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# Pandemic of coronavirus disease 19 (COVID-19): A comprehensive review

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**Abstract**

Coronaviruses are a group of enveloped viruses with non-segmented, single-stranded, and positive-sense RNA genomes. Coronavirus disease 2019 (COVID-19) caused by new coronavirus (COVID-19) was first identified in December 2019 in Wuhan, the capital of China's Hubei province and has rapidly spread all over the world. This virus has spread to more than 220 countries, and more than 21,549,706 confirmed cases and 767,158 deaths have been recorded, large global increases in the number of daily cases. COVID-19 is a serious disease which cause high mortality in human and also, contributed to the global economic downturn. Hence, control measures and precautions should be taken and developing effective treatment and vaccine to slow down the spread of the virus.

***Keywords:*** *COVID-19, SARS-CoV-2, Pneumonia, RNA, Pandemic, Outbreak*

## 1. Introduction

Coronavirus disease (COVID-19) is a highly infectious disease caused by a newly discovered coronavirus which has a great influence on public health worldwide. The disease was first emerged in December 2019 in Wuhan, Hubei province, China, and has spread globally, resulting in the ongoing COVID-19 pandemic. (Zhou *et al.*, 2020; and Huang *et al.*, 2020). The causative agent of this pneumonia was confirmed as the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), previously named 2019 Novel Coronavirus (2019-nCoV), and the diseases was termed coronavirus disease-2019 (COVID-19). Coronaviruses have ability to mutate rapidly, alter tissue tropism, cross the species barrier, and adapt to different epidemiological situations (Decaro *et al.*, 2010). Six human coronaviruses have been reported since the 1960s; four of them (OC43, 229E, NL63, and HKU1) cause mild illness similar to the common cold and gastrointestinal tract infection. The other two, SARS-CoV and Middle East Respiratory Syndrome Coronavirus (MERS-CoV), have raised significant public health concerns due to their zoonotic emergence and crossing of the species barrier, causing high pathogenicity and mortality in humans (Wu *et al.*, 2020). SARS- and MERS-CoVs were reported to be transmitted from the main host (bats) to palm civets or dromedary camels, respectively, then eventually to humans (Guan *et al.*, 2003; and Cui *et al.*, 2019). SARS-CoV-2 shares 96.3%, 89%, and 82% nucleotide similarity with bat CoV RaTG13, SARS-like CoV ZXC21, and SARS-CoV, respectively, which confirms its zoonotic origin (Chen *et al.*, 2020; and Paraskevis *et al.*, 2020).

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As of August 4, 2020, the disease has caused a worldwide pandemic in more than 220 countries, with more than 18,142,718 confirmed human cases and 691,013 deaths. As a result of the rapid spread of the virus. COVID-19 is reported to be transmitted between humans through direct contact, aerosol droplets, fecal–oral route, and intermediate fomites from both symptomatic and asymptomatic patients during the incubation period (Zhou *et al.*, 2020; and Li *et al.*, 2020). The disease is characterized by fever, dry cough, dyspnea, and diarrhea in 20-25% of patients who do not exhibit upper respiratory signs such as sneezing or sore throat (Huang *et al.*, 2020; and Chen *et al.*, 2020). In severe cases, the disease is characterized by pneumonia, metabolic acidosis, septic shock, and bleeding (Li *et al.*, 2020; and WHO, 2020).

This review provides an update information on a rapidly evolving global pandemic.

## 2. Historical background of coronaviruses outbreaks

Coronaviruses have repeatedly evolved during the past 1000 years (Forni *et al.*, 2007). Human coronaviruses were first characterized in the 1960s from respiratory tract infections (Kahn and McIntosh, 2005). The two first isolated viruses were B814 and 229E (Tyrrell and Bynoe, 1966; and Hamre *et al.*, 1966). Since then, several other coronavirus strains have been isolated from humans using tissue culture (OC16 and OC43) (Tyrrell *et al.*, 1975; and McIntosh *et al.*, 1967). The number of identified coronaviruses have continued to increase dramatically to include viruses of several additional species such as calves, dogs, cats, bats, sparrows, rabbits, and turkeys (Lai *et al.*, 2007). In 2002-2003, SARS-CoV caused a disease outbreak with deaths in 29 countries, most cases being in China and Hong Kong. The total number of reported cases was 8,096, of which 774 died, corresponding to a 9.6% fatality rate (WHO, 2020), before the disease died out in part due to strict quarantine protocols. Based on the genome sequence, SARS-CoV appeared to be very closely related to another virus from Himalayan palm civets, from which it may have emerged (Guan *et al.*, 2003). Later, civets were considered an intermediate host for SARS-CoV, with bats as the natural host (Cui *et al.*, 2019).

