# COVID-19 (Novel Coronavirus 2019) – recent trends

S. KANNAN<sup>1</sup>, P. SHAIK SYED ALI<sup>1</sup>, A. SHEEZA<sup>1</sup>, K. HEMALATHA<sup>2</sup>

Kannan Subbaram and Shaik Syed Ali Pakeer are equal contributors

**Abstract.** – The World Health Organization (WHO) has issued a warning that, although the 2019 novel coronavirus (COVID-19) from Wuhan City (China), is not pandemic, it should be contained to prevent the global spread. The COVID-19 virus was known earlier as 2019-nCoV. As of 12 February 2020, WHO reported 45,171 cases and 1115 deaths related to COVID-19. COVID-19 is similar to Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) virus in its pathogenicity, clinical spectrum, and epidemiology. Comparison of the genome sequences of COVID-19, SARS-CoV, and Middle East Respiratory Syndrome coronavirus (MERS-CoV) showed that COVID-19 has a better sequence identity with SARS-CoV compared to MERS CoV. However, the amino acid sequence of COVID-19 differs from other coronaviruses specifically in the regions of 1ab polyprotein and surface glycoprotein or S-protein. Although several animals have been speculated to be a reservoir for COVID-19, no animal reservoir has been already confirmed. COVID-19 causes COVID-19 disease that has similar symptoms as SARS-CoV. Studies suggest that the human receptor for COVID-19 may be angiotensin-converting enzyme 2 (ACE2) receptor similar to that of SARS-CoV. The nucleocapsid (N) protein of COVID-19 has nearly 90% amino acid sequence identity with SARS-CoV. The N protein antibodies of SARS-CoV may cross react with COVID-19 but may not provide cross-immunity. In a similar fashion to SARS-CoV, the N protein of COVID-19 may play an important role in suppressing the RNA interference (RNAi) to overcome the host defense. This mini-review aims at investigating the most recent trend of COVID-19.

Key Words:

Coronavirus, Pneumonia, Novel coronavirus 2019, 2019-nCoV, COVID-19, SARS, MERS.

## Introduction

In Wuhan (Hubei Province, China) several cases of pneumonia patients were admitted in

hospitals from December 2019<sup>1</sup>. 2019 Coronavirus (COVID-19) is the etiological agent in the reported cases2. The disease has been named as COVID-19 by World Health Organization (WHO). COVID-19 disease may manifest either as an asymptomatic infection or a mild to severe pneumonia. COVID-19 disease outbreaks caused significant mortality and morbidity in China compared to the rest of the world<sup>2</sup>. The COVID-19 strains are genetically related with (Severe Acute Respiratory Syndrome coronavirus) SARS-CoV and Middle East Respiratory Syndrome coronavirus (MERS-CoV)<sup>3</sup>. Surprisingly, the epidemiology of COVID-19 is similar to SARS-CoV<sup>4</sup>. The genome of COVID-19 shares sequence identity with both SARS-CoV and MERS-CoV5. With high incidence of COVID-19 cases in China and its spread to the other parts of the world, despite undertaking strict quarantine measures, the likelihood of WHO declaring COVID-19 a pandemic cannot be ruled out.

This mini-review is focused on recent and current trends on COVID-19 genome, morphology, clinical disease, epidemiology, laboratory diagnosis, and molecular aspects of Nucleocapsid protein.

## Genome of COVID-19

Comparison of the genome sequences of the COVID-19, SARS-CoV, and MERS-CoV showed that 2019-CoV has a better sequence identity with SARS-CoV than the MERS CoV<sup>6</sup>. The COVID-19 amino acid sequence varies from other coronaviruses exclusively in the regions of lab polyprotein and surface glycoprotein or S-protein. S-protein has two subunits with one subunit binding directly to the host receptor aiding the virus entry into cells. The RNA binding domain of the S-protein in COVID-19 has a higher homology with SARS-

<sup>&</sup>lt;sup>1</sup>School of Medicine, The Maldives National University, Male', Maldives

<sup>&</sup>lt;sup>2</sup>Department of Laboratory Sciences and Pathology, Jimma University, Jimma, Ethiopia

CoV. Though some of the residues critical for binding the receptor are different, overall the non-identical residues did not alter the structural conformation. Studies<sup>7,8</sup> suggest that the human receptor for COVID-19 could be angiotensin-converting enzyme 2 (ACE2). Other coronaviruses including SARS-CoV gain entry into human cells through ACE2<sup>9</sup>.

