

A CORONA VIRUS: - ENEMY FOR WORLD**Priyanka Suresh Ghuge, Mahesh M. Deshpande* and M. J. Chavan**

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Currently, the emergence of a novel human coronavirus, SARS-CoV-2, has become a global health concern causing severe respiratory tract infections in humans. Human-to-human transmissions have been described with incubation times between 2-10 days, facilitating its spread via droplets, contaminated hands or surfaces. We therefore reviewed the literature on all available information about the persistence of human and veterinary coronaviruses on inanimate surfaces as well as inactivation strategies with biocidal agents used for

chemical disinfection, e.g. in healthcare facilities. The analysis of 22 studies reveals that human coronaviruses such as Severe Acute Respiratory Syndrome (SARS) coronavirus, Middle East Respiratory Syndrome (MERS) coronavirus or endemic human coronaviruses (HCoV) can persist on inanimate surfaces like metal, glass or plastic for up to 9 days, but can be efficiently inactivated by surface disinfection procedures with 62e71% ethanol, 0.5% hydrogen peroxide or 0.1% sodium hypochlorite within 1 minute. Other biocidal agents such as 0.05e0.2% benzalkonium chloride or 0.02% chlorhexidine digluconate are less effective. As no specific therapies are available for SARS-CoV-2, early containment and prevention of further spread will be crucial to stop the ongoing outbreak and to control this novel infectious thread

KEYWORD: novel, severe respiratory tract infections, SARS-CoV-2 & a global health.**INTRODUCTION**

The coronavirus belongs to a family of viruses that may cause various symptoms such as pneumonia, fever, breathing difficulty, and lung infection.^[1] These viruses are common in animals worldwide, but very few cases have been known to affect humans. The World Health Organization (WHO) used the term 2019 novel coronavirus to refer to a coronavirus that affected the lower respiratory tract of patients with pneumonia in Wuhan, China on 29

December 2019.^[2-4] The WHO announced that the official name of the 2019 novel coronavirus is coronavirus disease (COVID-19).^[4] And the current reference name for the virus is severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It was reported that a cluster of patients with pneumonia of unknown cause was linked to a local Huanan South China Seafood Market in Wuhan, Hubei Province, China in December 2019.^[5] In response to the outbreak, the Chinese Center for Disease Control and Prevention (China CDC) dispatched a rapid response team to accompany health authorities of Hubei province and Wuhan city to conduct epidemiological and etiological investigations. The WHO confirmed that the outbreak of the coronavirus epidemic was associated with the Huanan South China Seafood Marketplace, but no specific animal association was identified.^[6] Scientists immediately started to research the source of the new coronavirus, and the first genome of COVID-19 was published by the research team led by Prof. Yong-Zhen Zhang, on 10 January 2020.^[7] Within 1 month, this virus spread quickly throughout China during the Chinese New Year – a period when there is a high level of human mobility among Chinese people. Although it is still too early to predict susceptible populations, early patterns have shown a trend similar to Severe Acute Respiratory Syndrome (SARS) and Middle East respiratory syndrome (MERS) coronaviruses. Susceptibility seems to be associated with age, biological sex, and other health conditions.^[8] COVID-19 has now been declared as a Public Health Emergency of International Concern by the WHO.^[9]

We conducted a scoping review to summarize and critically analyze all the published scientific articles regarding the new coronavirus in January 2020. This review aims to provide the evidence of early findings on the epidemiology, causes, clinical diagnosis, as well as prevention and control of COVID-19 in relation to time, location, and source of publication. This review can provide meaningful information for future research related to this topic and may support government decision making on strategies to handle this public health emergency at the community, national, and international levels.

Types

Coronaviruses belong to the subfamily Coronavirinae in the family Coronaviridae.^[10] Different types of human coronaviruses vary in how severe the resulting disease becomes, and how far they can spread. Doctors currently recognize seven types of coronavirus that can infect humans.

Common types^[11]

1. 229E (alpha coronavirus)
2. NL63 (alpha coronavirus)
3. OC43 (beta coronavirus)
4. HKU1 (beta coronavirus)

Rarer strains that cause more severe complications include MERS-CoV, which causes Middle East respiratory syndrome (MERS), and SARS-CoV, the virus responsible for severe acute respiratory syndrome (SARS). In 2019, a dangerous new strain called SARS-CoV-2 started circulating, causing the disease COVID-19.

