

## What is the Coronavirus pandemic?

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### Abstract:

A brand-new coronavirus, Prior until this, The severe acute respiratory syndrome coronavirus (SARS-CoV-2) has not been linked to any human cases. Wuhan was the first place where SARS-CoV-2 coronavirus infection appeared, Hubei Province, China. Later, it spread throughout the rest of China and the world, prompting the declaration of a new epidemic. The virus is extremely contagious and spreads among humans through intimate contact, mostly by respiratory droplets with an infected person. This boosts the virus' potential to infect more people.

Like other coronaviruses, There are 10 open reading frames in the SARS-CoV-2 genome (ORFs). The SARS-CoV-2 spike protein has a more favorable impact on the ACE2 receptor as compared to SARS-CoV. The discovery of the immune evasion mechanism linked to the pathophysiology Probably one of the most important developments in our knowledge of SARS-CoV-2 infection is the discovery of cytokine storm syndrome during infection. There are now various projects looking for COVID-19 prevention strategies.

**Keywords:** Coronavirus , Epidemic , Covid-19 , Wuhan China , Pneumonia , SARS. CoV.2 .

### ما هي جائحة فيروس كورونا؟

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### مستخلص:

قبل معرفة ووصف فيروس كورونا الجديد ، لم يتم ربط فيروس كورونا بالمتلازمة التنفسية الحادة الوخيمة (SARS-CoV-2) بأي من الحالات البشرية. كانت ووهان أول مكان ظهرت فيه عدوى فيروس كورونا (SARS-CoV-2) في مقاطعة هوبي بالصين. وفيما بعد ، انتشر في جميع أنحاء الصين والعالم ، مما دفع إلى إعلان وباء جديد. الفيروس شديد العدوى وينتشر بين البشر عن طريق الاتصال الحميم ، في الغالب عن طريق الرذاذ التنفسي مع الشخص المصاب. وهذا مما يزيد من قدرة الفيروس على إصابة المزيد من الناس.

ومثل الفيروسات التاجية الأخرى ، هناك 10 إطارات قراءة مفتوحة (ORFs) في الجينوم. وان بروتين الاشواك للفايروس له تأثير أكثر إيجابية على مستقبلات الإنزيم المحول للأنجيوتنسين (ACE2) مقارنة بـ SARS-CoV وان اكتشاف آلية الهروب المناعي المرتبطة بالفيزيولوجيا المرضية من المحتمل أن تكون أحد أهم التطورات في معرفتنا بعدوى SARS-CoV-2 هو اكتشاف متلازمة عاصفة السيتوكين أثناء الإصابة. هناك الآن العديد من المشاريع التي تبحث عن استراتيجيات الوقاية من COVID-19.

الكلمات الدالة: Covid-19 ، مدينة اوهان ، ذات الرئة ، المتلازمة التنفسية .

## Introduction:

Positive single-stranded DNA that is not segmented A coronavirus is an RNA virus. (Richman et al. 2016). They belong a large virus family usually targeting the respiratory organ (Bogoch et al. 2020). Many coronaviruses are zoonotic, which means they spread from animals to people (Zhou et al. 2020).

Due to the spiky fringe that surrounds these viruses, the name corona, which means “crown” or “wreath,” was derived from the Latin word corona (Li F., 2016). A subfamily of the Coronaviridae family of viruses called the Coronavirinae, which is a member of the Nidovirales order, the coronaviruses can be discovered there. The coronavirus subfamily known as Alpha, beta, Gamma, and Delta is made up of the four genera that make up the orthocoronavirinae family. (Cui *et.al.* 2019; Fehr and Perlman, 2015).

HCoV-229E and HCoV-NL63 are members of the genus Alpha, whereas the three The genus Beta includes the coronaviruses linked to MERS, SARS-CoV; and SARS-CoV.2.

## Historical Background

The severe respiratory infection of chickens that is today recognized as Avian Infection Bronchitis Coronavirus (IBV) was once thought to be the earliest coronavirus disease known to man in the mid-1930s (Yeager *et al.* 1992 ; McIntosh *et al.*, 1967).

In 1965, strain B814 of the human coronavirus (HCoV) was discovered. When Tyrrell and Bynoe discovered a virus, it had been found in a patient's nasal discharge from a British person who had a common cold in 1960. (named after a student specimen coded 229E) (1965, 1966, 1962; Tyrrell, Bynoe, and Kendall).

Before SARS emerged in 2002 as a new coronavirus, the first two HCoVs, HCoV-229E and HCoV-OC43, had been recognized since the 1960s (Birch *et al.*, 2005). The research on both of them was discontinued since it was determined that they were less dangerous because they only produced a mild flu-like illness.

