# Comparison Review between Sars-Cov-2 and Different Types of Viruses

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## Abstract

In this paper, we will focus our attention on Coronaviridae, a family of RNA viruses consisting of a sub-family "Coronavirinae" which by its turn consist on four genera, namely Al-phacoronaviruses (αCoV), Betacoronaviruses (βCoV), Gammacoronaviruses (γCoV), and Del-tacoronaviruses(δCoV). Beta Coronaviruses comprise the three most patho-genic coronaviruses known to date: the severe acute respiratory syndrome virus (SARS-CoV), the Middle East respiratory syndrome virus (MERS-CoV), and the SARS-CoV-2 virus, responsible for the currently ongoing (since December 2019). Although these deadly Coronaviruses (CoVs) are posing dreadful threats to humans.

The mildly pathogenic viruses infect the upper respiratory tract and cause seasonal, mild to moderate cold-like respiratory diseases in healthy individuals. In contrast, the highly pathogenic SARS-CoV infect the lower respiratory tract and cause severe pneumonia, sometimes leading to fatal acute lung injury (ALI) and acute respiratory distress syndrome (ARDS),The pathogenic SARS-CoV have high morbidity 9 and mortality and pose a major threat to public health

**Keywords:** SARS-CoV, COVID-19, Structural antigens, influenzaandSARS-CoV-2 variants.

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## I. Introduction

SARS-CoV-2 is identified as a third zoonotic human coronavirus [1]. SARS-natural CoV-2's host is bats, although the intermediate reservoir is still up for question [2]. According to the worldwide scenario, about 53.9 million persons test positive for COVID-19, with 1.31 million deaths verified and 34.7 million recovered as of November 14, 2020. With over 1.5 million instances through November 14, 2020, the top five worst COVID-19 impacted nations are the United States, India, Brazil, France and Russia [3].

SARS-CoV-2 infection is first reported in patients over 60 years of age in the United States, China, and Italy[4]. From June to August 2020, data show an elevated risk of infection (4.5 percent to 15 percent) among the 15-29-year-old age group [5]. This huge shift in infection cases among age groups can be attributable to the younger population returning to their places of employment, such as universities, colleges, and schools [5].

As a result, COVID-19-related mortality has a wide age range, ranging from 10 to 80 years old, with a higher number of instances recorded among patients with various co-morbid diseases. The case fatality rate (CFR) is calculated by dividing the total number of reported cases by the total number of fatalities. Because of variances in medical and health infrastructure, co-morbidities, and population age, the CFR for COVID-19 varies from nation to country [3].

COVID-19 severity is increased by 10.5 percent in patients with cardiovascular disease (CVD), 37.3 percent in patients with diabetes, 8.3 percent in patients with chronic obstructive pulmonary disease (COPD), 55.4 percent in patients with hypertension, and 8.1 percent in cancer patients [6].Men and females are virtually equally vulnerable to SARS-CoV-2 infection, according to sex-disaggregated COVID-19 data gathered from 26 countries, while males have a 2.4 times greater fatality rate than females [7].Male mortality rates may be linked to co-morbidities such as diabetes, hypertension, cardiovascular disease, and chronic renal disease, among other things [8]. Males with COVID show greater amounts of circulating angiotensin-converting enzyme (ACE2) than females in their plasma. This shows that the ACE2 receptor is expressed at higher levels on the skin. Virus internalization is aided by tissues[9].Due to variations in immunological, genetic, endocrinological, social, and behavioral variables, COVID19-related mortalities are higher in males than females in general [10].The transmission of SARS-COV-2 is most likely caused by a cross-species leap from animal to human, which begins at a wet animal market in Wuhan, China [11].The visitors to the Huanan animal market establish the person-to-person transmission [12].

As a result, the mechanism of transmission is either through direct human contact or by droplets produced by an infected individual's sneezing and coughing [13].Because there is no live virus in stool samples, the presence of viral RNA in stool samples suggests another route of transmission [14].

During the SARS-CoV-1 and MERS-CoV outbreaks, vertical virus transmission is recorded, but not in the case of SARS-COV-2. To break the chain of transmission of SARSCoV2, testing symptomatic and asymptomatic patients, containment procedures, and other preventive measures like wearing masks in public areas, maintaining social distance and regular use of handwash and hand sanitizers should be implemented [13].

## II. SARS-CoV-2

### II.1. Structure of SARS-CoV-2

SARS-CoV-2 has a double-layered lipid envelope that includes four main structural proteins (Fig.1): spike (S) glycoprotein, envelope (E) protein, nucleocapsid (N) protein, membrane (M) protein, and several accessory proteins [15].The spike proteins cover the viral genome that has a receptor-binding domain (RBD) for interacting with host cell receptors [16].

