IJPSR (2024), Volume 15, Issue 2 **(Review Article)**

INTERNATIONAL JOURNAL OF PHARMACEUTICAL SCIENCES AND RESEARCH

Received on 19 May 2023; received in revised form, 02 August 2023; accepted, 22 November 2023; published 01 February 2024

AREVIEW OF COVID-19 IDENTIFICATION, CLASSI-FICATION, THERAPY, PREVENTION AND VACCINATION

Najmeen Nisha [*1], Neda Fatima [2], Hira Moid [3] and Anil Kumar [4]

Dr. Shakuntala Mishra National Rehabilitation University [1], Mohan Rd, Lucknow - 226017, Uttar Pradesh, India.
Dr. Ram Manohar Lohia Avadh University [2], Faizabad - 224001, Uttar Pradesh, India.
Integral University [3], Kursi Rd, Lucknow - 226026, Uttar Pradesh, India.
Babasaheb Bhim Rao Ambedkar University [4], Lucknow - 226025, Uttar Pradesh, India.

Keywords:

Coronavirus, Prevention, Diagnosis, Treatment, Antiviral, Immune system

Correspondence to Author:
Najmeen Nisha

M. Sc,
Department of Microbiology, Dr. Shakuntala Mishra National Rehabilitation University, Mohan Rd, Lucknow - 226017, Uttar Pradesh, India.

E-mail: najmeenn@gmail.com

ABSTRACT: The population is currently under threat from a new global health emergency called COVID-19 (Coronavirus Disease-2019). The World Health Organization has classified the virus epidemic as a public health emergency of international concern since December 2019, when COVID-19 first surfaced at a seafood market in Wuhan, South China, and spread quickly throughout the world (WHO). In order to inform potential COVID-19 patients about COVID-19 prevention, diagnosis, treatments, and prevention, we have summarized the most recent clinical characteristic data below. We gathered information for this evaluation from a number of research reports, WHO recommendations, and other articles. It is crucial to remind readers that new information on clinical traits, diagnoses, treatment plans, and outcomes for COVID-19 is updated almost hourly. The ailment has affected people to varied degrees all across the world. The patient displays a variety of symptoms, most frequently a fever, cough, sore throat, shortness of breath, exhaustion and malaise. The condition is treated with general care, symptomatic care, antiviral medication, oxygen therapy and the immune system. To limit the potential spread of infection to other patients and medical personnel, it is essential to detect probable cases as soon as feasible and to isolate the suspected cases from the confirmed COVID-19 cases.

INTRODUCTION: The word "coronavirus" comes from the Latin corona, which is a derivation from the Greek v korn, which means "garland, wreath." When June Almeida and David Tyrrell discovered and researched human coronaviruses, they came up with the term. An unofficial group of virologists initially coined the term to describe the new family of viruses in the journal Nature in 1968. The term is a reference to the virions' distinctive appearance under electron microscopy, which is characterized by a fringe of enormous, bulbous surface projections that resembles the solar corona or halo. The viral spike peplomers, which are proteins on the surface of the virus, produce this shape [1].

The first COVID-19 incident was observed. In Wuhan, China, a well-known seafood market where many people come to buy or trade seafood, 27 COVID-19 pneumonia cases were recorded by the WMHC (Wuhan Municipal Health Commission) as of December 31 [2]. The International Committee for the Nomenclature of Viruses (later renamed the International Committee

QUICK RESPONSE CODE

DOI: 10.13040/IJPSR.0975-8232.15(2).353-71

This article can be accessed online on www.ijpsr.com

DOI link: https://doi.org/10.13040/IJPSR.0975-8232.15(2).353-71

on Taxonomy of Viruses) approved the scientific name Coronavirus as a genus name in 1971 [3]. Large, approximately spherical particles with distinctive surface projections are coronaviruses. They have a wide variation in size, often between 80 and 120 nm in diameter. Extreme sizes between 50 and 200 nm in diameter are known. The typical molecular weight is 40,000 kDa. They are contained in a package that contains several protein molecules [4]. When the virus is outside the host cell, it is shielded by the lipid bilayer envelope, membrane proteins, and nucleocapsid [5]. The membrane (M), envelope (E), and spike (S) structural proteins are embedded in a lipid bilayer that makes up the viral envelope [6]. The lipid bilayer and the structural proteins E and M work together to shape and preserve the size of the viral envelope. In order to connect with the host cells, S proteins are required. The M protein of the human coronavirus NL63, as opposed to the S protein, has the binding site for the host cell. The envelope has an 85-nm diameter. In electron micrographs, the virus's envelope is seen as a discrete pair of electron-dense shells (shells that are relatively opaque to the electron beam used to scan the virus particle) [7]. The M protein, a type III membrane protein, is the primary structural protein of the envelope and gives it its overall form. It creates a layer that is 7.8 nm thick and is made up of residues of 218 to 263 amino acids. A short N-terminal ectodomain, a triple-spanning transmembrane domain, and a C-terminal endodomain make up its three domains. The C-terminal domain creates a lattice-like structure that increases the envelope's additional thickness. The amino-terminal region of a protein may contain either N- or O-linked glycans, depending on the species. The assembly, budding, envelope formation, and pathogenic phases of the virus lifecycle depend on the M protein [8].

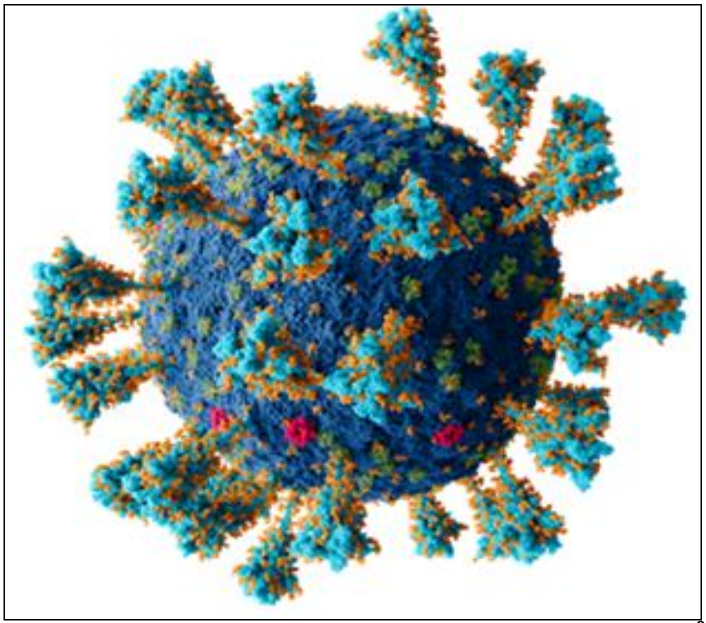

FIG. 1: ILLUSTRATION OF SARS-COV-2, THE VIRUS THAT CAUSES COVID-19 [8]. Blue: lipid bilayer envelope, Light blue: spike (S) glycoprotein, Red: envelope (E) proteins, Green: membrane (M) proteins, Orange: glycan.

A new human coronavirus illness since the 1918 flu pandemic, COVID-19, has been identified as the fifth pandemic. After being first discovered in Wuhan, China, COVID-19 quickly spread throughout the world. Based on a phylogenetic study, the coronavirus was given the name severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses. SARS-CoV-2 is thought to have evolved from an animal coronavirus through spillover and later picked up the capacity for human-to-human transmission. The virus spreads quickly among humans and is constantly evolving since it is so contagious. We analyze the fundamental characteristics, conceivable origin, and evolutionary history of the novel human coronavirus in this review article. The development of vaccines against the virus and research on pathogenicity may both depend on these elements [9].

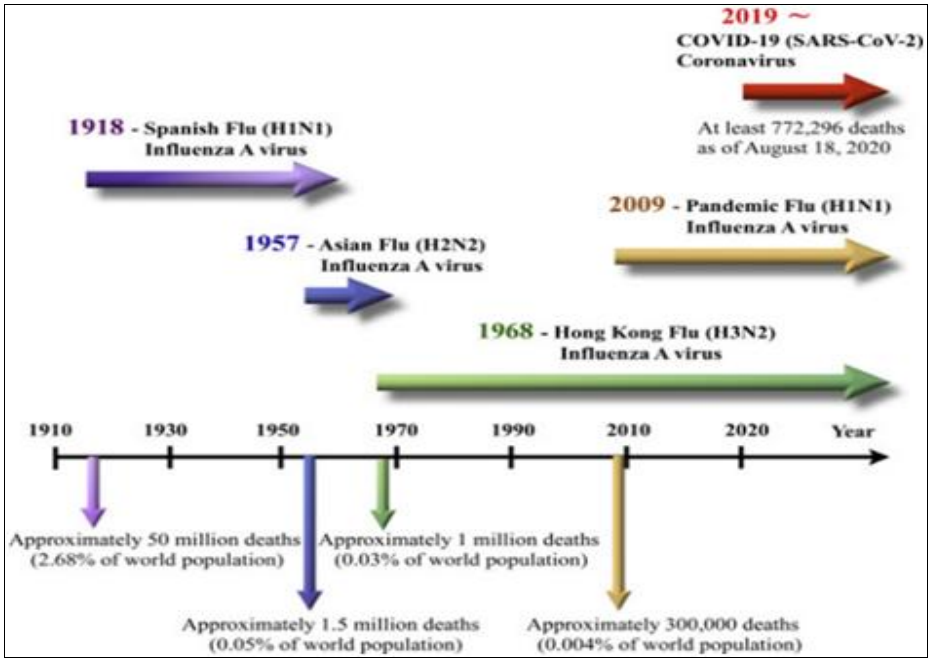

FIG. 2: A TIMELINE OF FIVE PANDEMICS SINCE 1918 AND THE GLOBALLY CIRCULATING VIRUSES AFTERWARD [9]

The fifth pandemic after the 1918 flu pandemic, coronavirus disease 2019 (COVID-19), is currently affecting individuals all over the world. Since late December 2019, we have been able to trace the first complaint and subsequent epidemic to a cluster of unique human pneumonia cases in Wuhan City, China. The earliest symptomatic date was December 1, 2019. Viral pneumonia was diagnosed based on these individuals' symptomatology, which included fever, lethargy, dry cough, and dyspnea [10]. Because of the location and the symptoms of pneumonia, the disease was initially referred to as Wuhan pneumonia by the media. A new coronavirus was identified as the cause by whole-genome sequencing data. Consequently, this virus is the eighth coronavirus family member to infect humans [11].

The World Health Organization (WHO) initially called the new virus 2019 novel coronavirus (2019-nCoV) on January 12, 2020, and coronavirus illness 2019 (COVID-19) on February 12, 2020, respectively. Later, the virus was officially designated SARS-CoV-2 by the International Committee on Taxonomy of Viruses (ICTV) based on phylogeny, taxonomy, and accepted practice [12]. Humans contract common colds from coronaviruses (CoV), which are also to blame for the Middle East and Severe Acute Respiratory Syndromes (SARS and MERS, respectively). Live attenuated vaccines (LAVs), some of which target the envelope (E) protein, a tiny membrane protein that creates ion channels, are a promising method of prophylaxis. Unfortunately, SARS-CoV E still has very little information, and other CoV E proteins have no precise structural information. Here, we present a structural model of a SARS-CoV E construct in LMPG micelles that contains clear intermolecular NOEs for the first time. The model for the detergent-embedded area agrees with orientational restrictions previously discovered in lipid bilayers and *in-vivo* escape mutants. The majority of the C-terminal domain is helical, and extramembrane intermolecular NOEs point to interactions that could influence the conformation of the TM channel [13].