With southern China serving as its hub, Late in 2002, SARS-CoV (Severe Acute Respiratory Syndrome Coronavirus) initially surfaced in South East

Asia and quickly spread around the world (Wit et al.2016). Following the admission that a novel human coronavirus (SARS-CoV) is what causes SARS, it has been discovered to be more virulent and to cause major respiratory complications. The World Health Organization documented 8096 instances in one year, with 774 fatalities occurring in 30 countries across five continents (Luk et al. 2019). Since 2003, there have been no reports of SARS cases due to the outbreak's containment. (Yin and Wunderink., 2018).

Two other contemporary human coronaviruses, HCoV-NL63 and HCoV-HKU1, were subsequently discovered in connection with respiratory illness. While HKU1 (Hong Kong University) was isolated from a patient with pneumonia in Hong Kong in 2005, and NL63 (National Library of Medicine) was discovered in the bronchiolitis aspirate of a 7-month-old child with bronchiolitis in 2004. SARS-CoV, MERS-CoV, and SARS-CoV-2 are three newly discovered zoonotic HCoVs that are connected to severe respiratory illness. The four of the seven prevalent HCoVs (229E, OC43, NL63, and HKU1) that often cause mild to moderate upper re-

spiratory tract illness are those four.

2012 saw the emergence of that in Jordan, then the virus was isolated from a patients in Kingdom of Saudi Arabic (KSA) (Assiri *et al.*, 2016). Following then, MERS-CoV outbreaks appeared in numerous parts of the world. From September 2012 through July 2014, the World Health Organization (WHO) reported 288 fatalities and at least 834 cases of MERS with laboratory confirmation (Ramadan and Shaib 2019).

According to Guan et al. (2003) and Chu et al. (2018), dromedary camels and feline animals, notably the civet, were the primary vectors for the direct transmission of SARS-CoV and MERS-CoV to humans. The biological characteristics and distinctive appearance of human coronaviruses have been better described as a result of in-depth research on these two viruses. The COVID-19 imaging signs, a novel virus found in December 2019, may aid in predicting. (WHO 2020).

### Covid-19

In December 2019, a brand-new coronavirus emerged in Wuhan, Hubei Province, China. 2020 (Lu et al.) and 2020 (Zhu et al.) This respiratory

ailment was first categorized as pneumonia with an uncertain etiology since the underlying cause could not be determined. To identify the bacteria in concern, the local Chinese Center for Disease Control and Prevention did more investigation, which was given the tentative designation 2019 new coronavirus (nCoV) for the virus (Tang et al. 2020).

Following the initial reports of a pneumonia case that was incorrectly diagnosed in Wuhan on December 8, China sent a warning to the World Health Organization (WHO) on December 30 regarding a cluster of pneumonia patients. (Huang *et al.*, 2020). On January 3, 2020, a new coronavirus was isolated. The World Health Organization (WHO) refers to the illness brought on by as of January 30, February 11, 2020, The abbreviation COVID-19 will be used to refer to this new coronavirus “coronavirus disease 2019.” (Phan 2020). (Zhu *et al.*, 2019). The eighth coronavirus to infect humans is SARS-CoV-2, is the culprit that causes COVID-19. There are six other coronavirus types that are known to harm people. The World Health Organization classified the threat posed

by this CoV pandemic as “extremely high” in February 2020. Despite the installation of severe quarantine measures and travel restrictions, the virus spread fast outside of China. On March 12, a pandemic was declared as a result of several confirmed cases being reported in different countries (WHO 2020) .

### **Virus source (Covid-19)**

It is known that coronaviruses spread among animals, and some of them can spread to humans. (Chan *et.al.* 2020). However , the initial source or the animal reservoir of SARS.CoV.2 is unknown, Although the early instances had a connection to Wuhan City’s Huanan Large Seafood and Live Animal Market in Hubei Province, China (Li Q et al. 2020).

On January 1st, a Huanan wholesale fish market, which also sold live animals, closed, and thus cut off the source of many of the first cases. The exact species has not been discovered, although more recent investigations have suggested that bats or snakes might be the SARS-CoV-2 virus’s possible natural hosts (Holshue and DeBolt ,2020).

### SARS-CoV-2 taxonomy

Continent:	Orthornavirae
The phylum is:	Pisuviricota.
The correct order is :	Nidovirales
The Suborder is:	Cornido virineae
The Family is :	Coronavirida.
Subfamilyis:	Orthocoronavirina.
Genus:	Betacoronavirus.
Subgenus:	Sarbecovirus.
Species:	SARS-CoV-2.

