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The emergence of severe acute respiratory syndrome-coronavirus 2 epidemic and pandemic

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1.1 Introduction

In the history of travel and tourism, a microscopic creature wrote a dark note, which interrupted the fast pace of globalization. In December 2019, in the seafood market of Wuhan city of China, a severe viral pneumonia-like infection was initiated, and which was new to the world and resulted in the emergence of a global health emergency. Thousands of passengers traveled through the city without knowing that one travel can change not only their lives but the future of the world. When WHO declared the severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) outbreak as a global emergency, still no one thought of the conversion of the epidemic into the worst pandemic of the ongoing decade (Cucinotta & Vanelli, 2020). Initially, the spread of SARS-CoV-2 infection over a wide area with a lot of patients at the same time declared it as a global epidemic, but the rapid escalation of the infection at more comprehensive geographical locations with a significant portion of the infected population soon turned the epidemic into the pandemic. The imported cases soon spread to their native places and turn the disease pandemic. While many countries are imposing partial or complete lockdown for the safety of travelers and civilians, the vacant human-made spaces and tourist architectures are asking that where the lacunae were, which has put the globe in such a devastating phase (Wu et al., 2020). The emergence of SARS-CoV-2 created a colossal health crisis for the entire world. From a provincial health concern to a global meltdown, the impact of SARS-CoV-2 has undeniably impacted the world medically, socially, financially, and psychologically (Ali et al., 2020; Preti et al., 2020). The footprints of SARS-CoV-2 are impactfully imprinted on the decade that will require a lot of time for global recovery.

1.2 Severe acute respiratory syndrome-coronavirus 2: the member of the coronavirus family

SARS-CoV-2 is the pathogen of zoonotic origin that belongs to the family “Coronaviridae,” order “Nidovirales” and realm “Riboviria.” coronavirus is not a new entity as four categories of the existing coronaviruses are already known to the world. The alpha, beta, delta, and gamma coronaviruses...
are the classes among which two categories, alpha and beta coronaviruses, have the potential to infect human beings. The mutational changes in these unharmful viruses make them capable of being a threat to human health. To date, seven human coronaviruses (HCoVs) are known, named as severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS), SARS-CoV-2, HCoV-229E, HCoV-OC43, HCoV-NL63, and HCoV-HKU1 (Alsaad et al., 2018; Anderson et al., 2004; Chan et al., 2014; Li et al., 2005; Sexton et al., 2016). SARS-CoV-2 was initially termed as “Wuhan virus” or “China virus” but later, on February 11, 2020, the WHO announced that the name for the disease would be COVID-19. In the name, CO refers to the virus family “Corona,” VI stands for “Virus,” D for “disease,” and 19 refers to the year of the outbreak “2019.” Later on, based on genetic similarity with the SARS virus the “The International Committee on Taxonomy of Viruses” named it “severe acute respiratory syndrome-coronavirus 2,” or SARS-CoV-2.

1.2.1 SARS-CoV-2 in connection with severe acute respiratory syndrome-coronavirus and Middle East respiratory syndrome-coronavirus