Transmission

Limited research is available on how HCoV spreads from one person to the next. However, researchers believe that the viruses transmit via fluids in the respiratory system, such as mucus.^[12-15]

Coronaviruses can spread in the following ways

Coughing and sneezing without covering the mouth can disperse droplets into the air. Touching Touching or shaking hands with a person who has the virus can pass the virus between individuals. Making Making contact with a surface or object that has the virus and then touching the nose, eyes, or mouth. Some animal coronaviruses, such as feline coronavirus (FCoV), may spread through contact with feces. However, it is unclear whether this also applies to human coronaviruses. The National Institutes of Health (NIH) suggest that several groups of people have the highest risk of developing complications due to COVID-19.

These groups include^[16-17]

1. Young children
2. People aged 65 years or older
3. Women who are pregnant

Coronaviruses will infect most people at some time during their lifetime. Coronaviruses can mutate effectively, which makes them so contagious. To prevent transmission, people should stay at home and rest while symptoms are active. They should also avoid close contact with other people. Covering the mouth and nose with a tissue or handkerchief while coughing or

sneezing can also help prevent transmission. It is important to dispose of any tissues after use and maintain hygiene around the home.

COVID-19

In 2019, the Centers for Disease Control and Prevention (CDC) started monitoring the outbreak of a new coronavirus ^[18-21], SARS-CoV-2, which causes the respiratory illness now known as COVID-19. Authorities first identified the virus in Wuhan, China. More than 74,000 people have contracted the virus in China. Health authorities have identified many other people with COVID-19 around the world, including many in the United States. On January 31, 2020, the virus passed from one person to another in the U.S. The World Health Organization (WHO) have declared a public health emergency relating to COVID-19.

Since then, this strain has been diagnosed in several U.S. residents. The CDC have advised that it is likely to spread to more people. COVID-19 has started causing disruption in at least 25 other countries. The first people with COVID-19 had links to an animal and seafood market. This fact suggested that animals initially transmitted the virus to humans. However, people with a more recent diagnosis had no connections with or exposure to the market, confirming that humans can pass the virus to each other.

Epidemiology

In December 2019, many pneumonia cases that were clustered in Wuhan city were reported and searches for the source have shown Huanan Seafood Market as the origin.^[22-25] The first case of the COVID-19 epidemic was discovered with unexplained pneumonia on December 12, 2019, and 27 viral pneumonia cases with seven being severe, were officially announced on December 31, 2019. Etiologic investigations have been performed in patients who applied to the hospital due to similar viral histories of these patients has strengthened the likelihood of an infection transmitted from animals to humans. On January 22, 2020, novel CoV has been declared be originated from wild bats and belonged to Group 2 of beta-coronavirus that contains Severe Acute Respiratory Syndrome Associated Coronavirus (SARS-CoV).

Although COVID-19 and SARS-CoV belong to the same beta corona virüs subgroup, similarity at genome level is only 70%, and the novel group has been found to show genetic differences from SARS-CoV. Similar to the SARS epidemic, this outbreak has occurred during the Spring Festival in China, which is the most famous traditional festival in China,

during which nearly 3 billion people travel countrywide. These conditions caused favorable conditions for the transmission of this highly contagious disease and severe difficulties in prevention and control of the epidemic. The period of the Spring Festival of China was between January 17 and February 23 in 2003, when the SARS epidemic peaked, while the period of the festival was between January 10 and February 18 in 2020. Similarly, there was a rapid increase in COVID-19 cases between January 10-22. Wuhan, the center of the epidemic with 10 million population, is also an important center in the spring festival transportation network. The estimated number of travelers during the 2020 spring festival has risen 1.7 folds when compared with the number traveled in 2003 and reached to 3.11 billion from 1.82 billion. This large-scale travel traffic has also created favorable conditions for the spread of this difficult-to-control disease.