### Structure

Coronaviruses are large pleomorphic spherical particles with protruding surface projections. Virus particles are generally 120 nm in diameter. 2020 (Park and Kwon). The spikes are 20 nm long and the envelope's diameter is about 80 nm figure 1 (Zhou et al. 2020).

The zoonotic origin of positive-sense, single-stranded RNA SARS CoV-2 viruses is indicated by the presence of an envelope. These spherical to pleomorphic particles range in size from 80 to 160 nm (Kumar *et al.*, 2029). The nucleocapsid, spike, membrane, and envelope structural proteins are all present in SARS.CoV-2 (N).

The proteins S, M, and E make up

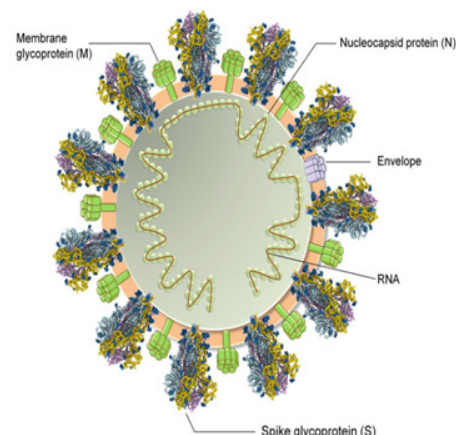
the virus's envelope. The most common protein type, M, controls the envelope's form primarily. The E protein is the smallest structural protein. For viral replication and assembly, two transmembrane proteins called S and M are required. 2020 (Wu et al). (Wu et al.). The RNA inside the envelope is joined by N proteins to create a nucleocapsid (Forni *et al.*, 2017).

N proteins participates in a number of viral genome-related functions, include the cycle of CoV replication and the host's biological reaction to viral infection, as well as assembly and budding. The S protein polymers that are still present in the envelope and give the coronavirus its name are what give the envelope the appearance of a crown. (Yan *et al.*, 2020).



SARS-structure is shown in Fig. 1.

The SARS-CoV.2 spikeglycoprotein (S) interacts with ace2 cell surface receptor via surface viral proteins. The glycoprotein (M) of the SARS-membrane CoV-2 and the envelope form a lipid bilayer from the host membrane that covers the helical nucleocapsid that contains the viral RNA (E).



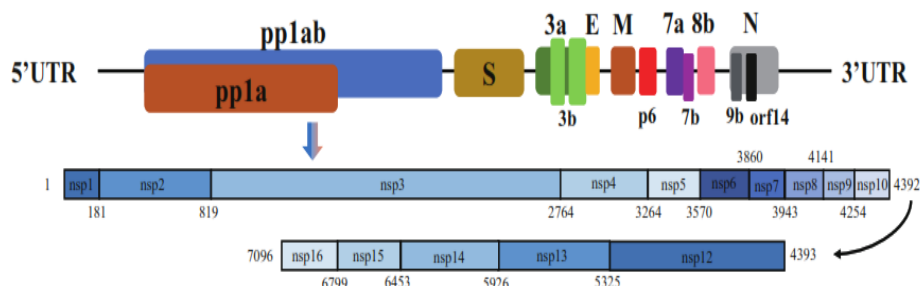
### Genome:

The positive-sense RNA genome of SARS-single-stranded CoV-2 is 30 kb in size (29891 nucleotides) and comprises 9860 amino acids. 38% of the substance is made up of G+C. (Guo *et al.*,2020). The 12 relevant open reading frames are composed of the 9 sub genomic mRNAs with a conserved leader sequence, nine transcription-regulatory domains, and two terminal untranslated regions. (ORFs). (Zhou *et al.*, 2020).

The hemagglutinin-esterase gene, which is frequently seen in lineage A

CoV.s, is absent from the genome of this virus. two polyproteins, 16 non-structural proteins, and almost 2/3 of the viral RNA are produced by the pp1a and pp1b gene (NSP). The remaining ORFs make structural and support proteins. (Paraskevis *et al.*,2020) .

The sixteen non-structural proteins (main protease) include NSP13 The 2 viral cysteine proteases known as NSP3 (papain-like protease) and NSP5 (helicase), as well as NSP12 (RNA-dependent RNA polymerase), are likely involved in the transcription and replication of the virus. (Chan *et.al.*, 2020).



**Fig (2). The SARS-CoV-2 genome's and its encoded proteins' organization.**

The remaining section of the viral genome encodes 4 structural proteins (E, M, S, and E) and a number of auxiliary proteins that inhibit the host immune response. (Walls *et al.* 2020).