CoVs were named after a viral particle with an envelope that resembles a crown. The CoV genome is the second-largest RNA virus genome and is a positive-sense, single-strand RNA (+ssRNA) with a size of 27–32 kb. Normally, two major overlapping polyproteins, ORF1a and ORF1b, which are processed into the viral polymerase (RdRp) and other nonstructural proteins involved in RNA synthesis or host response modulation, are encoded by two thirds of the genomic RNA. Four structural proteins (spike (S), envelope (E), membrane (M), and nucleocapsid (N)) and additional accessory proteins are encoded in the remaining part of the genome. The ORF1a/ORF1b and the four structural proteins are rather stable. However, the size and quantity of accessory proteins strongly influence the length of the CoV genome [14]. There are four primary structural proteins found in coronavirus particles. These are the proteins that are encoded at the 3′ end of the viral genome: the spike (S), membrane (M), envelope (E), and nucleocapsid (N). The 150 kDa S protein is extensively N-linked glycosylated and uses an N-terminal signal sequence to enter the ER. The unique spike structure on the surface of the virus is made up of homotrimers of the S protein expressed by virus [15]. A class I fusion protein is the trimeric S glycoprotein [16]. And facilitates a host receptor's adhesion [17]. In the majority of coronaviruses, S is split into two distinct polypeptides called S1 and S2 by a host cell furin-like protease. S2 makes up the stalk of the spike molecule, whereas S1 makes up the major receptor-binding domain of the S protein [18].

The M protein dominates the virion's structural protein composition. It is a Scientific term protein (about 25–30 kDa) with three transmembrane domains that is hypothesized to form the virion. Its C-terminal endodomain extends 6–8 nm inside the viral particle and possesses a significantly bigger N-terminal glycosylated ectodomain [19]. Most M proteins lack a signal sequence despite being co-translationally placed in the ER membrane. According to recent research, the M protein may exist as a dimer in the virion and may take on two distinct conformations that enable it to bind to the nucleocapsid and enhance membrane curvature [5].

The virion contains trace amounts of the E protein (8–12 kDa). Despite their significant divergence, the coronavirus E proteins share a similar design [20]. Although the E protein's membrane topology is not entirely clear, the majority of the available data points to it being a transmembrane protein. The E protein functions as an ion channel and has an N- and C-terminal ectodomain. Recombinant viruses lacking the E protein are not invariably fatal, in contrast to other structural proteins, however, virus type affects this [21]. The E protein helps the virus assemble and spread, but it also serves other purposes. For instance, the SARS-CoV E protein's ion channel function is needed for pathogenesis but not for viral replication [22].

The nucleocapsid contains solely the N protein as its protein. It is made up of two distinct domains, an N-terminal domain (NTD) and a C-terminal domain (CTD), both of which can bind RNA in vitro using various processes. It has been proposed that both domains are necessary for efficient RNA binding [23]. The N protein is also extensively phosphorylated, and it has been proposed that phosphorylation causes a structural alteration that increases the affinity for viral RNA as opposed to nonviral RNA. The N protein forms a conformation resembling beads on a string to bind the viral DNA. The genomic packing signal and the TRSs have been identified as two of the N protein's distinct RNA substrates [24]. It has been discovered that the genomic packing signal binds selectively to the second, or C-terminal, RNA binding domain. Additionally, the M protein and nsp3, a crucial part of the replicase complex, are bound by the N protein. These protein interactions probably aid in binding the viral DNA to the RTC and packaging the encapsulated genome into viral particles [25].

General Classification of Human Coronaviruses: Coronaviruses (CoVs) are positive-sensed single-stranded RNA viruses (ssRNA) encased in an envelope. They are members of the family Coronaviridae in the order Nidovirales. The word "Corona," which means "crown" in Latin, refers to the spike proteins that give the virus its distinctive crown-like appearance and enable it to engage with host cell receptors, a crucial stage in the process of penetrating the host cell membrane.

Based on differences in the protein sequence, this group of viruses is split into four genera: There are four different types of coronaviruses: alpha, beta, gamma, and delta [26]. Seven different coronavirus strains, including the alpha- and beta-coronaviruses HCoV-229E, HCoV-NL63, HCoV-OC43, HCoV-HKU1, SARS-CoV, MERS-CoV, and SARS-CoV-2, are known to infect people. Human coronavirus is abbreviated as HCoV; alpha-CoVs include HCoV-229E and HCoV-NL63, whereas beta-CoVs include HCoV-OC43 and HCoV-HKU1. The stomach flu, severe rhinitis, or common cold infections that result in diarrhea are only a few of the minor symptoms that these human coronaviruses typically produce [27].

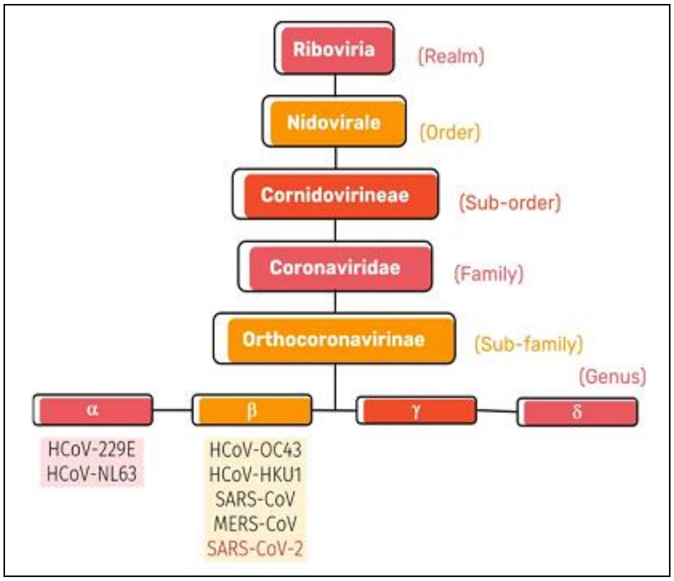

FIG. 3: CLASSIFICATION OF HUMAN CORONA-VIRUSES, SARS-COV, MERS-COV, AND SARS-COV-2 [24]

SARS-CoV, MERS-CoV and SARS-CoV-2, which are beta-CoVs, on the other hand are very contagious and pathogenic, increasing the risk that patients will contract severe acute respiratory infections such as pneumonia. SARS-CoV and MERS-CoV are zoonotic diseases that can be spread from animal to human during intimate contact, according to epidemiological evidence. It was discovered in 2002 that the SARS-CoV outbreak in Guangdong Province, China, was brought on by a bat-to-human transmission route using civet cats as the intermediary host. Ten years later, in 2012, it was determined that people and camels were the sources of the Middle East respiratory syndrome (MERS) outbreak caused by MERS-CoV from Saudi Arabia [28].

In China's Hubei Province, Wuhan, saw an outbreak of an unnamed pneumonia sickness in December 2019 that was brought on by a new coronavirus (nCoV) [29]. The novel coronavirus strain, which hasn't been discovered in people before, is known by the provisional designation nCoV. Prior to being given the name severe acute respiratory syndrome coronavirus 2 (SAR-CoV-2) by the International Committee on Taxonomy of Viruses, this novel strain of the virus was known as 2019-nCoV (ICTV) [25]. As of July 1, 2022, there were more than 545 million verified COVID-19 cases, including more than 6 million fatalities, according to the WHO. There were formerly four SARS-CoV-2 variants of concern (VOC): Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1), and Delta (B.1.617.2). However, on November 26, 2021, the WHO identified the Omicron variation, a new variety of concern that was initially revealed by experts in South Africa (B.1.1.529). Omicron is now the most common form in circulation worldwide as a result. These are brought on by mutations, particularly those that affect the spike protein's receptor-binding domain (RBD), which promotes viral replication in the upper respiratory tract and *in-vivo* transmission [30].

Replication Cycle:

Cell Entry: When the viral spike protein binds to the complementary host cell receptor, infection starts. The host cell's protease cleaves and activates the receptor-attached spike protein after attachment. Cleavage and activation enable the virus to enter the host cell via endocytosis or direct fusing of the viral envelope with the host membrane depending on the kind of host cell protease present [31]. Contacts between the S protein and its receptor start the initial attachment of the virion to the host cell. Different coronaviruses have different locations for their receptor binding domains (RBD), with some having them at the N-terminus of S1 (MHV), while others (SARS-CoV) have them at the C-terminus of S1 [32].

The S-protein-receptor interaction is the key factor in coronavirus infection of a host species and controls the virus's tissue tropism. Peptidase is used by many coronaviruses as their cellular receptor. Given that entrance happens even when these proteins' enzymatic domains are absent, it is unclear why peptidases are used. Many coronaviruses bind to aminopeptidase N (APN), SARS-CoV and HCoV-NL63 bind to angiotensin-converting enzyme 2 (ACE2), MHV enters through CEACAM1, and the recently discovered MERS-CoV binds to dipeptidyl-peptidase 4 (DPP4) to enter human cells [33]. Aminopeptidase N (APN), ACE2 (angiotensin-converting enzyme 2), DPP4 (dipeptidyl peptidase 4), mCEACAM (murine carcinoembryonic antigen-related adhesion molecule 1), TGEV (transmissible gastroenteritis virus), and PEDV (porcine epidemic diarrhea virus) are some examples of viruses; MHV (murine hepatitis virus), CCoV (canine coronavirus), BCoV (bvine coronavirus), FIPV (feline infectious peritonitis virus), the coronaviruses responsible for

SARS and MERS are both severe acute respiratory syndrome viruses [33].

Genome Translation: The non-segmented, 30-kb positive-sense RNA genome of coronaviruses is non-translated. The genome functions as an mRNA for the translation of the replicase polyproteins because it has a 5′ cap structure and a 3′ poly (A) tail. Contrary to the structural and accessory proteins, which make up only approximately 10 kb of the viral genome, the replicase gene for the non-structural proteins (nsps) takes up around two-thirds of the genome, or about 20 kb. A leader sequence and an untranslated region (UTR) with numerous stem loop structures necessary for RNA replication and transcription can be found near the 5′ end of the genome. Transcriptional regulatory sequences (TRSs), which are necessary for the expression of each of these genes, are also present at the start of each structural or auxiliary gene. RNA structures needed for viral RNA production and replication are also present in the 3′ UTR. The coronavirus genome is structured as a 5′-leader-UTR-replicase. At the 3′ end of the genome, there are structural genes with a 3′ UTR-poly (A) tail and auxiliary genes scattered throughout. In tissue culture, accessory proteins are almost entirely non-essential for replication, although several have been found to play crucial roles in viral pathogenesis [34].