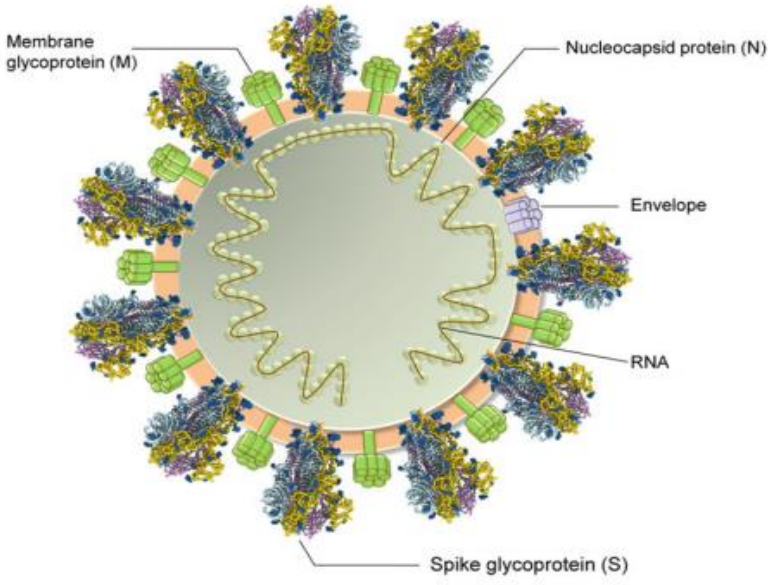


**Fig. 1: Structure of SARS-CoV-2 [17].**

The S protein is a transmembrane protein with a molecular weight of about 150 KDa. It forms a homotrimer in the viral surface. This protein gives virions the appearance of a solar corona or medieval crown, which gives rise to the virus family's name. The S protein also facilitates binding the envelope with the host cell by attraction withACE2 [18].

The nucleocapsid protein known as N protein is the structural component of the virus. It is localized in the endoplasmic reticulum-Golgi region and also packs the viral genome into a ribonucleoprotein complex. The N protein plays a role in the genome replication and cell-signaling pathway [19,20].

The M protein plays a role in determining the shape of the virus envelope. This protein can bind to all structural proteins. Binding with M protein aids in the stabilization of nucleocapsids or N proteins and facilitates viral assembly completion by stabilizing the N protein-RNA complex inside the internal virion. The last component is the envelope protein, which is the smallest protein in the SARS-CoV-2 structure and plays a function in the virus's generation and maturation[19].

### II.2. Genomic organization of SARS-CoV2

The genome of SARS-CoV-2 is typical for beta coronaviruses, comprised of a single strand of positive-sense RNA. The SARS-CoV-2 has 13-15 open reading frames (ORFs) (12 functional), which encode for different proteins [21].It has a 5′ untranslated region (UTR), replication complex

(ORF1a and ORF1b), Spike (S) gene, Envelope (E) gene, Membrane (M) gene, Nucleocapsid (N) gene,3′ UTR, several unidentified non-structural ORFs and poly adenosine (A) tail [22,23].

The ORF1a gene is located at the 5′UTR, encodes for polyprotein pp1a, which contains 10 nonstructural proteins (nsps). The ORF1b gene (Fig.2), located next to ORF1a, encodes for polyprotein pp1ab, which contains 16 nsps. The autoproteolytic cleavage of the pp1ab and pp1a proteins leads to the formation of the viral replication complex [21].

The nsps contains two viral cysteine proteases: papain-like protease (nsp3), chymotrypsin-like,3C-like, or main protease (nsp5), as well as RNA-dependent RNA polymerase (nsp12), helicase (nsp13), and others that are primarily engaged in SARS-CoV-2 transcription and replication [24].

The 3′UTR contains four structural genes (S, E, M and N) and eight accessory genes (Fig.2). The accessory genes distributed between the structural genes and their function is unknown [21,23].