Hu *et al.* (2017) conducted a five-year surveillance study of SARS-related coronaviruses isolated from horseshoe bats in Yunnan province, China, where 11 SARS-like CoVs were identified. Genome comparisons revealed high genetic diversity among these viruses in several genes, including S, ORF3, andORF8. Despite the differences in S protein sequences, all 11 SARS-like CoVs are still able to use the same human angiotensin-converting enzyme-2 (hACE2) receptor, demonstrating a close relationship with SARS-CoV. Therefore, SARS-CoV likely emerged through recombination of bat SARS-like CoVs before infecting civets, from which the recombinant virus spread to humans, causing the SARS epidemic (Cui *et al.*, 2019; and Hu *et al.*, 2017). Over past 10 years, MERS-CoV emerged in Middle Eastern countries where the virus was transmitted to humans from dromedary camels (Zaki *et al.*, 2012). As of January 2020, MERS-CoV has resulted in 2,519 laboratory-confirmed cases and 866 deaths (34.3% fatality rate), with more than 80% of the cases reported from Saudi Arabia (WHO, 2020). The human and camel MERS-CoV strains share more than 99% identity with variations (substitutions) located in the S, ORF3, and ORF4b genes (Chu *et al.*, 2018). Phylogenetically, MERS-CoV is very close to bat coronaviruses HKU4 and HKU5 (Lau *et al.*, 2013). A comprehensive analysis of the evolutionary relationships indicated that MERS-CoV may have originated from bats as a result of recombination events within ORF1ab and S genes (Dudas and Rambaut, 2016; and Wang *et al.*, 2015). To gain access into the cell, MERS-CoV uses the human dipeptidyl peptidase 4 (DPP4) receptor (Raj *et al.*, 2013). This is also the case for MERS-related CoVs isolated from bats in China, whose spike proteins are able to bind to the same receptor as MERS-CoV, confirming the possibility of a bat origin for MERS-CoV (Luo *et al.*, 2018).

In December 2019, SARS-CoV-2 emerged in Wuhan city, China, causing severe respiratory illness and mortality. Early studies reported that it may have evolved from bats, as revealed by phylogenetic analysis and its high identity (96.3%) with the bat coronavirus RaTG13 (Zhou *et al.*, 2020).

## 3. Causative agent of coronaviruses

Comparative phylogenetic analysis of SARS-CoV-2, single stranded RNA viruses exhibit a faster biological mutation rate due to the lack of proof-reading activity of viral RNA polymerase (Elena and Sanjuán, 2005); however, unlike other mutation-prone RNA viruses, with the exception of the Arenaviridae family, CoVs do have limited proof-reading capabilities, with the nsp14 protein allowing for the improved genome size of CoV family members (Ferron *et al.*, 2018). Recombination is another mechanism of evolution in coronaviruses (Lau *et al.*, 2011: and Makino *et al.*, 1986). Recombination was reported for MERS-CoV and SARS-CoV. Seven recombination regions were detected in ORF1ab and S protein between SARS-CoV and six other coronaviruses by in silico analysis of their genomes (Zhang *et al.*, 2005). Similarly, bioinformatic analysis of MERS-CoV

genomic data revealed 28 recombinant sequences from humans and camels (Zhang *et al.,* 2016). Primary studies proposed that it may have occurred in the course of SARS-CoV-2 evolution (Zhou *et al.,* 2020; and Zheng *et al.,* 2020), while other researchers excluded the possibility of recombination based on a full genome evolutionary analysis investigating putative recombination events (Paraskevis *et al.,* 2020).