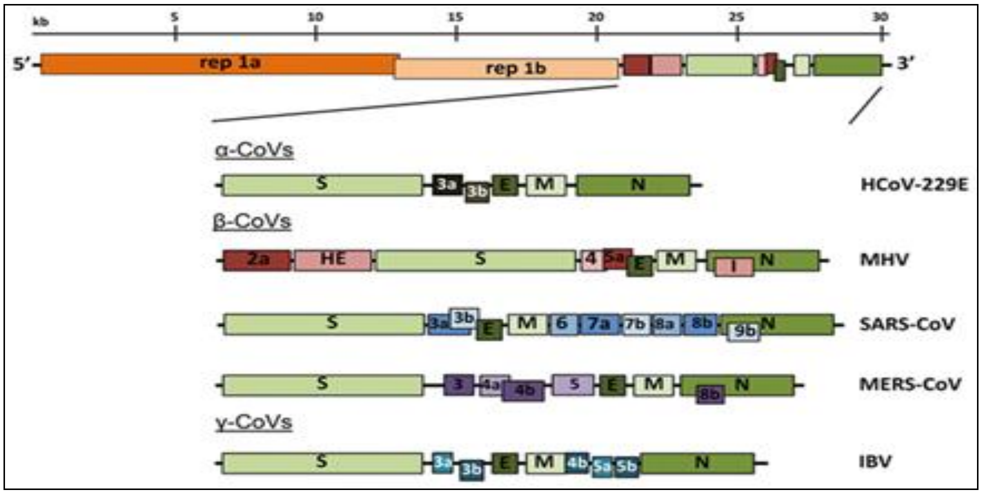

FIG. 4: GENOMIC ORGANIZATION OF REPRESENTATIVE Α, Β, AND Γ COVS. THE TOP OF THE IMAGE SHOWS A REPRESENTATION OF THE MHV GENOME. THE STRUCTURAL AND AUXILIARY PROTEINS IN THE 3′ SECTIONS OF THE HCOV-229E, MHV, SARS-COV, MERS-COV, AND IBV ARE VISIBLE IN THE PORTIONS BELOW THAT HAVE BEEN ENLARGED. SIZE OF THE GENOME AND INDIVIDUAL GENES ARE APPROXIMATED USING THE LEGEND AT THE *TOP* OF THE DIAGRAM BUT ARE NOT DRAWN TO SCALE. HUMAN CORONAVIRUS 229E (HCOV-229E), MOUSE HEPATITIS VIRUS (MHV), SEVERE ACUTE RESPIRATORY SYNDROME (SARS-COV), MIDDLE EAST RESPIRATORY SYNDROME (MERS-COV), AND INFECTIOUS BRONCHITIS VIRUS (IBV) ARE SOME EXAMPLES OF CORONAVIRUSES [32]

Replicase-transcriptase: A multi-protein replicase-transcriptase complex is created when a number of the non-structural proteins come together (RTC). The RNA-dependent RNA polymerase (RdRp) is the primary protein involved in replicase transcription. It participates directly in the transcription and replication of RNA from an RNA strand.

The complex's other non-structural proteins contribute to the processes of transcription and replication. For example, the exoribonuclease non-structural protein increases replication fidelity by performing a proofreading role that the RNA-dependent RNA polymerase is unable to do [35].

Replication: The translation of the replicase gene from the virion genomic RNA is the next phase in the coronavirus lifecycle. The replicase gene produces two co-terminal polyproteins, pp1a and pp1ab, by encoding two big ORFs, rep1a and rep1b.

The virus uses a slippery sequence (5′-UUUAAAC-3′) and an RNA pseudoknot to drive ribosomal frameshifting from the rep1a reading frame into the rep1b ORF in order to express both polyproteins. The ribosome typically unravels the pseudoknot structure and carries on translating until it comes across the rep1a stop codon. Sometimes the pseudoknot prevents the ribosome from extending translation into rep1b, forcing it to stall on the slippery sequence and move the reading frame back one nucleotide, or a -1 frameshift, before the ribosome is able to melt the pseudoknot structure and extend translation into pp1ab [36]. Ribosomal frameshifting may occur up to 25% of the time, according to *in-vitro* research; however, this hasn't been confirmed in relation to viral infection. Although the precise purpose of these viruses' use of frameshifting to regulate protein expression is unknown, it is believed to be either to precisely regulate the ratio of rep1b to rep1a proteins or to postpone the production of rep1b until the environment for RNA replication has been sufficiently prepared by rep1a's products [37].

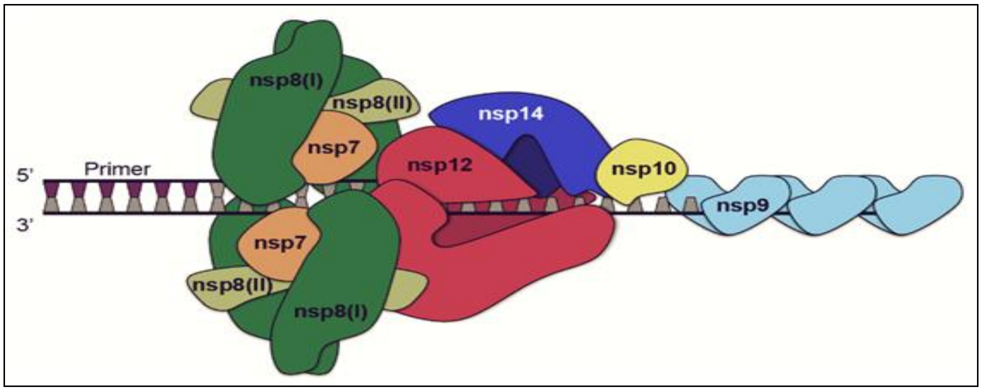

FIG. 5: REPLICATION COMPLEX OF RNA[38]

After that, a large number of NSPS come together to form the replicase-transcriptase complex (RTC), which is ultimately in charge of RNA replication and transcription of the sub-genomic RNAs. Other enzyme domains and activities, such as those necessary for RNA replication, are also encoded by the NSPS. For instance, nsp12 encodes the RNA-dependent RNA polymerase (RdRp) domain, nsp13 encodes the RNA helicase domain and RNA 5′-triphosphatase activity, nsp14 encodes the exoribonuclease (ExoN) involved in replication fidelity, and N7: Some of the NSPS have been found to perform additional actions outside replication, such as suppressing innate immunological responses (nsp1; nsp16-2′-O-methyl transferase; nsp3-deubiquitinase), while others have completely unidentified roles (nsp3-ADP-ribose-1′′-phosphatase; nuclease (Nendo). Non-structural proteins and their envisioned uses. Interestingly, the Nidovirales order is the only one that has the ribonucleases nsp15-NendoU and nsp14-ExoN activities, which are regarded as genetic identifiers for these viruses [39].

TABLE 1: FUNCTIONS OF CORONAVIRUS NON-STRUCTURAL PROTEINS (NSPS)

Protein	Function	References
nsp1	Promotes cellular mRNA degradation and blocks host cell translation, results in blocking innate immune response	39
nsp2	No known function, binds to prohibitin proteins	
nsp3	Large, multi-domain transmembrane protein, activities include: Ubl1 and Ac domains, interact with N protein. ADRP activity, promotes cytokine expression, PLPro/Deubiquitinase domain, cleaves viral polyprotein and blocks host innate immune response, Ubl2, NAB, G2M, SUD, Y domains, unknown functions	
nsp4	Potential transmembrane scaffold protein, important for proper structure of DMVs	
nsp5	Mpro, cleaves viral polyprotein	
nsp6	Potential transmembrane scaffold protein	
nsp7	Forms hexadecameric complex with nsp8, may act as processivity clamp for RNA polymerase	
nsp8	Forms hexadecameric complex with nsp7, may act as processivity clamp for RNA polymerase; may act as primase	
nsp9	RNA binding protein	
nsp10	Cofactor for nsp16 and nsp14, forms heterodimer with both and stimulates ExoN and 2-O-MT activity	
nsp12	RdRp	

nsp13	RNA helicase, 5′ triphosphatase	
nsp14	N7 MTase and 3′-5′ exoribonuclease, ExoN; N7 MTase adds 5′ cap to viral RNAs, ExoN activity is important for proofreading of viral genome	39
nsp15	Viral endoribonuclease, NendoU	
nsp16	2′-O-MT; shields viral RNA from MDA5 recognition	

Transcription: Viral replicase complexes are assembled and translated before being translated into viral RNA. Genomic and sub-genomic RNAs are both produced during viral RNA production. The structural and auxiliary genes located downstream of the replicase polyproteins are transcribed into messenger RNAs (mRNAs) by sub-genomic RNAs. A distinguishing characteristic of the order Nidovirales is that all positive-sense sub-genomic RNAs are 3′ co-terminal with the full-length viral genome and so constitute a set of nested RNAs. Negative-strand intermediates are used to create both genomic and sub-genomic RNAs. These poly-uridylate and anti-leader sequence-containing negative-strand intermediates are just 1% as prevalent as their positive-sense counterparts [40]. It takes a lot of cis-acting sequences for viral RNAs to replicate. Seven stem-loop structures that may extend into the replicase 1a gene can be found in the genome's 5′ UTR [41]. Transcription of the viral genome is the complex's additional significant function. RdRp directly mediates the conversion of positive-sense genomic RNA into negative-sense subgenomic RNA molecules. The transcription of these negative-sense subgenomic RNA molecules into their corresponding positive-sense mRNAs occurs after this step. The "nested set" of subgenomic mRNAs has a shared 5'-head and a largely duplicated 3'-end [42].

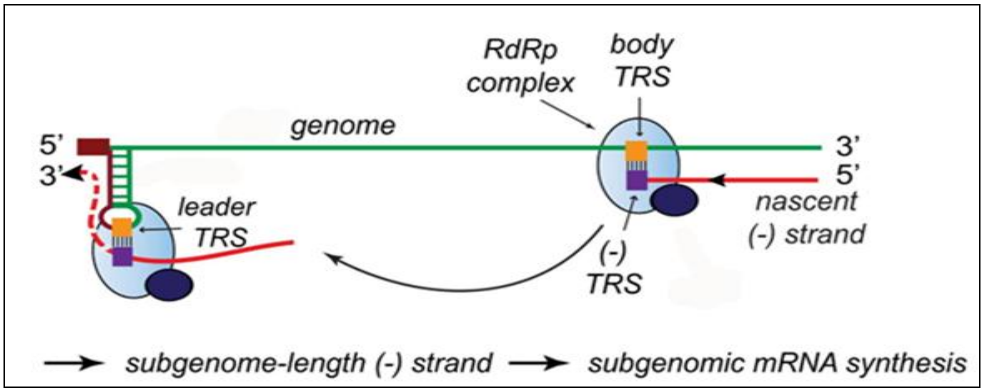

FIG. 6: EAV REPLICATION AND TRANSCRIPTION MODEL. CONTINUOUS MINUS-STRAND RNA SYNTHESIS, WHICH NSP1 IS NOT REQUIRED FOR, PRODUCES A GENOME-LENGTH NEGATIVE STRAND TEMPLATE FOR GENOME REPLICATION. A NESTED COLLECTION OF SUB GENOME-LENGTH MINUS STRANDS PRODUCED BY DISCONTINUOUS MINUS-STRAND RNA SYNTHESIS ACT AS TEMPLATES FOR THE PRODUCTION OF SG MRNA. NSP1 IS ESSENTIAL FOR THIS PROCESS, WHICH IS ALSO CONTROLLED BY A BASE PAIRING INTERACTION BETWEEN THE GENOMIC LEADER TRS, CONTAINED IN AN RNA HAIRPIN STRUCTURE (LTH), AND THE TRS COMPLEMENT [() TRS] AT THE 3′ END OF THE DEVELOPING MINUS-STRAND [43]

Recombination: When at least two viral genomes are present in the same infected cell, the replicase-transcriptase complex is also capable of genetic recombination. When it comes to the genetic diversity within a coronavirus species, the ability of a coronavirus species to jump from one host to another, sporadically, the formation of novel coronaviruses, RNA recombination appears to be a primary driving force. Although the precise mechanism of recombination in coronaviruses is unknown, template swapping probably occurs during genome replication [44].