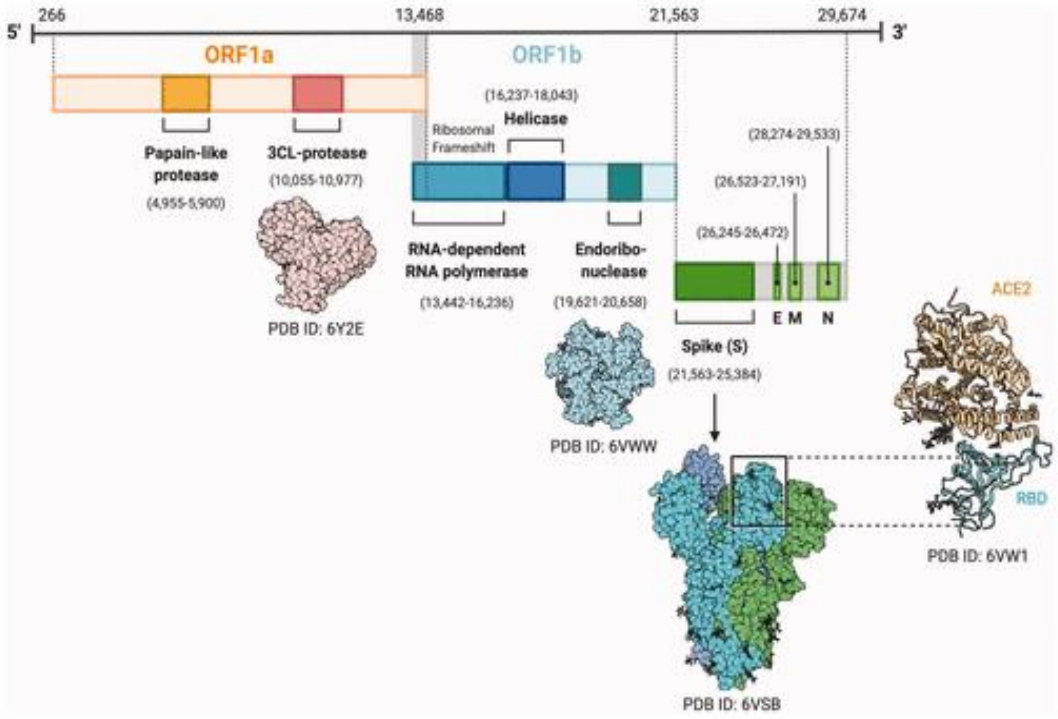


**Fig. 2: Genomic structure of sars-cov-2 [15].**

## II.3. SARS-CoV-2 life cycle

### II.3.1. Attachment and entry

SARS-CoV-2 can hijack the cell in two ways, either via endosomes or via plasma membrane fusion. In both ways, Spike proteins (S1, S2) of SARS-CoV-2 mediate attachment to the membrane of a host cell and engage ACE2 as the entry receptor[25]. This receptor can be found in many organ cells such as the respiratory tract, heart, kidney, intestine, testis, and vascular endothelium [26]. This attachment occurs in the binding domain of S protein of SARS CoV-2 receptors (RBD)

which are present at 331 to 524 residues and can bind strongly to human ACE2 and bat ACE2. Cell surface vimentin (VIM) acts as a critical co-receptor and is essential for successful ACE-2 binding. The binding of heparan sulfate (HS) to the receptor-binding domain (RBD) enhances binding to ACE2 as well [27].

Alternatively, the spike protein can be cleaved between the S1 and S2 domains by the type II transmembrane serine protease (TMPRSS2) near the ACE2 receptor, which activates the receptor attached spike-like, S proteins [28]. S1 segment binds the extracellular N-terminus of ACE2 while conformational changes in S2 subunit facilitate fusion between the host cell membrane and viral envelope to initiate internalization of the virus/receptor complex by endocytose [29]. Both of these proteins (TMPRSS2 and ACE2) are the main determinants of the entry of this virus (Fig.3).