Coronaviruses mutations and their effects, based on the whole-genome sequence alignment, SARS-CoV-2 shares 89% identity with bat SARS-like CoVZXC21, 82% with SARS-CoV, and 96.3% with bat CoVRaTG13 (Paraskevis *et al.,* 2020; and Chen *et al.,* 2020). Alignment of the predicted protein sequences of SARS-CoV-2 to those of SARS-CoV or SARS-like coronaviruses revealed a total of 380 amino acid substitutions between these viruses (Wu *et al.,* 2020). These amino acid substitutions were distributed as follows: 348 mutations in nonstructural proteins (ORF1ab, 3a, 3b, 7a, 7b, 9b, and ORF14), 27 in S protein, and 5 in N protein. No amino acid substitutions were detected in E or M proteins, indicating that E and M proteins are highly conserved among these viruses. Some studies have been reported that SARS-CoV-2 uses the same cellular receptor, hACE2, as SARS-CoV to gain entry in to the cell. The analysis of the Receptor-Binding Domains (RBD) of SARS-CoV and SARS-CoV-2 S protein revealed similar binding affinities (Walls *et al.,* 2020). Wu *et al.* (2020) found a total of 27 amino acid substitutions in the S protein but not in the Receptor-Binding Motif (RBM) that directly interacts with hACE2, which may affect host tropism. These 27 substituted residues were distributed as follows: 17 in the S1subunit [6 in the RBD and 6i n the subdomain (SD)] and 10 in the S2 subunit. Wan *et al.* (2020) reported similarity in the spike protein RBD, including RBM, of both SARS-CoV and SARS-CoV-2, in addition to the presence of several residues in SARS-CoV-2 RBM that favor the interaction with human ACE2. The results of these studies compatible with the genomic analysis of SARS-CoV-2, according to which the S2 subunit of the spike protein shares 99% identity with those of two bat SARS-like CoVs (SL-CoVZXC21 and ZC45) and of human SARS-CoV (Chen *et al.,* 2020). The S1 subunit of COVID-19 and SARS- share with overall 70% identity with those of bat and human SARS-CoV. The S1 is strongly conserved, with most of the amino acid differences located in the external subdomain that is responsible for the direct interaction with host receptors (Chen *et al.,* 2020). Researchers have also reported the presence of a polybasic cleavage site and predicted O-linked glycans that are unique to SARS-CoV-2 S protein. Differences in SARS-CoV-2 S protein and the high contagious nature of this virus propose that SARS-CoV-2 has evolved via natural selection for binding to human ACE2 receptor (Andersen *et al.,* 2020). ORF3b also differs in SARS-CoV-2. ORF3b deletion mutations in SARS-CoV do not affect viral replication in vitro (Yount *et al.,* 2005). ORF3b may play a role in viral pathogenicity in addition to its Inhibitory Effects on Interferon (IFN) expression and signaling (Khan *et al.,* 2006; and Kopecky-Bromberg *et al.,* 2007). Now, a novel short putative protein was recognized in ORF3b of SARS-CoV-2 (Chen *et al.,* 2020); however, the function of this novel protein is remains unknown. SARS-CoV-2 ORF8 is closer to those of bat SARS CoV ZXC21 and ZC45 and distant from that of human SARS-CoV (Chen *et al.,* 2020).

Genetic diversity of COVID-19, the evaluation of genetic diversity among 86 complete or semi-complete genomes of SARS-CoV-2 viruses revealed three deletions in the genome of isolates from Japan, USA, and Australia in addition to many other substitution mutations. The deletion mutations were in the ORF1abgene (3-nucleotide and 24-nucleotide deletion) and at the 30 end of the genome (10-nucleotide deletion). There are 93 substitution mutations, 42 changed the amino acid sequence of structural and non-structural proteins (Phan, 2020). The 3 and 24-nucleotide deletions in ORF1ab are anticipated to reduce the protein sequence by 1 and 8 amino acid residues respectively, without changing the reading frame, but the functional effects have yet to be studied.