Assembly and Release: Membranes are where virion assembly occurs. N protein binds to genomic RNA, which then connects with M protein and buds into the ER and Golgi membranes. M is assumed to be responsible for the membrane curvature that promotes budding because it packs densely into membranes. The membrane proteins S and E are also acquired during the budding process. The viroporin-like ion channel activity of E modifies cell secretory pathways to encourage virus release. E could improve the pH of the transport vesicles as one of its functions.

Exocytosis is the process by which membrane-bound vesicles containing virus particles are discharged from cells [45].

How Variants are classified: To improve coordination between the CDC, National Institutes of Health (NIH), Food and Drug Administration (FDA), Biomedical Advanced Research and Development Authority (BARDA), and Department of Defence, the U.S. Department of Health and Human Services (HHS) established a SARS-CoV-2 Interagency Group (SIG) (DOD). This interagency team is concentrated on the quick characterization of novel variations and actively tracks their potential influence on crucial SARS-CoV-2 countermeasures, such as vaccinations, treatments, and diagnostics. The SIG meets frequently to assess the threat posed by SARS-CoV-2 variants present in the US and to offer suggestions about variant classification. A team of experts in the field evaluates the information that is currently available, including variant proportions at the national and regional levels and the potential or known effects of the constellation of mutations on the efficacy of medical interventions, the severity of the illness, and the capacity for contagion. Variants may be reclassified based on their characteristics and prevalence in the United States in light of the fact that SARS-CoV-2 is a living organism that is constantly evolving and our understanding of how variants affect public health (CDC.gov.2021). https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html [46].

- Variants being monitored (VBM)
- Variant of interest (VOI)
- Variant of Concern (VOC)
- Variant of high consequence (VOHC)

TABLE 2: CLASSIFICATION OF COVID-19 VARIANTS

WHO Label	Pango Lineage	Date of Designation		
Alpha	B.1.1.7 and Q lineages	VOC: December 29, 2020		VBM: September 21, 2021
Beta	B.1.351 and descendent lineages	VOC: December 29, 2020		VBM: September 21, 2021
Gamma	P.1and descendent lineages	VOC: December 29, 2020		VBM: September 21, 2021
Delta	B.1.617.2 and AY lineages	VOC: June 15, 2021		VBM: April 14, 2022
Epsilon	B.1.427 B.1.429	VOC: March 19, 2021	VOI: February 26, 2021 VOI: June 29, 2021	VBM: September 21, 2021
Eta	B.1.525		VOI: February 26, 2021	VBM: September 21, 2021
Iota	B.1.526		VOI: February 26, 2021	VBM: September 21, 2021
Kappa	B.1.617.1		VOI: May 7, 2021	VBM: September 21, 2021
N/A	B.1.617.3		VOI: May 7, 2021	VBM: September 21, 2021
Zeta	P.2		VOI: February 26, 2021	VBM: September 21, 2021
Mu	B.1.621, B.1.621.1			VBM: September 21, 2021
Omicron	(B.1.1.529, BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5, BF.7 lineages)	VOC: November 24, 2021		

https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html [46].

Covid-19 Vaccine: A COVID-19 vaccination is a shot meant to protect against the coronavirus illness 2019 (COVID-19), also known as the severe acute respiratory syndrome coronavirus type 2 (SARS-CoV2). The structure and operation of coronaviruses that cause diseases like Middle East respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS) were well understood before the COVID-19 pandemic (MERS). This information sped up the creation of several vaccine platforms in early 2020 [47]. The SARS-CoV-2 vaccines initial goal was to avoid symptoms of the frequently serious sickness [48]. The genetic sequence data for SARS-CoV-2 was made available through GISAID in January-March 2020 and by March 2020, the global pharmaceutical sector had made a significant investment to combat COVID-19. The initial COVID-19 vaccinations were created and distributed to the general population in 2020 thanks to emergency authorizations and conditional approvals. With the Janssen COVID-19 vaccine being the lone exception, the majority of COVID-19 vaccinations were initially two-dose vaccines. However, it has been discovered that vaccine immunity wanes over time, necessitating booster doses of the vaccine to maintain protection against COVID-19. The genetic sequence data for SARS-CoV-2 was made available through GISAID in January 2020, and by March 2020, the global pharmaceutical sector had made a significant investment to combat COVID-19. The initial COVID-19 vaccinations were created and distributed to the general population in 2020 thanks to emergency authorizations and conditional approvals. With the Janssen COVID-19 vaccine being the lone exception, the majority of COVID-19 vaccinations were initially two-dose vaccines. However, it has been discovered that vaccination immunity wanes with time, necessitating booster doses of the vaccine in order to retain protection against COVID-19. The COVID-19 vaccines are largely recognized for helping to stop the disease spread as well as its severity and fatality rates [49]. Ten vaccines, including those produced by Pfizer-BioNTech, Oxford-AstraZeneca, Sinopharm BIBP, Moderna, Janssen, CoronaVac, Covaxin, Novavax, Convidecia, and Sanofi-GSK, have received approval for either emergency use or full use. Sputnik V, Sinopharm WIBP, Abdala, Zifivax, Corbevax, COVIran Barekat, and SCB-2019 are the other seven drugs that the WHO is currently evaluating. Out of the 40 vaccines, 16 have full or emergency approval in just one nation, 12 in ten or fewer nations, and 12 in more than ten. Be aware that in some countries, vaccinations may only be permitted for travel. They might not be accepted for use by the general public. The CoronaVac, Covishield, BBIBP-CorV, and Covaxin vaccines, for instance, are recognized for travel to Australia but are not included in Australia's national vaccination program. COVID-19 vaccines are authorized for emergency use or approved for full use [50].

TABLE 3: LIST OF COVID-19 VACCINE AUTHORIZATIONS [51]

Common name	Type (Technology)	Country of origin	First authorization	Notes
QazCovid-in	Inactivated	Kazakhstan	April 2021	
Valneva	Inactivated	France, Austria	April 2022	
Sputnik V	Adenovirus vector	Russia	April 2022	
CoronaVac	Inactivated	China	April 2022	
Soberana Plus	Subunit	Cuba	August 2021	
ZyCoV-D	DNA	India	August 2021	
Oxford–AstraZeneca	Adenovirus vector	United Kingdom, Sweden	December 2020	
Corbevax	Subunit	India,United States	December 2021	
Turkovac	Inactivated	Turkey	December 2021	
Janssen	Adenovirus vector	United States, Netherlands	February 2021	
Sinopharm WIBP	Inactivated	China	February 2021	
CoviVac	Inactivated	Russia	February 2021	
CoVLP	Virus-like particle	Canada, United Kingdom	February 2022	
Covaxin	Inactivated	India	January 2021	
Sinopharm BIBP	Inactivated	China	July 2020	
Abdala	Subunit	Cuba	July 2021	
Medigen	Subunit	Taiwan	July 2021	
Convidecia	Adenovirus vector	China	June 2020	
Soberana 02	Subunit	Cuba, Iran	June 2021	
COVIran Barekat	Inactivated	Iran	June 2021	
Chinese Academy of Medical Sciences	Inactivated	China	June 2021	
Skycovione	Subunit	South Korea	June 2022	
Zifivax	Subunit	China	March 2021	

Noora	Subunit	Iran	March 2021	
Sputnik Light	Adenovirus vector	Russia	May 2021	
Minhai	Inactivated	China	May 2021	
EpiVacCorona	Subunit	Russia	October 2020	
COVAX-19	Subunit	Australia, Iran	October 2021	
RaziCov Pars	Subunit	Iran	October 2021	
IndoVac	Subunit	Indonesia	October 2022	
FAKHRAVAC	Inactivated	Iran	September 2021	
Walvax	RNA	China	September 2022	
V-01	Subunit	China	September 2022	
Novavax	Subunit/virus-like particle	United States	December 2021	
Sanofi–GSK	Subunit	France, United Kingdom	November 2022	Based on Beta variant
Sinopharm CNBG	Subunit	China	December 2021	Based on original, Beta, and Kappa variants
Pfizer–BioNTech	RNA	Germany, United States	December 2020	Both original and Omicron variant versions
Moderna	RNA	United States	December 2020	Both original and Omicron variant versions
iNCOVACC	Adenovirus vector	India	September 2022	Nasal vaccine
Gemcovac	RNA	India	October 2022	Self-amplifying RNA vaccine

Prevention: Information on the COVID-19 vaccination, COVID-19 workplace hazard controls, Non-pharmaceutical intervention, and pandemic prevention COVID-19 preparations, COVID-19 monitoring, and COVID-19 applications Pathogens can spread rapidly in the absence of pandemic containment measures such as social isolation, immunization, and face masks. This diagram demonstrates how early adoption of containment measures typically tends to protect larger segments of the population. Vaccination, staying at home, wearing a mask in public, avoiding crowded areas, keeping a distance from others, ventilating indoor spaces, controlling potential exposure durations, washing hands frequently and for at least 20 seconds, practicing good respiratory hygiene, and avoiding touching the eyes, nose, or mouth with unwashed hands are all preventive measures to lessen the likelihood of infection.

The CDC advises people with COVID-19 or those who think they may be infected to stay at home unless they need medical attention, call ahead before going to the doctor's office, wear a face mask when in a shared room or vehicle, cover coughs and sneezes with tissues, frequently wash their hands with soap and water, and avoid sharing personal household items. On December 2, 2020, the UK pharmaceutical authority MHRA (Medicines and Healthcare Products Regulatory Agency) gave the first COVID-19 vaccination regulatory approval. The US FDA and numerous other nations assessed it for emergency use authorization (EUA) status. In the beginning, the US National Institutes of Health guidelines did not suggest any medication for COVID-19 prophylaxis, either before or after exposure to the SARS-CoV-2 virus. One of the most important aspects of managing COVID-19 is attempting to lessen and delay the epidemic peak, sometimes known as "flattening the curve," in the absence of a vaccine, other preventative measures, or efficient treatments. This is accomplished by reducing the rate of infection to lower the possibility that health systems would become overburdened, allowing for better treatment of cases that are already active, and postponing the onset of new instances until cures or vaccines are developed [52].

