Human Coronaviruses: Overview and Comparison of Biological and Clinical Characteristics

Tasiu Mahmud1, Ibrahim Alhaji Sabo2, Dauda Danlami Tsakuwa3, Shuaibu Isah4, Zakari Nuhu Lambu5, Adamu Abdullahi Shehu6, Rabiu Adamu Tsakuwa7, Ibrahim Adamu Karfi8, Abdulwahid Isah Adamu9, Isma’ila Ahmed10, Naziru Dahiru11, Jamilu Isyaku12 and Sadisu Umar Farouk13

1,5,6,7,8,9,10,12& 13 Department of Microbiology, Kano University of Science and Technology, Wudil. Nigeria.

4Department of Microbiology, Gombe State University, Nigeria.

2Department of Microbiology, Federal University Wukari, Nigeria.

3&11 National Biotechnology Development Agency Abuja, Nigeria.

Email: tasiu.microlabs@gmail.com

Abstract
An overview of biological and clinical characteristics of the seven human coronaviruses (HCoVs) including the novel coronavirus SARS-CoV-2, was carried out in response to the on-going pandemic which raised public health concerns and necessitated the imposition of stays at home order by national authorities at different levels and close down of all socio-economic activities, including religious gathering worldwide. The coronavirus disease 2019 (Covid-19) originated from bats and was transmitted to humans through an unknown intermediate host in the Wuhan seafood market, China in December 2019. Due to high sequencing similarity with SARS-CoV, this virus was named SARS-CoV-2 and was classified under beta coronavirus. There are 115,653,459 numbers of laboratory-confirmed cases of Covid-19 globally, including 2,571,823 death reported to WHO as at 6th March 2021 and a total of 249,160,837 vaccine doses was administered. The SARS-CoV-2 causes severe respiratory infection as SARS-CoV and MERS-CoV, presented as fever, cough, and dyspnea. In this review, we provided an overview and updates on human coronavirus (HCoVs) under the headings of history, origin, classification, structure, genomic organization, clinical symptoms, and epidemiology with a strong focus on SARS-CoV-2, the causative agent of Covid-19. We also summarized the comparison of characteristics among the seven human coronaviruses (HCoVs).