## 4. Epidemiology of COVID-19

The COVID-19 outbreak emerged from Wuhan city, Hubei province, in China. 50% of the infected cases before January 1, 2020 were associated to the Huanan seafood wholesale market. However, the first human-to-human case of COVID-19 infection reported in the first of December 2019 did not have any exposure to this market (CDC, 2020; and WHO, 2020). In the middle of January 2020, SARS-CoV-2 spread to other provinces of China due to the Spring Festival travel season. SARS-CoV-2 was transmitted from China to other countries via international passengers. By January 13, 2020, the first case of SARS-CoV-2 infection was confirmed outside China in Thailand, and then January 16, 2020 the first infected case was confirmed in Japan. These cases were linked to the seafood wholesale market as well.

For the week ending 16 August, over 1.8 million new COVID-19 cases and 39,000 new deaths were reported to WHO. This brings the cumulative total to 21.2 million confirmed COVID-19 cases including 761,000 deaths.

In the past seven days, the number of reported daily cases rapidly increased with an average of 260,000 cases and 5,500 deaths.

By August 17, 2020, the number of confirmed cases in the global had risen to 21,549, 706, including 767,158 deaths. The number of confirmed cases in the United State of America reached up to 5,312,940 which represent the highest number, following by Brazil, 3,317,096, India, 2,647,663, Russian Federation 927,745, South Africa 587,345, Peru 525,803, Mexico 517,714, Colombia 456,689, Chile, 385,946, Iran 343,203, Spain, 342,813 and the United Kingdom, 318,488 confirmed cases respectively. Therefore, WHO declared the COVID-19 outbreak to be a Public Health Emergency of International Concern in last January due to the global spread (Cowling and Leung, 2020; and WHO, 2020).

As of 16 August, in the Region of the Americas, over 53% newly confirmed cases and 75% deaths have been reported in the past week compared to this week, with a less than 1% increase in the number of newly confirmed cases. However, during the same period, the number of deaths increased by 13%.

The United States of America of Americas region, reported 360,000 new cases, a 4% decrease from the previous week. This decrease may in part be attributable to an underreporting of cases in California due to technology issues with the electronic laboratory reporting system which reports into the state's disease registry system. The number of deaths reported in Peru increased by 220% in the past seven days to a total of 25,800 and a cumulative death rate of 784 deaths per 1 million population, which is currently the highest in the region and the United States of Americas region remains the most affected regions (WHO, 2020).

In South-East Asian region, South-East Asia, is the second most affected region and currently accounts for a respective 26% and 19% of newly reported cases and deaths globally in the past seven days. The region has seen a steady increase in reported cases and deaths, with a 9% increase in the past seven days, compared to the previous week. India continues to report the majority of cases, accounting for 85% of all confirmed cases in the region as of 16 August and 92% of cases in the past seven days. The Maldives has recorded the highest incidence rate globally as cases continue to increase in the country (WHO, 2020).

The European region, the number of cases reported in the European region has gradually increased in recent weeks, however, there was no substantial change in the number of cases reported this week compared to the previous week. Nevertheless, a number of countries in the region are showing a resurgence in cases including France, Germany, Netherlands, Spain and the United Kingdom. Several COVID-19 clusters, which have contributed to the resurgence of cases, have been reported in meat processing and packaging facilities in a number of countries including Belgium, Denmark and Germany. A total of 2,480 deaths were reported across the region in the past seven days, which is a 21% decrease from the previous week. However, following a retrospective review process in the United Kingdom, over 5,000 deaths were deducted from the country's total COVID-19 deaths, resulting in a decrease of 2,728 deaths in the European region (WHO, 2020).

In the African region, The African region reported the largest decrease in the number of newly reported cases (27%) and deaths (21%) in the past seven days, primarily due to a decrease in cases reported in South Africa, Kenya, Algeria, Nigeria and Ghana. Conversely, Ethiopia reported a 56% and 12% increase in the number of cases and deaths respectively, with more than half of the cases reported in Addis Ababa. Due to the increase in cases, a month-long testing and prevention campaign will be implemented with a plan to carry out 400,000 tests.

There are increasing reports of healthcare worker infections across the region, resulting in an overburdened health care system in several countries including Gambia, Kenya, Nigeria and Zimbabwe (WHO, 2020).