Vaccine: The coronavirus disease 2019 (COVID19) is caused by the SARS-CoV2 virus, and a COVID19 vaccine is a vaccination designed to induce acquired immunity against this virus. Before the COVID-19 pandemic, a corpus of knowledge regarding the structure and operation of coronaviruses responsible for illnesses including Middle East respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS) already existed. The creation of numerous vaccination platforms during the first half of 2020 was sped up by this information [47]. The main goal of SARS-CoV-2 vaccinations was to prevent symptomatic illness, which is frequently very serious. The genetic sequence data for SARS-CoV-2 was made available through GISAID in January 2020, and by March 2020, the global pharmaceutical sector had made a significant investment to combat COVID-19. The first COVID-19 vaccinations were created and distributed to the public in 2020 thanks to conditional permissions and emergency authorizations. However, it has been discovered that vaccine immunity wanes over time, necessitating booster doses of the vaccine to maintain protection against COVID-19 [48].

Face Masks and Respiratory Hygiene: The WHO and the US CDC advise people to use non-medical face coverings in public places where there is a higher risk of transmission and when it is challenging to maintain social distance practices. This advice is supposed to supplement proven preventive measures like social seclusion and is intended to lessen the transmission of the illness by asymptomatic and presymptomatic patients. Face covers reduce the amount and dispersion of exhalatory droplets released during breathing, speaking, and coughing. A face mask without vents or holes can help reduce the risk of infection by filtering out virus-carrying particles from the air breathed in and exhaled. Nevertheless, if the mask has an exhalation valve, an infected (and possibly asymptomatic) wearer could pass the virus through the valve. To stop the spread of the virus, several nations and local governments promote or require that people cover their faces with cloth or face masks [53].

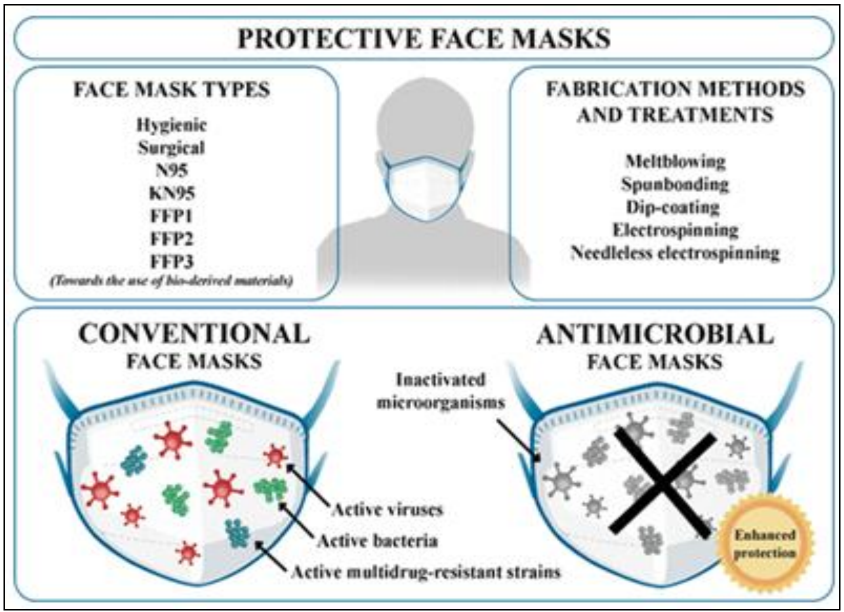

FIG. 7: A SELECTION OF PROTECTIVE MASKS [54]

Hand-washing and Hygiene: It is necessary to thoroughly wash your hands when you cough or sneeze. Additionally, the WHO advises people to often wash their hands with soap and water for at least 20 seconds, especially after using the restroom, before eating, after blowing their noses, and otherwise when their hands are obviously dirty. The CDC advises using an alcohol-based hand sanitizer with at least 60% alcohol when soap and water are not readily available. The WHO offers two formulations for local manufacturing in regions where commercial hand sanitizers are not easily accessible. Ethanol or isopropanol are the sources of the antibacterial action in these compositions. Hydrogen peroxide helps remove bacterial spores from alcohol but is "not an active agent for hand antisepsis." Added as a humectant is glycerol [55].

Social Distancing: Physical and social barriers are used in infection control to prevent intimate contact between people, which is meant to inhibit the spread of disease. Quarantines, travel restrictions, and the closure of workplaces, schools, stadiums, theatres, or retail malls are a few examples of methods. Staying at home, restricting travel, avoiding crowded places, utilizing no-contact greetings, and physically separating themselves from others are all examples of social distancing techniques that people can use. Many governments are requiring or advising social seclusion in areas where the pandemic is occurring [56].

Self-isolation: For those with a diagnosis of COVID-19 or who believe they may be infected, self-isolation at home has been advised. Health organizations have published comprehensive guidelines for appropriate self-isolation. Many governments have required or advised population-wide self-quarantine.

Those who are members of high-risk categories have received the strictest self-quarantine guidelines. It has been suggested that persons who may have come into contact with someone who has COVID-19 and those who have recently visited a place where the disease is being widely transmitted self-quarantine for 14 days starting from the time of their last probable exposure [57].

International Travel-related Control Measures: According to a 2021 Cochrane quick assessment, cross-border travel restrictions and other international travel-related control measures may assist in slowing the spread of COVID-19. Additionally, border screening procedures based on symptoms or exposure may fail to detect many positive cases.

Test-based border screening procedures may be more successful, but if they are just used once at the border and are not followed up on, they risk missing many positive instances. The study found that a minimum 10-day quarantine might help stop the spread of COVID-19 and might be even more effective if used in conjunction with another management approach like border screening [58].

Death Rate Depends on Age, Health, and Sexes: According to Tedros Adhanom Ghebreyesus, director-general of the World Health Organization, around 3.4% of recorded COVID-19 instances have resulted in fatalities worldwide. According to Matt Hancock, the health secretary for the UK government, the fatality rate is "2% or, possibly, lower." However, it varies depending on a number of variables, including general health, age, sex, and the healthcare system in your area. Women were the first to be greatly affected by the coronavirus. Nevertheless, from country to country, the figures vary slightly. It doesn't always correspond to biological differences. Scientists are still unsure for sure, but it's possible that men engage in unhealthy behaviors like drinking and smoking more frequently than women on average [55].

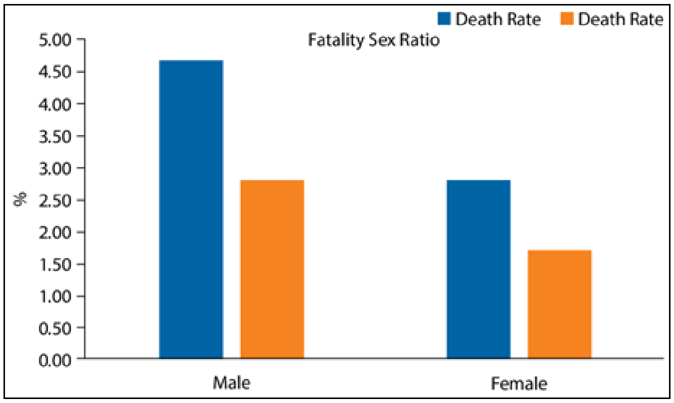

FIG. 8: A GRAPH SHOWED ON DEATH RATE DEPENDS ON AGE, HEALTH, AND GENDERS [55]

Countries or Territories with Reported Cases and Deaths: 229 nations and territories are currently impacted by the COVID-19 coronavirus. The day is restarted at 00:00 GMT. The United Nations Geoscheme is the foundation for the list of nations and their regional categorization. Under "Latest News," sources are listed. Learn more about the COVID-19 statistics from World meter [https://www.worldometers.info/coronavirus/] [59].

TABLE 4: THE NATIONS OR TERRITORIES WHERE CASES AND DEATHS HAVE BEEN REPORTED

S. no.	Country, Other	Total cases	New Cases	Total Deaths	New Deaths	Total Recovered	New Recovered	Active Cases	Total Tests	Population
1	China	5,03,302		5,272		3,79,053		1,18,977	16,00,00,000	1,44,84,71,400
2	India	4,46,81,884		5,30,726		4,41,47,983		3,175	91,23,62,106	1,40,66,31,776
3	USA	10,34,82,187		11,25,020		10,02,65,118		20,92,049	1,15,68,31,187	33,48,05,269
4	Indonesia	67,25,458		1,60,719		65,57,313		7,426	11,41,58,919	27,91,34,505
5	Pakistan	15,76,054	16	30,640	1	15,38,689		6,725	3,05,70,862	22,94,88,994
6	Nigeria	2,66,463		3,155		2,59,850		3,458	57,08,974	21,67,46,934
7	Brazil	3,66,23,217		6,95,334		3,54,74,747		4,53,136	6,37,76,166	21,53,53,593