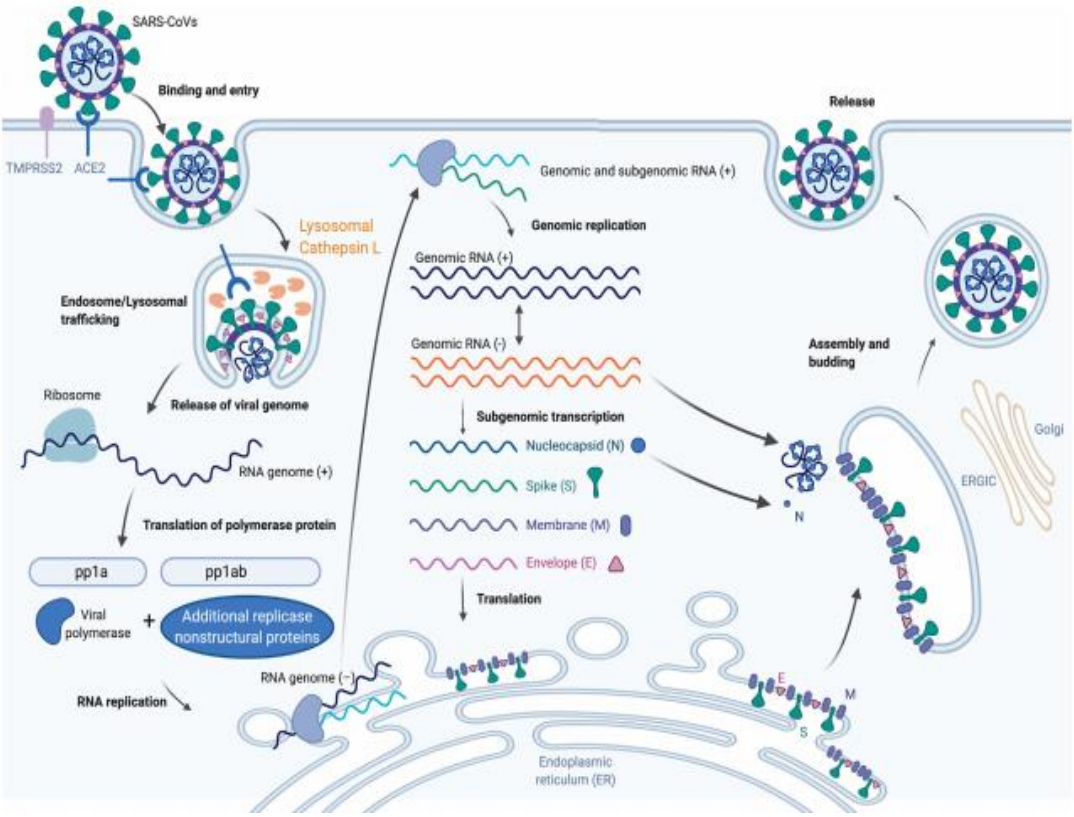


**Fig. 3: Severe Acute Respiratory Syndrome Coronavirus 2 Lifecycle [29].**

### II.3.2. Translation and replication

After the viral RNA is released into the host cell, polyproteins are translated. The coronavirus genomic RNA encodes nonstructural proteins (NSPs) that have a critical role in viral RNA synthesis, and structural proteins, which are important for virion assembly. The virus uses the host ribosomes to translate RNA code to viral proteins [24]. First, polyproteins are translated into ORF1a and ORF1b to produce two large overlapping polyproteins pp1a and pp1ab which are cleaved by the Papain-like protease ($Pl^{pro}$) and 3C-like protease ($3CL^{pro}$) to form functional NSPs which play an important role in many processes in viruses and host cells (Fig.3), as Helicase or the

RNA replicase–transcriptase complex (RdRp). RdRp is responsible for replication of structural protein RNA [30].

Many of the NSPs subsequently form replicase-transcriptase complex (RTC) in double-membrane vesicles (DMVs), which are mainly an assembly by RNA-dependent RNA polymerase (RdRp) and helicase-containing subunits, the canonical RdRp domain residing of CoV nsp12 and AV nsp9[31].

This complex can multiply the viral genome by attachment to the genomic RNA called $RNA^{+}$ and creates a copy of it. The complimentary copy is called $RNA^{-}$, the minus strand is then copied back to make additional $RNA^{+}$ for packaging into new viruses (Fig.3). Furthermore, small minus RNA strands are first produced by the replicase transcriptase complex. The RT Complex copies the small minus strands to produce small plus strands called sub genomic messenger RNAs. Next, the subgenomic proteins become translated into structural and accessories proteins such as M, S, and E proteins that subsequently are insulated in the endoplasmic reticulum and then moved to the endoplasmic reticulum-Golgi intermediate compartment (ERGIC). Both genomic and sub-genomic RNAs are produced through negative-strand intermediates [32].

### II.3.3. Virion assembly and release

The previous replicated genome program can directly join the N protein to the nucleocapsid form and move into the ERGIC. In this compartment, nucleocapsids will meet with several other structural proteins and form small wallet vesicles to be exported out of the cell through exocytosis [29].

The generated virions release out of the cell by exocytosis or cell death. Some virions are released into environment to infect others, while others remain in the body and interact with ACE2 receptors to trigger the invasive infection [24].

### II.4.Virus transmission

SARS-CoV-2 has been recognized as a coronavirus by several research organizations, with a genome that is almost identical to that of bat coronavirus. According to this research, bats may be the virus's natural host [15]. The new coronavirus travels mostly through the respiratory system and employs the same receptor as SARS-CoV-2 [(ACE2)].

### II.4.1. Contact and droplet transmission

SARS-CoV-2 can spread through infected fluids such as saliva and respiratory secretions or their respiratory droplets, which are released when an infected person coughs, sneezes, talks, or sings. Respiratory droplets are >5-10 m in diameter, whereas droplets 5 m in diameter are called to as droplet nuclei or aerosols [32].

Human-to-human aerosol transmission, which occurs mostly through contaminated droplets, hands, or surfaces, is without a doubt the most common cause of infection (Fig.4). Virus particles found in secretions from an infected person's respiratory system infect others by direct contact with mucosal membranes [33], with an incubation period ranging from 2 to 12 days. It is worth noting that viral transmission by asymptomatic or affected persons has been well characterized during the incubation phase. Despite evidence of RNA-laden aerosols discovered near toilet bowls, as well as detectable SARS-CoV-2 RNA in rectal swabs during the antecedent pandemic of COVID-19 in China (Fig.4), fecal-oral transmission has been suggested as a possible route of human dissemination [34].

