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Review Article

Transmission, entry and pattern of infection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)

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ABSTRACT: Ever since the first case of SARS-CoV-2 infection was detected, the World Health Organization (WHO) has been working intimately with clinicians and other health care workers to provide care for affected COVID-19 patients. Transmission of the virus occurs through the spread of respiratory and salivary droplets from persons to persons. It is expected that an infected person can transmit the disease to at least two other people because WHO estimated the transmission rate *R0* to be between 2.0-2.5. One of the strategies adopted by WHO in the eradication of the virus is to interrupt human-to-human transmission. This article aims at providing scientific view on transmission, entry and pattern of SARS-CoV-2 with a perspective that brings more clarity about the novel coronavirus using knowledge and in-depth analysis of the existing data and facts on COVID-19 disease. It has been reported that the genomic sequence analysis of COVID-19 showed 88% identity with two bat-derived severe acute respiratory syndromes (SARS)-like coronaviruses and this explains the animal to human transmission in Wuhan, China. Meanwhile, human-to-human transmission of the infection is the most popular since the outbreak of the disease. Importantly, the sequence of the receptor-binding domain of COVID-19 spikes is like that of SARS-CoV and the entry of the virus into the host cells is most likely via the Angiotensin Converting Enzyme (ACE2) receptor. In conclusion, understanding the mode of transmission, immunogenicity of COVID-19 and exploring the pattern of viral infection is essential in determining the virulence and developing the most effective treatment regimens and vaccine towards the eradication of the virus.

Keywords: Coronavirus, COVID-19, pathogenesis, transmission, virulence.

BACKGROUND

Coronavirus is one of the microorganisms that affect the human respiratory system (Li et al., 2020). In the twenty-first century, before COVID-19, there has been severe acute respiratory syndrome coronavirus (SARS-CoV) and the Middle East respiratory syndrome coronavirus (MERS-CoV) (Li et al., 2020). The World Health Organization named the disease Coronavirus disease 2019 on February 11, 2020 (Li et al., 2020) and the organization has since the first case of COVID-19 been working intimately with clinicians to provide care for patients with COVID-19. This article aims at providing scientific view on transmission, entry and pattern of SARS-CoV-2 with a perspective that brings more clarity about the novel coronavirus using knowledge and in-depth analysis of the existing data and facts on COVID-19 disease. Basically**,** analysis of the existing data and facts on COVID-19 disease was done in this study to bring about more clarity about the novel coronavirus.

TRANSMISSION AND PATTERNS OF COVID 19 AS A VIRAL INFECTION

Among the various reports on the reproduction number of COVID19 include a report that stated that the reproduction number of COVID19 is between 2.2 to 2.7 (Sanche et al., 2020), and another report that stated that the reproduction number is 5.7 (Healthline, 2020). Transmission of the virus occurs through the spread of respiratory and salivary droplets from persons to persons (Sanche et al., 2020). One of the strategic objectives of the World Health Organization (WHO) in the eradication of COVID-19 is to interrupt human-human transmission (WHO, 2020a,b,c). An individual can be asymptomatic and still transmit the virus (Cascella et al., 2020; Ghinai et al., 2020). Meanwhile, current information recommends that the infection can develop within a person within three to seven days of contact which means symptoms may not develop in some infected people until the seventh day (Li et al., 2020). Genomic sequence analysis of COVID-19 showed 88% identity with two bat-derived severe acute respiratory syndromes (SARS)-like coronaviruses (Lu et al., 2020; Wan et al., 2020). This suggests the possibility of animal-human transmission. Although human-to-human transmission of the infection is the most popular since the first case was identified. In this manner, human-to-human transmission is currently thought about as the primary type of transmission.

Some domestic and wild animals such as camels, battles, cats, and bats, may serve as hosts for coronaviruses but it has been reported that most of these coronaviruses do not spread among humans (Adhikari et al., 2020). Meanwhile, early patients in China were reported to have visited Huanan Seafood Market in Wuhan, China and this supports the suggestion that the early infections in China were due to animal-to-person transmission. However, later cases after that were reported among medical staff and others with no history of exposure to that Huanan Seafood Market in Wuhan, which was taken as an indication of human-to-human transmission (Liu et al., 2020).

Finally, on the pattern of infection, the global outbreak of SARS-CoV-2 may be due to lack of full understanding about molecular mechanisms of viral binding and entry manners of the virus which may be an obstacle to the development of targeted therapies. Also, the fact that available data suggest that the SARS-CoV-2 is more virulent may also be another factor for the global outbreak and manner of spread of the virus (WHO, 2020a,b,c).

