–188.
22. Ge, X.-Y.; Li, J.-L.; Yang, X.-L.; Chmura, A.A.; Zhu, G.; Epstein, J.H.; Mazet, J.K.; Hu, B.; Zhang, W.; Peng, C.; et al. Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature*, 2013; 503: 535–538.
23. Lau, S.K.P.; Woo, P.C.Y.; Li, K.S.M.; Huang, Y.; Tsoi, H.-W.; Wong, B.H.L.; Wong, S.S.Y.; Leung, S.-Y.
24. Chan, K.-H.; Yuen, K.-Y. Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proc. Natl. Acad. Sci. USA*, 2005; 102: 14040–14045.
25. Lam, T.T.-Y.; Shum, M.H.-H.; Zhu, H.-C.; Tong, Y.-G.; Ni, X.-B.; Liao, Y.-S.; Wei, W.; Cheung, W.Y.-M.; Li, W.-J.