Before the eruption of the deadly SARS-CoV-2 epidemic, various similar outbreaks had happened in the past. These viruses infected lives at a large scale, with a little less global expansion (Azhar et al., 2019; Ba Abduallah & Hemida, 2020; Yan et al., 2020). SARS-CoV and also the MERS-CoV outbreaks that happened in China and the Kingdom of Saudi Arabia have a powerful correlation with SARS-CoV-2 in terms of similarity of bat origin or ordination similarity compared to the other human epidemic virus (Table 1.1). Several members of the coronaviruses (alpha-coronaviruses: HCoV-229E and HCoV-NL63; beta-coronaviruses; HCoV-OC43 and HCoV-HKU1) present self-limiting delicate virulence entities, but the severity of the SARS-CoV-2 virus irruption is increased because of the self-modifying nature of the strain. The respiratory disorder caused by SARS-CoV-2 features a potential similarity to SARS-CoV and MERS-CoV in composition, genome sequence, immunological response identification, and other symptoms (Gu et al., 2005; Memish et al., 2020). SARS-CoV-2 prefers pyrimidine-rich codons to purines (Kandeel et al., 2020). At the early stage of the epidemic, the similarities with the preexistent viruses facilitate the investigations related to drug targeting and immunogen preparation against SARS-CoV-2 infection (Hui & Zumla 2019). SARS epidemic began in Guangdong Province, China, in November 2002. Several observations supported the hypothesis of a wild animal origin for SARS. On March 12, 2003, the WHO issued a global alert about SARS cases in Guangdong Province, which subsequently spread rapidly worldwide (Leung et al., 2004). Several studies suggested that the SARS probably originated in the horseshoe bats, and later passed through palm civets before reaching humans. Similarly, MERS-CoV was found to possess similarity with two bat coronaviruses, HKU4 and HKU5 with confirmed infection in camels be the intermediate host and humans as a possible host (Zhu et al., 2020). In December 2019, SARS-CoV-2 infection originated in an exceedingly similar approach from a food market in an urban center, Hubei Province, China, that at first showing the symptoms of respiratory disorder. Undoubtedly, SARS-CoV-2 is an extremely infectious virus compared to the SARS-CoV associate degreeed MERS-CoV because it has already killed millions of people worldwide with the unsurpassed epidemic potential in an uncontrolled pattern (Rabaan et al., 2020).
1.3 Virion structure of severe acute respiratory syndrome-coronavirus 2

SARS-CoV-2 is a type of beta coronavirus consisting a single positive-strand RNA of 32 kb length as the genetic material (Fig. 1.1). The high recombination frequency of the RNA strand makes SARS-CoV-2 quite remarkable with the largest known RNA viral genome pathogenic to mankind (Alsaad et al., 2018; Anderson et al., 2004; Chan et al., 2014; Li et al., 2005; Sexton et al., 2016). It is made up of various proteins, including structural proteins, including spike (spike glycoprotein), envelope protein, matrix protein, and nucleocapsid protein, along with various accessory proteins, which are responsible for the initiation of host innate immune response (Cui et al., 2019; Sainz et al., 2005). The spikes of SARS-CoV-2 contain S protein that has two functional units named the S1 and S2 subunits. On the N terminus of the S protein, there is a signal peptide that exists composed of 1–12 amino acids. The S protein contains an extracellular domain (amino acid residues 13–1195), a transmembrane domain (amino acid residues 1196–1215), and an intracellular domain (amino acid residues 1216–1255). A fragment at the S1 subunit (318–510 amino acids) is termed as the minimal receptor-binding domain (RBD) involved in the interaction with the angiotensin-converting enzyme 2 (ACE2) receptor during infection. Open reading frames (ORFs) proteins are the segments that play a vital role in initiating an immune response (Sui et al., 2005). Nucleocapsid proteins mediate virus replication, transcription, and assembly. The oligomeric transmembrane spike protein (S1 and S2 subunits) mediates the attachment of the virus into host cells. The SARS-CoV-2 primarily attaches to the ACE2 present on the lung epithelium cells. The alteration of thermoregulation, reactive oxygen species (ROS) production, and associated phenomena result in
enhancement of cytokine storm, which ultimately leads to the virion host response and results in a runny nose, fever, sore throat, fever, chest congestion, and difficulty in breathing like symptoms (Ashour et al., 2020; Tian, Xiong, et al., 2020).