8	Bangladesh	20,37,331		29,441		19,89,139		18,751	1,51,70,888	16,78,85,689
9	Russia	2,18,46,722		3,94,309		2,12,67,545		1,84,868	27,34,00,000	14,58,05,947
10	Mexico	73,09,154	5,554	3,31,510	58	65,36,180	3,428	4,41,464	1,91,98,152	13,15,62,772
11	Japan	3,11,76,281		61,761		2,12,96,635		98,17,885	8,83,89,228	12,55,84,838
12	Ethiopia	4,99,041		7,572		4,84,834		6,635	54,39,982	12,08,12,698
13	Philippines	40,69,734		65,553		39,91,690		12,491	3,41,39,206	11,25,08,994
14	Egypt	5,15,645		24,613		4,42,182		48,850	36,93,367	10,61,56,692
15	Vietnam	1,15,26,089		43,186		1,06,12,049		8,70,854	8,58,26,548	9,89,53,541
16	DRC	95,173		1,462		84,159		9,552	8,46,704	9,52,40,792
17	Iran	75,62,446		1,44,723		73,36,655		81,068	5,44,20,785	8,60,22,837
18	Turkey	1,70,42,722		1,01,492		N/A	N/A	N/A	16,27,43,369	8,55,61,976
19	Germany	3,76,05,135		1,63,775		3,70,17,500	8,100	4,23,860	12,23,32,384	8,38,83,596
20	Thailand	47,24,916		33,727		46,90,108		1,081	1,72,70,775	7,00,78,203
21	UK	2,42,43,393		2,02,157		*2,39,11,930*		1,29,306	52,25,26,476	6,84,97,907
22	France	3,94,42,176		1,63,347		*3,89,96,410*		2,82,419	27,14,90,188	6,55,84,518
23	Tanzania	42,467		846		N/A	N/A	N/A		6,32,98,550
24	South Africa	40,51,243		1,02,568		39,12,506		36,169	2,64,73,049	6,07,56,135
25	Italy	2,53,63,742		1,85,993		2,48,24,106		3,53,643	26,41,82,282	6,02,62,770
26	Kenya	3,42,672		5,688		3,36,824		160	39,63,314	5,62,15,221
27	Myanmar	6,33,741		19,490		6,14,199		52	98,71,462	5,52,27,143
28	Colombia	63,49,971		1,42,259		61,70,360		37,352	3,69,51,507	5,15,12,762
29	S. Korea	2,97,74,321	36,552	32,912	45	*2,87,39,329*	87,550	10,02,080	1,58,04,065	5,13,29,899
30	Uganda	1,70,279		3,630		1,00,431		66,218	30,12,408	4,84,32,863
31	Spain	1,37,11,251		1,17,759		1,35,22,850		70,642	47,10,36,328	4,67,19,142
32	Argentina	1,00,04,679		1,30,249		*97,34,360*	8,843	1,40,070	3,57,16,069	4,60,10,234
33	Sudan	63,702		4,995		*58,275*		432	5,62,941	4,59,92,020
34	Algeria	2,71,286		6,881		1,82,682		81,723	2,30,861	4,53,50,148
35	Ukraine	53,64,322		1,10,920		*52,45,191*		8,211	3,26,03,805	4,31,92,122
36	Iraq	24,65,545		25,375		24,39,497		673	1,95,44,451	4,21,64,965
37	Afghanistan	2,07,900		7,854		1,85,772		14,274	11,81,872	4,07,54,388
38	Canada	45,08,275		49,566		*44,00,717*	2,361	57,992	6,63,43,123	3,83,88,419
39	Morocco	12,72,022		16,295		12,55,456		271	1,28,91,382	3,77,72,756
40	Poland	63,72,901		1,18,640		53,35,940		9,18,321	3,80,46,705	3,77,39,785
41	Saudi Arabia	8,27,358		9,540		8,14,983		2,835	4,49,85,521	3,58,44,909
42	Angola	1,05,095		1,930		1,03,050		115	14,99,795	3,50,27,343
43	Uzbekistan	2,50,137		1,637		2,41,486		7,014	13,77,915	3,43,82,084
44	Peru	44,73,821		2,18,490		*42,41,294*	1,106	14,037	3,75,44,705	3,36,84,208
45	Malaysia	50,32,146		36,908		49,84,301		10,937	6,73,76,375	3,31,81,072
46	Mozambique	2,31,219		2,232		2,28,801		186	13,71,127	3,30,89,461
47	Ghana	1,71,088		1,462		1,69,612		14	25,25,773	3,23,95,450
48	Yemen	11,945		2,159		9,124		662	3,29,592	3,11,54,867
49	Nepal	10,01,046		12,020		9,88,998		28	59,96,192	3,02,25,582
50	Venezuela	5,50,881		5,834		5,44,423		624	33,59,014	2,92,66,991
51	Madagascar	67,760		1,418		66,316		26	5,23,108	2,91,78,077
52	Cameroon	1,23,993		1,965		1,18,616		3,412	17,51,774	2,79,11,548
53	Ivory Coast	87,960		833		87,121		6	16,67,605	2,77,42,298
54	Niger	9,931		312		8,890		729	2,54,538	2,60,83,660
55	Australia	1,12,47,412		17,712		1,11,46,950		82,750	7,88,35,048	2,60,68,792
56	DPRK	47,72,813		74		47,72,739		0		2,59,90,679
57	Taiwan	91,88,207	20,412	15,802	47	*86,83,645*	17,675	4,88,760	2,97,02,483	2,38,88,595
58	Burkina Faso	22,025		396		21,596		33	2,48,995	2,21,02,838
59	Sri Lanka	6,71,959		16,822		6,55,127		10	64,86,117	2,15,75,842
60	Mali	32,772		743		31,951		78	7,86,195	2,14,73,764
61	Malawi	88,220		2,685		85,065		470	6,24,784	2,01,80,839
62	Zambia	3,36,955		4,035		3,30,907		2,013	38,14,053	1,94,70,234
63	Syria	57,435		3,164		54,267		4	1,46,269	1,93,64,809
64	Chile	50,81,862		63,466		50,09,385		9,011	4,78,99,274	1,92,50,195
65	Kazakhstan	14,04,865	111	13,695		13,83,020		8,150	1,15,75,012	1,92,05,043
66	Romania	33,16,192		67,460		*32,41,020*		7,712	2,61,58,689	1,90,31,335
67	Guatemala	12,17,439		20,045		11,85,961		11,433	66,40,347	1,85,84,039
68	Ecuador	10,40,463		35,940		*10,04,523*		0	30,82,403	1,81,13,361
69	Senegal	88,900		1,968		86,915		17	11,46,543	1,76,53,671
70	Chad	7,651		194		4,874		2,583	1,91,341	1,74,13,580
71	Netherlands	85,76,523		22,989		*85,31,247*	1,017	22,287	2,59,84,435	1,72,11,447
72	Cambodia	1,38,659		3,056		1,35,581		22	30,91,420	1,71,68,639
73	Somalia	27,310		1,361		13,182		12,767	4,00,466	1,68,41,795
74	Zimbabwe	2,59,981		5,637		2,53,677		667	25,25,756	1,53,31,428

75	Guinea	38,210		466	37,292		452	6,60,107	1,38,65,691
76	Rwanda	1,33,063		1,468	1,31,112		483	59,59,042	1,36,00,464
77	Benin	27,982		163	27,817		2	6,04,310	1,27,84,726
78	Burundi	52,162		38	51,393		731	3,45,742	1,26,24,840
79	Tunisia	11,47,729		29,288	N/A	N/A	N/A	49,86,390	1,20,46,656
80	Bolivia	11,77,361		22,329	11,25,932		29,100	27,05,422	1,19,92,656
81	Haiti	33,969		860	32,977		132	1,32,422	1,16,80,283
82	Belgium	46,86,147		33,478	*46,23,545*		29,124	3,64,81,740	1,16,68,278
83	South Sudan	18,368		138	18,115		115	4,10,280	1,16,18,511
84	Cuba	11,12,252		8,530	11,03,573		149	1,42,76,770	1,13,05,652
85	Dominican Republic	6,50,990		4,384	6,44,785		1,821	37,40,928	1,10,56,370
86	Czechia	45,84,611		42,242	45,37,187		5,182	5,68,34,894	1,07,36,784
87	Greece	55,48,487		34,779	*55,13,708*		0	10,22,28,365	1,03,16,637
88	Jordan	17,46,997		14,122	17,31,007		1,868	1,72,01,885	1,03,00,869
89	Azerbaijan	8,27,228		10,042	8,16,647		539	74,53,564	1,03,00,205
90	Honduras	4,69,230		11,095	N/A	N/A	N/A	16,08,989	1,02,21,247
91	Sweden	26,87,840		22,610	*26,29,138*	2,427	36,092	1,93,69,173	1,02,18,971
92	Portugal	55,57,941		25,805	*55,26,851*	509	5,285	4,58,55,210	1,01,40,570
93	UAE	10,47,936		2,348	10,31,091		14,497	19,82,29,191	1,00,81,785
94	Tajikistan	17,786		125	17,264		397		99,57,464
95	Hungary	21,90,334		48,578	21,30,407		11,349	1,13,94,556	96,06,259
96	Belarus	9,94,037		7,118	9,85,592		1,327	1,36,46,641	94,32,800
97	Israel	47,75,264		12,111	47,53,341		9,812	4,13,73,364	93,26,000
98	Papua New Guinea	46,663		669	43,982		2,012	2,49,149	92,92,169
99	Austria	57,38,797		21,558	56,88,197		29,042	20,50,12,497	90,66,710
100	Switzerland	43,83,648		14,407	*43,41,532*	2,435	27,709	2,33,04,439	87,73,637
101	Togo	39,350		290	39,053		7	8,05,428	86,80,837
102	Serbia	24,58,228		17,590	*24,23,678*		16,960	1,19,90,447	86,53,016
103	Sierra Leone	7,760		126	N/A	N/A	N/A	2,59,958	83,06,436
104	Hong Kong	28,17,707		12,693	*21,91,097*		6,13,917	7,53,75,235	76,04,299
105	Laos	2,17,927	5	758	N/A	N/A	N/A	12,33,207	74,81,023
106	Paraguay	8,00,163		19,746	N/A	N/A	N/A	26,57,506	73,05,843
107	Libya	5,07,154		6,437	5,00,697		20	24,83,446	70,40,745
108	Bulgaria	12,94,070		38,138	12,52,218		3,714	1,09,37,902	68,44,597
109	Nicaragua	18,491		225	4,225		14,041		67,79,100
110	Kyrgyzstan	2,06,586		2,991	1,96,406		7,189	19,07,195	67,28,271
111	Lebanon	12,25,047		10,759	10,87,587		1,26,701	47,95,578	66,84,849
112	El Salvador	2,01,785		4,230	1,79,410		18,145	26,10,114	65,50,389
113	Singapore	22,11,131		1,717	21,37,821		71,593	2,47,56,374	59,43,546
114	Denmark	31,71,515		7,982	*31,57,088*		6,445	12,90,94,301	58,34,950
115	Congo	25,375		386	24,006		983	3,47,815	57,97,805
116	Finland	14,48,656		8,431	*14,28,985*	2,143	11,240	1,19,97,419	55,54,960
117	Norway	14,76,876		4,571	*14,69,946*		2,359	1,10,02,430	55,11,370
118	Slovakia	18,60,041		20,866	*18,38,217*		958	73,81,362	54,60,193
119	Palestine	6,21,008		5,404	6,15,445		159	30,78,533	53,45,541
120	Oman	3,99,154		4,260	3,84,669		10,225	2,50,00,000	53,23,993
121	Liberia	8,043		294	7,741		8	1,39,824	53,05,117
122	Costa Rica	11,71,802		9,104	8,60,711		3,01,987	46,59,757	51,82,354
123	Ireland	16,97,775		8,388	*16,76,786*		12,601	1,29,53,855	50,20,199
124	CAR	15,351		113	14,615		623	81,294	50,16,678
125	Mauritania	63,435		997	62,423		15	10,09,957	49,01,981
126	New Zealand	21,38,754		3,621	21,14,718		20,415	77,10,637	48,98,203
127	Panama	10,27,247		8,584	10,16,577		2,086	74,22,622	44,46,964
128	Kuwait	6,62,747		2,570	6,60,095		82	84,47,300	43,80,326
129	Croatia	12,66,259		17,752	12,47,174		1,333	54,48,800	40,59,286
130	Moldova	5,97,216		11,940	5,04,142		81,134	32,16,305	40,13,171
131	Georgia	18,11,015		16,909	17,76,548		17,558	1,69,20,079	39,68,738
132	Eritrea	10,189		103	10,086		0	23,693	36,62,244
133	Uruguay	10,25,810		7,586	10,13,059		5,165	61,14,822	34,96,016
134	Mongolia	10,07,821		2,179	*10,05,087*		555	40,30,048	33,78,078
135	Bosnia and Herzegovina	4,01,187		16,241	3,78,908		6,038	18,83,099	32,49,317
136	Jamaica	1,52,968		3,465	1,02,116		47,387	11,83,986	29,85,094
137	Qatar	4,91,177		685	4,89,892		600	40,65,369	29,79,915
138	Armenia	4,45,976		8,716	4,35,162		2,098	32,42,901	29,71,966