The coronavirus genome is organized as follows: The 3' end of the genome also has various auxiliary genes, such as 5'-leader-UTR-replicase-S. (Spike), E (Envelope), M (Membrane), N (Nucleocapsid), and 3'UTR-poly (A) tail, in addition to structural genes. SARS-whole CoV-2's genomic sequence is more comparable to SARS-like CoVs. found in bats in 2020 in Wrapp *et al.* Spike proteins NSP2 and NSP3, which are necessary for the SARS-CoV-2 virus's capacity to infect cells and its differentiation strategy, have undergone modifications. (Chan *et al.*, 2020). There are several strains of both the L-type and the S-type. It has been established that the L-S-offspring type is more aggressive and contagious.

### Replication and Transcription

2020 Angiotensin converting enzyme 2 (ACE2) is where the SARS-CoV-2 (COVID-19) hooks onto and enters cells. Throughout the host's cy-

toplasm, this starts translation of the replicase polyprotein pp1a (Wrapp *et al.*, 2020). The spike protein must next be activated by an enzyme called a protease for the virus to effectively enter the cell after this initial phase. This is how SARS-CoV-2 (COVID-19) uses transmembrane serine protease 2 (TMPRSS2) as its protease. (Hoffman *et al.*, 2020). SARS-CoV-2 distributes extrapulmonarily, like SARS-CoV, and it is believed that this is because the ACE2 receptor is widely expressed in many tissues. The viral receptor (spike protein) has to be activated as a protease before it can interact with its biological ligand (ACE2). Graph 3 from (Guo *et al.*, 2020).

When the spike protein, which entered the host cell via the endosomal pathway, connects with the ACE2 receptor, the host cell membrane is joined with the viral envelop protein.. (Matsuyama *et al.*, 2009).

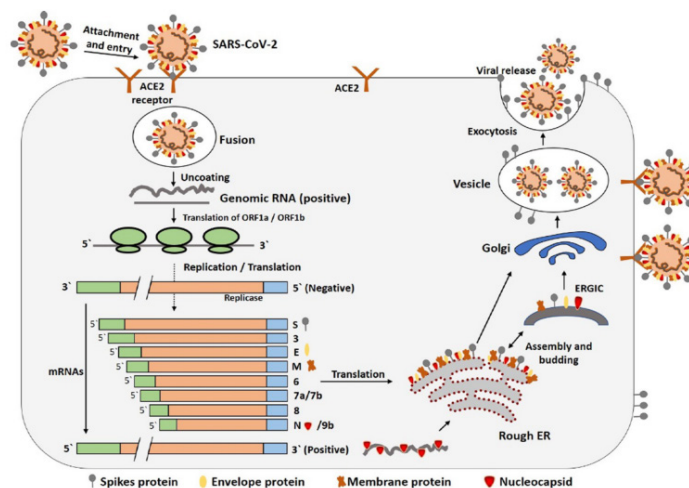
After then, pp1b and viral RNA are released. Proteinases that are encoded by viruses further degrade these into little proteins. (Hoffmann *et al.*, 2020).

When a coronavirus replicates, ribosomal frame shifting occurs during translation, resulting in the creation of

genomic RNA as well as many copies of sub genomic RNA species that code for important viral proteins. (Simmons *et al.*, 2013).

To create the virion, viral RNA and

protein interact in the endoplasmic reticulum (ER) and Golgi complex. The viruses are subsequently expelled from the cells via vesicles (figure 4).



**Fig.:(3).** Following infection, SARS-CoV-2 replication occurs in host cells. For SARS-CoV-2 to infect host target cells, the spike glycoprotein has to be absorbed by the cellular receptor ACE2. Viral RNA is uncoated during internalization and enters it is translated into the replicase polyproteins pp1a and pp1b in the cytoplasm. Then, this is divided into smaller proteins by virus-encoded proteinases. Ribosomal frame shifting takes place during translation during SARS-CoV-2 replication, resulting in the generation of multiple sub-genomic RNA species and genomic copies of the virus. To

create the virion, In the Golgi complex and endoplasmic reticulum (ER), viral RNA and protein interact. Then, by use of vesicles, these virions are exocytotically ejected from the cells.

### Transmission

According to Ghinai et al. (2020), COVID-19 is mostly transmitted by close contact and inhalation of microscopic droplets produced by an infected person's talking, sneezing, and coughing, as well as through airborne particles and surface particles. Less frequently, infected droplets that land on floors or other surfaces may contin-



ue to be contagious if individuals touch those surfaces with unwashed hands before touching their eyes, nose, or mouth. Surfaces are not regarded to be the primary means by which the virus spreads since the amount of active virus on them gradually diminishes until it can no longer induce infection. (Ji *et al.*, 2020 ; Phan *et al.*, 2020).