1.4 Pathophysiology of severe acute respiratory syndrome-coronavirus 2 infection

The most likely way of transmission of the SARS-CoV-2 viral infection is person-to-person transmission. Once any person gets exposed to the SARS-CoV-2 virus, it enters within the human body and continues to secrete in various secretions including saliva, nasal droplets, mucus, sweat, feces, etc. The primary pathophysiology involved in the development of a disease is the binding of the RBD of viral spike protein with the host ACE2 receptor of lung epithelial cells followed by the membrane fusion similar to SARS (Hui & Zumla 2019; Lai et al., 2003; Polak et al., 2020). The respiratory distress syndrome that is the marked symptom of the SARS-CoV-2 infection slowly comes into the light, once the host’s innate and adaptive immune system starts the response against the infection (Long et al., 2020). With the binding and insertion of the virus genome into the host, the virus further replicates to form new virus copies. The matured virions that formed within the host then extend the infection to another level and bind to many new target cells Fig. 1.2. After the damage to lung tissue, SARS-CoV-2 continues to infect several other tissues, including intestinal mucosal cell lines, renal tubular epithelial cells, immune cells, and the central nervous system (Kato et al., 2020). The associated symptoms can be classified as immune responses, upper respiratory tract symptoms, lower
airways congestion, gastrointestinal symptoms. The clinical spectrum is diverse and multidimensional that resulting in moderate to severe health implications. Histopathological data from the lungs of COVID-19 patients revealed hyperplasia, edema, proteinaceous exudates along the protein globule congestion combined with inflammatory clusters and fibrinoid necrosis. The proinflammatory chemokines, cytokines, and interleukin rush become noticeable in the infected body, which indicates the deterioration of lung function due to the progression of atypical pneumonia and rapid respiratory distress. Interleukin 1 beta (IL1-β), interleukin-1 receptor antagonist (IL1RA), interleukin-7 (IL7),
interleukin-8 (IL8), interleukin-9 (IL9), interleukin-10 (IL10), basic fibroblast growth factor (basic FGF2), granulocyte-colony stimulating factor (GCSF), granulocyte-macrophage colony-stimulating factor (GMCSF), interferon γ (IFNγ), interferon gamma-induced protein 10 (IP10), monocyte chemotactic protein-1 (MCP1), macrophage inflammatory proteins α (MIP1α), macrophage Inflammatory Proteins β (MIP1β), platelet-derived growth factor-B (PDGFB), tumor necrosis factor α (TNFα), and vascular endothelial growth factor A (VEGFA) are some of the important factors that alter the disease progression in the existing patients. In severe cases of COVID-19, an increment in blood C-reactive protein and erythrocyte sedimentation rate and D-dimer values were also reported (Lei et al., 2020). As a severity indicator after the incubation period (approximately 5.2 days) the symptoms of the viral infection start to appear (Rothan & Byrareddy 2020).

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### 1.5 Transmissibility of severe acute respiratory syndrome-coronavirus 2

SARS-CoV-2 has the highest genetic similarity with bat coronavirus that suggests the possibility of interspecies virus transmission, but the exact cause and pathway of the virus origin are still unidentified. The possible introduction of SARS-CoV-2 in a human chain from bats is suggested to have pangolins as a mediator animal source (Lam et al., 2020). The primary transmission occurs primarily due to person-to-person contact and salivary droplets within a narrow range of distance (1 m). The exchange of salivary droplets is considered the primary mode of transmission around the globe.
United States of America, Brazil, India, France, Russia, United Kingdom and are some of the countries that have been suffered mainly in comparison to other countries (Lavezzo et al., 2020). The transmission of infection is divided into different phases for better understanding. When a direct visitor got infected after visiting Wuhan city directly, it was considered stage I transmission. In stage II local transmission, these infected visitors transmitted the infection to the local civilians. In stage III of transmission, which is also termed as community transmission, the indirect transmission got started without any direct contact with primary infected patients. In the last stages, named stage IV transmission, the uncontrolled epidemic spread in an uncontrolled fashion. In India, the local transmission spread once the imported cases slowly came in contact with the local citizens (Zhao et al., 2020).

The measure of transmissibility index for any infectious disease is expressed using the term “R naught” which specifically indicates the average number of persons that could possibly get the infection as a fresh case from one infected individual. The transmission potential of SARS-CoV-2 in early outbreak during January was estimated to be around 2.24 (eighthfold) to 3.58 (twofold), which is in connection with the R naught value of SARS (2–5) (Bauch et al., 2005; Wallinga & Teunis 2004; Zhou et al., 2020) and MERS (2.7–3.9) (Lin et al., 2018; Zhao et al., 2020). According to WHO, the basic reproduction number (for the human-to-human direct transmission) is from 1.4 to 2.5 and other available studies reported the mean R naught ranging from 2 to 5 (Read et al., 2001). The change in initial “R naught” (1.4–2.5) increased further by about 3.3–5.5 in late January 2020. This value indicates the severity of the disease that is even higher than the SARS and the MERS virus which have a low “R naught” value than coronavirus. On 30th January 2020, the WHO declared the COVID-19 to be a Public Health Emergency of International Concern posing a high risk to countries with vulnerable health systems (Zumla et al., 2020).