139	Albania	3,34,018	3,595	3,28,751		1,672	19,41,032	28,66,374
140	Lithuania	12,92,278	9,514	12,76,655		6,109	1,03,31,999	26,61,708
141	Namibia	1,70,369	4,082	1,66,197		90	10,62,663	26,33,874
142	Gambia	12,586	372	12,189		25	1,55,686	25,58,482
143	Botswana	3,28,230	2,795	3,23,747		1,688	20,26,898	24,41,162
144	Gabon	48,980	306	48,668		6	16,21,909	23,31,533
145	Lesotho	34,790	723	25,980		8,087	4,31,221	21,75,699
146	North Macedonia	3,46,095	9,623	3,36,215		257	22,10,818	20,81,304
147	Slovenia	13,16,918	7,032	12,98,423		11,463	28,14,897	20,78,034
148	Guinea-Bissau	8,947	176	8,656		115	1,45,231	20,63,367
149	Latvia	9,74,872	6,195	9,67,881		796	78,53,541	18,48,837
150	Bahrain	6,99,473	1,539	6,97,398		536	1,06,56,620	17,83,983
151	Equatorial Guinea	17,186	183	16,880		123	3,65,697	14,96,662
152	Trinidad and Tobago	1,86,685	4,297	1,82,182		206	8,82,325	14,06,585
153	Timor-Leste	23,405	138	23,102		165	2,78,529	13,69,429
154	Estonia	6,12,829	2,885	5,24,990		84,954	36,43,453	13,21,910
155	Mauritius	41,584	1,042	39,861		681	3,58,675	12,74,727
156	Cyprus	6,38,062	1,270	*6,27,239*		9,553	96,40,118	12,23,387
157	Eswatini	74,053	1,422	72,603		28	10,48,081	11,84,817
158	Djibouti	15,690	189	15,427		74	3,05,941	10,16,097
159	Fiji	68,793	883	66,752		1,158	6,67,116	9,09,466
160	Réunion	4,83,818	917	4,18,572		64,329	16,03,660	9,08,061
161	Comoros	8,986	161	8,822		3		9,07,419
162	Guyana	72,638	1,293	70,996		349	7,13,856	7,94,045
163	Bhutan	62,551	21	61,564		966	23,03,734	7,87,941
164	Solomon Islands	24,575	153	N/A	N/A	N/A		7,21,159
165	Macao	3,416	106	3,140		170	7,850	6,67,490
166	Luxembourg	2,97,757	1,133	2,88,991		7,633	44,12,567	6,42,371
167	Montenegro	2,85,483	2,794	2,82,163		526	26,86,929	6,27,950
168	Western Sahara	10	1	9		0		6,26,161
169	Suriname	82,020	1,398	N/A	N/A	N/A	2,39,603	5,96,831
170	Cabo Verde	63,220	412	62,742		66	4,01,622	5,67,678
171	Maldives	1,85,702	311	1,63,687		21,704	22,13,831	5,40,985
172	Brunei	2,72,646	225	2,43,601		28,820	7,17,784	4,45,431
173	Malta	1,16,781	822	1,15,149		810	21,04,197	4,44,033
174	Belize	70,397	688	69,605		104	5,76,016	4,12,190
175	Bahamas	37,491	833	36,366		292	2,57,839	4,00,516
176	Guadeloupe	2,00,965	1,003	N/A	N/A	N/A	9,38,039	3,99,794
177	Martinique	2,28,171	1,085	N/A	N/A	N/A	8,28,928	3,74,087
178	Iceland	2,08,459	229	N/A	N/A	N/A	19,96,384	3,45,393
179	Vanuatu	12,014	14	11,976		24	24,976	3,21,832
180	French Guiana	97,982	416	11,254		86,312	6,51,257	3,14,169
181	New Caledonia	79,724	314	79,234		176	98,964	2,90,915
182	Barbados	1,05,905	569	1,05,314		22	7,88,414	2,88,023
183	Mayotte	42,002	188	N/A	N/A	N/A	1,76,919	2,86,259
184	French Polynesia	77,957	649	N/A	N/A	N/A		2,84,164
185	Sao Tome and Principe	6,279	77	6,202		0	29,036	2,27,679
186	Samoa	16,008	29	1,605		14,374	1,87,397	2,02,239
187	Saint Lucia	29,759	409	29,095		255	2,10,983	1,85,113
188	Channel Islands	1,00,738	219	1,00,043		476	12,52,808	1,76,463
189	Curaçao	45,986	295	44,720		971	4,96,693	1,65,529
190	Kiribati	4,921	17	2,703		2,201		1,23,419
191	Micronesia	22,247	58	N/A	N/A	N/A	54,967	1,17,489
192	Grenada	19,680	238	19,358		84	1,82,981	1,13,475
193	St. Vincent Grenadines	9,563	121	9,429		13	1,13,272	1,11,551
194	Tonga	16,590	13	15,638		939	5,35,009	1,07,749
195	Aruba	43,936	236	42,438		1,262	1,77,885	1,07,609

196	Antigua and Barbuda	9,106		146		8,954		6	18,901	99,509
197	Seychelles	50,355		172		50,026		157		99,426
198	Isle of Man	38,008		116		N/A	N/A	N/A	1,50,753	85,732
199	Andorra	47,781		165		47,563		53	2,49,838	77,463
200	Dominica	15,760		74		15,673		13	2,29,344	72,344
201	Cayman Islands	31,472		37		8,553		22,882	2,22,773	67,277
202	Bermuda	18,718		155		18,529		34	10,23,546	61,939
203	Marshall Islands	15,554		17		15,528		9		60,057
204	Greenland	11,971		21		2,761		9,189	1,64,926	56,973
205	Saint Kitts and Nevis	6,578		46		6,523		9	1,26,861	53,871
206	Faeroe Islands	34,658		28		N/A	N/A	N/A	7,78,000	49,233
207	Sint Maarten	11,005		89		10,905		11	62,056	43,966
208	Monaco	16,021		65		15,936		20	78,646	39,783
209	Turks and Caicos	6,479		36		6,423		20	6,11,527	39,741
210	Saint Martin	12,222		63		1,399		10,760	1,12,382	39,730
211	Liechtenstein	21,311		88		21,186		37	1,12,457	38,387
212	San Marino	23,290		121		23,034		135	1,57,634	34,085
213	Gibraltar	20,379		111		16,579		3,689	5,34,283	33,704
214	British Virgin Islands	7,305		64		N/A	N/A	N/A	1,07,339	30,596
215	Caribbean Netherlands	11,646		38		10,476		1,132	30,126	26,647
216	Palau	5,976		9		5,965		2	68,587	18,233
217	Cook Islands	6,926		2		6,826		98	19,690	17,571
218	Anguilla	3,904		12		3,879		13	51,382	15,230
219	Tuvalu	2,805						2,805		12,066
220	Wallis and Futuna	3,427		7		438		2,982	20,508	10,982
221	Nauru	4,621		1		4,609		11	20,509	10,903
222	St. Barth	5,418		6		N/A	N/A	N/A	78,646	9,945
223	Saint Helena	1,806				2		1,804		6,115
224	Saint Pierre Miquelon	3,368		2		2,449		917	25,400	5,759
225	Montserrat	1,403		8		1,376		19	17,762	4,965
226	Falkland Islands	1,930				1,930		0	8,632	3,539
227	Niue	709				618		91		1,622
228	Tokelau	5						5		1,378
229	Vatican City	29				29		0		799
	World	67,08,79,580	62,650	67,28,418	151	64,20,60,993	1,36,979	2,20,90,169		
230	Diamond Princess	712		13		699		0		
231	MS Zaandam	9		2		7		0		

Highlighted in green= all cases have recovered from the infection. Highlighted in grey = all cases have had an outcome (there are no active cases).

CONCLUSION: People all across the world are currently being affected by the COVID-19 pandemic. Current management focuses on stopping the spread of the virus and giving sick patients supportive care without fundamental therapeutic procedures.

Future COVID-19 vaccines should take into consideration factors such as the creation of heat-stable vaccinations that are simple to give in tropical environments with limited resources. Regardless of political differences, nations may come together and collaborate to quickly and effectively implement the COVID-19 vaccination internationally.

ACKNOWLEDGEMENT: The Corresponding author would like to thanks Neda Fatima, Hira Moid, Anil Kumar for encouraging and supporting the manuscript's preparation.

CONFLICT OF INTEREST: The authors have no conflict of interest to declare.

REFERENCES:

