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SARS-CoV-2

New Member In Coronavirus Family

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Introduction

- ❑ Coronaviruses are a group of related viruses that cause diseases in mammals and birds.
- ❑ In humans, coronaviruses cause respiratory tract infections that can range from mild to lethal.
- ❑ Symptoms in other species vary: in chickens, they cause an upper respiratory tract disease, while in cows and pigs they cause diarrhea. There are yet to be vaccines or antiviral drugs to prevent or treat human coronavirus infections

History



- ❑ Coronaviruses were first discovered in the 1930s when an acute respiratory infection of domesticated chickens was shown to be caused by infectious bronchitis virus (IBV)
- ❑ Human coronaviruses were discovered in the 1960s.
- ❑ The earliest ones studied were from human patients with the common cold, which were later named human coronavirus 229E and human coronavirus OC43.
- ❑ They were first imaged by Scottish virologist [June Almeida](#) at St. Thomas Hospital in London.

Taxonomy



Virus classificatione

(unranked) : Virus

Realm : Riboviria

Phylum : incertae sedis

Order : Nidovirales

Family : **Coronaviridae**

Subfamily : Orthocoronavirinae

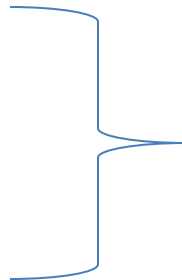
Genera

Alphacoronavirus

Betacoronavirus

Gammacoronavirus

Deltacoronavirus



40 Species

Human Coronaviruses



Four human coronaviruses produce symptoms that are generally mild:

1. Human coronavirus OC43 (HCoV-OC43), β -CoV
2. Human coronavirus HKU1 (HCoV-HKU1), β -CoV
3. Human coronavirus 229E (HCoV-229E), α -CoV
4. Human coronavirus NL63 (HCoV-NL63), α -CoV

Three human coronaviruses produce symptoms that are potentially severe:

1. Middle East respiratory syndrome-related coronavirus (MERS-CoV), β -CoV
 2. Severe acute respiratory syndrome coronavirus (SARS-CoV), β -CoV
 3. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), β -CoV
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Outbreaks of human coronavirus diseases



Viruses	Diseases	Outbreaks	Location of identified	Confirmed cases	Death	CFR
MERS-CoV	MERS	2012,2105, 2018	Jeddah Saudi Arabia	2494	585	37%
SARS-CoV	SARS	2002-2004	Shundi China	8096	774	9.2%
SARS-CoV-2	COVID-19	2019-2020 Pandemic	Wuhan China	2,397,216 21th Apr. 2020	162,956 21th Apr. 2020	14.7% 21th Apr. 2020