Diagnosis, treatment & prevention

In most cases of self-limited infection, diagnosis of coronaviruses is unnecessary, as the disease will naturally run its course.^[26] However, it may be important in certain clinical and veterinary settings or in epidemiological studies to identify an etiological agent. Diagnosis is also important in locations where a severe CoV outbreak is occurring, such as, at present, in the Middle East, where MERS-CoV continues to circulate. The identification of cases will guide the development, of public health measures to control outbreaks. It is also important to diagnose cases of severe veterinary CoV-induced disease, such as PEDV and IBV, to control these pathogens and protect food supplies. RT-PCR has become the method of choice for diagnosis of human CoV, as multiplex real-time RT-PCR assays have been developed, are able to detect all four respiratory HCoVs and could be further adapted to novel CoVs. Serologic assays are important in cases where RNA may be difficult to isolate, is no longer present, and for epidemiological studies.

To date, there are no anti-viral therapeutics that specifically target human coronaviruses, so treatments are only supportive. In vitro, interferons (IFNs) are only partially effective against coronaviruses. IFNs in combination with ribavirin may have increased activity in vitro when compared to IFNs alone against some coronaviruses; however, the effectiveness of this combination in vivo requires further evaluation [coronavirus] The SARS and MERS outbreaks have stimulated research on these viruses and this research has identified a large number of suitable anti-viral targets, such as viral proteases, polymerases, and entry proteins.

Significant work remains, however, to develop drugs that target these processes and are able to inhibit viral replication.

Only limited options are available to prevent coronavirus infections. Vaccines have only been approved for IBV, TGEV, and Canine CoV, but these vaccines are not always used because they are either not very effective, or in some cases have been reported to be involved in the selection of novel pathogenic CoVs via recombination of circulating strains. Vaccines for veterinary pathogens, such as PEDV, may be useful in such cases where spread of the virus to a new location could lead to severe losses of veterinary animals. In the case of SARS-CoV, several potential vaccines have been developed but none are yet approved for use. These vaccines include recombinant attenuated viruses, live virus vectors, or individual viral proteins expressed from DNA plasmids. Therapeutic SARS-CoV neutralizing antibodies have been generated and could be retrieved and used again in the event of another SARS-CoV outbreak. Such antibodies would be most useful for protecting healthcare workers. In general, it is thought that live attenuated vaccines would be the most efficacious in targeting coronaviruses. This was illustrated in the case of TGEV, where an attenuated variant, PRCV, appeared in Europe in the 1980s. This variant only caused mild disease and completely protected swine from TGEV. Thus, this attenuated virus has naturally prevented the reoccurrence of severe TGEV in Europe and the U.S. over the past 30 years. Despite this success, vaccine development for coronaviruses faces many challenges. First, for mucosal infections, natural infection does not prevent subsequent infection, and so vaccines must either induce better immunity than the original virus or must at least lessen the disease incurred during a secondary infection. Second, the propensity of the viruses to recombine may pose a problem by rendering the vaccine useless and potentially increasing the evolution and diversity of the virus in the wild. Finally, it has been shown in FIPV that vaccination with S protein leads to enhanced disease. Despite this, several strategies are being developed for vaccine development to reduce the likelihood of recombination, for instance by making large deletions in the nsp1 or E proteins. rearranging the 3' end of the genome. modifying the TRS sequences. mutant viruses with abnormally high mutation rates that significantly attenuate the virus.

Owing to the lack of effective therapeutics or vaccines, the best measures to control human coronaviruses remain a strong public health surveillance system coupled with rapid diagnostic testing and quarantine when necessary. For international outbreaks, cooperation of

governmental entities, public health authorities and health care providers is critical. During veterinary outbreaks that are readily transmitted, such as PEDV, more drastic measures such as destruction of entire herds of pigs may be necessary to prevent transmission of these deadly viruses.

Symptoms

Cold- or flu-like symptoms usually set in from 2–4 days after a coronavirus infection and are typically mild. However, symptoms vary from person-to-person, and some forms of the virus can be fatal.