ENTRY AND REPLICATION

Importantly, the sequence of the receptor-binding domain of SARS-CoV-2 spikes is similar to that of SARS-CoV (Li et al., 2020). It has been suggested that entry into the host cells is via the ACE2 receptor which is found on the cells of the heart, lungs, kidneys, and gastrointestinal tract just like in the case of SARS-CoV (Li et al., 2020; Wan et al., 2020). Meanwhile, the lung epithelial cells are the primary target of the SARS-CoV-2 virus (Rothan and Byrareddy, 2020). SARS-CoV-2 viruses after infection find their way to the oropharyngeal and move from there to the lungs and then into the blood (Zhou et al., 2020). This is according to an analysis of the COVID19 progression in 191 patients from Wuhan (Zhou et al., 2020). The S protein has been reported to be the main protein involved in the entry of the SARS-CoV virus into host cells (De Wit et al., 2016) and the envelope spike glycoprotein of SARS-CoV virus binds to a cellular ACE2 receptor during the process (Li et al., 2003). This similar behaviour is expected of SARS-CoV-2 virus as SARS-CoV and SARS-CoV-2 viruses are variants of coronaviruses (Jeffers et al., 2004). Furthermore, CD209L (a C-type lectin, also called L-SIGN) is a receptor identified for SARS-CoV attachment to host cells (Jeffers et al., 2004) and Dipeptidyl peptidase-4 (DPP4) is another receptor for the attachment of MERS-CoV virus to the host cells (Raj et al., 2013). These two receptors are also expected to be involved in SARS-CoV-2 entry into host cells.

Also, another behaviour of SARS-CoV expected of SARS-CoV-2 is the critical proteolytic cleavage event that occurs at position (S2') of SARS-CoV S protein which leads to membrane fusion (Li et al., 2020). The membrane fusion is possible by direct membrane fusion between the virus and plasma membrane of the cell (Xia et al., 2020). Apart from using membrane fusion (Xia et al., 2020; Yu et al., 2020), the clathrin-dependent and independent endocytosis are also involved in the entry and replication of the SARS-CoV virus (Wang et al., 2008). The viral genome is released and after the viral RNA genome is released, it is then translated into two polyproteins and structural proteins (Li et al., 2020).

After this, the virus then continues to replicate (Li et al., 2020). The newly formed glycoproteins possess envelopes and they are inserted into the membrane of the endoplasmic reticulum or Golgi. The nucleocapsid is formed by the combination of genomic RNA and the nucleocapsid protein. Afterwards, viral particles enter the endoplasmic Reticulum-Golgi intermediate compartment (ERGIC) and the vesicles containing the virus particles then join with the plasma membrane for viral release (De Wit et al., 2016; Xia et al., 2020). Importantly, the sequence of the receptor-binding domain of COVID-19 spikes is like that of SARS-CoV and it is suggested that SARS-CoV-2 follows the same pattern of entry and replication like SARS-CoV (Li et al., 2020; Wan et al., 2020).

Majorly, the virus replicates to spread the infection by increasing the number of infecting viruses and as the virus keeps replicating, it reaches the lungs and causes inflammation in the alveoli or lung sacs. The alveoli and lung sacs are filled with fluid and pus that results in pneumonia, then followed by the inflammation of the lung tissues, and the person experience difficulty in breathing leading to acute respiratory distress (Wan et al., 2020).

TROPISM AND VIRULENCE

In a study conducted to determine population genetic analyses of 103 SARS-CoV-2 genomes, 2 different prevalent types of SARS-CoV-2 were classified out. The two types are the L type (~ 70%) and S type (~ 30%) (Guo et al., 2020). These two types were the most prevalent strains of SARS-CoV-2 after the study. Meanwhile, there are dart reports on the virulence of the virus (Guo et al., 2020; Huang et al., 2020).

The genome of SARS-CoV-2 has 89% nucleotide homology with bat SARS-like-CoVZXC21 and 82% with human SARS-CoV (Chan et al., 2020) and for the fact that the virus is related to the SARS-CoV virus, the new virus was called SARS-CoV-2. The virus is an RNA virus and its genome is single-stranded (Cascello M., 2020). The virus contains 29891 nucleotides for 9860 amino acids (De Soto et al., 2020). Mutation in the original strain of the virus could have directly triggered virulence towards human (Cascello M., 2020). SARS-CoV-2 is genetically similar to SARS-COV but more infectious. This is because the spike protein of SARS-COV-2 has accumulated mutations which increase its binding affinity with ACE2 (Guo et al., 2020).

HOST FACTORS

It has been reported that the survival rate for SARS-CoV-2 disease is dependent on the age of infected persons as persons below the age of 60 and even younger have more chance of surviving the disease (Huang et al., 2020). This may be because more T cells are produced by younger people than older people (Huang et al., 2020). The immune response of the human body is vital in the control and resolution of SARS-CoV-2 and the interaction between the virus and a cell of the body can produce a diverse set of immune mediators against the virus. Meanwhile, innate immunity is necessary in precise regulation in order to eliminate the SARS-CoV-2 virus (CDC, 2020). Furthermore, the SARS-CoV-2 viral particles invade the respiratory mucosa and then infect more cells, triggering immune responses, this then leads to the production of a cytokine storm in the body and of which production of cytokines may be a contributory factor to the critical condition of COVID-19 infected patients (Liu et al., 2020). Also, people with severe underlying medical conditions and immunocompromised individuals seem to be at higher risk for developing serious complications to SARS-CoV-2 infection (CDC, 2020).

CONCLUSION

In conclusion, understanding the mode of transmission, immunogenicity of COVID-19 and exploring pattern of viral infection is essential in determining the virulence and developing the most effective treatment regimens and vaccine towards the eradication of the virus.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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