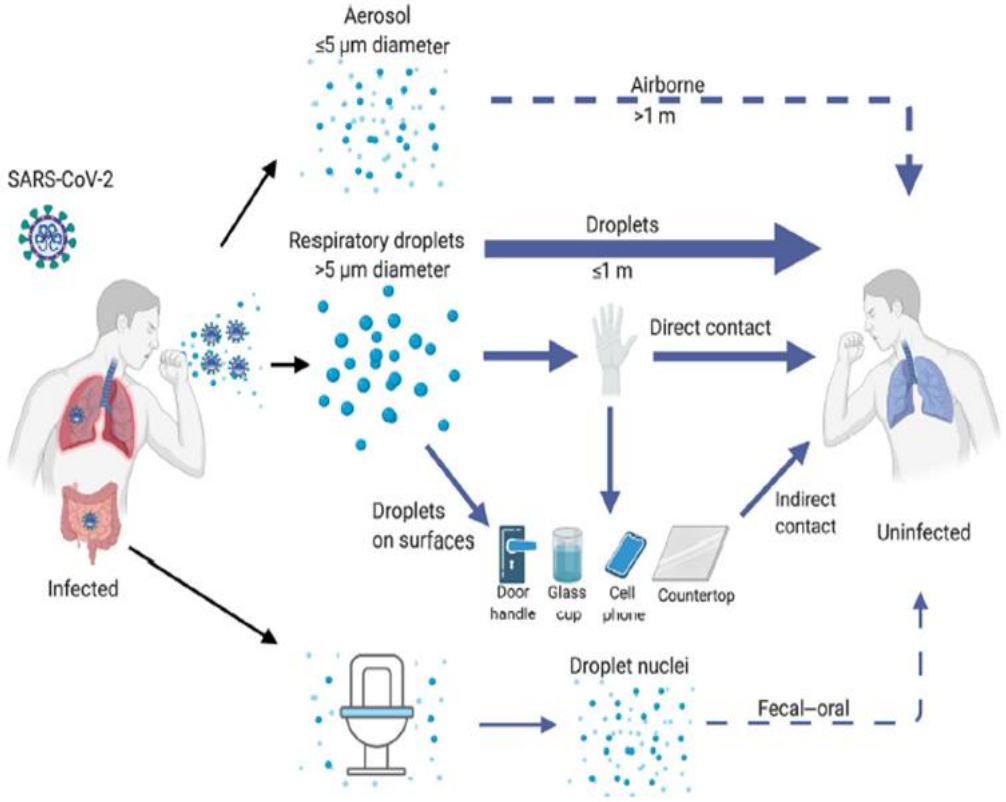


**Fig. 4: Proposed Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV2) Transmission Routes [29].**

Human coronaviruses, including MERS-CoV and endemic human coronaviruses, may survive for up to 9 days on surfaces like metal, glass, or plastic (Fig.4), but maybe effectively inactivated in 1 minute using 62–71 % ethanol, 0.5 % hydrogen peroxide, or 0.1 % sodium hypochlorite, according to a review of 22 research. Furthermore, the majority of existing research supports the hypothesis that a social distance of 1.5 m is sufficient to avoid airborne transmission [35].

Transmission appears to be possible for around 8 days after symptoms start. Patients may have a positive pharyngeal swab for several weeks after remission of symptoms, although the active virus

cannot be found after roughly 8 days of illness, implying that extended polymerase chain reaction (PCR) test positivity is unlikely to correlate with the clinical transmission [36].

Several mechanisms of transmission, such as aerosol, surface contamination, and the fecal-oral route, fomite, bloodborne, mother-to-child, and animal-to-human transmission, have been hypothesized as confounding variables in the current COVID-19 epidemic; hence, their relative importance is still being researched [37].

### II.4.2. Airborne transmission

Airborne transmission of SARS-CoV-2 is defined as the propagation of an infectious agent by the dissemination of droplet nuclei (aerosols) that stay infectious when suspended in the air for lengthy periods. Airborne transmission of SARS-CoV-2 can occur during medical procedures that produce aerosols (aerosol-generating operations) [38].

Another recent experimental model indicates that healthy people can emit aerosols by coughing and talking and another model reveals that particle emission rates during speaking vary widely between people [39], with higher rates correlating with higher vocalization amplitude. Transmission of SARS-CoV-2 by this type of aerosol pathway has yet to be demonstrated; considering the potential consequences of such a mode of transmission, much more investigation is needed [40].

### II.4.3. Fomite transmission

Infected people's secretions or droplets can contaminate surfaces and objects, leading to the formation of fomites (contaminated surfaces). Depending on the ambient environment (including temperature and humidity) and the type of surface, viable SARS-CoV-2 virus and/or RNA identified by RT-PCR can be discovered on those surfaces for periods ranging from hours to days [41].