Keywords: Animal, Bat, Coronavirus, Genome, Origin.
INTRODUCTION
The ability of human coronaviruses to cross-species barriers and cause serious infections of the lower and upper respiratory tract in humans and animals has become the world's biggest challenge resulting in an increasing number of pathogenic human coronaviruses (Lau & Chan, 2015). Among the coronaviruses identified so far, seven have shown their ability to infect humans and cause serious infections including the newly emerged coronavirus disease 2019 (Tomasi, 2020). Before December 2019, only 6 strains of coronaviruses (CoVs) were known to infect humans and cause respiratory disease (Hamre & Procknow, 1966). Several researchers have extensively reviewed the six strains of human coronaviruses (HCoVs) discovered in a human before the emergence of 2019-nCoV, these include Human coronavirus -229E, Human coronavirus-OC43, Human coronavirus-NL63, Human coronavirus-HKU1, Severe acute respiratory syndrome coronavirus, and Middle east respiratory syndrome coronavirus (Hamre & Procknow, 1966; Hendley, 1972; Gerna et al., 2007; McIntosh & Periris, 2009; Abdul-Rasool & Fielding, 2010; King et al., 2011; Lau & Chan, 2015; Fehr & Perlman, 2015; Chan et al., 2015; Gao et al., 2016 and Aly et al., 2017). HCoV-229E, HCoV-OC43, HKU1, and HCoV-NL63 are coronaviruses that infect infants and elderly people and cause mild upper respiratory disease (McIntosh & Periris, 2009). However, SARS-CoV, and MERS-CoV are the most dangerous human coronaviruses which infect the lower respiratory tract and causes a severe respiratory condition that can result in death of human (Fehr & Perlman, 2015). On December 31, 2019, the world health organization (WHO) reported another infection of the lower respiratory tract that resulted in pneumonia from Wuhan, China, which is different from that of SARS-CoV and MERS-CoV infections (WHO, 2020b). After laboratory investigations, a novel coronavirus was identified as the causative agent, on 7 January 2020. The international committee on taxonomy of virus named the novel coronavirus SARS-CoV-2 and the disease was also named covid-19 (Zhang et al., 2020; Wu et al., 2020). By March 2020 around 20 nations were battling with the covid-19 outbreak (Tomasi, 2020). Covid-19 cases were detected in every country of the globe with an unprecedented record of transmission, number of cases, and death (WHO, 2020a). To date, there are seven human coronaviruses of public health concern following the recent emergence of SARS-CoV-2 (Tomasi, 2020; Zu et al., 2020). In December 2020, the United Kingdom detected a new variant of SARS-CoV-2, which was named as variant of concern 01 (SARS-CoV-2 VOC 202012/01). This UK variant is more transmissible than the wild type of SARS-CoV-2, however, there is no change in disease severity and it spread quickly in December 2020 and cause a significant increase in the number of confirmed cases of covid-19 worldwide (Public health England, 2020). Meanwhile, on 18 December 2020, the government of South Africa announced the detection of another new variant of SARS-CoV-2 which is different from that of the UK variant, the South African authorities have named it variant 501Y.V2. Phylogenetic analyses have shown that both the UK and South Africa's variants have the N501Y mutation and were largely in circulation worldwide (WHO, 2021). The outbreak of covid-19 is still on-going as at March 2021, despite all the responses from health workers and national authorities which resulted in the imposition of the lockdown of socioeconomic activities and precautionary measures worldwide. Covid-19 was declared pandemic with more than 115,653,459 laboratory-confirmed cases and 2,571,823 death reported to WHO globally as at 6th March, 2021 (WHO, 2021). In Tables 1 and 2 we reviewed and summarized biological and clinical characteristics of seven human coronaviruses (HCoVs) that are of public health importance with a greater focus on the similarities and differences observed among them. We also present the most recent findings related to the newly emerged human coronaviruses (SARS-CoV-2). The objective of the study is to establish more understanding of human coronaviruses (HCoVs) which could stimulate more future research and help specialists working in this field.
Taxonomy and Classification of Human Corona Viruses
Shortly after the emergence of 2019-nCoV (SARS-CoV-2), the classification of human coronaviruses was reviewed and updated (Roujian et al., 2020; Wang et al., 2020; Yasmin, 2020). Based on genetic composition, coronaviruses (CoVs) has been classified into four groups: alpha coronaviruses (α-CoV), beta coronavirus (β-CoV), gamma coronavirus (γ-CoV), and delta coronavirus (δ-CoV) (Woo et al., 2012). Before the emergence of SARS-CoV-2, in December 2019, six known strains of the human coronavirus caused infections in humans; HCoV-229E and HCoV-NL63 belong to the alphacoronaviruses, HCoV-OC43 and HKU1 belong to lineage A beta coronaviruses. MERS-CoV belongs to lineage C of beta coronaviruses and SARS-CoV belongs to lineage B of beta coronaviruses (Lu et al., 2020). However, the recent genomic analysis of 2019-nCoV, shows 79% homology to SARS-CoV and phylogenetic analysis has placed 2019-nCoV under beta coronaviruses, lineage B, and hence the name SARS-CoV-2. (Roujian et al., 2020; Guo et al., 2020). Figure 1 Shows updated classification of human coronaviruses with SARS-CoV-2 inclusive (Roujian et al., 2020).

Overview of Human Corona Virus (HCoVs) Infections
Several human coronaviruses have caused serious problems in humans and animals from 1960 to date. According to Weiss & Navas (2005) urbanization and frequent interactions between different animals and humans may have facilitated the emergence and re-emergence of some of these coronaviruses. Some studies show that the rate of mutation and recombination of coronaviruses in general is very high due to their genomic organization which can allow them to cross the species barrier and adapt to another host (Lau & Chan, 2015). The first human coronavirus to have caused infection in a human was HCoV-229E which was first isolated in 1965 by Dorothy Hamre, a researcher at the University of Chicago (Bradburne et al., 1967). The second human coronavirus is HCoV-OC43, which was first reported in 1967 from patients with upper respiratory tract infection (McIntosh, 1967a). The third human coronavirus is HCoV-NL63 which was first isolated in 2004 from clinical samples of infants suffering from pneumonia in the Netherland, HCoV-NL63 was similarly isolated from a seven-month-old baby (Van der Hoek et al., 2004). The fourth human coronavirus is HKU1, which was isolated and identified in Hong Kong in 2005 from 71 years old man with pneumonia, fever, and cough (Hamre & Procknow 1966; Woo et al., 2005; Chiu, 2005). These four human coronaviruses (HCoV-229E, HCoV-OC43, HCoV-NL63, and HKU1) are the most common pathogens which cause mild upper respiratory tract infections.
and they rarely cause lower respiratory tract infections (Myint, 1994; Woo et al., 2005; Kim et al., 2017).