Symptoms include

1. Sneezing
2. Runny nose
3. Cough
4. Watery diarrhea
5. Fever in rare cases
6. Sore Throat
7. Exacerbated asthma

Scientists cannot easily cultivate human coronaviruses in the laboratory unlike the rhinovirus, which is another cause of the common cold. This makes it difficult to gauge the impact of the coronavirus on national economies and public health. There is no cure, so treatments include self-care and over-the-counter (OTC) medication. People can take several steps, including:

1. Resting and avoiding overexertion
2. Drinking enough water
3. avoiding smoking and smoky areas
4. Taking acetaminophen, ibuprofen, or naproxen for pain and fever
5. Using a clean humidifier or cool mist vaporizer
6. A doctor can diagnose the virus responsible by taking a sample of respiratory fluids, such as mucus from the nose, or blood.
7. Standard recommendations to prevent infection spread

Its include regular hand washing, covering mouth and nose when coughing and sneezing, thoroughly cooking meat and eggs. Avoid close contact with anyone showing.

CONCLUSION

Over the past 50 years the emergence of many different coronaviruses that cause a wide variety of human and veterinary diseases has occurred. It is likely that these viruses will continue to emerge and to evolve and cause both human and veterinary outbreaks owing to their ability to recombine, mutate, and infect multiple species and cell types.

Future research on coronaviruses will continue to investigate many aspects of viral replication and pathogenesis. First, understanding the propensity of these viruses to jump between species, to establish infection in a new host, and to identify significant reservoirs of coronaviruses will dramatically aid in our ability to predict when and where potential epidemics may occur. As bats seem to be a significant reservoir for these viruses, it will be interesting to determine how they seem to avoid clinically evident disease and become persistently infected. Second, many of the non-structural and accessory proteins encoded by these viruses remain uncharacterized with no known function, and it will be important to identify mechanisms of action for these proteins as well as defining their role in viral replication and pathogenesis. These studies should lead to a large increase in the number of suitable therapeutic targets to combat infections. Furthermore, many of the unique enzymes encoded by coronaviruses, such as ADP-ribose-1-phosphatase, are also present in higher eukaryotes, making their study relevant to understanding general aspects of molecular biology and biochemistry. Third, gaining a complete picture of the intricacies of the RTC will provide a framework for understanding the unique RNA replication process used by these viruses. Finally, defining the mechanism of how coronaviruses cause disease and understanding the host immune pathological response will significantly improve our ability to design vaccines and reduce disease burden.

REFERENCES

1. Woo PC, Huang Y, Lau SK, Yuen KY. Coronavirus genomics and bioinformatics analysis. *Viruses*, 2010; 2: 1804-20.
2. Drexler, J.F., Gloza-Rausch, F., Glende, J., Corman, V.M., Muth, D., Goettsche, M., Seebens, A., Niedrig, M., Pfefferle, S., Yor-danov, S., Zhelyazkov, L., Hermanns, U., Vallo, P., Lukashev, A., Muller, M.A., Deng, H., Herrler, G., Drosten, C., Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences. *J. Virol*, 2010; 84: 11336–11349.

3. Yin, Y., Wunderink, R. G. MERS, SARS and other coronaviruses as causes of pneumonia. *Respirology*, 2018; 23(2): 130-137.
4. Peiris, J. S. M., Lai S. T., Poon L. et. al. Coronavirus as a possible cause of severe acute respiratory syndrome. *The Lancet*, 2003; 361(9366): 1319-1325.
5. Zaki AM, van Boheemen S, Bestebroer TM, Osterhaus AD, Fouchier RA. Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *N. Engl. J. Med*, 2012; 367: 1814–20.
6. Seven days in medicine: 8-14 Jan 2020. *BMJ*, 2020; 368-132.31948945.
7. Imperial College London. Report 2: estimating the potential total number of novel coronavirus cases in Wuhan City, China. *Jan. disease-analysis/news--wuhan-coronavirus*, 2020.
8. European Centre for Disease Prevention and Control data. Geographical distribution of 2019- nCov cases. Available online: (<https://www.ecdc.europa.eu/en/geographical-distribution-2019-ncov-cases>) (accessed on 05 February 2020).
9. World Health Organization, nCoV Situation, 2020; 22: 12. [source/coronaviruse /situation-reports/](https://www.who.int/situation-reports/), 2019.
10. Gralinski L.; Menachery V; Return of the Coronavirus: 2019- nCoV, *Viruses*, 2020; 12(2): 135.
11. Chen Z.; Zhang W.; Lu Y et. al.. From SARS-CoV to Wuhan 2019-nCoV Outbreak: Similarity of Early Epidemic and Prediction of Future Trends.: *Cell Press*, 2020.
12. Luk H. K., Li X., Fung J., Lau S. K., Woo P. C. (Molecular epidemiology, evolution and phylogeny of SARS coronavirus. *Infection, Genetics and Evolution*, 2019; 71: 21-30.
13. Coronavirinae in *ViralZone*. [expaty.org/785](https://www.ebi.ac.uk/ViralZone/expaty.org/785) (accessed on 05 February 2019).
14. Subissi, L.; Posthuma, C.C.; Collet, A.; Zevenhoven-Dobbe, J.C.; Gorbalenya, A.E.; Decroly, E.; Snijder, E.J.; Canard, B.; Imbert, I. One severe acute respiratory syndrome coronavirus protein complex integrates processive RNA polymerase and exonuclease activities. *Proc. Natl. Acad. Sci. USA*, 2014; 111: E3900–E3909.
15. Zhao L, Jha BK, Wu A, Elliott R, Ziebuhr J, Gorbalenya AE, Silverman RH, Weiss SR. Antagonism of the interferon-induced OAS-RNase L pathway by murine coronavirus ns2 protein is required for virus replication and liver pathology. *Cell host & microbe*, 2012; 11(6): 607–616.
16. Barcena M, Oostergetel GT, Bartelink W, Faas FG, Verkleij A, Rottier PJ, Koster AJ, Bos BJ. Cryo-electron tomography of mouse hepatitis virus: Insights into the structure of