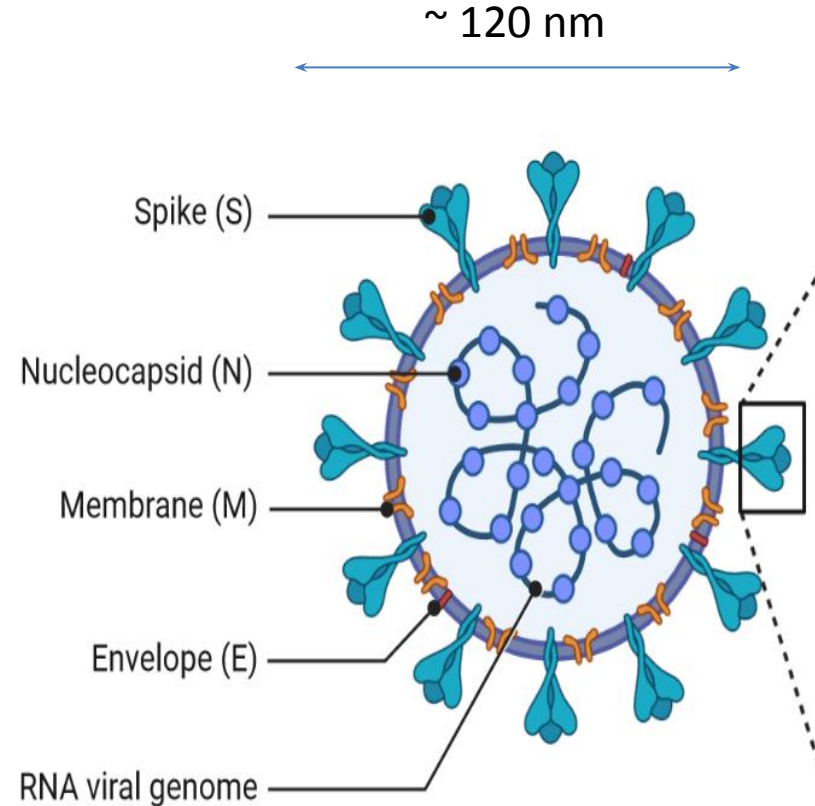
SARS-CoV-2



- ❑ SARS CoV-2 virus is a betacoronavirus which was discovered in Wuhan City, Hubei Province, China in December 2019
- ❑ They are enveloped, positive-sense, single-stranded RNA viruses.
- ❑ They are spherical to pleomorphic particles
- ❑ four structural proteins, namely:

Envelope (E)
Spike (S)
Membrane (M)
Nucleocapsid (N)

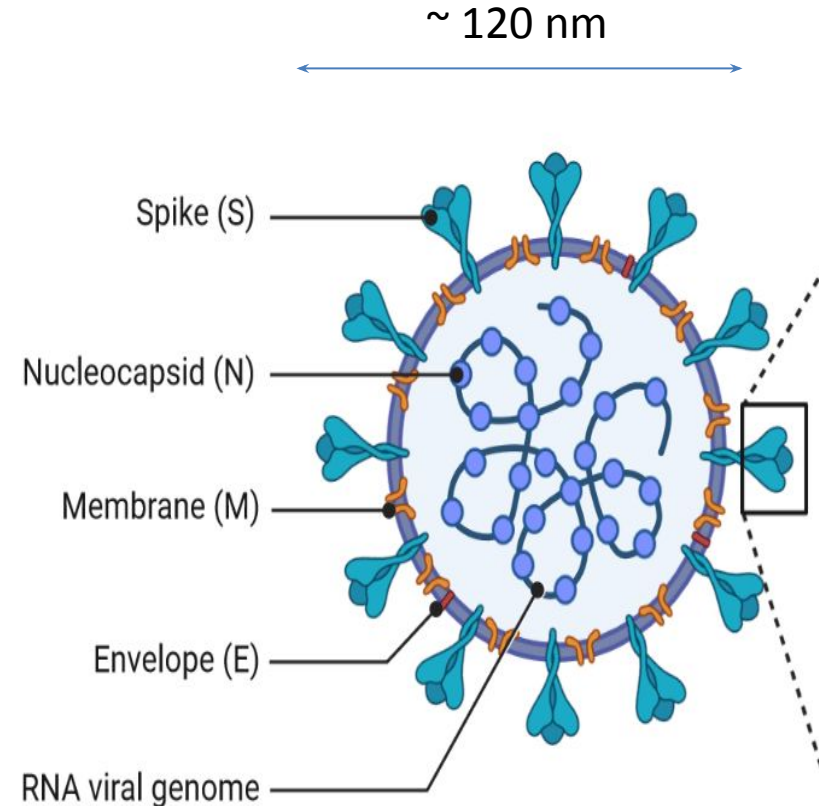
} Envelop



SARS-CoV-2



- ❑ The S and M proteins are also the transmembrane proteins that are involved in virus assembly during replication.
- ❑ N proteins remain associated with the RNA forming a nucleocapsid inside the envelope.
- ❑ Although N protein is largely involved in processes relating to the viral genome, it is also involved in other aspects of the CoV replication cycle (assembly and budding) and the host cellular response to viral infection.



