Biological Property of Novel Coronavirus SARS-CoV-2 (2019-nCoV)

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**Abstract**

Novel coronavirus (2019-nCoV) is a positive-sense RNA virus that possesses four genes that encode the spike (S), membrane (M), nucleocapsid (N), and envelope (E) proteins. The virus was originated in seafood market selling live animals and responsible for coronavirus disease 2019 (COVID-19). The initial case was traced to the city of Wuhan in the province of Hubei, China, reported as an emerging respiratory virus, the outbreak was reported to WHO on December 31, 2019, and soon after identified the causative pathogen as a beta coronavirus named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2); Furthermore, It is a highly contagious virus that spreads swiftly outside of China in March and the World Health Organization had to declare COVID-19 pandemic on March 11, 2020, and as of August 15, 2020, more than 21 million confirmed cases have been reported, with > 755 786 deaths worldwide. This day’s novel coronavirus-2019 is the most infectious virus with high infectivity and low mortality rate where a high mortality rate was observed among people above the age of sixteen (60) years and with the pre-existing health condition. To date, there is no clinically approved antiviral drug or vaccine available to be used against COVID-19. However, Preventive measures such as masks, hand hygiene practices, avoidance of public contact, case detection, contact tracing, and quarantines have been discussed as ways to reduce transmission. Therefore, the purpose of this review is to summarize the basic biological properties of novel coronavirus 2019.

**Introduction**

Novel coronavirus-2019 is a member of a large family of viruses that are known to cause illness ranging from the common cold to more severe diseases like Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndromes SARS-CoV (Tok and Tar, 2017; Li et al., 2020). At the end of December 2019, a new infectious respiratory disease known as 2019-novel coronavirus (2019-nCoV) or the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, Hubei province, China (Ahn et al., 2020). Later on, February 11, 2020, the World Health Organization named the disease as coronavirus disease 2019 (COVID-19) (Adhikari et al., 2020).
It is one of the emerging respiratory viruses which is originated in seafood market selling live animals and was transmitted to humans through yet unknown intermediary animals in Wuhan, Hubei province, China (Singhal, 2020). This novel virus is responsible for the current pandemic; its diverse biological and epidemiological characteristics make this virus more contagious than other Human coronaviruses (HCoVs); it has affected more people in a short period of time. Therefore, the purpose of this review is to highlighted the basic biological properties of 2019-nCoV or SARS-CoV-2.

**Viral Composition and Structure**

2019-nCoV is an enveloped, non-segmented, single-stranded, positive-sense RNA virus belong to order Nidovirales, family Coronaviridae, subfamily Coronavirinae, genus Coronavirus and subgenus sarbecovirus (Chen et al., 2020). Similar, to SARS-CoV and MERS-CoV, SARS-CoV-2 belongs to the beta-genus Coronavirus and possesses the largest genome, 26.4–31.7 kilobases in size (Mousavizadeh and Ghaseimi, 2020; Schoeman and Fielding, 2019). The viral genome is packed inside a capsid with a helical symmetry, which is built by the nucleocapsid protein (N) and further surrounded by an envelope which is also associated with at least three structural proteins namely the membrane protein (M), envelope protein (E) and the spike protein (S) where the first two involved in virus assembly. Whereas, the S protein mediates virus entry into host cells and forms large protrusions from the virus surface, giving the appearance of having crowns (hence their name; corona in Latin means crown) (Li, 2016). In addition to mediating virus entry, the spike is a critical determinant of viral host range, tissue tropism and it is a major inducer of host immune responses; which implies that currently it is the most promising antigen formulation for SARS-CoV-2 vaccine research (Fig.1) (Zhang et al., 2020).

According to the findings of Lu et al. (2020), it was found that the genome sequence of SARS-CoV-2 is closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21, collected in 2018 in Zhourshan, eastern China, but were more distant from SARS-CoV (about 79%) and MERS-CoV (about 50%).

**Fig. 1:** The overall structure of SARS-CoV-2 shown with structural proteins: - N: Nucleocapsid protein; S: Spike protein; M: Membrane protein and E: Envelop protein.

At the 5′ terminal two-thirds of the genome contains two open reading frames (ORFs), ORF1 and ORF2 which encodes non-structural proteins (such as 3-chymotrypsin-like protease, papain-like protease (pp1a and pp1b), helicase, and RNA-dependent RNA polymerase) which are key enzymes in the viral life cycle and the last third of the genome encodes primarily structural proteins namely S, E, M and N located at the one-third 3′ terminal of the genome (Fig.2) (Malik et al., 2020).