# Morphology of COVID-19

Coronaviruses are enveloped, pleomorphic or spherical particles, 150 to 160 nm in size, associated with positive single stranded RNA, unsegmented, nucleoprotein, capsid, matrix, and S-protein (Figure 1). Important viral proteins are nucleocapsid protein (N), membrane glycoprotein (M), and spike glycoprotein (S)<sup>10</sup>. COVID-19 differs from other coronaviruses by encoding an additional glycoprotein that has acetyl esterase and hemagglutination (HE) properties<sup>6</sup>.

# Nucleocapsid (N) Protein of COVID-19

Antibodies generated against the N protein of SARS-CoV may cross react with COVID-19<sup>11</sup>. The heterophilic antibodies of SARS-CoV may not provide cross protection to COVID-19. Nevertheless, they can be used for diagnostic purpos-

es. Another potential role of SARS-CoV N protein is its ability to counter host immune response as a viral suppressor protein of RNA*i* (VSR)<sup>12</sup>. The VSRs suppress the RNA*i* at the pre-dicer or post-dicer level to overcome the host defense to establish infection<sup>13-16</sup>.

# VSR Activity of COVID-19 N-Protein

We performed a Clustal W analysis of N-protein of SARS-CoV and COVID-19 by NCBI amino acid blast that demonstrated more than 90% sequence identity with each other (Figure 2). Therefore, the N-protein of COVID-19 may act in a similar fashion to SARS-CoV as a VSR to counter the host defense mechanism.

#### Clinical Presentation

The most convincing mode of transmission of COVID-19 is inhalation of infectious aerosols<sup>17</sup>. The incubation period is approximately 3-14 days. COVID-19 may cause disease ranging from asymptomatic to fatal disease. In elderly patients, COVID-19 infects the lower respiratory tract with the potential of leading to fatal pneumonia<sup>18-22</sup>. Other non-specific symptoms include fever, cough, myalgia, dyspnea with or without diarrhea<sup>5,22</sup>. In the second week of infection, it

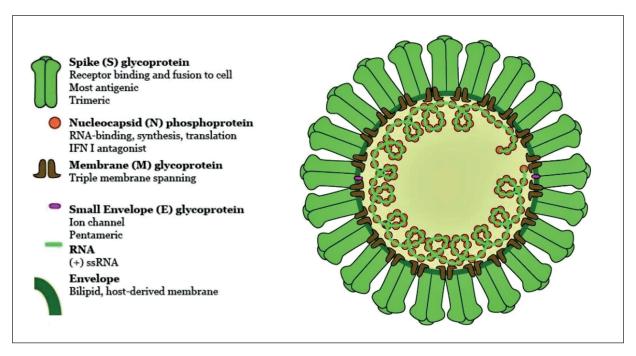


Figure 1. Coronavirus schematic diagram. (Courtesy from Dr. Ian M Mackay, Ph.D.).

CLUSTAL 2.1 multiple sequence alignment		
SARS-CoV-Nprotein 2019-nCoV-Nprotein	MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNTASWFTALTQH MSDNGPQ-NQRNAPRITFGGPSDSTGSNQNGERSGARSKQRRPQGLPNNTASWFTALTQH ****** ***.***************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	GKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFYYLGTGPEA GKEDLKFPRGQGVPINTNSSPDDQIGYYRRATRRIRGGDGKMKDLSPRWYFYYLGTGPEA ***:*:*******************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	SLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVLQLPQGTTLPKGFYAEGSRGG GLPYGANKDGIIWVATEGALNTPKDHIGTRNPANNAAIVLQLPQGTTLPKGFYAEGSRGG .******:**	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	SQASSRSSSRSRGNSRNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVSGKGQ SQASSRSSSRSRNSSRNSTPGSSRGTSPARMAGNGGDAALALLLLDRLNQLESKMSGKGQ ***********************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	QQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYK QQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYK ************************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDA HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDA ************************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	YKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLLPAADMDDFSRQLQNSMSGASADST YKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA ************************************	
SARS-CoV-Nprotein 2019-nCoV-Nprotein	QA 	