Severe acute respiratory syndrome (SARS) coronavirus is the fifth human coronavirus that first emerged in 2002 from Guangdong province, China. The virus spread rapidly to Hong Kong and other provinces of China and then to 28 countries (Zhong et al., 2003). Severe acute respiratory syndrome coronavirus was documented as the first human coronavirus that caused acute lower respiratory tract infection which resulted in a 10% fatality rate. Severe acute respiratory syndrome coronavirus was characterized with onset of respiratory symptoms including dyspnea, cough, and pneumonia. It’s also highly transmissible compared to other human Coronaviruses that cause upper respiratory tract infections (Susan & Sonia 2005). SARS-CoV was detected in 29 countries with 8,098 confirmed cases and over 774 death (Du et al., 2009). However, the second outbreak of SARS-CoV occurs in 2004 with only four cases and no mortality (Song et al., 2005; Du et al., 2009). Middle east respiratory syndrome coronavirus became the sixth human coronavirus that emerged in June 2012 from Jeddah, Kingdom of Saudi Arabia (KSA). The first patient was reported to have symptoms similar to that of SARS–CoV, however, it is less transmissible compared to SARS (Zaki et al., 2012). There are 2,494 laboratory confirmed cases of MERS and 858 death from 27 countries which were reported to the world health organization as of December 2019, however, a study revealed that 80% of the cases reported were from Saudi Arabia. People infected with MERS-CoV had a history of contact with infected dromedary camels or persons and they are in the median age of 50 years (Du et al., 2009; Zaki et al., 2012; Hu et al., 2015). Comparatively, the fatality rate of MERS (34.4%) is much high than that of SARS (9.6%).

In December 2019, another new strain of human coronavirus (HCoV) has emerged, which became the seventh pathogenic human coronavirus, novel coronavirus 2019 is an unusual and unprecedented human coronavirus that does not recognize or respect any barrier such as sex, geographical, tribal, race, etc. It was first identified in Wuhan, China in December 2019 from 40 years old patient who presented symptoms of fever, chest tightness, cough, pain, weakness, and pneumonia (Zu et al., 2020; Wang et al., 2020). Phylogenetic analysis of the novel coronavirus 2019 (2019-nCoV) showed that it was closely related to two sequences of severe acute respiratory syndrome coronavirus (SARS-CoV) which were isolated from bats in 2005 (Zhang et al., 2020; Hu et al., 2015). Similarly, some studies revealed that 2019-nCoV showed 88% homology with the bat-SL-CoVZC45 and bat-SL-CoVZC21 which are all SARS-related coronavirus (Zhang et al., 2020; Lu et al., 2020). Therefore, 2019n-CoV was considered as SARS-like coronavirus and hence the name SARS-CoV-2, it’s also believed that they all shared a common ancestral origin of bat coronavirus (Zhang et al., 2020).

**Origin of Human coronavirus (HCoVs)**

The origin of the human coronavirus was previously reviewed (Woo et al., 2012; Li et al., 2020a; Wuhan municipal health commission, 2020). Similarly, several studies have shown that all the seven human coronaviruses (HCoVs) including the novel coronavirus 2019 have zoonotic origin from bats and or other animals. Several studies have supported what was already in the literature that all human coronaviruses have evolutionary origin from bats where they are well adapted and non-pathogenic (Li et al., 2020a; Wei et al., 2020). Tracing the zoonotic origin of the human coronavirus could help in preventing species jumping, emergence, and re-emergence of the human coronavirus (Lo’ai et al., 2020). It’s very important to note that the WHO has sent a team of scientists to investigate the origin of Covid-19 pandemic including how and when SARS-CoV-2 infected the first person from Wuhan city where the virus was first identified (Wei et al., 2020). Five human coronaviruses,
including; HCoV-229E, SARS-CoV,HCoV-NL63,MERS-CoV, and SARS-CoV-2 have bats as their common natural host, however, the intermediate host differs, HCoV-229E has camels as its intermediate host (Han et al., 2006), SARS-CoV has palm civets as its intermediate host (Hu et al., 2015), the intermediate host for HCoV-NL63 is unidentified, while, the intermediate host for MERS-CoV is dromedary camels (Van et al., 2012; Cotton et al., 2013), the intermediate host for SARS-CoV-2 is pangolins (Lam et al., 2020; Zhou et al., 2020). HCoV-OC43 and HCoV-HKU1 have rodents as their natural host, however, the intermediate host for HCoV-OC43 is bovines and for HCoV-HKU1 is unidentified (Bucknall et al., 1972; Donaldson et al., 2010; Huyunj et al., 2012).