As a result, transmission can happen inadvertently by contacting surfaces in the local area or devices contaminated with virus from an infected person (stethoscope or thermometer), then contacting the mouth, nose, and eyes [33].

### II.4.4. Other modes of transmission

SARS-CoV-2 RNA has also been detected in other biological samples, including the urine and feces of some patients. SARS-CoV-2 RNA is in plasma and serum in some tests. The virus can reproduce in blood cells, according to the researchers. The function of blood-borne transmission, on the other hand, is unclear, and low virus titers in plasma and serum suggest that the danger of infection by this route is weak[16, 22].Several studies are being conducted, to better understand SARS-CoV-2 susceptibility in various animal species. According to current research, individuals infected with SARS-CoV-2 can infect other mammals such as dogs, cats, and farmed mink.

However, it is uncertain if these diseased mammals constitute a major danger of human infection [42].

## II.5.Symptoms of SARS-CoV-2

People with COVID-19 have had a wide range of symptoms reported-ranging from mild symptoms to severe illness. Symptoms may appear 2-14 days after exposure to the virus. Anyone can have mild to severe symptoms. People with these symptoms may have COVID-19:Fever or chills, Cough, Shortness of breath or difficulty breathing, Fatigue, Muscle or body aches, Headache, New loss of taste or smell, Sore throat, Congestion or runny nose, Nausea or vomiting and Diarrhea [21,34,43].

This list does not include all possible symptoms. CDC will continue to update this list as we learn more about COVID-19. Older adults and people who have severe underlying medical conditions like heart or lung disease or diabetes seem to be at higher risk for developing more serious complications from COVID-19 illness [42].

## II.6.Pathogenesis and clinical manifestation

People infected with SARS-CoV-2 show a wild variety of clinical symptoms. It varies from minor sickness to severe pneumonia. Covid19 evaluated in three stages: The first stage is asymptotic, the second is upper airway responses and the last is hypoxia and progression to acute pneumonia [20].

Patients are asymptomatic yet contagious during stage 1 (the first two days of infection) within two days after being breathed, the virus seems to attach to epithelial cells in the nasal cavity and begins replicating. Although the viral load is generally low in the early stages of infection, SARS-CoV-2 may be identified by nasal and throat swabs, which may help determine the following clinical course [43].

The virus migrates down into the lower respiratory tract during the next several days (stage 2), inducing more innate immune responses. The clinical signs are observed at stage 2. Some innate response cytokine (XCL10) might be useful prognostic and predictive markers for subsequent infectivity and clinical course [44]. These prognostic indicators may also assist clinicians in determining whether patients require intensive monitoring. More than 80% of infected patients have minor symptoms and should be followed at home; approximately 20% progress to stage 3 infection and even suffer severe pneumonia. According to estimates, the general population's COVID-19 mortality rate is around 2%, however, this changes significantly among the elderly and people with underlying illnesses [14]. It should be mentioned that some infected persons are asymptomatic and go undetected by healthcare systems since they do not visit hospitals or clinics to be inspected by doctors. As a result, the mortality and morbidity rates must be updated [45].

At stage three, SARS-CoV-2 reaches the functional or gas exchange unit of the lung, which consists of alveolar ducts, alveolar sacs, and alveoli [32].

In comparison to other cells, it appears that this virus preferentially infects alveolar type II cells. The propagation of the virus within type II cells and consequently release several viral particles causes these cells to undergo apoptosis and die. Most scientists base their opinions on the pathogenesis of COVID-19 on the concept that SARS-CoV-2 enters the cell in the same way as SARS-CoV does. Overall, there are gaps in existing knowledge of COVID-19 pathogenesis that must be discovered [46].

## III.Comparison between different types of viruses

### III.1. Comparison between SARS-CoV, MERS-CoV and COVID19

To better understand the current COVID-19 pandemic caused by SARS-CoV-2, we have performed a comparative study between SARS-CoV-2 and past epidemic/pandemic viral infections that primarily affect the respiratory system: the two coronaviruses SARS-CoV and MERS-CoV (Table I).