The virus enters target cells via receptor-mediated endocytosis driven by the spike (S) glycoprotein, which protrudes from the surface of the virion; The S protein serves as the major viral attachment protein, critical to virus binding and fusion of the viral envelope (Schoeman and Fielding, 2019; Li, 2016). Angiotensin-converting enzyme 2 (ACE-2) and Cluster of Differentiation two hundred nine ligand (CD209L) were identified as functional receptors for SARS CoV-2 (Fig: 3). However, Angiotensin-Converting Enzyme 2 serves as a more efficient receptor (Zhang et al., 2020).

**Fig. 2:** Genome organization of novel coronavirus. Comparative spike (S) protein sequence length of different Beta-coronaviruses is depicted.
nCoV-19 Related HCoVs

Human coronaviruses (HCoVs) are common viral respiratory pathogens that primarily cause symptoms in the upper respiratory and gastrointestinal tracts; they have long been considered inconsequential pathogens, causing the “common cold”. SARS-CoV-2 became the seventh member of the human coronaviruses (HCoVs) identified as HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1, SARS-CoV, MERS-CoV and now SARS-CoV-2 (Rabaan et al., 2020; Zhou et al., 2020). However, in the 21st century, 2 highly pathogenic HCoVs named as SARS-CoV and MERS-CoV emerged from animal reservoirs to cause global epidemics with alarming morbidity and mortality. Currently, four different genera exist, including Alphacoronavirus-(α) Betacoronavirus-(β) Gammacoronavirus-(γ) and Deltacoronavirus-(δ) where α- and β-CoV are able to infect mammals, while γ- and δ-CoV tend to infect birds; whereas, the other two known β-CoVs; SARS-CoV and MERS-CoV leads to severe and potentially fatal respiratory tract infections (Meo et al., 2020; Shen et al., 2019).

SARS-CoV first identified in 2002 and diagnosed in Southern China, occurred from a human CoV. Then, exactly 10 years after the SARS-CoV emergence, a new emerging Coronavirus named MERS-CoV has infected people with a high mortality rate of nearly 50% in the Middle East (Zhou et al., 2020).

Host Range

A wide range of species; such as, dogs, cats, pigs, mice, bats, and humans are infected by CoVs. However, most strains of corona viruses exhibits a narrow host range (Meo et al., 2020). They cause a variety of diseases in mammals and birds ranging from enteritis in cows and pigs and upper respiratory disease in chickens to potentially lethal human respiratory infections (Meo et al., 2020; Shen et al., 2019). Rarely, animal CoVs can infect humans and; as a result; may spread among humans during epidemics such as MERS, SARS, and COVID-19. Additionally, at the onset of major outbreaks caused by CoVs, palm civet has been proposed to be a natural reservoir of Human CoVs for SARS and dromedary camels for MERS. However, more advanced virological and genetic studies have shown that bats are reservoir hosts of both SARS-CoV and MERS-CoV (Shen et al., 2019).

Infection and Replication

Initially for SARS-CoV-2 to replicate it starts with an infection. Infection begins when the virus enters the host cell, via receptors mainly by spike protein and its ligand host cell receptor called ACE2 which is found in various organs such as heart, lungs, kidneys; and gastrointestinal tract. Thus, facilitating viral entry into target cells (Shen et al., 2019). Then entered-SARS-CoV-2 will subsequently release its genetic material in the cytoplasm via uncoating and get translated in the host nuclei (Hafeez et al., 2020; Guo et al., 2020). Virus-specific RNA and proteins are synthesized entirely in the cytoplasm. During this process protein synthesizing and viral expression starts with translation of two polyproteins, namely, pp1a and pp1ab, which undergo cotranslational proteolytic processing into the proteins that form the replicas complex and lastly, new virions are assembled by budding into intracellular membranes and released through vesicles by the cell secretory mechanisms (Fig. 4) (Astuti, 2020).
Transmission and Symptoms
In spite of the belief that 2019-nCoV was introduced into humans from an animal species (i.e. zoonotic transmission); According to the latest guidelines from Chinese health authorities human-to-human transmission is possible by three different ways ; these transmission routes includes droplets transmission, contact transmission, and aerosol transmission:- In droplets transmission viral transmission occurs when respiratory droplets produced when an infected person coughs or sneezes are ingested or inhaled by individuals nearby proximity and while during contact transmission it occurs when a subject touches a surface or object contaminated with the virus and subsequently touch their mouth, nose, or eyes; and lastly in the aerosol transmission it occurs when respiratory droplets mix into the air, forming aerosols and may cause infection when inhaled high dose of aerosols into the lungs in a relatively closed environment (Jin et al., 2020). Viral incubation period ranges from 2 to 14 days with a mean day of 6.4 and the usual symptoms include fever, cough, shortness of breath, and muscle ache. In cases of some patients they may have sore throat, rhinorrhea, headache and confusion, a few days before the onset of fever. This indicates that fever is a critical symptom, but not the only initial manifestation of infection (Huang et al., 2020; Tu et al., 2020).