Virion Structure and Genomic Organization

Generally, the virion structure of coronavirus (CoVs) consists of club-shaped protein spikes projecting from the surface, resembling a solar corona (Xin & Hayes, 2020). Human coronavirus possesses four structural proteins; Large trans-membrane spike protein, small envelop protein, integral membrane glycoprotein, and heavily phosphorylated-nucleocapsid protein (Chen et al., 2020). Similarly, some of the components of the virion structure of coronavirus were considered as a basis for their earlier classification, these component include; spike proteins (S), membrane proteins (M), and nucleocapsid proteins (N) (Roujian et al., 2020; Chen et al., 2020). According to some genomic analysis of human coronaviruses, the genome consists of a single-stranded positive RNA (+SSRNA) which is 27-32kbp in length (Cui et al., 2018; Guo et al., 2020; Xin & Hayes, 2020). Similarly, the size of the genome of seven human coronavirus ranges from 26 to 36kb. The particular genomic size of HCoV-229E, HCoV-NL63, HCoV-OC43, HKU1, SARS-CoV, and MERS are 27.3, 27.5, 30.5, 29.9, 29.7, and 30.1 kb respectively. However, recent genomic analysis revealed the genomic size of SARS-CoV-2 as 36 kb (Roujian et al., 2020; Guo et al., 2020).

Symptoms and Pathogenesis

The general symptoms of HCoV-229E include; malaise, headache, nasal discharge, sore throat, and sneezing. However, some patients experience fever and cough (McIntosh, 1967a; Tyrrell, 1993; Li, 2020b). Laboratory studies of HCoV-229E show how it has grown well in WI-38 lung fibroblast cell line. HCoV-OC43 presents clinical symptoms similar to that of HCoV-229E (Li, 2020b). The clinical symptoms of SARS-CoV include; fever, myalgia (muscular pain), headache, malaise, cough, dyspnea, respiratory distress, and infection of the internal organs, these symptoms last for 5-7 days and may result in death in some cases, similarly, infection of the lungs have also been reported (Weiss & Navas, 2005; Li, 2020b).