The United States advises a distance of three feet, although the World Health Organization (WHO) recommends one meter. Although the incidence of this is unclear, it is possible for people to transfer the virus even when they are symptomless. The Centers for Disease Control (CDC) advises a distance of 2 meters (6 ft). It is estimated that 40% of those infected are asymptomatic.

Despite the fact that presymptomatic transmission can happen up to two days before symptoms manifest, even minor or nonspecific symptoms might increase a person's contagiousness. (Li Q *et al.* 2020). In mild cases, they keep their contagiousness for an average of seven to twelve days, whereas in severe cases, they do so for an average of two weeks. Being a novel disease, COVID-19, many elements of its transmission are actively being studied

(Ji *et al.*, 2020).

## Pathogenesis

### Virus Entry and Spread

Respiratory droplets, direct touch, and perhaps fecal-oral transfer are the primary SARS-CoV-2 transmission methods. Prior to affecting the stomach mucosa and lower respiratory system, it is believed that the virus first replicates in the mucosal epithelium of the upper respiratory tract (pharynx and nasal cavity). (Xiao *et.al.*;2020), causing a moderate viremia to develop. At this time, few infections are under control and are still asymptomatic. All of these human organs are susceptible to SARS because they express ACE2 widely, encompasses the mucosa of the bronchi, lungs, and nose as well as the kidney, stomach, bladder, and ileum. – CoV.2 (Zou;X,*et.*.*al.* 2020).

Recently, doctors have made the claim that SARS-CoV-2 could damage testicular tissues, raising questions regarding young patients' fertility (Fan *et .(al.*,2020

### Pathological Findings

By Xu Z *et al.* in 2020, pathological outcomes from a severe COVID-19

were first described. They revealed bilateral widespread lung injury and cellular fibromyxoid exudates. Pneumocyte desquamation and hyaline membrane development in the right lung were both plainly visible, indicating acute respiratory distress syndrome. Early-stage pulmonary edema and the emergence of a hyaline membrane connected the tissue of the acute respiratory distress syndrome symptoms were seen in the left lung (ARDS) (Liu Q *et al.*, 2020).

These lung pathology findings have striking similarities to those found in MERS and SARS. Massive mucus flow was observed in both lungs in COVID-19 fatality patients, in contrast to SARS (Ding *et al.*, 2003) and MERS (Ng *et al.*, 2014) cases.

### Strategies for COVID-19 prevention

The method utilized to treat individuals with illnesses associated to coronavirus because there is currently no particular medication for this condition. The outbreak, however, which at one point appeared to be completely out of control, might now be controlled (Liu *et al.*, 2020).

It is advised to adhere to certain

fundamental precautions against the COVID-19

(WHO 2020).

- Follow local and national health authorities for the most recent information on the COVID-19 epidemic.
- Wash your hands often with a soap and the water or an alcohol-based handwashing product.
- Remain at least one meter away from someone who is sniffing or sneezing.
- Refrain from touching your mouth, nose, or eyes.
- Retain proper respiratory care.
- As soon as you get a fever, cough, or breathing issues, see a doctor.
- Maintain knowledge and heed the physician's recommendations.
- When greeting, avoid physical touch.

Supportive, cautious, watchful, compassionate, and prepared to combat COVID-19.

### Conclusion:

There is considerable doubt that coronaviruses can adapt to new hosts and traverse species boundaries, making it easy to anticipate that more will appear in the future. However, it is un-

clear why coronaviruses have this ability in comparison to certain other RNA viruses.

It is crucial that animals be included in the monitoring of animal coronaviruses since they presumably play a significant role in the virus's ability to infect humans indirectly through intermediate hosts. Limiting our exposure to animal diseases as much as possible is probably the easiest and most economical strategy to lower the danger of future outbreaks given the wide diversity of viruses in animals and their continual development.

Understanding the mechanics of the newly emerging coronavirus's pathogenicity and transmission, There is a critical need for more research. In order to perhaps only transmit to simple animals or people, it must be possible to clearly demonstrate the evolutionary process from the first host to cross-species transmission. Additionally, to solve the puzzle of the molecular mechanism of viral entrance and reproduction, which serves as the foundation for further study into the creation of vaccines and medications with specific antiviral effects.

Finally, we draw the conclusion

that each component of a coronavirus is distinct and whole. Due to its immune-evasion mechanisms, which help it avoid immune system detection, the host is infected and dies as a result.

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