

Isiaka safinat yunusa (028)

Corona virus was discovered in 2019. It is similar to the SARS virus. Bats are the reservoir for the SARS virus and in 2002, it was believed that the virus mutated and infected an animal host (civet) and then mutated again and infected humans. In 2012, it was believed that the mutated SARS virus became MERS which also was transmitted from the bats (reservoirs) to camels and then also mutated and infected humans. In 2019, it was believed that the mutated MERS virus became COVID-19 which also was transmitted from bats (reservoirs) to pangolins and then mutated and infected humans.

The symptoms of COVID-19 infection appear after an incubation period of approximately 5 days. The period from the onset of COVID-19 symptoms to death ranges from 6 to 41 days with an average of 14 days. This period is dependent on the age of the patient and status of the

patient's immune system. It was shorter among patients above 70-years old compared with those under the age of 70. The most common symptoms at onset of COVID-19 illness are fever, cough, and fatigue, while other symptoms include sputum production, headache, haemoptysis, diarrhoea, dyspnoea, and lymphopenia. Clinical features revealed by a chest CT scan presented as pneumonia, however, there were abnormal features such as RNAemia, acute respiratory distress syndrome, acute cardiac injury, and incidence of ground-glass opacities that led to death. In some cases, the multiple peripheral ground-glass opacities were observed in subpleural regions of both lungs that likely induced both systemic and localized immune response that led to increased inflammation. Regrettably, treatment of some cases with interferon inhalation showed no clinical effect and instead appeared to worsen the condition by progressing

pulmonary opacities.

Genomic sequence analysis of COVID-19 showed 88% identity with two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses indicating that mammals are the most likely link between COVID-19 and humans. Several reports have suggested that person-to-person transmission is a likely route for spreading COVID-19 infection. Person-to-person transmission occurs primarily via direct contact or through droplets spread by coughing or sneezing from an infected individual. In a small study conducted on women in their third trimester who were confirmed to be infected with the coronavirus, there was no evidence that there is transmission from mother to child. However, all pregnant mothers underwent cesarean sections, so it remains unclear whether transmission can occur during vaginal birth. This is important because pregnant mothers are relatively more susceptible to infection by respiratory pathogens and

severe pneumonia.

The binding of a receptor expressed by host cells is the first step of viral infection followed by fusion with the cell membrane. It is reasoned that the lung epithelial cells are the primary target of the virus.

Thus, it has been reported that human-to-human

transmissions of SARS-CoV occurs by the binding between the receptor-binding domain of virus spikes and the cellular receptor which has been identified as angiotensin-converting enzyme 2 (ACE2) receptor. Importantly, the sequence of the receptor-binding domain of COVID-19 spikes is similar to that of SARS-CoV. This data strongly suggests that entry into the host cells is most likely via the ACE2 receptor.

World Health Organisation (WHO) has classified COVID-19 as a β CoV of group 2B. Ten genome sequences of COVID-19 obtained from a total of nine patients exhibited 99.98% sequence identity. Another study showed

there was 99.8–99.9% nucleotide identity in isolates from five patients and the sequence results revealed the presence of a new beta-CoV strain .The genetic sequence of the COVID-19 showed more than 80% identity to SARS-CoV and 50% to the MERS-CoV and both SARS-CoV and MERS-CoV originate in bats.Thus, the evidence from the phylogenetic analysis indicates that the COVID-19 belongs to the genus betacoronavirus, which includes SARS-CoV, that infects humans, bats, and wild animals. COVID-19 represents the seventh member of the coronavirus family that infects humans and has been classified under the orthocoronavirinae subfamily. The COVID-19 forms a clade within the subgenus sarbecovirus .Based on the genetic sequence identity and the phylogenetic reports, COVID-19 is sufficiently different from SARS-CoV and it can thus be considered as a new betacoronavirus that infects humans. The COVID-19 most likely developed from bat

origin coronaviruses. Another piece of evidence that supports the COVID-19 is of bat origin is the existence of a high degree of homology of the ACE2 receptor from a diversity of animal species, thus implicating these animal species as possible intermediate hosts or animal models for COVID-19 infections. Moreover, these viruses have a single intact open reading frame on gene 8, which is a further indicator of bat-origin CoVs. However, the amino acid sequence of the tentative receptor-binding domain resembles that of SARS-CoV, indicating that these viruses might use the same receptor