Eastern Mediterranean region, following five weeks of decline in the number of cases reported in the Eastern Mediterranean region, a total of 88,700 new cases were reported in the last seven days, a 10% increase in the number of newly reported cases compared to the previous week. While countries in the Gulf state are reporting a decline in incidence, Iraq, Morocco, occupied Palestinian territory, Lebanon and Libya are reporting an increase in cases (WHO, 2020). The number of cases and deaths reported in Pakistan in the past seven days decreased by 20% and 24% respectively from the previous week, resulting in the lifting of lockdown restrictions across the country. The number of confirmed cases, deaths, and infected regions are shown in Table 1.

The Western Pacific region, the number of cases reported in the region decreased by 5% as the number of new cases reported in Japan, Australia, Singapore and Viet Nam decreased in the past seven days. However, the number of deaths reported increased by 90% mainly due to increases reported in the Philippines, Japan, Viet Nam, China and Australia. The Republic of Korea continues to report cases associated with religious clusters and reported an increase of 210% in the number of cases compared to last week. On August 11, New Zealand reported a new locally acquired case, after recording 102 days with no community transmission. A

**Table 1: The number of confirmed and deaths cases of COVID-19 outbreaks according to WHO situation reports August 17, 2020 by region**

| Region | Number of confirmed cases | Number of deaths |
|---|---|---|
| America | 11,561,554 | 417,699 |
| Europe | 3,779,672 | 214,355 |
| South-East Asia | 3,103,018 | 60,929 |
| Eastern Mediterranean | 1,737,027 | 46,067 |
| Africa | 953,088 | 18,708 |
| Western Pacific | 414,606 | 9,387 |

total of 52 new cases have been reported in the past seven days resulting in a temporary lockdown of the northern part of the country. New Zealand is the third country in the region to report a resurgence in cases after a period of little or no known community transmission. Other countries include Australia and Viet Nam.

## 5. COVID-19 transmission

Coronaviruses were and are reported to spread from an infected person to a non-infected person via direct or indirect contact. SARS-CoV-2 infection was reported to be transmitted directly from person to person like most respiratory viruses through close contact with an infected person or via respiratory droplets (aerosol) produced when an infected person coughs or sneezes. These droplets can be inhaled through respiratory tract to the lung. The virus can be indirectly transmitted via touching a surface or an object that was previously contaminated with the virus and then touching the face, eyes, or mouth (CDC, 2020) and possibly through the fecal-oral route (Lai *et al.*, 2020; and Holshue *et al.*, 2020). Asymptomatic carriers (during the incubation period of the virus 2 – up to 14 days) and patients after recovery from the acute form of the disease are also considered a potential source of virus transmission to healthy persons (Chan *et al.*, 2020; and Rothe *et al.*, 2020). Human coronaviruses have ability to survive on steel, metal, wood, aluminum, paper, glass, plastic, ceramic, disposable gowns, and surgical gloves for 2-9 days. High temperature ($\geq 30$ °C) can reduce the persistence period, while low temperature (4 °C) increases the persistence time up to 28 days (Kampf *et al.*, 2020). Transmission of the virus vertically from mother to fetus or via breast milk has not been confirmed yet (Chen *et al.*, 2020). The transmission cycle of coronavirus among animals and humans is shown in Figure 1.
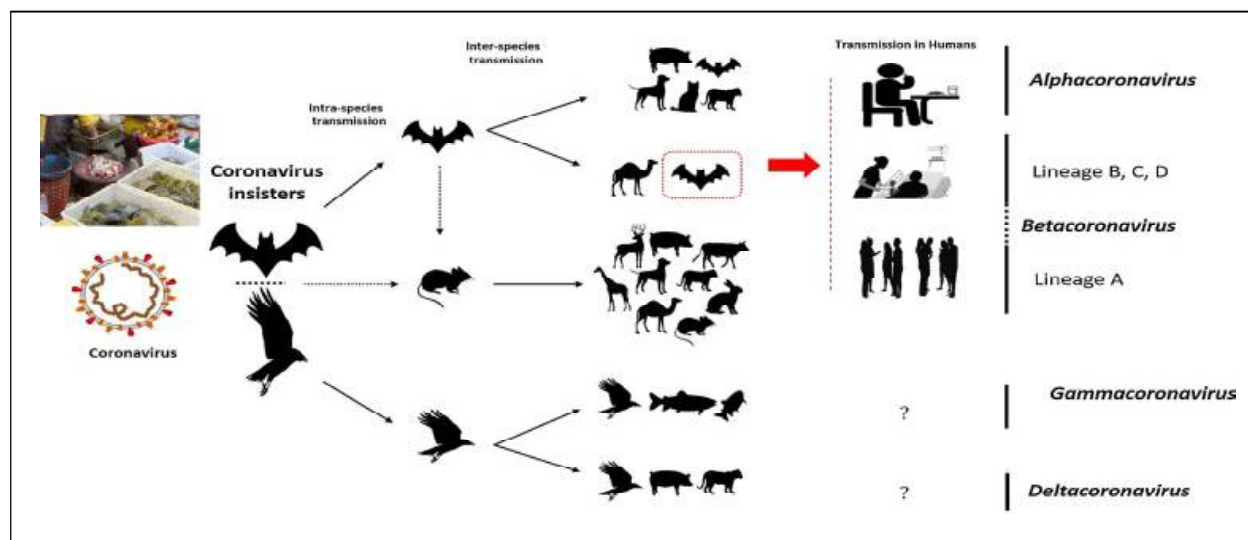


