SARS CoV-2, a betacoronavirus arose for the first time in Wuhan, China in December 2019. Due to a close similarity in the genomic structure of the virus, to that of Severe Acute Respiratory Syndrome related coronaviruses (SARS-CoV), the virus got named as SARS-CoV-2. <https://www.mdpi.com/1999-4915/12/5/498>. The first genome of this novel coronavirus was isolated and sequenced in January from an affected individual from the seafood market in Wuhan, China.

Structurally, SARS CoV-2 is spherical andenveloped with particles containing the linear, single stranded, positive sense RNA of around 30kb encoding 9860 amino acids. The genome is associated with nucleoprotein which is confined within the capsid made of matrix protein. <https://www.sciencedirect.com/science/article/pii/S1684118220300827>Fundamentally, the genome consists of a total of 12 functional Open Reading Frames (ORFs) along with a set of nine sub-genomic mRNAs carrying a conserved leader sequence, nine transcription-regulatory sequences, and 2 terminal untranslated regions. Particularly, the orf1ab and orf1a genes in the 5’-terminus encode the pp1ab and pp1a proteins respectively. Together, they encode 16 non-structural proteins including two viral cysteine proteases, namely, NSP3 (papain-like protease) and NSP5 (main protease), whereas, NSP12 (RNA-dependent RNA polymerase), NSP13 (helicase), and other NSPs are likely involved in the transcription and replication of the virus. The 3′-terminus of the genome contains four structural proteins (S, E, M, and N) and eight accessory proteins that interfere with the host immune response. <https://www.europeanreview.org/wp/wp-content/uploads/4576-4584.pdf>

<https://microbenotes.com/structure-and-genome-of-sars-cov-2/>

In order to understand the virus evolution of SARS-CoV-2, it is important to investigate the genotype changes during its transmission. These mutations might be associated with the changes in transmissibility and virulence of the virus. The mutations can be in the S protein, RNA polymerase, RNA primase, and nucleoprotein, which are fundamental proteins for vaccine efficacy. Mutations have been observed in NSP2,NSP3 and spike proteins that play a significant role in the infectious capability and differentiation mechanism of SARS-CoV 2.