The SARS-CoV-2 was first isolated from cases of severe pneumonia in Wuhan city, Hubei province, China in December 2019 (Zhou et al., 2020). On 11 March, SARS-CoV-2 was declared as a pandemic with millions of laboratory-confirmed cases and resulted in losing of life of about one million victims worldwide. However, the only the visible tip of the iceberg represents the laboratory confirmed cases, a huge number of infected people passed without laboratory confirmation is assumed (Hosein et al., 2020). A novel coronavirus 2019 (nCoV-2019) was the initial name of the virus while SARS-CoV-2 is the current official name as described by the ICTV and currently used in NCBI taxonomy database. The Chinese virologist suggested HCoV-19 as an alternate name which is currently used in GISAID EpiCoV database. The WHO named the disease caused by the virus to be coronavirus disease 2019 (COVID-19) (Gorbalenya et al., 2020). SARS-CoV-2 belongs to family Coronaviridae, subfamily Orthocoronavirinae, genus Betacoronavirus, subgenus Sarbecovirus. The virus possesses a single stranded RNA positive polarity genome surrounded by a helical symmetry and envelope obtained from the host cell Golgi and endoplasmic reticulum. The viral genome encodes structural proteins including: S, E, M, and N proteins as well as non-structural proteins (NSPs 1-16). The latter play an important role in virus replication (Fehr and Perlman, 2015). The S protein binds to ACE-2 receptor of the target cell. It is cleaved by TMPRSS2 into S1 and S2 subunits. The S1 of the SARS-CoV-2 binds to the ACE2 receptor for virus entry while S2 induces the fusion of viral envelope with cell membrane (Hoffmann et al., 2020). The M protein is important for virus morphology, E protein helps in virus assembly and release while N protein encapsidates the viral RNA genome. Based on the full-length genome, the SARS-CoV-2 is classified into G, GH, GR, L, O, S and V clades with many lineages. Nextstrain database introduced a nomenclature based on the timely emerged strains with about 20% genome variations[https://nextstrain.org/sars-cov-2/]. Currently, five clades do exist: 19A (the root clade in China and of Asia), 19B (Wuhan original strain), 20A, 20B, and 20C. SARS-CoV-2 is closely related to a bat coronavirus called RaTG13 (Zhou et al., 2020) and recently, the receptor binding domain of Malayan pangolins coronaviruses were found to share 97% amino acid identity to SARS-CoV-2 (Wong et al., 2020, Xiao et al., 2020). This finding together with the detection of multiple coronavirus lineages in pangolin delineates that pangolin could be a potential intermediate host of SARS-CoV-2 (Lam et al., 2020).
A furin cleavage was found in the SARS-CoV-2 spike, that was assumed to increase its transmissibility and virulence probably by increasing the affinity of virus to infect cells with reduced ACE2 expression (Belouzard et al., 2009). Although, RaTG13 bat coronavirus and pangolin coronaviruses showed high genome similarity to SARS-CoV-2 (Zhou et al., 2020) (Wong et al., 2020), none of these viruses, so far possess polybasic cleavage sites. However, this fact cannot abrogate the presence of polybasic cleavage sites in not yet identified viruses from these species. Polybasic cleave sites may probably be acquired through adaptation in humans, however, this scenario assumes a sufficient extended period of time between the first spillover of the virus from the animal host and the adaptation among humans that probably lead to the acquisition of the polybasic cleavage site. SARS-CoV-2 strains from Singapore showed a 382 nucleotide removal of the transcription regulatory sequence (TRS) of the ORF8 (Su et al., 2020). Intriguingly, analogous deletion in SARS-CoV was discovered before its fading.

The virus is transmitted via both direct and indirect contact with infected patients. It was found that SARS-CoV-2 can be aerosolized and remains infectious for 3 hours and in the environment for 3 days (van Doremalen et al., 2020). The signs of the disease includes flu-like signs that may precede dyspnoea and pneumonia (Zhu et al., 2020). Diarrhoea was rarely reported and less frequently than in SARS-CoV (Huang et al., 2020). More than 80% of the infected cases suffered from asymptomatic, mild or moderate diseased conditions, 15 % of the patients suffer from severe respiratory disease conditions while the remaining 5% suffered from critical diseased conditions with high fatal consequences (WSV, 2020). The critical form of the disease is mainly detected among elderly persons and in immunocompromised or in persons who have pre-existing conditions. Seroconversion begins in the second week of infection (Wölfel et al., 2020).

It is not accurate to estimate the case fatality of the disease since the current published case fatality rate is based only on the laboratory confirmed cases, however, the fact that there are huge number of cases that could inapparently infected, render published case fatality case is inaccurate and is expected to be decreased by at least 10 fold (Hosein et al., 2020).

The SARS-CoV-2 was found to infect dogs, cats, large cats (tigers and lions). The infected dogs were asymptomatic however, the virus was detected in the nasal sections of infected dogs. In contrast, the domestic and wild cats showed clinical disease manifestations. Both ferrets and cats were found to be highly susceptible to experimental infection in comparison to dogs. The cats were found able to transmit infection to contact animals. Meanwhile, SARS-CoV-2 was not able to replicate in pigs, chickens, or ducks. Interestingly, Egyptian fruit bats was found to experimentally susceptible to SARS-CoV-2, however, the virus did not be transmitted to contact bats as reviewed in (Abdel-Moneim and Abdelwhab, 2020).

Standard hygienic measures include washing of hands, covering mouth and nose when sneezing or coughing and avoid close contact with individuals showing symptoms of respiratory illness. There are no available vaccines, however there are currently dozens of candidate vaccines in different clinical trials phases. Three types of vaccines including RNA vaccine (RNA-1273), adenovirus-based vaccine (non-replicating Ad5), and inactivated vaccine are in clinical phase III (WSV, 2020). These vaccines are expected to be commercially available within few months. Meanwhile, convalescent plasma from COVID-19 recovered patients were used successfully in the treatment of severe cases of COVID-19 in differed countries as recently.
reviewed (Alghamdi and Abdel-Moneim, 2020).

Although no current drugs recommended by the FDA against SARS-CoV-2, many drugs showing promising antiviral activities. Both chloroquine phosphate/hydroxychloroquine (an old antimalarial drug) and remdesivir were found to possess the highest in vitro antiviral activities in comparison to ribavirin, penciclovir, nitazoxanide, nafamostat and favipiravir (Wang et al., 2020). Interestingly, remdesivir and chloroquine phosphate/hydroxychloroquine were found effective with acceptable safety against SARS-CoV-2 patients in multicentre clinical trials (Gao et al., 2020, Chiotos et al., 2020). Ivermectin, an antiparasitic drug, was recently found to possess potent in-vitro anti-viral activity against SARS-CoV-2 (Caly et al., 2020). Camostat mesylate, a serine protease inhibitor, inhibits TMPRSS2 might be a possible drug for treatment of SARS-CoV-2 since it inhibited SARS-CoV replication in mice (Zhou et al., 2015). Additionally, bromhexine hydrochloride, a mucolytic drug, also inhibits TMPRSS2 and found to be effective for both influenzaviruses and coronaviruses (Shen et al., 2017).

It is important to adopt all possible efforts to mitigate the spread of infection without transferring panic among community. Early detection with subsequent quarantine measures of infected and contact persons can limit further propagation of the pandemic are highly recommended.

Conflict of Interest

No conflict of interest.

References