Figure 2. Clustal W analysis for nucleocapsid (N) protein of SARS-CoV and COVID-19.

progresses to hypoxemia, difficulty in breathing and acute respiratory distress syndrome (AR-DS)<sup>23</sup>. Patients at this stage may require mechanical ventilation in Intensive Care Unit (ICU) with quarantine facilities. Secondary bacterial infections may set in leading to secondary bacterial pneumonia.

## Epidemiology

Outbreaks of COVID-19 have been documented to have originated from 'wet markets' in South China from wild animals. It is very intriguing to note that the SARS outbreak in Southern China in 2002 and the current outbreak of COVID-19 happened in winter due to exposure to live animals sold in markets. Primary examinations revealed some environmental specimens were positive for COVID-19 in Huanan Seafood Market, Wuhan<sup>11</sup>. Based on the WHO report, although the market-place was deemed positive for COVID-19, no specific association with an animal is confirmed yet. Snake was found to be a possible reservoir but it was dismissed by some scholars<sup>24</sup>. Many researchers speculated that these viruses have wide

range of animal and bird reservoirs<sup>3</sup>. Researchers are working to establish a possible animal reservoir for COVID-19<sup>25</sup>.

Initially the patients that contracted the disease had activities related to the market. Surprisingly some confirmed COVID-19 positive patients did not visit the suspected market. Health care workers in various countries are affected from the infected patients. This indicates that human to human transmission of COVID-19 is highly likely<sup>26-28</sup>. In addition to aerosol and large respiratory droplets, COVID-19 may also be present in the stool and urine of affected patients with diarrheal symptoms. As of 12 February 2020, WHO reported 45,171 cases and 1115 deaths globally related to COVID-19. Statistical data demonstrate that 99% of the infections and 99.9% of deaths related to COVID-19 occurred in China. Measures are being undertaken by WHO to contain the spread of COVID-19<sup>29</sup> WHO situation reports as of 12 February 2020 indicates that COVID-19 is spreading globally in a rapid manner (Figure 3) (Table I). Scientists are trying to develop drugs for COVID-19 by conducting drug trials on animals in Wuhan, China<sup>30</sup>.

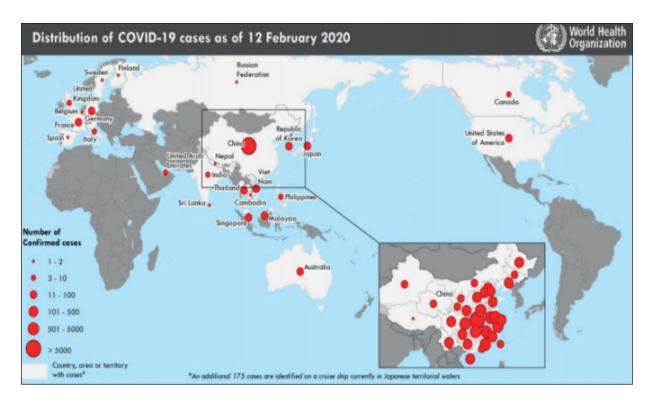


Figure 3. WHO Situation report dated 12 February 2020. (Adapted from WHO).

Table I. Confirmed COVID-19 cases and deaths (WHO data as of 10 February 2020).

WHO region	Confirmed cases	Total cases
Western specific region		
China	44,730	1114
Other than China	155	1
South-East region	38	0
Region of the Americas	20	0
European region	45	0
Eastern Mediterranean region	8	0
Other (Cruise ship cases in Japanese territorial water)	175	0

#### Laboratory Diagnosis

Nasal secretions, blood, sputum, and bronchoalveolar lavage (BAL) collected from suspected patients are used as clinical specimens. The samples are subjected to specific serological and molecular tests specific for COVID-19 for laboratory diagnosis. Serological tests employ enzyme linked immunosorbent assay (ELISA) or Western blots that detects specific COVID-19 proteins. Molecular approaches are based on Real Time-PCR (RT-PCR) or Northern blot hybridization targeting specific COVID-19 genes<sup>31</sup>. Viral antigens present in the clinical specimens are detected by using direct immune fluorescent assay (IFA).