**Table I: Differences and similarities between SARS-CoV, MERS-CoV and COVID19[41,42,43, 47, 48]**

| Type of virus / Comparison | SARS | MERS | COVID-19 |
|---|---|---|---|
| Name of the virus(pathogen) | SARS-CoV | MERS-CoV | SARS-CoV-2 |
| Disease | Severe acute respiratory syndrome | Middle east respiratory syndrome | Severe acute respiratory syndrome |
| Possible natural reservoir | Bat | Bat | Bat |
| Possible intermediate host | Palm civets | Camel | Malayan pangolins and turtles |
| Genomic properties of the virus | Giant, enveloped-positive stranded RNA virus with a genome of 29.727 nucleotides and two large genes ORF1a and ORF1b, which | Genome size of 30.119 nucleotides that encode for two replicase polyproteins, four structural proteins | RNA genome size is 29.9 nucleotides. Shares 80% nucleotides sequence identity with SARS-CoV. |

| | | | |
|---|---|---|---|
| | encode for 2 large polyproteins. | and 4 nonstructural proteins. | |
| The lineage of beta coronaviruses | **B** | **C** | **B** |
| Predominant cellular receptor (Host receptor) | ACE2. | Dipeptidyl peptidase 4 ($DDP_4$) known as $CD_{26}$ | ACE2 |
| Dominant cell entry pathway | Clathrin-and cavedae independent endocytic pathway | Cell membrane fusion | Endocytosis and plasma membrane fusion |
| Average Incubation period (days) | 4 to 5 | 6 to 7 | 1 to 14 |
| Symptoms | Fever, headache, dry cough, body aches, pain malaise. | Fever, dry cough, shortness of breath, diarrhea, nausea, vomiting. | Fever, dry cough, shortness of breath, fatigue, shortness of breath, loss of taste or smell, a rash on skin |
| Case fatality rate | 11% | 34% | 4.2% |
| Primary modes of transmission | Droplets discharged through cough or sneeze and by touching infected objects or surface. | Droplets discharged through cough or sneeze and by touching infected objects or surface. | Droplets discharged through cough or sneeze and by touching infected objects or surface. |
| Risk groups | People aged 65 years and above & people with medical conditions. | People aged 65 years and above & people with medical conditions. | People aged 65 years and above & people with medical conditions. |
| Treatment | Supportive medical care | Supportive medical care | Supportive medical care |

| | | | |
|---|---|---|---|
| Blood test results | Lymphopenia, thrombocytopenia and leukopenia. | Leucocytosis, monocyosis and low CRP. | Lymphopenia, thrombocytopenia, leukopenia, leucocytosis, monocytosis and low *C-reactive protein* (CRP). |
| Vaccination | No vaccines | No vaccines | 6 approved vaccines by WHO |

### III.2. Difference between COVID-19 and influenza

Both influenza (Flu) and COVID-19 are contagious respiratory infections, but the viruses that cause them are different. Infection with a novel corona virus (named SARS-CoV-2) causes COVID-19, while influenza viruses cause flu. COVID-19 appears to be more contagious than flu and can cause more serious disease in certain people. It may also take longer for patients to develop symptoms, and they may be contagious for extended period. Because certain flu and COVID-19 symptoms are similar, it may be difficult to distinguish between them based on symptoms alone, and testing may be required to help confirm a diagnosis [49].

## IV. SARS-CoV-2 variants

All viruses, including SARS-CoV-2, the virus that causes COVID-19, change over time. They constantly change through mutations; a variant has one or more mutation that differentiate it from other variants. Multiple variants of SARS-CoV-2 are circulating around the world through the pandemic[47].

The majority of the modifications have little or no effect on the virus's characteristics (properties). However, some modifications may have an impact on the virus properties, such as how quickly it spreads, the associated disease severity, or the performance of vaccines, therapeutic medicines, diagnostic tools, or other public health and social measures [50].

The established nomenclature systems for naming and tracking SARS-CoV-2 genetic lineages by GISAID, Nextstrain and Pango are currently and will remain in use by scientists and scientific research. To assist with public discussions of variants, WHO convened a group of scientists from the WHO Virus Evolution Working Group, the WHO COVID-19 reference laboratory network, representatives from GISAID, Nextstrain, Pango and additional experts in virological, microbial nomenclature and communication from several countries and agencies to consider easy-to-pronounce and non-stigmatising labels for Variants. There are the 3 variants [41].

### IV. 1. Variant of Concern (VOC)

A SARS-CoV-2 variant that meets the definition of a variant of interest (VOI). Through a comparative assessment is demonstrated to be associated with one or more of the following changes at a degree of global public health significance (table II): Increase in transmissibility, Cause more

severe disease, Significant reduction in neutralization by antibodies generated during previous infection or vaccination and Reduced effectiveness of treatments or vaccines, or diagnostic detection failures [35].