1.6 Origin and etiology of severe acute respiratory syndrome-coronavirus 2

The list of zoonotic events resulting in an infection includes SARS and MERS (Table 1.1). Earlier, the SARS infection was initiated from a bat, transmitted via a palm civet; similarly, MERS originated from a bat transmitted via a camel to a human (Alsaad et al., 2018; Bradley & Bryan 2019) (Fig. 1.4). The origin of SARS-CoV-2 was itself a matter of controversy among the researchers and nation heads. This virus not only put billions of lives at threat but it turned the flow of power and economy in a devastating manner (Chevance et al., 2020). The possible influence and loss caused due to SARS-CoV-2 would be difficult to be calculated exactly, however, implementation of complete lockdown in several countries brought economic activity to a near-standstill. The SARS-CoV-2 forced the countries to reassess the existing clinical facility, medical facility, and research potential. China was the country, where the virus starts to spread but on the benefit meter, many superpowers bore much high losses than China at the economic and political front (Ali et al., 2020; Li et al., 2005). These issues give an idea of genetically engineered and intentionally transmitted the virus to the world. The possibility of an inadvertent laboratory release of SARS-CoV-2 was a strong point initially which further can not rest the scientific arguments. The overall controversy that exists on the origin of SARS-CoV-2 can be summarized under three possible categories. The first theory suggests that the virus was artificially synthesized or modified through laboratory manipulation. Before that
This theory goes for and be the cause of another war, sufficient scientific investigation refused the theory and declared the possibility of natural genetic selection. Now only two possibilities exist to justify the pathogenic evolution of SARS-CoV-2 either the virus has transferred from animals to humans through a mediator via natural selection, prior to zoonotic transfer, or the virus has encountered the humans and acquired the natural selection to create its pathogenicity in humans through natural selection in human followed by the zoonotic transfer. The first theory suggests that the higher similarity of SARS-CoV-2 with bat coronavirus gives the clue that bats are the possible host reservoirs that work as a progenitor. RaTG13 bat virus is the closest genome that matches SARS-CoV-2 (Zhou et al., 2020). In addition, the pangolin coronavirus also exhibits a higher genetic similarity with human coronaviruses (Lam et al., 2020). Pangolin coronaviruses show 85.5 to 92.5 sequence similarity with SARS-CoV-2. Pangolins are ant-eating animals that are illegally smuggled into China for meat and scales. The present theory suggests that this intermediate host facilitated the zoonotic transfer of SARS-CoV-2 from bats to humans by providing a possibility of natural selection before the zoonotic transfer of SARS-CoV-2 in humans. A study suggests that the SARS-CoV-2 interaction with human ACE2 is quite consistent between Pangolin-CoV with an exceptional mutation of four amino acids. The binding capacity of SARS-CoV-2 with the human ACE receptor is quite more efficient than any

**FIGURE 1.4**

Possible transmission pathway of severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2). The key reservoirs and mode of transmission of coronaviruses); only a and b coronaviruses can infect humans, the consumption of infected animals as a source of food is the major cause of animal to human transmission of the virus and due to close contact with an infected person, the virus is further transmitted to healthy persons. The dotted black arrow shows the possibility of viral transfer from bat whereas the solid black arrow represents the confirmed transfer.

*Reproduced with permission from Shereen, M. A., Khan, S., Kazmi, A., Bashir, N., & Siddique, R. (2020). COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses. Journal of Advanced Research, 24, 91–98. https://doi.org/10.1016/j.jare.2020.03.005.*
predicted virus. Apart from that, the virus backbone of SARS-CoV-2 makes it unique with years of natural selection to be a human pathogen (Zhang et al., 2020; Zhao et al., 2020). Investigations revealed that SARS-CoV-2 shares sequence similarity with coronaviruses derived from five wild animals, including Paradoxurus hermaphroditus, Civet, Paguma larvata, Aselliscus stoliczkanus and Rhinolophus sinicus with similar branch sharing on the phylogenetic tree. However, the exact genome homology and ORF1a homology further revealed that none of the animals is the originator of SARS-CoV-2 as it has the highest genome similarity with a bat coronavirus isolate RaTG13 (Li et al., 2020). The possible mutations, especially insertions and deletions play a vital role in the rise of polybasic binding sites in a natural evolutionary process. In contrast, the theory that suggests the natural selection in humans followed by the zoonotic transfer indicates the possibility of adaptation of the virus within the humans after the progenitor jump. It states that the expression of acquired human pathogenicity gives rise to the clinical symptoms followed by a further human-to-human transmission which results in the progression of the pandemic. Among all the possibilities, no direct progenitor of SARS-CoV-2 is confirmed yet.