### Conclusions

COVID-19 outbreak from China has the potential to reach pandemic proportion if it is not appropriately contained. COVID-19 symptoms are milder, but infectivity is higher compared to SARS-CoV and MERS-CoVCOVID-19; it may be considered as a severe public health threat of this decade. The drug for COVID-19 is distant and therefore COVID-19 spread may be contained by following strict quarantine protocols.

## **Conflict of Interest**

The Authors declare that they have no conflict of interests.

## References

- MUNSTER VJ, KOOPMANS M, VAN DOREMALEN N, VAN RIEL D, DE WIT E. A novel coronavirus emerging in china key questions for impact assessment. N Engl J Med. 2020 Jan 24. doi: 10.1056/NE-JMp2000929. [Epub ahead of print].
- 2) ZHU N, ZHANG D, WANG W, LI X, YANG B, SONG J, ZHAO X, HUANG B, SHI W, LU R, NIU P, ZHAN F, MA X, WANG D, XU W, WU G, GAO GF, TAN W; CHINA NOVEL CORONAVIRUS INVESTIGATING AND RESEARCH TEAM. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med. 2020 Jan 24. doi: 10.1056/NEJMoa2001017. [Epub ahead of print].
- ZHOU P, YANG XL, WANG XG, Hu B, ZHANG L, ZHANG W. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin. Nature 2020. https:// doi.org/10.1038/s41586-020-2012-7.
- FRAIRE AE, WODA BA, WELSH RM, KRADIN RL (EDS.). Coronavirus. In: viruses and the lung: infections and non-infectious viral-linked lung disorders. Springer-Verlag Berlin Heidelberg 2014; pp. XIV, 243.
- Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020; 20: 30183-30185.
- Wu F, Zhao S, Yu B, Chen YM, Wang W, Hu Y. Complete genome characterisation of a novel coronavirus associated with severe human respiratory disease in Wuhan, China. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.24.919183.
- ZHAO Y, ZHAO Z, WANG Y, ZHOU Y, MA Y, ZUO W. Single-cell RNA expression profiling of ACE2, the putative receptor of Wuhan 2019-nCov. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.26.919985.
- LETKO M, MUNSTER V. Functional assessment of cell entry and receptor usage for lineage B β-coronaviruses, including 2019-nCoV. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.22.915660.
- Dong N, Yang X, Ye L, Chen K, Chan EW, Yang M. Genomic and protein structure modelling analysis depicts the origin and infectivity of 2019-nCoV, a new coronavirus which caused a pneumonia outbreak in Wuhan, China. bioRxiv 2020. doi: https:// doi.org/10.1101/2020.01.20.913368.
- 10) PERLMAN S. Another decade, another coronavirus. N Engl J Med 2020. doi: 10.1056/NEJMe2001126. [Epub ahead of print] No abstract available.
- Gralinski LE, Menachery VD. Return of the Coronavirus: 2019-nCoV. Viruses 2020; 12. pii: E135.
- 12) Cui L, Wang H, Ji Y, Yang J, Xu S, Huang X, Wang Z, Qin L, Tien P, Zhou X, Guo D, Chen Y. The nucleocapsid protein of coronaviruses acts as a viral suppressor of RNA silencing in nammalian nells. J Virol 2015; 89: 9029-9043.
- DING SW. RNA-based antiviral immunity. Nat Rev Immunol 2010; 10: 632-644.