**Figure 1: The life cycle of coronaviruses transmission including MERS-CoV, SARS-CoV, and COVID-19. The virus transmission to humans occurs by direct contact with infected animals. The continuous line represents direct transmission**

## 6. Risk factors of COVID-19

The Center for Diseases Control (CDC) suggest that several groups of people with medical conditions are at increase risk factors and developing complications due to COVID-19. These factors include:

1.  People aged 65 years or older

2.  Pregnant women

3.  Chronic kidney diseases

4.  Cancer

5.  Diabetes mellitus

6.  Asthma

7.  Liver disease

8.  Cardiovascular diseases

9.  Smoking

10. Immunocompromised state (weakened immune system) from blood or bone marrow transplant, immune deficiencies, HIV, use of corticosteroids or other immune weakening medicine.

## 7. Clinical manifestations

People affected with COVID-19 develop clinical signs ranging from mild to severe illness. Symptoms may appear 2-14 days after exposure to the virus (WHO, 2020). The most common and serious symptoms of COVID-19 are fever, dry cough, tiredness, shortness or difficulty breathing, persistent pressure or pain in the chest pain or and the loss of speech or movement in severe cases. Muscle or body ached, headache, sore throat, loss of taste or smell, congestion or runny nose, nausea or vomiting and diarrhea are slighter common symptoms (WHO, 2020).

## 8. Pathogenesis of coronaviruses

Coronaviruses are enveloped, non-segmented, positive-sense RNA viruses. They are characterized by club-like spikes that project from their surface and the largest identified RNA genomes, containing approximately 30 kilobase (kb) genome and unique replication strategy. The strategy of replication of coronaviruses involves a nested set of messengers RNAs with common polyadenylated 3-ends. Only the unique protein of the 5-end is translated. Mutations are common in nature. In addition, coronaviruses are capable of genetic recombination if two viruses infect the same cell at the same time (Lai and Holmes, 2001). The name of coronavirus is derived from Latin, corona, meaning crown. Due to characteristic appearance of virions by electron microscopy on the surface of the virus creating an image reminiscent of a crown or of a solar corona, coronavirus has acquired its name.

Tang *et al.* Reported the patterns of molecular divergence between SARS-CoV-2 and other related coronaviruses by studying the population genetic analyses of 103 genomes of SARS-CoV-2. The study showed that SARS-CoV-2 viruses evolved into two major types (L and S types) with the S type being the more ancient version of SARS-CoV-2. L type was shown to be more aggressive than the S type and more prevalent in the early stages of the outbreak in China, the frequency of the L type decreased after early January 2020 possibly due to human intervention (Tang Xiaolu*et al.*, 2020).