Spike Glycoprotein

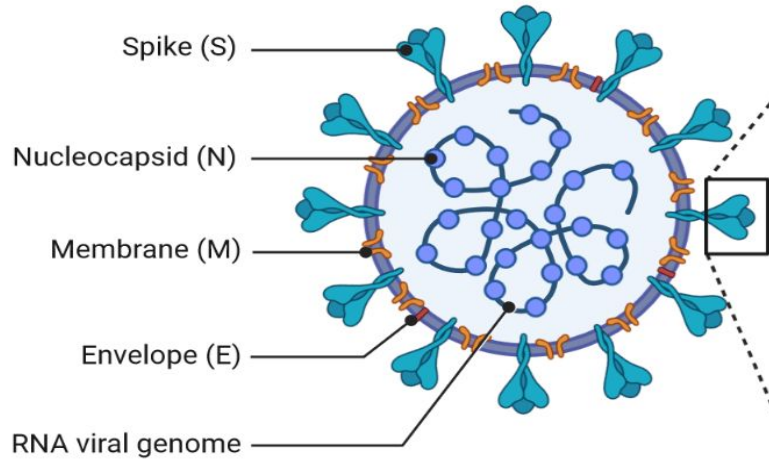
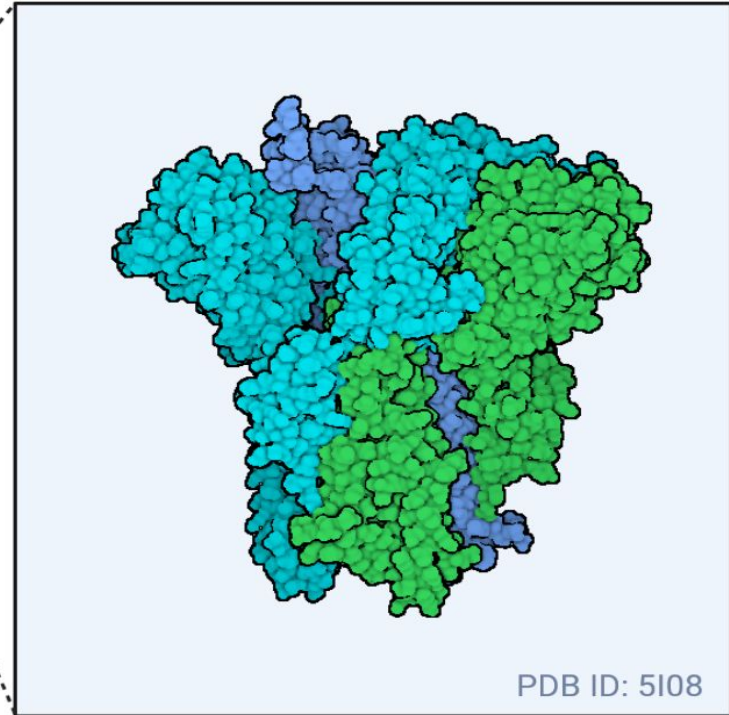
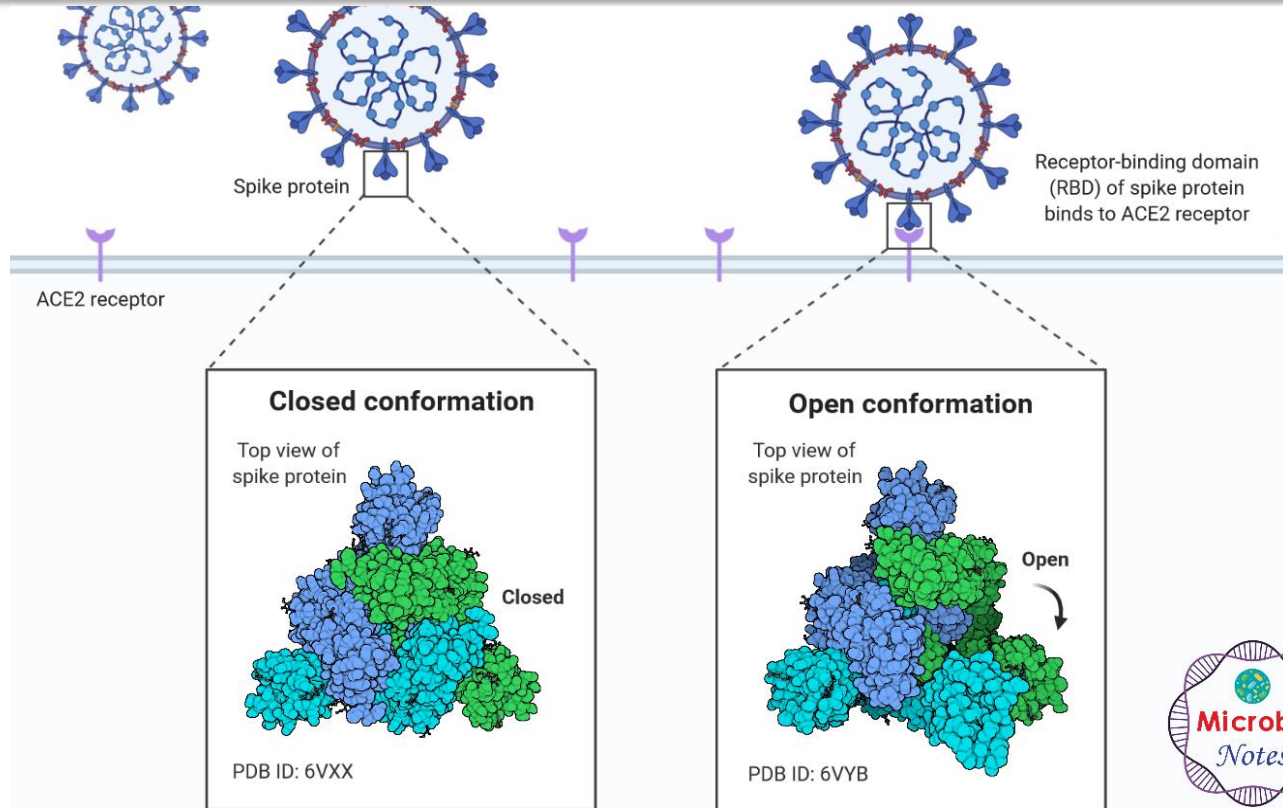


