



Alignment and phylogenetic tree analysis of some corona and influenza type A viruses based on nucleocapsid protein sequences

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Background

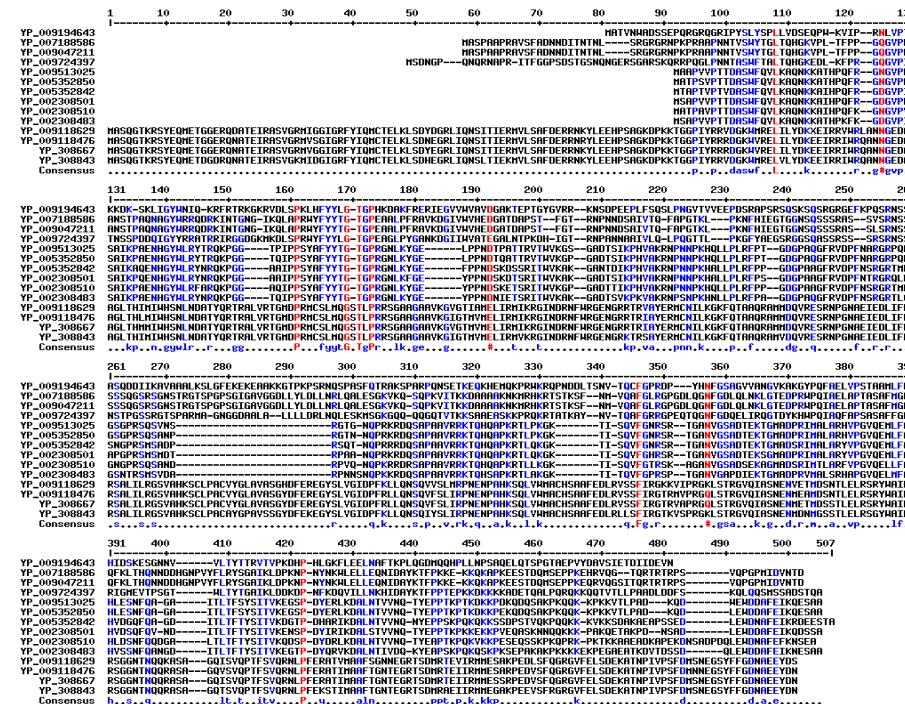
The nucleocapsid (N) proteins of viruses, as with most enveloped viruses, have received less attention than the surface glycoproteins and generally have been perceived to be of lesser concern. Interest in this class of proteins, however, has been stimulated in recent years especially in this pandemic age. The nucleocapsid phosphoprotein of the severe acute respiratory syndrome coronavirus (SARS-CoV N protein) packages the viral genome into a helical ribonucleocapsid (RNP) and plays a fundamental role during viral self-assembly.

Materials and Methods

In this article by using multalin software and their phylogenetic tree by neighbor-joining method protein sequence of 10 subfamily of corona viruses and four subfamily of influenza A viruses from *National Center for Biotechnology Information (NCBI) GenBank* were analyzed. This method is a special case of the star decomposition method. In contrast to cluster analysis neighbor-joining keeps track of nodes on a tree rather than taxa or clusters of taxa. The raw data are provided as a distance matrix and the initial tree is a star tree.

Results

Alignment showed low similarity in consensus. The phylogenetic tree displayed that influenza and corona virus have a common ancestor and delta corona virus subfamily has more difference compare to other types of corona virus.



Conclusion

According to the low similarity of alignment approves the fact that RNA viruses are perhaps the most intriguing biological entities in which to study mutation rates. They encode their replication machinery, and thus their mutation rates can be optimized for their fitness (in comparison to small DNA viruses that use the polymerases of their host cells). Their inherently high mutation rates yield offspring that differ by 1–2 mutations each from their parent, producing a mutant cloud of descendants that complicates our conception of a genotype's fitness. Their ability to rapidly change their genome underlies their ability to emerge in novel hosts and escape vaccine-induced immunity. The phylogenetic tree displayed that influenza and corona virus have a common ancestor and delta corona virus subfamily has more difference compare to other types of corona virus.

References

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