

# Genomic analysis and comparative multiple sequences of SARS-CoV2



## Abstract:-

**Background:** On December 31, 2019, China announced the outbreak of a new coronavirus in Wuhan, and the virus has since spread globally. The development of antiviral strategies depends on understanding the molecular mechanisms of genome selection. We define the correlation of ten coronavirus (SARS-CoV2) sequences from various countries to analyze the genomic patterns of disease origin.

**Methods:** We apply a *Clustalw web service* for *Multiple sequence alignment* (<https://www.genome.jp/tools-bin/clustalw>) and apply genomic analysis to sequence SARS-CoV2 from GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>)

**Results:** Using (NCBI) database and genome alignment for *protein sequencing* we found no differences in amino acid sequences between M and N proteins. The spike (S) protein has two amino acid variations.

## INTRODUCTION:-

Infections such as (SARS-CoV) and (MERS-CoV), which are spread from animals to humans, have caused pneumonia all over the world. SARS was first discovered in Guangdong, China, in 2002, and has since spread around the world, resulting in 8096 infected cases and 774 deaths. Then a coronavirus appeared in Wuhan, named SARS-CoV2 (International Committee on Taxonomy of Viruses).

Coronaviruses are classified into four genera ( $\alpha$ ,  $\beta$ ,  $\gamma$  and  $\delta$ ). SARS-CoV2 (2019) and SARS-CoV1 (2003) are belong to coronaviruses. Coronaviruses contain four proteins: *The spike (S)* protein helps the virus bind to the host cell's membrane, while *the N* (nucleocapsid) protein protects the virus's RNA genome. The *E* (envelope) and *M* (membrane).

the coronavirus start transmission when attaches to host cell membrane receptors and enters the host cell. The virus genome's RNA gene 1 then starts to replicate. After that, the virus synthesises subgenomic RNAs with new transcription. and make a lot of copy of virus which attack human body and its Lung. (<https://youtu.be/5DGwOIXsqg>)

SARS-CoV1 is thought to spread from bats and civets to humans, where it causes extreme respiratory illness and a 10% mortality rate. Before being transmitted to humans, Wuhan SARS-CoV2 is thought to be transmitted from a bat (Ra TG13).

The s protein is consist two subunit s1 and s2 on the s1 there is receptor binding domain is for ability of binding to human cell and effect him it bind with ACE2 which lung is produce ([https://youtu.be/OVDaq\\_vOQ48](https://youtu.be/OVDaq_vOQ48))

in this paper, We compared SARS-CoV2 sequences from various countries to examine disease origin and evolution genomic providing genomic knowledge for the creation of new control methods against the worldwide SARS-CoV2 pandemic.