- the coronavirus. Proceedings of the National Academy of Sciences of the United States of America, 2009; 106(2): 582–587.
17. Neuman BW, Adair BD, Yoshioka C, Quispe JD, Orca G, Kuhn P, Milligan RA, Yeager M, Bucheier MJ. Supramolecular architecture of severe acute respiratory syndrome coronavirus revealed by electron cryomicroscopy. *Journal of virology*, 2006; 80(16): 7918–7928.
 18. Beniac DR, Andonov A, Grudeski E, Booth TF. Architecture of the SARS coronavirus prefusion spike. *Nature structural & molecular biology*, 2006; 13(8): 751–752.
 19. Delmas B, Laude H. Assembly of coronavirus spike protein into trimers and its role in epitope expression. *Journal of virology*, 1990; 64(11): 5367–5375.
 20. Bosch BJ, van der Zee R, de Haan CA, Rottier PJ. The coronavirus spike protein is a class I virus fusion protein: structural and functional characterization of the fusion core complex. *J Virol*, 2003; 77(16): 8801–8811.
 21. Collins AR, Knobler RL, Powell H, Buchmeier MJ. Monoclonal antibodies to murine hepatitis virus-4 (strain JHM) define the viral glycoprotein responsible for attachment and cell–cell fusion. *Virology*, 1982; 119(2): 358–371.
 22. Abraham S, Kienzle TE, Lapps W, Brian DA. Deduced sequence of the bovine coronavirus spike protein and identification of the internal proteolytic cleavage site. *Virology*, 1990; 176(1): 296–301.
 23. Luytjes W, Sturman LS, Bredenbeek PJ, Charite J, van der Zeijst BA, Horzinek MC, Spaan WJ. Primary structure of the glycoprotein E2 of coronavirus MHV-A59 and identification of the trypsin cleavage site. *Virology*, 1987; 161(2): 479–487.
 24. De Groot RJ, Luytjes W, Horzinek MC, van der Zeijst BA, Spaan WJ, Lenstra JA. Evidence for a coiled-coil structure in the spike proteins of coronaviruses. *J Mol Biol*, 1987; 196(4): 963–966.
 25. Armstrong J, Niemann H, Smeekens S, Rottier P, Warren G. Sequence and topology of a model intracellular membrane protein, E1 glycoprotein, from a coronavirus. *Nature*, 1984; 308(5961): 751–752.
 26. Nal B, Chan C, Kien F, Siu L, Tse J, Chu K, Kam J, Staropoli I, Crescenzo-Chaigne B, Escriou N, van der Werf S, Yuen KY, Altmeyer R. Differential maturation and subcellular localization of severe acute respiratory syndrome coronavirus surface proteins S, M and E. *The Journal of general virology*, 2005; 86(5): 1423–1434.