Chapter 3
Comparing Proteomics of NCoV 19 and MERS Corona Virus

In order to develop any diagnostic or therapeutic protocol for COVID19 it is necessary to study the genome and proteome of the NCoV and annotate the proteins to identify its phylogeny and evolutionary relation with the other known organisms. The SARS NCoV and MERS Corona Virus belong to the Corona group of viruses and both are known to cause Respiratory illness. There is a very close similarity in the disease manifestation and mode of transmission in MERS and COVID forming basis for the comparison between the two organisms. Hence the proteins of novel Corona virus are compared with those of MERS Corona Virus (Fig. 3.1).

Inference: The above BLAST result shows that only 14% (**13,670–17,861)** of the Query genome can be aligned with the MERS Corona Virus genome (Middle East respiratory syndrome-related coronavirus isolate Bat-CoV/P.khulii/Italy/206645-63/2011, complete genome: **MG596803.1** [1]). However the identity in the aligned region is 70.58%. This reveals a close evolutionary relation between the two organisms.

The aligned gene region with 14% of the query gene region was from 13,670 to 17,861(4192 bp) in MERS CoV which is found to share the similarity with Novel Corona Virus 2019. This region codes for ORF1ab poly protein. Thus it can be concluded that the only region that shares the highest identity between MERS CoV and Novel Corona virus 2019 is the ORF1ab polyprotein.

A. Kumar et al., *Novel Coronavirus 2019*,
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