In general, SARS-CoV-2 similar to other coronaviruses in the subgenus Sarbecovirus, a clade of beta-coronavirus that causes SARS (SARS-CoV-2) and other SARS-CoV-like coronavirus found in bats. Recombination between coronaviruses are common, and SARS-CoV is believed to be a recombinant between bat sarbecoronaviruses. Generally, the genome of SARS-CoV-2 is highly similar to that of a bat >96% sequence identity), which suggests that the immediate ancestor of SARS-CoV-2 has been circulating in bats at least several years (Lu *et al.*, 2020). ACE2 has been identified as a functional receptor for coronaviruses, including SARS-CoV-2 and SARS-CoV-2.
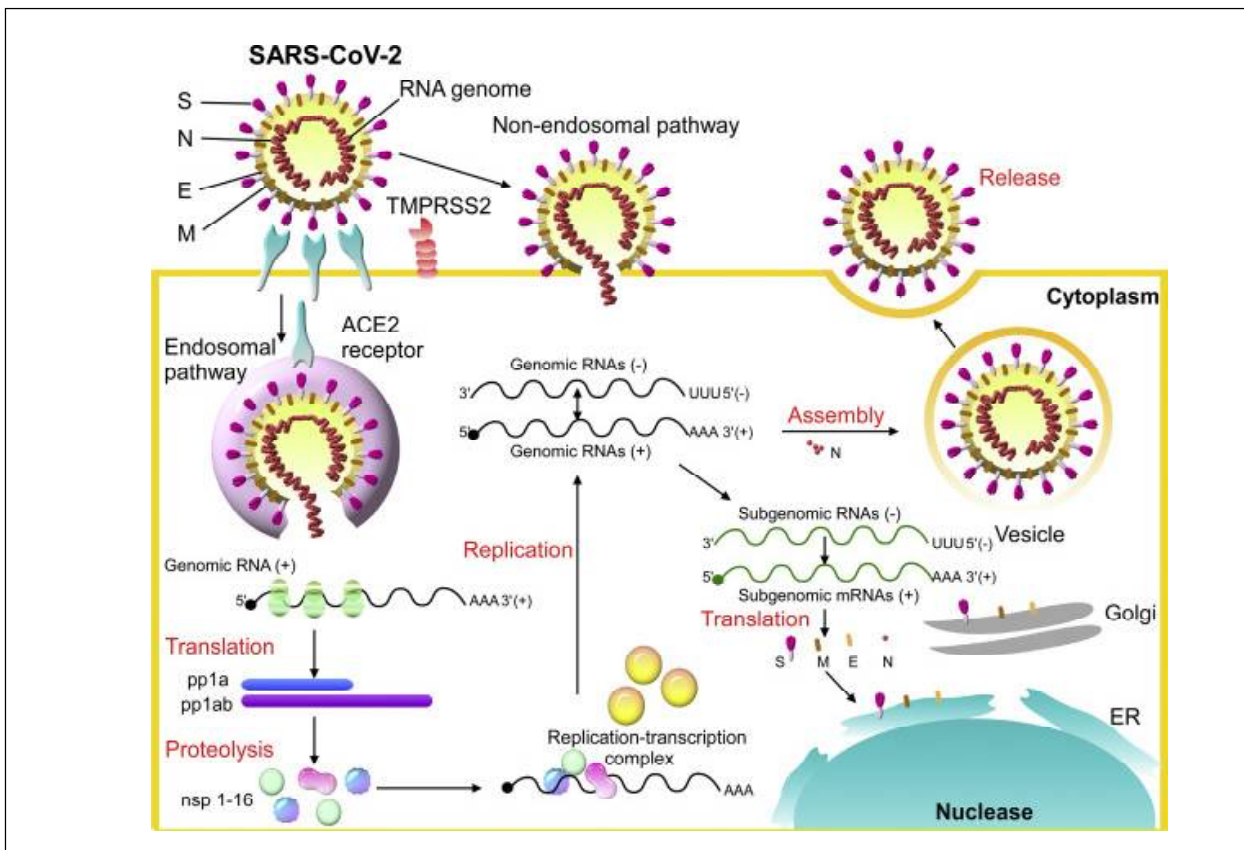
**Figure 2: Corona virus entry**

| Table 2: The Director-General also noted that the risk of serious complications increases with age. According to the WHO | |
| --- | --- |
| **Stage of severity** | **Rough percentage of people with COVID-19** |
| Mild disease from which a person can recover | More than 80% |
| Severe disease, causing breathlessness and pneumonia | Around 14% |
| Critical disease, including septic shock, respiratory failure, and the failure of more than one organ. | About 5% |
| Fatal disease | 2% |