Table II: Selected characteristics of SARS-Cov-2 variants of concern [12, 35, 41, 45].

| WHO label | Panglo lineage (a) | GISAID clade/lineage | Lixtstrain (b) | Earliestdocumented samples | Date of disintegration | Attributes |
|---|---|---|---|---|---|---|
| Alpha | B.1.1.7 | GRY5formerly GR/501Y.V1) | 20I (V1) | United Kingdom Sep-2020 | 18/12/2020 | ~50% increased transmission. Potential increased severity based on hospitalizations and case fatality rates. No impact on susceptibility to EUA monoclonal antibody treatments. |
| Beta | B.1.351 | GH/501Y.V2 | 20H (V1) | South Africa May-2020 | 18/12/2020 | ~50% increased transmission Significantly reduced susceptibility to the combination of bamlanivimab and etesevimab monoclonal |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | antibody treatment, but other EUA monoclonal antibody treatments are available. Reduced neutralizatio n by convalescent and post-vaccination sera |
| Gam ma | P.1 | GR/501Y.V 3 | 20J (V3) | Brazil Nov-2020 | 11/01/2021 | Significantly reduced susceptibility to the combination of bamlanivima b and etesevimab monoclonal antibody treatment,bu t other EUA monoclonal antibody treatments are available. Reduced neutralizatio n by convalescent and post- |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | vaccination sera |
| Delta | B.1.617.2 | G/478.V1 | 21A | India Oct-2020 | VOI:4-Apr-2021 VOC:11-May-2021 | Increased transmissibility Potential reduction in neutralization by some EUA monoclonal antibody treatments potential reduction in neutralization by post vaccination sera. |

EUA: Emergency Use Authorization; VOC: variant of concern; VOI: variant of interest;

**(a):** Phylogenetic Assignment of Named Global Outbreak (PANGO) Lineages is software tool developed by members of the Rambaut Lab. The associated web application was developed by the Centre for Genomic Pathogen Surveillance in South Cambridgeshire and is intended to implement the dynamic nomenclature of SARS-CoV-2 lineages, known as the PANGO nomenclature

**(b):** Nextstrain, a collaboration between researchers in Seattle, USA and Basel, Switzerland, provides open-source tools for visualizing the genetics of outbreaks. The goal is to support public health surveillance by facilitating understanding of the spread and evolution of pathogens.

## IV.2. Variant of interest (VOI)

A SARS-CoV-2 isolate is a Variant of Interest (VOI), when compared to a reference isolate; its genome has mutations with known or suspected phenotypic implications. These mutations [47]:

- reduce neutralization by antibodies generated against past infections or vaccinations
- reduce therapeutic efficacy
- potential diagnostic impact
- predicted increase in transmissibility or disease severity

The table below shows the monitored and characterized the current variants around the world.

**Table III:** Selected Characteristics of SARS-CoV-2 Variants of interest [22,36,41,45,50]

| WHO label | Pango lineage (a) | GISSAID clade | Lixtstrain (b) | Earliestdocumented samples | Date of designation | Attributes |
|---|---|---|---|---|---|---|
| Epsilon | B.1.427 / B.1.429 | GH/452R.V1 | 21C | United States of America, Mar-2020 | 3/2020 | _____ |
| Zeta | P.2 | GR/484K.V2 | 20B/S.484K | Brazil, Apr-2020 | 17/3/2021 | Potential reduction in neutralization by some EUA monoclonal antibody treatments. Reduced neutralization by post-vaccination sera. |
| Eta | B.1.525 | G/484K.V3 | 21D | Multiple countries, Dec-2020 | 17/3/2021 | Potential reduction in neutralization by some EUA monoclonal antibody treatments. Potential reduction in neutralization by convalescent and post-vaccination sera* |

| | | | | | | |
|---|---|---|---|---|---|---|
| Theta | P.3 | GR/1092K.V1 | 21E | Philippines, Jan-2021 | 24/3/2021 | _____ |
| Lota | B.1.526 | GH/253G.V1 | 21F | United States of America, Nov-2020 | 24/3/2021 | Reduced susceptibility to the combination of bamlanivimab and etesevimab monoclonal antibody treatment; however, the clinical implications of this are not known.Alternative monoclonal antibody treatments are available.Reduced neutralization by convalescent and post-vaccination sera |
| Kappa | B.1.617.1 | G/452R.V3 | 21B | India, Oct-2020 | 4/3/2021 | Potential reduction in neutralization by some EUA monoclonal antibody treatments. |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | Potential reduction in neutralization by post-vaccination sera |
| Lambda | C.37 | GR/452Q.V1 | 20D | Peru, Aug-2020 | 14/6/2021 | _____ |

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### IV.3. Variant of high consequence (VOHC)

In comparison to previously circulating variations, a variant of high significance has clear evidence that preventive interventions or medical countermeasures (MCMs) are considerably less effective. In addition, to the possible attributes of a variant of concern [41].

- Impact on Medical Countermeasures (MCM)
  - Demonstrated Failure of diagnostics
  - Evidence of a substantial decrease in vaccination efficacy, a disproportionately proportion of vaccine breakthrough cases, or low vaccine-induced protection against severe disease.
  - Significantly reduced susceptibility to multiple EUA or approved therapeutics
  - More severe clinical disease and increased hospitalizations

Currently there are no SARS-CoV-2 variants that rise to the level of high consequence.

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