1.7 From epidemic to pandemic

Emerging infectious diseases are a major public health issue with considerable uncertainty and threat potential. Within 10 months time frame, the virus has infected several people with a huge death toll (Figs. 1.5–1.7). The first case of SARS-CoV-2 induced severe respiratory distress was reported in December 2019 in Wuhan city of Hubei province, China (Simone et al., 2020). After the first report of the SARS-CoV-2 infection that originated from the seafood market of Wuhan, the case of severe pneumonia of unknown etiology started spreading fast (Zafar, 2020). After Wuhan, Thailand, Japan, and Korea were the countries that found the suspected cases of infection. On January 12, 2020, China shared the genetic sequence of the novel coronavirus available for other countries, and on the very next day, the first case of novel coronavirus was confirmed by the Ministry of Public Health, Thailand. Two days later on January 15, 2020, the Ministry of Health, Labour and Welfare, Japan (MHLW) reported the first case of SARS-CoV-2 infection with laboratory confirmation. With an exponential increment, on January 26, 2020, 2033 cases were identified with a similar infection and symptoms (National Health Commission of the People’s Republic of China. 2020. “Definition of Suspected Cases of Unexplained Pneumonia,” the National Health Commission of the People’s Republic of China, n.d.). In the investigation of the outbreak, it was reported that the patient zero of the infection belonged to the seafood market in Wuhan. This outbreak brought light to the potential of a viral spill-over with an international concern. The potential of the virus spread and transmissibility was primarily underestimated and so, the millions of lives paid off the price by losing their lives (Yang et al., 2020). Very soon, on January 20, 2020, the National IHR Focal Point (NFP) for the Republic of Korea also confirmed the presence of infection in their country as an imported case. On the same day, the number of cases was already reached two hundred eighty-two confirmed cases globally. In China, there were 278 confirmed cases along with a few critically ill patients and a few deaths. Although the maximum number of patients belongs to Hubei Province, Guangdong Province, Beijing Municipality, and Shanghai. After the establishment of the Center for Disease Control and Prevention (CDC) management
1.7 From epidemic to pandemic

system, the United States of America has also found the patient one of SARS-CoV-2 infection (Suthar et al., 2021). In January, the confirmed cases raised up to 10,000 cases worldwide with a maximum number of confirmed cases in China alone. The highest number of suspected cases of death in China indicated the alarming condition that brought attention to the emergence of the epidemic with a probable potential of the pandemic. By the end of January, the imported cases were already reached Japan, the Republic of Korea, Viet Nam, Singapore, Australia, Malaysia, Cambodia, Philippines, Thailand, Nepal, Sri Lanka, India, United States of America, Canada, France, Finland, Germany, Italy, and the United Arab Emirates. The consistently increasing number of patients forced the WHO to declare COVID-19 as a Public Health Emergency of International Concern. In February 2020, the imported cases were continuing to report in many new countries with a high occurrence of the new report of cases in each of the countries with existing infections. By the end of February, the total number of confirmed cases globally raised close to one hundred thousand with maximum cases in China alone. The high transmission and the presence of local transmission in many places clearly stated the emergence of the epidemic, which was confirmed by the WHO officially. Although, initially the WHO started to design the wonderful strategy, precautionary measures, knowledge tools, awareness material, and management capacities but still the infection continues to grow due to the unresponsiveness of many countries towards that alarming issue. On March 11, 2020, WHO Director-General, Dr. Tedros Adhanom Ghebreyesus briefed in a press conference that the novel coronavirus, COVID-19 (SARS-CoV-2) outbreak is a health threat