1. Almeida JD, Berry DM, Cunningham CH, Hamre D, Hofstad MS, Mallucci L, McIntosh K and Tyrrell DA: Coronaviruses. Nature 1968; 220(5168): 650.
2. Bo W, Ahmad Z, Alanzi AR, Al-Omari AI, Hafez EH and Abdelwahab SF: The current COVID-19 pandemic in China: An overview and corona data analysis. Alexandria Engineering Journal 2022; 61(2): 1369-81.
3. Lalchhandama K: The chronicles of coronaviruses: the bronchitis, the hepatitis and the common cold. Science Vision 2020; 20(1): 43-53.
4. Goldsmith CS, Tatti KM, Ksiazek TG, Rollin PE, Comer JA, Lee WW, Rota PA, Bankamp B, Bellini WJ and Zaki SR: Ultrastructural characterization of SARS coronavirus. Emerging Infectious diseases 2004; 10(2): 320.
5. Neuman BW, Kiss G, Kunding AH, Bhella D, Baksh MF, Connelly S, Droese B, Klaus JP, Makino S, Sawicki SG and Siddell SG: A structural analysis of M protein in coronavirus assembly and morphology. Journal of Structural Biology 2011; 174(1): 11-22.
6. Lai MM and Cavanagh D: The molecular biology of coronaviruses. Advances in Virus Research 1997; 48: 1-00.
7. Naskalska A, Dabrowska A, Szczepanski A, Milewska A, Jasik KP and Pyrc K: Membrane protein of human coronavirus NL63 is responsible for interaction with the adhesion receptor. Journal of Virology 2019; 93(19): 00355-19.
8. Schoeman D and Fielding BC: Proteína de envoltura de coronavirus: conocimiento actual. Virol J 2019; 16: 69.
9. Liu YC, Kuo RL and Shih SR: COVID-19: The first documented coronavirus pandemic in history. Biomedical Journal 2020; 43(4): 328-33.
10. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X and Cheng Z: Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. The Lancet 2020; 395(10223): 497-506.
11. Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei YY and Yuan ML: A new coronavirus associated with human respiratory disease in China. Nature 2020; 579(7798): 265-9.
12. Gorbalenya AE, Baker SC, Baric RS, de Groot RJ, Drosten C, Gulyaeva AA, Haagmans BL, Lauber C, Leontovich AM, Neuman BW and Penzar D: Severe acute respiratory syndrome-related coronavirus: The species and its viruses–a statement of the Coronavirus Study Group. BioRxiv 2020.
13. Surya W, Li Y and Torres J: Structural model of the SARS coronavirus E channel in LMPG micelles. Biochimica et Biophysica Acta (BBA)-Biomembranes 2018; 1860(6): 1309-17.
14. Fan Y, Zhao K, Shi ZL and Zhou P: Bat coronaviruses in China. Viruses 2019; 11(3): 210.
15. Beniac DR, Andonov A, Grudeski E and Booth TF: Architecture of the SARS coronavirus prefusion spike. Nature Structural & Molecular Biology 2006; 13(8): 751-2.
16. Bosch BJ, Van der Zee R, De Haan CA and Rottier PJ: The coronavirus spike protein is a class I virus fusion protein: structural and functional characterization of the fusion core complex. Journal of Virology 2003; 77(16): 8801-11.
17. Collins AR, Knobler RL, Powell H and Buchmeier MJ: Monoclonal antibodies to murine hepatitis virus-4 (strain JHM) define the viral glycoprotein responsible for attachment and cell-cell fusion. Virology 1982; 119(2): 358-71.
18. Luytjes W, Sturman LS, Bredenbee PJ, Charite J, van der Zeijst BA, Horzinek MC and Spaan WJ: Primary structure of the glycoprotein E2 of coronavirus MHV-A59 and identification of the trypsin cleavage site. Virology 1987; 161(2): 479-87.
19. Nal B, Chan C, Kien F, Siu L, Tse J, Chu K, Kam J, Staropoli I, Crescenzo-Chaigne B, Escriou N and van Der Werf S: Differential maturation and subcellular localization of severe acute respiratory syndrome coronavirus surface proteins S, M and E. Journal of General Virology 2005; 86(5): 1423-34.
20. Godet M. L Haridon R and Vantherot JF: TGEY coronavirus oRF encodes a membrane protein that is incorporated into virions. J Vird 1992; 188: 666-75.
21. Chang CK, Sue SC, Yu TH, Hsieh CM, Tsai CK, Chiang YC, Lee SJ, Hsiao HH, Wu WJ, Chang WL and Lin CH: Modular organization of SARS coronavirus nucleocapsid protein. Journal of Biomedical Science 2006; 13: 59-72.
22. Tuñón-Molina A, Takayama K, Redwan EM, Uversky VN, Andrés J and Serrano-Aroca Á: Protective face masks: current status and future trends. ACS Applied Materials & Interfaces 2021; 13(48): 56725-51.
23. Hurst KR, Koetzner CA and Masters PS: Identification of *in-vivo*-interacting domains of the murine coronavirus nucleocapsid protein. Journal of Virology 2009; 83(14): 7221-34.
24. Molekamp R and Spaan WJ: Identification of a specific interaction between the mouse hepatitis virus A59 nucleocapsid protein and packaging signal. Virology 1997; 239: 78-86.
25. Sturman LS, Holmes KV and Behnke J: Isolation of coronavirus envelope glycoproteins and interaction with the viral nucleocapsid. Journal of Virology 1980; 33(1): 449-62.
26. Khan MM, Goh YW, Ahmad N and Siddique MM: Understanding and combating COVID-19 using the biology and chemistry of SARS-CoV-2. Bioprocess and Biosystems Engineering 2022; 45(11): 1753-69.
27. Ye ZW, Yuan S, Yuen KS, Fung SY, Chan CP and Jin DY: Zoonotic origins of human coronaviruses. International Journal of Biological Sciences 2020; 16(10): 1686.
28. Shereen MA, Khan S, Kazmi A, Bashir N and Siddique R: COVID-19 infection: Emergence, transmission, and characteristics of human coronaviruses. Journal of Advanced Research 2020; 24: 91-8.
29. Amin SA and Jha T: Fight against novel coronavirus: a perspective of medicinal chemists. European Journal of Medicinal Chemistry 2020; 201: 112559.
30. Escalera A, Gonzalez-Reiche AS, Aslam S, Mena I, Laporte M, Pearl RL, Fossati A, Rathnasinghe R, Alshammary H, van de Guchte A and Farrugia K: Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission. Cell Host & Microbe 2022; 30(3): 373-87.
31. Simmons G, Zmora P, Gierer S, Heurich A and Pöhlmann S: Ativaçãoproteolítica de pico de proteína SARS-coronavírus: enzimas de cortenavanguarda da pesquisa antiviral. Antiviral Res 2013; 100: 605-14.
32. Kubo H, Yamada YK and Taguchi F: Localization of neutralizing epitopes and the receptor-binding site within the amino-terminal 330 amino acids of the murine coronavirus spike protein. Journal of Virology 1994; 68(9): 5403-10.

33. Cheng PK, Wong DA, Tong LK, Ip SM, Lo AC, Lau CS, Yeung EY and Lim WW: Viral shedding patterns of coronavirus in patients with probable severe acute respiratory syndrome. The Lancet 2004; 363(9422): 1699-700.
34. Fehr AR, Perlman S, Maier HJ, Bickerton E and Britton P: An overview of their replication and pathogenesis; section 2 genomic organization. Methods in Molecular Biology 2015; 1282: 1-23.
35. Sexton NR, Smith EC, Blanc H, Vignuzzi M, Peersen OB and Denison MR: Homology-based identification of a mutation in the coronavirus RNA-dependent RNA polymerase that confers resistance to multiple mutagens. Journal of Virology 2016; 90(16): 7415-28.
36. Baranov PV, Henderson CM, Anderson CB, Gesteland RF, Atkins JF and Howard MT: Programmed ribosomal frameshifting in decoding the SARS-CoV genome. Virology 2005; 332(2): 498-510.
37. Araki K, Gangappa S, Dillehay DL, Rouse BT, Larsen CP and Ahmed R: Pathogenic virus-specific T cells cause disease during treatment with the calcineurin inhibitor FK506: implications for transplantation. Journal of Experimental Medicine 2010; 207(11): 2355-67.
38. Smith EC and Denison MR: Coronaviruses as DNA wannabes: a new model for the regulation of RNA virus replication fidelity. PLoS Pathogens 2013; 9(12): 1003760.
39. Snijder EJ, Bredenbeek PJ, Dobbe JC, Thiel V, Ziebuhr J, Poon LL, Guan Y, Rozanov M, Spaan WJ and Gorbalenya AE: Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. Journal of Molecular Biology 2003; 331(5): 991-1004.
40. Sethna PB, Hofmann MA and Brian DA: Minus-strand copies of replicating coronavirus mRNAs contain antileaders. Journal of Virology 1991; 65(1): 320-5.
41. Raman S, Bouma P, Williams GD and Brian DA: Stem-loop III in the 5′ untranslated region is a cis-acting element in bovine coronavirus defective interfering RNA replication. Journal of Virology 2003; 77(12): 6720-30.
42. Bentley K, Keep SM, Armesto M and Britton P: Identification of a noncanonically transcribed subgenomic mRNA of infectious bronchitis virus and other gammacoronaviruses. Journal of Virology 2013; 87(4): 2128-36.
43. Nedialkova DD, Gorbalenya AE and Snijder EJ: Arterivirus Nsp1 modulates the accumulation of minus-strand templates to control the relative abundance of viral mRNAs. PLoS Pathogens 2010; 6(2): 1000772.
44. Su S, Wong G, Shi W, Liu J, Lai AC, Zhou J, Liu W, Bi Y and Gao GF: Epidemiology, genetic recombination, and pathogenesis of coronaviruses. Trends in Microbiology 2016; 24(6): 490-502.
45. Gonzalez JM, Gomez-Puertas P, Cavanagh D, Gorbalenya AE and Enjuanes L: A comparative sequence analysis to revise the current taxonomy of the family Coronaviridae. Archives of Virology 2003; 148(11).
46. https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html
47. Li YD, Chi WY, Su JH, Ferrall L, Hung CF and Wu TC: Coronavirus vaccine development: from SARS and MERS to COVID-19. Journal of Biomedical Science 2020; 27(1): 1-23.
48. Subbarao K: The success of SARS-CoV-2 vaccines and challenges ahead. Cell Host & Microbe 2021; 29(7): 1111-23.
49. Mallapaty S, Callaway E, Kozlov M, Ledford H, Pickrell J and Van Noorden R: How COVID vaccines shaped 2021 in eight powerful charts. Nature 2021; 600(7890): 580-3.
50. Yan Y, Pang Y, Lyu Z, Wang R, Wu X, You C, Zhao H, Manickam S, Lester E, Wu T and Pang CH: The COVID-19 vaccines: recent development, challenges and prospects. Vaccines 2021; 9(4): 349.
51. https://www.ema.europa.eu/en/human-regulatory/overview/public-health-threats/coronavirus-disease-covid-19/treatments-vaccines/vaccines-covid-19/covid-19-vaccines-authorised#originally-authorised-covid-19-vaccines-section
52. Anderson RM, Heesterbeek H, Klinkenberg D and Hollingsworth TD: How will country-based mitigation measures influence the course of the COVID-19 epidemic. The Lancet 2020; 395(10228): 931-4.
53. Greenhalgh T, Schmid MB, Czypionka T, Bassler D and Gruer L: Face masks for the public during the covid-19 crisis. BMJ 2020; 369.
54. Tuñón-Molina A, Takayama K, Redwan EM, Uversky VN, Andrés J and Serrano-Aroca Á: Protective face masks: current status and future trends. ACS Applied Materials & Interfaces 2021; 13(48): 56725-51.
55. Hafeez A, Ahmad S, Siddqui SA, Ahmad M and Mishra S: A review of COVID-19 (Coronavirus Disease-2019) diagnosis, treatments and prevention. EJMO 2020; 4(2): 116-25.
56. Qian M, Peng R, Yue C, Yang Z, Zhu H, Liu B and Xie M: A Comparison Study of ChaihuShugan San and Fluoxetine on Antidepression and Regulating Blood Rheology Effects with Chronic Restrained Stress Rats. Evidence-Based Complementary and Alternative Medicine 2020; 2020: 1-8.
57. Chtourou H, Trabelsi K, H'mida C, Boukhris O, Glenn JM, Brach M, Bentlage E, Bott N, Shephard RJ, Ammar A and Bragazzi NL: Staying physically active during the quarantine and self-isolation period for controlling and mitigating the COVID-19 pandemic: a systematic overview of the literature. Frontiers in Psychology 2020; 11: 1708.
58. Burns J, Movsisyan A, Stratil JM, Biallas RL, Coenen M, Emmert-Fees KM, Geffert K, Hoffmann S, Horstick O, Laxy M and Klinger C: International travel-related control measures to contain the COVID-19 pandemic: a rapid review. Cochrane Database of Systematic Reviews. 2021(3).
59. [https://www.worldometers.info/coronavirus/

How to cite this article:
Nisha N, Fatima N, Moid H and Kumar A: A review of covid-19 identification, classification, therapy, prevention and vaccination. Int J Pharm Sci & Res 2024; 15(2): 353-71. doi: 10.13040/IJPSR.0975-8232.15(2).353-71.