Epidemiology
According to updated world health organization (WHO) reports, the number of confirmed cases is constantly increasing worldwide even a steep increase in cases is currently being observed in low-income countries. As of 09 August 2020, based on the WHO reports; globally 19,462,112 confirmed cases and 722,285 deaths distributed as per (Table.1) (WHO, 2020).
Table 1: COVID-19 situational report as of August 15, 2020.

| Situation in numbers (by WHO Region) | Total (new cases in last 24 hours) |
|-------------------------------------|-----------------------------------|
| Globally                            | 21 026 758 cases (294 237)        |
|                                     | 755 786 deaths (9 985)            |
| Africa                              | 936 062 cases (10 765)            |
|                                     | 18 286 deaths (382)              |
| Americas                            | 11 271 215 cases (161 772)       |
|                                     | 410 483 deaths (7 749)           |
| Eastern Mediterranean               | 1 710 272 cases (13 382)         |
|                                     | 45 361 deaths (357)              |
| Europe                              | 3 733 965 cases (29 260)         |
|                                     | 213 674 deaths (365)             |
| South-East Asia                     | 2 971 104 cases (70 757)         |
|                                     | 58 844 deaths (1 088)            |
| Western Pacific                     | 403 399 cases (8 301)            |
|                                     | 9 125 deaths (44)                |

Diagnosis

Clinical specimens used to diagnose novel coronavirus nucleic acid includes nasal secretions, sputum, lower respiratory tract secretions, blood, feces, broncho alveolar lavage (BAL) and in order to increase the positive rate of nucleic acid detection. It is recommended to take as much sample as possible; the aforementioned samples are subjected to specific serological and molecular tests specific for COVID-19 where serological tests employ enzyme linked immunosorbent assay (ELISA) or Western blots that detects specific COVID-19 proteins while molecular approaches are based on Real Time-PCR (RT-PCR) or Northern blot hybridization targeting specific COVID-19 genes. Further, viral antigens present in the clinical specimens are detected by using direct immune fluorescent assay (IFA) (Kannan et al., 2020).

Treatment

SARS-CoV-2 continues to spread around the globe without any approved therapies. Researchers are urgently searching for effective prophylactic and therapeutic interventions. For instance, type I Interferons-alpha/beta (IFNs-α/β) are regulatory proteins that have broad-spectrum antiviral activities that work to directly block viral replication and support immune responses to clear virus infection. “Interferons are our first line of defence against any and all viruses, but viruses such as coronaviruses have co-evolved to very specifically block an interferon response (Weiss et al., 2020). However, the Current 2019-nCoV treatment strategies includes bed rest, supportive treatments, physical cooling for patients with body temperature exceeds 38.5°C, oxygen therapy like nasal catheter, mask oxygen, nasal high-flow oxygen therapy, antiviral therapy including interferon-α, favipiravir and ribavirin. In addition to this, remdesivir, galidesivir, lopinavir, and litchi syrup, convalescent plasma, and mAbs some situations where there is systemic inflammatory responses glucocorticoids can be used for a short period (Shen et al., 2019; Li and Declercq, 2020; Li et al., 2020).

Control and Prevention

Till to date, even thought, there is no clinically licensed vaccine against COVID-19, Prevention or slowing down the transmission was the first choices to reduce the pandemic. Currently, the best solution is to follow Infection preventive and control (IPC) measures that may reduce the risk of exposure. This IPC measures includes:- avoiding being exposed to the virus, case isolation, identification and follow-up of contacts, environmental disinfection, use of face masks; covering coughs and sneezes with tissues that are then safely disposed of (or, if no tissues are available, use a flexed elbow to cover the cough or sneeze); regular hand washing with soap or disinfection with hand sanitizer containing 60-80% alcohol (if soap and water are not available); avoidance of contact with infected people and maintaining an appropriate distance as much as possible; and refraining from touching eyes, nose, and mouth with unwashed hands (Ou et al., 2020 ; Wei and Ren, 2020).

Conclusion

Beginning from the end of December 2019, SARS CoV 2 outbreak has challenged the economic, medical and public health infrastructure of the globe; this day, the largest challenge is being observed in low-income countries. Up to date, there is no effective treatment and vaccine; time alone will tell how the virus will impact our lives; yet there is an urgent need to develop new strategies to prevent or control infections. Therefore, the review provides an insight into the basic biological properties and increase the knowledge about the virus that helps for understanding the nature and current status of SARS-CoV-2 this plays a vital role in determining effective treatment and prevention strategies.

Authors’ Contribution

All authors have contributed equally to the manuscript.

Conflict of interest

All authors declare that there exist no commercial or financial relationships that could in any way leads to a potential conflict of interest.
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