FIGURE 1.5
Comparison of the number of severe acute respiratory syndrome-coronavirus 2 death reports from December 2019 to September 2020. Monthly Statistics of death of coronavirus disease 2019 patients (December 2019 to September 2020).
for the globe with expected potential to further spread as a global pandemic (Naik et al., 2021). At the end of April 2020, within the globe, there were more than 3 million confirmed cases of SARS-CoV-2 infection with a high death toll of more than 200,000 deaths. With a very high global risk, SARS-CoV-2 infection continued to grow and remains a matter of worry and threat for the entire globe. In countries like Italy and France the infection turned out as a curse that not only spread death but an enormous amount of fear and emotional trauma were also spread (Wu et al., 2020). Including all the clusters of cases, community transmissions, and reported sporadic cases the number of infected cases jumped high at the end of May 2020. According to the WHO situation report 132 released on May 31, 2020, nearly 6 million cases have existed globally with more than 300,000 deaths. In June 2020, the alarms raised the bar with more than 10 million positive cases were confirmed worldwide. The number of patient’s death by the respective infection broke all the existing records with a high number of deaths (Seitz et al., 2020; Wang, Tang, et al., 2020). The pandemic data suggest the ongoing disastrous phase of SARS-CoV-2 infection overall the world. However, many countries have been saved their population by the virulence on time, very wisely with strategic organization and determination. As per the WHO COVID-19 dashboard, on March 31, 2021, there have been 130 million confirmed cases of COVID-19, including 2.5 million deaths globally (WHO COVID-19 dashboard, n.d.).
1.8 Perspective

The coronavirus epidemic is not something new to the world. Earlier, few coronavirus members, namely SARS and MERS have shown the world their life-threatening potential. The loss of lives and peace through a pandemic is not new to the human world. The world has already overcome various previously emerged epidemics and pandemics, but the unidentified potential within the coronavirus allows this virus family to undergo various mutations and self-resisting mutations with the capability to the interspecies exchange of infection. In the current status where, unlike the war, the risk is quite higher for the health security of children, older people, pregnant and newborns, and people with comorbidities. This status puts many debatable questions in front of the world. This is the time to rethink whether we have intercalated the space required for the forests, animals, and natural resources (Seitz et al., 2020; Suthar et al., 2021). On the one side, we urbanized everything but is there anything wrong that contributes to unnecessary exposures to animals and their parasites to let them jump over species. Backyard farming of wild animals, unhygienic slaughtering of any animals, unprotected and unorganized flesh market, unbothered exposures are some of the prime causes that play a vital role in the early hour silent spread of the infection. The improvement of basic management and travel monitoring are important precautions that are the need of the hour.

**FIGURE 1.7**

Distribution of severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) confirmed cases as of October 11, 2020. Distribution of SARS-CoV-2 confirmed cases as of October 2020.
In the past, a few countries were fighting against the epidemics; the rest of the nations did not pay heed to those alarming signals and did not prepare themselves for the tough times. The lack of global unity in health services made the entire world suffer from the worst pandemic of recent times. Few countries could overcome the pandemic smoothly with their excellent management action plan and timely efforts. The good thing about coronaviruses is that they are not usually fatal to humans until they undergo mutations, and the bad thing is that they have a high potential to undergo mutations due to species shift. Not only the coronaviruses but there are many more existing and potentially upcoming forms of viruses on this planet named “disease X.” The repetitive mutation potential states that even though the globe won the fight against SARS-CoV-2, there are still many chances left for modulation and reoccurrence of existing, upcoming, or mutated viruses. The end of the ongoing confinement and the possibility of the reemergence of any new or modified threat is an avoidable question among us (Lopez & Rodo 2020). The safety of travelers would be another agenda of perfect management of epidemic for the next decades. The assurance of advancement, monetization, modernization, and power in which the powerful countries of the world were busy enough to enjoy was demolished like anything, and that is one of the biggest learning that we all have learned. The biggest investment is to make the health care sector strong with enormous possibilities of fast pace accurate research advancements. The world has to rethink, redesign, and justify the role of anthropogenic activities in the progression of such epidemics that are still unmanageable despite all the advancements. The alarming rate of transmission of SARS-CoV-2 infection also raised various questions on the fast pace of globalization and travel medicine. The biggest question mark is asking mankind, “is this the last virus of the decade, or are there more possibilities of interspecies jump or virus modifications that could result in another epidemic and pandemic”? The unpredicted unknown answer is something that will have the fate of the urbanized globe in its hands. An intelligent survival is the only power of mankind over any other organism of nature and the SARS-CoV-2 infection again proves that the survival of the fittest is what that nature is likely to support.

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