FIGURE 1: Coronaviruses belong in the family *Coronaviridae* and can cause disease in mammals and birds. The coronavirus spike (S) protein mediates membrane fusion by binding to cellular receptors.



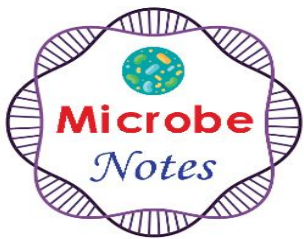
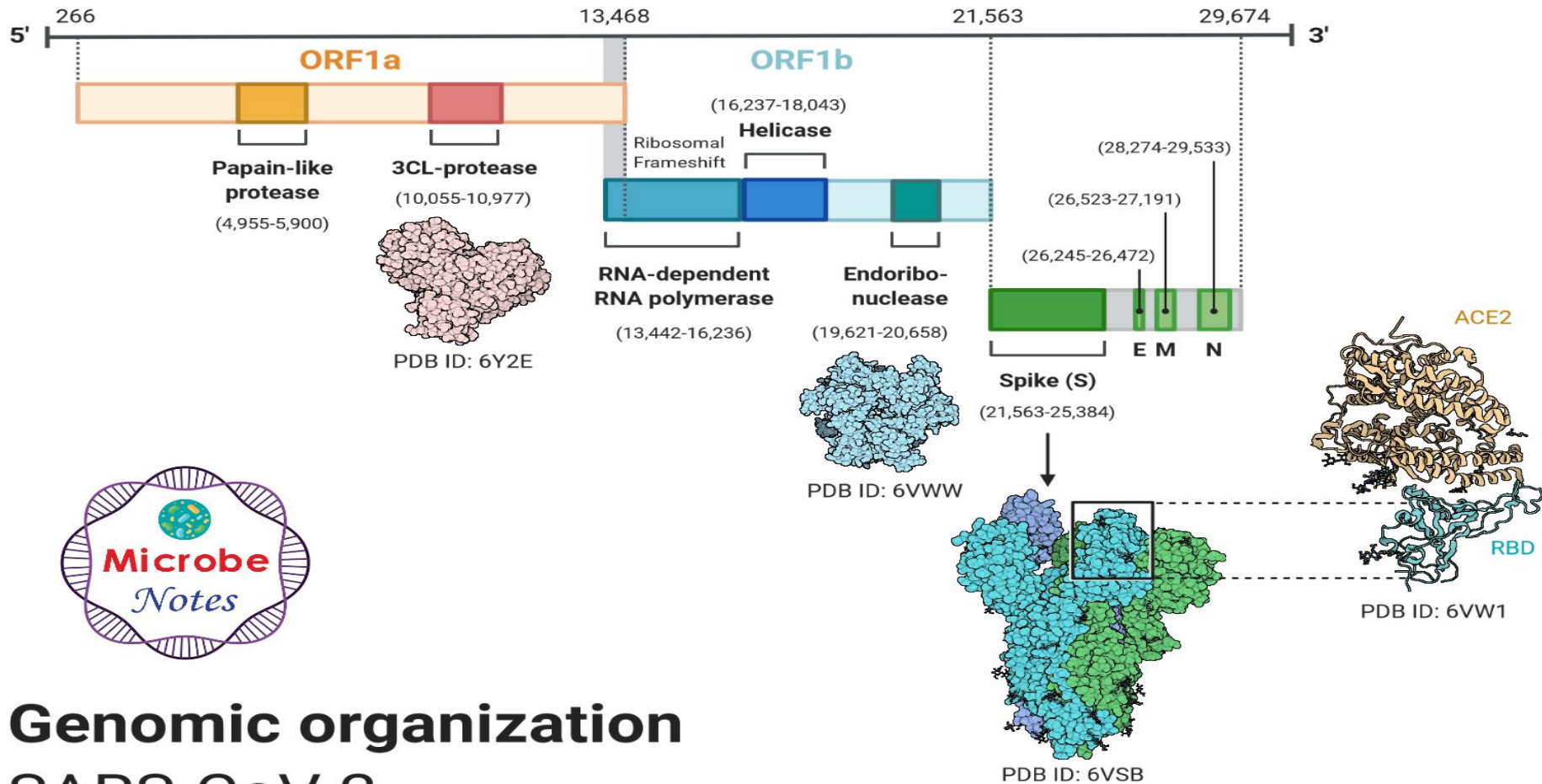
Spike Protein Conformation