Human coronavirus NL63 has clinical symptoms similar to a common cold, which include; cough, rhinorrhea, laryngitis, tachypnea, fever, and hypoxia (Van der Hoek, 2006; Li, 2020b). The typical clinical symptoms of MERS-CoV infection include; fever cough, myalgia, arthralgia sore throat, and pneumonia (Arabi, 2014). Some patients present symptoms that are associated with gastrointestinal tract infections (diarrhoea and vomiting) and acute renal impairment. However, MERS-CoV infection is asymptomatic in some patients (Zumla, 2015; Drosten, 2015). The clinical symptom of SAR-CoV-2 include common colds, cough, fever, chills sore throat, pain, loss of taste or smell. However, few patients experience an asymptomatic infection. Other symptoms of Covid-19 include raise in body temperature, dry cough and pneumonia (Bendix, 2020). According to research conducted by the Chinese centre for disease control, 80% of covid-19 cases are mild while 15% are severe and 5% of patients are critically ill (Bendix, 2020). At the initial stage, the symptoms of Covid-19 are mild however, after 10 days patient may experiences the worst symptoms including; diarrhoea, difficulty in breathing, and acute respiratory Syndrome which ultimately may lead to death (Bendix 2020; Xu et al., 2020).
Epidemiology
The epidemiology of diseases caused by seven human coronaviruses including the novel coronavirus 2019-nCoV was recently reviewed (Wang et al., 2020; Lai et al., 2020; Rothe et al., 2020). HCoV-NL63, HCoV-229E, and HCoV-OC43 are all distributed globally and predominantly transmitted during the winter season (Hendley, 1972). But HCoV-NL63 infection becomes peaks from spring to summer period, this is according to a study conducted in Hong Kong (Chiu, 2005; Hofmann et al., 2005). HCoV-HKU1 and HCoV-OC43 infections were reported to be predominant from March 2012 to September 2012 (Maryam et al., 2006; Dare et al., 2007). However, other findings reported that the prevalence of HCoV-HKU1 and HCoV-OC43 infections peaks during the winter season (Furuse et al., 2010). The outbreaks of MERS-CoV are distributed in the middle east and South Korea, during the Summer period, however, the highest global seasonal occurrence took place from June 2012 to 2017 (Nassar et al., 2018; Wei et al., 2020). SARS-CoV infections are globally distributed with seasonal variation, however, the transmission becomes peaks during the winter season (Wei et al., 2020; Chen et al., 2020). The outbreak of the novel coronavirus 2019-nCoV was first experience during the winter seasons of 2019, since then the virus was incessantly transmitted globally and have affected more than 199 countries without geographical boundaries (Wei et al., 2020; Huang, 2020). Novel coronavirus 2019-nCoV infection is still ongoing with 115,653,459 numbers of laboratory-confirmed cases globally, including 2,571,823 death reported to WHO as at 6th March 2021, and a total of 249,160,837 vaccine doses have been administered (WHO, 2021).

Receptor
Several kinds of research have shown the existence of different types of receptors among the human coronavirus (HCoVs). Receptors play a crucial role in the interaction between a virion and host cell, before the establishment of any viral infection, the attachment of the S-protein of the Virion to specific receptors of the host cell is necessary. Similarly, several studies revealed the diversity of receptor usage by the human coronavirus (Cavanagh & Britton, 2008). Previous findings have reported that SARS-CoV, SARS-CoV-2, and HCoV-NL63 uses angiotensin-converting enzyme 2 (ACE2) as their common receptor (Huang, 2020). While MERS-CoV recognized and binds to dipeptidyl peptidase-4 (DPP4), and HCoV 229E recognized and binds to aminopeptidase N (APN) However, HCoV-OC43 and HCoV-HKU1 recognized and bind 9-O-acetylated sialic acid as their receptor (Li, 2020b). Similarly, another finding showed that HCoV-OC43 and HCoV HKU1 can also recognized and bind to dipetidyl peptidase 4 (DPP4) and sugars respectively (Chen et al., 2007).
## Table 1: Comparison of clinical characteristics of HCoVs

<table>
<thead>
<tr>
<th>Strain</th>
<th>Fatality rate</th>
<th>Incubation period</th>
<th>Transmission</th>
<th>Clinical symptoms</th>
<th>Epidemiology</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCoV-229E</td>
<td>N/A</td>
<td>2-5 days</td>
<td>Respiratory droplets</td>
<td>Headache, sneezing, fever, cough, malaise</td>
<td>Globally peak in winter</td>
<td>(Bradburne et al., 1967)</td>
</tr>
<tr>
<td>HCoV-OC43</td>
<td>N/A</td>
<td>2-5 days</td>
<td>Respiratory droplets</td>
<td>Headache, sneezing, fever, nasal discharge</td>
<td>Globally, peak in winter</td>
<td>(McIntosh, 1967a)</td>
</tr>
<tr>
<td>SARS-CoV</td>
<td>9.6%</td>
<td>2-11 days</td>
<td>Respiratory droplets</td>
<td>Fever, headache, Malaise</td>
<td>Globally, peak in winter</td>
<td>(Cheng et al., myalgia 2007)</td>
</tr>
<tr>
<td>HCoV-NL63</td>
<td>N/A</td>
<td>2-4 days</td>
<td>Respiratory droplets</td>
<td>Cough, rhinorrhea, hypoxia, tachypneaor</td>
<td>Globally, peak in winter</td>
<td>(Vander Hoek et al., 2004)</td>
</tr>
<tr>
<td>HCoV-HKU1</td>
<td>N/A</td>
<td>2-4 days</td>
<td>Respiratory droplets</td>
<td>Fever, running nose, cough, dyspnea</td>
<td>Globally, peak in winter</td>
<td>(Woo et al., 2005)</td>
</tr>
<tr>
<td>MERS-CoV</td>
<td>34.4%</td>
<td>2-13 days</td>
<td>Respiratory droplets</td>
<td>Fever, cough, chills, myalgia, arthralgia</td>
<td>Middle east, S. Korea during summer</td>
<td>(Hilgenfeld &amp; Peiris, 2013)</td>
</tr>
<tr>
<td>SARS-CoV-2</td>
<td>3.5%</td>
<td>3-6 days</td>
<td>Respiratory droplets</td>
<td>Fever, dry cough, myalgia, runny nose, headache</td>
<td>China then Globally</td>
<td>(Huang 2020)</td>
</tr>
</tbody>
</table>

