

- 26523–27191 codes for Membrane Glycoprotein or M structural protein.
- ORF6 gene is coded from 27202–27387.
- 27394–27759 is coded for ORF 7a.
- 27894–28259 is coded for ORF8.
- The gene coding for Nucleocapsid phosphoprotein N lies in the region 28274–29533.
- Region from 29558–29674 codes for ORF10 protein.
- Finally the region from 29675–29903 ends as 3 prime UTR.

2.2 Linking NCoV with SARS and determining its genomic conservation

The genomic sequence of Novel Corona Virus (NCoV) was retrieved from NCBI which was subjected to BLAST run to detect the organisms sharing similarity. According to the data mining related to NCoV it was found that the organism belongs to the family of SARS which are known to cause severe acute respiratory syndrome (Fig. 2.1).

Inference: The above BLAST analysis for the complete genome of NCoV reveals its association with all the other SARS Corona virus of class 2 and share an identity of 99% to 100% with most of them.

Furthermore to understand the conservation pattern among the functional protein coding genes of NCoV genome their nucleotide sequences were retrieved from NCBI. A similarity search was performed using BLAST. Among them the major gene covering the maximum length of the genome is ORF1ab polyprotein (Gene region:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1 complete genome	55221	55221	100%	0.0	100.00%	NC_045512.2
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/GH01/2020 complete genome	55210	55210	100%	0.0	99.99%	MT121215.1
Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/PRCAMS-WH-03/2019 complete genome	55208	55208	99%	0.0	100.00%	MT019531.1
Severe acute respiratory syndrome coronavirus 2 TKYE6182_2020 RNA complete genome	55204	55204	100%	0.0	99.99%	LC529905.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/VT-0010/2020 complete genome	55201	55201	100%	0.0	99.99%	MT334520.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/CA-CZB-IX00095/2020 complete genome	55199	55199	99%	0.0	100.00%	MT385430.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/UKA/COV486/2020 complete genome	55199	55199	100%	0.0	99.99%	MT371050.1
Severe acute respiratory syndrome coronavirus 2 TKYE6968_2020 RNA complete genome	55199	55199	100%	0.0	99.99%	LC542978.1
Severe acute respiratory syndrome coronavirus 2 TKYE6947_2020 RNA complete genome	55199	55199	100%	0.0	99.99%	LC542809.1
Synthetic construct ORF1ab_sarbs_ORF3_E_M_ORF8_ORF9_and_N_genes complete cds	55199	55199	99%	0.0	100.00%	MT108784.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/HN/195/2020 complete genome	55199	55199	100%	0.0	99.99%	MT135041.1
Severe acute respiratory syndrome coronavirus 2 isolate MW04 complete genome	55199	55199	99%	0.0	100.00%	MN996528.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/CA-CZB-IX00045/2020 complete genome	55197	55197	99%	0.0	99.99%	MT385425.1
Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/PRCAMS-WH-04/2019 complete genome	55197	55197	99%	0.0	100.00%	MT019532.1
Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/PRCAMS-WH-01/2019 complete genome	55197	55197	99%	0.0	99.99%	MT019529.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/CA-CZB-EX00458/2020 complete genome	55195	55195	99%	0.0	100.00%	MT385431.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/TW/NCGMH-CGU-09/2020 complete genome	55193	55193	99%	0.0	99.99%	MT374150.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/HKG/HKU-802b/2020 complete genome	55193	55193	99%	0.0	100.00%	MT114413.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/VNM/Cov-19-01S/2020 complete genome	55193	55193	99%	0.0	100.00%	MT192772.1
Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/GZ33/2020 complete genome	55193	55193	100%	0.0	99.98%	MT135043.1

Fig. 2.1 BLAST analysis for the evolutionary study of NCoV