SARS-CoV-2 is a member of the Coronavirus family.

CoVs are positive-stranded RNA viruses with a crown-like appearance under an electron microscope (coronam is the Latin term for crown) due to the presence of spike glycoproteins on the envelope.

The subfamily Orthocoronavirinae of the Coronaviridae family classifies into four genera of CoVs:
- Alphacoronavirus (alphaCoV)
- Betacoronavirus (betaCoV)
- Deltacoronavirus (deltaCoV)
- and Gammacoronavirus (gammaCoV)

Full-genome sequencing has indicated that the coronavirus that causes COVID-19 is a betacoronavirus in the same subgenus as the severe acute respiratory syndrome (SARS) virus (as well as several bat coronaviruses).

Members of this large family of viruses can cause respiratory, enteric, hepatic, and neurological diseases in different animal species, including camels, cattle, cats, and bats.

To date, seven human CoVs (HCoVs) capable of infecting humans have been identified.

Common human CoVs include HCoV-OC43, and HCoV-HKU1 (betaCoVs); HCoV-229E, and HCoV-NL63 (alphaCoVs). They can cause common colds and self-limiting upper respiratory infections in immunocompetent individuals. In immunocompromised subjects and the elderly, lower respiratory tract infections can occur.

For SARS-CoV, MERS-CoV, the mortality rates are up to 10% and 35%, respectively.

The Middle East respiratory syndrome (MERS) virus, another beta-coronavirus, appears more distantly related.

Estimates suggest that 2% of the population are healthy carriers of a CoV and that these viruses are responsible for about 5% to 10% of acute all respiratory infections.

Other human CoVs are SARS-CoV, SARS-CoV-2, and MERS-CoV (betaCoVs of the B and C lineage, respectively). These cause epidemics with variable clinical severity featuring respiratory and extra-respiratory manifestations.

The structure of the receptor-binding gene region for SARS-CoV-2 is very similar to that of the SARS coronavirus, and the virus has been shown to use the same receptor, the angiotensin-converting enzyme 2 (ACE2), for cell entry.

Different strains?
In a phylogenetic analysis of 103 strains of SARS-CoV-2 from China, two different types of SARS-CoV-2 were identified, designated type L (accounting for 70 percent of the strains) and type S (accounting for 30 percent). The L type predominated during the early days of the epidemic in China, but accounted for a lower proportion of strains outside of Wuhan than in Wuhan. The clinical implications of these findings are still uncertain.

E protein
M protein
S protein

"Disclaimer drawn up based on the best available evidence at the time, but may be subject to change."