- SULLIVAN CS, GANEM D. A virus-encoded inhibitor that blocks RNA interference in mammalian cells. J Virol 2005; 79: 7371-7379.
- Maillard PV, Ciaudo C, Marchais A, Li Y, Jay F, Ding SW, Voinnet O. Antiviral RNA interference in mammalian cells. Science 2013; 342: 235-238.
- ALI PS, JOHN J, SELVARAJ M, KEK TL, SALLEH MZ. Nodamura virus B2 amino terminal domain sensitivity to small interfering RNA. Microbiol Immunol 2015; 59: 299-304.
- 17) READ JM, BRIDGEN JR, CUMMINGS DA, Ho A, Jewell CP. Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions. medRxiv 2020. doi: https://doi.org/10.1101/2020.01.23.20018549
- 18) Mahase E. China Coronavirus: what do we know so far? BMJ 2020; 368: m308.
- Lu H, Stratton CW, Tang Y. Outbreak of pneumonia of unknown etiology in Wuhan China: the mystery and the miracle. J Med Virol 2020. doi: 10.1002/jmv.25678. [Epub ahead of print].
- 20) NISHIURA H, JUNG SM, LINTON NM, KINOSHITA R, YANG Y, HAYASHI K, KOBAYASHI T, YUAN B, AKHMETZHANOV AR. The extent of transmission of novel Coronavirus in Wuhan, China, 2020. J Clin Med 2020; 9. pii: E330.
- CHEN Y, LIU Q, GUO D. Emerging coronaviruses: genome structure, replication, and pathogenesis. J Med Virol 2020. doi: 10.1002/jmv.25681. [Epub ahead of print].
- 22) Chan JF, Yuan S, Kok KH, To KK, Chu H, Yang J, Xing F, Liu J, Yip CC, Poon RW, Tsoi HW, Lo SK, Chan KH, Poon VK, Chan WM, Ip JD, Cai JP, Cheng VC, Chen H, Hui CK, Yuen KY. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. Lancet 2020. pii: S0140-6736(20)30154-9. [Epub ahead of print].
- 23) Hui DS, I Azhar E, Madani TA, Ntoumi F, Kock R, Dar O, Ippolito G, Mchugh TD, Memish ZA, Drosten C, Zumla A, Petersen E. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health the latest 2019 novel coronavirus outbreak in Wuhan, China. Int J Infect Dis 2020; 91: 264-266.
- 24) Ji W, Wang W, Zhao X, Zai J, Li X. Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission from snake to human. J Med Virol 2020. doi: 10.1002/jmv.25682. [Epub ahead of print].
- 25) Guo Q, Li M, Wang C, Fang Z, Wang P, Tan J. Host and infectivity prediction of Wuhan 2019 novel coronavirus using deep learning algorithm. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.21.914044.
- 26) RIOU J, ALTHAUS CL. Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January

- 2020. Euro Surveill 2020; 25. doi: 10.2807/1560-7917.ES.2020.25.4.2000058.
- 27) CHEN TM, RUI J, WANG QP, ZHAO ZY, CUI JA, YIN L. A mathematical model for simulating the transmission of Wuhan novel Coronavirus. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.19.911669
- 28) Wu P, Hao X, Lau EHY, Wong JY, Leung KSM, Wu JT, Cowling BJ, Leung GM. Real-time tentative assessment of the epidemiological characteristics of novel coronavirus infections in Wuhan, China, as at 22 January 2020. Euro Surveill 2020; 25. doi: 10.2807/1560-7917.ES.2020.25.3.2000044.
- WORLD HEALTH ORGANIZATION. WHO: Novel Coronavirus (2019-nCoV) advice for the public. Nov-

- el Coronavirus (2019-nCoV) advice for the public, 2020.
- CYRANOSKI D. This scientist hopes to test coronavirus drugs on animals in locked-down Wuhan. Nature 2020; 577: 607.
- 31) CORMAN VM, LANDT O, KAISER M, MOLENKAMP R, MEIJER A, CHU DK, BLEICKER T, BRÜNINK S, SCHNEIDER J, SCHMIDT ML, MULDERS DG, HAAGMANS BL, VAN DER VEER B, VAN DEN BRINK S, WIJSMAN L, GODERSKI G, ROMETTE JL, ELLIS J, ZAMBON M, PEIRIS M, GOOSSENS H, REUSKEN C, KOOPMANS MP, DROSTEN C. Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Euro Surveill 2020; 25. doi: 10.2807/1560-7917. ES.2020.25.3.2000045.