### Abbreviations

HCoV-human coronavirus, MERS-middle east respiratory syndrome, SARS-severe acute respiratory syndrome, CoV-coronavirus, NA-not available

## Table 2: Comparison of biological characteristics of HCoVs

<table>
<thead>
<tr>
<th>Strain</th>
<th>Classification</th>
<th>First identified in</th>
<th>Animal Origin</th>
<th>Genomic size (kb)</th>
<th>Receptor</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCoV-229E</td>
<td>alpha-CoV</td>
<td>Chikago, 1966</td>
<td>Bats</td>
<td>27.3</td>
<td>APN</td>
<td>(Bradburne et al., 1967)</td>
</tr>
<tr>
<td>HCoV-OC43</td>
<td>beta-CoV</td>
<td>Asia, 1967</td>
<td>Rodents</td>
<td>30.5</td>
<td>DPP4</td>
<td>(McIntosh, 1967a)</td>
</tr>
<tr>
<td>SARS-CoV</td>
<td>beta-CoV</td>
<td>Guangdong, 2002</td>
<td>Bats</td>
<td>29.7</td>
<td>ACE2</td>
<td>(Cheng et al., 2007)</td>
</tr>
<tr>
<td>HCoV-NL63</td>
<td>alpha-CoV</td>
<td>Netherlands, 2004</td>
<td>Bats</td>
<td>27.5</td>
<td>ACE2</td>
<td>(Vander Hoek et al., 2004)</td>
</tr>
<tr>
<td>HCoV-HKU1</td>
<td>beta-CoV</td>
<td>Hong Kong, 2004</td>
<td>Rodents</td>
<td>29.9</td>
<td>DPP4</td>
<td>(Woo et al.; 2005)</td>
</tr>
<tr>
<td>MERS-CoV</td>
<td>beta-CoV</td>
<td>Saudi Arabia, 2012</td>
<td>Camels</td>
<td>30.1</td>
<td>DPP4</td>
<td>(Gao et al., 2016)</td>
</tr>
<tr>
<td>SARS-CoV-2</td>
<td>beta-CoV</td>
<td>Wuhan, China, 2019</td>
<td>Bats</td>
<td>36</td>
<td>ACE2</td>
<td>(Huang 2020)</td>
</tr>
</tbody>
</table>

### Abbreviation

HCoV-human coronavirus, MERS-middle east respiratory syndrome, SARS-severe acute respiratory syndrome, CoV-coronavirus, APN-aminopeptidase-N, DPP4-dipeptidylpeptidase-4, ACE-2-angiotensin converting enzyme 2
CONCLUSION
This review specifically focused on the biological and clinical characteristics of the seven human coronaviruses (HCoVs), from HCoV-229E to SARS-CoV-2. The review was in response to the current outbreak of COVID-19, which needs urgent and enormous studies that could serve as a framework for the control and prevention of this outbreak. The study identified the emergence and re-emergence of pathogenic human coronaviruses (HCoVs) as the biggest challenge to the public health system globally. Similarly, the study revealed that all the seven human coronaviruses (HCoVs) are zoonotic pathogens originating from animals and they were transmitted to humans through direct contact. According to our investigation, bats are the most common host of many coronaviruses and some of these pathogenic human coronaviruses (HCoVs) migrated from bats to humans through an intermediate host.

REFERENCES


Human Coronaviruses: Overview and Comparison of Biological and Clinical Characteristics


Human Coronaviruses: Overview and Comparison of Biological and Clinical Characteristics


T. Mahmud et al., DUJOPAS 7 (2b): 253-264, 2021