Spike Protein Conformation



- ❑ Spike glycoprotein comprised of S1 and S2 subunits. The S1 subunit contains a signal peptide, followed by an N-terminal domain and receptor-binding domain.
- ❑ The S2 subunit of 2019-nCoV is highly conserved and shares 99% identity with those of the two bats SARS-like CoVs and human SARS-CoV.
- ❑ The S1 subunit shares 70% to these CoVs but the core receptor binding domain is highly conserved. These amino-acid differences are responsible for the direct interaction of spike protein with the host receptor.
- ❑ Spike glycoprotein binds to the human ACE2 receptor present in the target cells in the respiratory tract. This protein has a compact ridge that allows the virus to attach more strongly than other viruses of the same origin.



Genomic organization SARS-CoV-2

Genomic organization of SARS-CoV-2



- ❑ The genome of SARS-CoV-2 is a single-stranded positive-sense RNA of 30kb (29891 nucleotides) encoding 9860 amino acids. The G + C content is 38%
 - ❑ There are 12 functional open reading frames (ORFs) along with a set of nine subgenomic mRNAs carrying a conserved leader sequence, nine transcription-regulatory sequences, and 2 terminal untranslated regions.
 - ❑ The genome of this virus lacks the haemagglutinin-esterase gene, which is characteristically found in lineage A β CoV.
 - ❑ Two-thirds of viral RNA, mainly located in the first ORF translates two polyproteins, pp1a and pp1ab, and encodes 16 non-structural proteins (NSP), while the remaining ORFs encode accessory and structural proteins.
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Genomic organization of SARS-CoV-2



- ❑ The genome of SARS-CoV-2 is a single-stranded positive-sense RNA of 30kb (29891 nucleotides) encoding 9860 amino acids. The G + C content is 38%
- ❑ The 16 non-structural proteins include two viral cysteine proteases, namely, NSP3 (papain-like protease) and NSP5 (main protease), NSP12 (RNA-dependent RNA polymerase, NSP13 (helicase), and other NSPs which are likely involved in the transcription and replication of the virus.
- ❑ The rest part of the viral genome codes for four structural proteins E, M, S, and E along with a number of accessory proteins that interfere with the host immune response.

Genomic organization of SARS-CoV-2



- ❑ The organization of the coronavirus genome is 5'-leader-UTR-replicase-S (Spike)-E (Envelope)-M (Membrane)-N (Nucleocapsid)-3'UTR-poly (A) tail with accessory genes interspersed within the structural genes at the 3' end of the genome.
- ❑ SARS-CoV-2 is closer to the SARS-like bat CoVs in terms of the whole genome sequence.
- ❑ However, mutations are observed in NSP2 and NSP3 and the spike protein, that play a significant role in infectious capability and differentiation mechanism of SARS-CoV-2
- ❑ Besides, two strains, namely L-type and S-type, are discovered. The L-type, derived from the S-type, is found to be more aggressive and contagious.

Thank you

