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Basic neurological highlights of COVID-19: Role of imaging strategies and biosensors for powerful finding

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Abstract
COVID-19 is a respiratory infection that has been declared as a global health crisis by the WHO. It mainly affects the respiratory system. Apart from respiratory system, it also affects other organs as well including the brain. Numerous emerging reports have demonstrated that the COVID-19 has detrimental effects on neurological functions, and can lead to severe impairment of the central nervous system (CNS). The neurological manifestations linked with COVID-19 include headache, anosmia, encephalitis, epileptic seizures, Guillain-Barre syndrome, stroke and intracerebral hemorrhage alongwith multiple others complications. The CNS related complications may be severe and are linked with poor diagnosis which may worsen the condition. Therefore, there is a need to precisely understand the neurological sequelae along with upcoming clinical outcomes. Here, we present a brief review of the neurological complications and symptoms associated with COVID-19 along with brain imaging findings. Further, we have discussed about the emerging biosensing approaches which may aid in rapid, precise and mass diagnosis of COVID-19.

By the end of year 2019, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged as a novel pathogenic virus causing severe pulmonary infection affecting millions of people. It has killed more than three million people worldwide till April 28, 2021. In a short duration, it spread globally, evolved as a pandemic and was declared as a communal health emergency by the World Health Organization (WHO). In view of this pandemic, the infection caused by the SARS-CoV-2, the WHO termed it as Corona Virus Disease 2019 (COVID-19). COVID-19 has created global angst because of its novelty, communicability, and rapid mutation rate. Coronaviruses belong to the Torovirinae subfamily that combined with Coronavirinae falls under the Coronaviridae family of order Nidovirales. At present, a total of seven different human coronaviruses have been reported namely, 229E, HKU1, NL63, OC43, middle east respiratory syndrome (MERS)-CoV, SARS-CoV and SARS-CoV-2 (COVID-19). Among these seven different strains, 2019-nCoV, SARS-CoV and MERS-CoV evinced to be extremely pathogenic. Before SARS-CoV and MERS-CoV outburst, CoV was considered to seed milder disease. However, these two outbursts spotlighted their potential to cause serious infections and thus, they were distinguished under emerging viruses. The COVID-19 is considered as the most fatal one among all the coronaviruses.

Coronaviruses are spherical, pleiomorphic or enveloped viruses which have a single-stranded, positive sense RNA genome size ranging from 26.2 to 31.7 kb. The RNA genome of SARS-CoV-2 is one of the biggest among all the RNA viruses. They contain six to ten open reading frames (ORFs) in their genome. The viral genome contains four different proteins encoding Viz. spike (S), nucleocapsid (N), membrane (M), and envelope (E) proteins and several non-structural proteins as well [8]. The genome of CoV is receptive for recurrent recombination evolving into new strains with revision in virulence [9]. COVID-19 is distinguished by severe clinical exhibition of the lower respiratory tract infection that includes common cold, pneumonia, rhinitis, bronchiolitis, pharyngitis, and sinusitis along with other indications such as vomiting, infrequent watery diarrhea etc.. The epithelial cells of the respiratory tract are preyed by the coronavirus, evolving into diffused alveolar damage. It is mainly transmitted via droplets produced while sneezing, coughing and close individual-to-individual contact Upon entering into the host, the spike protein S1 of SARS-CoV-2 attaches to the cellular receptor angiotensin-converting enzyme 2 (ACE2). The attachment is favored by the spike receptor-binding domain (RBD) which allows direct connection with ACE2, and a S1/S2 cleavage site that is cleaved by the transmembrane protease serine 2 (TMPRSS2) as shown in Fig. 1. This mediates the entry of the virus through surface of the plasma membrane which leads to arrival of the RNA genome of the virus inside the host cell followed by the translation of structural and non-structural proteins. The polyproteins pp1a and pp1ab are produced from the translation of ORF1a and ORF1ab, which are then cleaved to form 16 non-structural proteins. It is accompanied by grouping and enters into the lumen of the ERGIC (Endoplasmic Reticulum Golgi Intermediate Compartment) and finally via exocytosis the virions are released from the infected cell