The COVID-19 infection is triggered by binding of the spike protein of the virus to ACE2, which is strongly expressed in the heart and lungs. Binding of the S1 unit of the viral S protein to the host ACE2 cellular facilitates viral attachment to the surface of target host cells. Viral host protein priming then requires S protein cleavage of S1 from S2 (and at another S2 site) by the host cell serine protease TMPRSS2. The viral S2 subunit then drives fusion of the viral and host cell membranes (Zhang *et al.,* 2020). Additionally, cytokine storm triggered by an imbalanced response by type 1 and type 2 helper cells and respiratory dysfunction and hypoxemia caused by COVID-19 can result in damage to myocardial cells (Huang *et al.,* 2020). Pangolins, protected animals that are targeted illegally in Asia and elsewhere, have been proposed as a potential amplifying host by some studies (Tsan-Yuk Lam Tommy *et al.,* 2020). And the virus enters the body by the following steps:

1. Attachment and entry
2. Replicase protein expression
3. Replication and transcription
4. Assembly and release.

## 9. Diagnosis of COVID-19

The rapid diagnosis of COVID-19 infection is the cornerstone of disease control. The detection of the virus depends on numerous criteria including case history, clinical symptoms, serology, molecular diagnosis, and computed tomography (CT) imaging. The World Health Organization (WHO) published interim guidance for laboratory testing of suspected human cases on March 2, 2020, with precautions for specimen collection, packing, shipment, and amplification of nucleic acid to detect viral genes (N, E, S, and RdRp) (WHO, 2020). COVID-19 uses the same cell entry receptor, hACE2, as SARS-CoV. Therefore, oral swabs, Bronchoalveolar Lavage Fluid (BALF), blood, as well as anal swabs are the best samples used for virus diagnosis (Zheng *et al.,* 2020).

## 10. Control of COVID-19

Many control measures are being imposed by communities around the global to slow down the COVID-19 pandemic, including the issuance of travel advisories or even flight bans to and from infected countries, strict quarantine measures and traveler screenings, implementation of mitigation measures by healthcare specialists, application of social distancing measures for popular gatherings and schools, emphasis of personal hygiene such as wearing face masks and frequent handwashing to limit the virus spread (Cowlingand Leung, 2020).

Currently, there is no vaccine or approved treatment to prevent COVID-19 infection, and trials for vaccine development are in the preliminary stages of research. Several vaccine candidates such as live attenuated, adenovirus-vectored, recombinant protein and nucleic acid (DNA and mRNA) vaccines are in the pipeline (Chen *et al.*, 2020).

## 11. Conclusion

The COVID-19 pandemic spreads rapidly among people and across the countries due to the high potential of the virus. This virus causes high morbidity and mortality rate in human. In addition to, this pandemic has greatly impacted the global economy.

## 12. Recommendations

The control of the COVID-19 outbreak and future epidemics requires global efforts and collaboration among medical and veterinary clinicians, diagnosticians, virologists, physicians, epidemiologists, public health experts, vaccineologists, pharmaceutical industries, economists, and governments to implement a One-Health approach. These measures should include:

1. Writing policies and supporting funds required for the implementation of One Health, prevention, and control measures.

2. Hiring well-trained and professional personnel and performing rapid and accurate diagnosis and treatment of infected people.

3. Developing and providing vaccines for virus control as well as providing antiviral drugs for the treatment of the disease in humans.

4. Conducting surveillance among domestic and wild life animals for the identification and characterization of possible reservoirs and surveillance among people who are in contact with wildlife to identify risk factors in human behaviors and living environment as well as assessing the social and economic impacts of COVID-19 on the population.

5. Utilizing veterinary experiences in the disinfection of premises and gatherings under the supervision of health authorities to decrease outbreaks in humans.

## Conflicts of Interest

The authors declare that there is no conflict of interest.

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