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(https://www.ncbi.nlm.nih.gov/genbank/)

Results: Using (NCBI) database and genome alignment for protein sequencing 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(MERSCoV), 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 (α, β, ρ and δ). SARSCoV2 (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/5DGwOJXSxqg)*

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)

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.

Related work:-

- *COVID-19 Genome Analysis using Alignment-Free Methods:-*
  The genome sequences for COVID-19 strains, taken from NCBI's GenBank, are compared and analyzed with AF methods for: (1) extracting frequent patterns of nucleotides in COVID-19 genome sequences, (2) finding the similarity/dissimilarity between COVID-19 genome sequences by using difference distance measure and (3) Phylogeny construction with various AF methods for COVID-19 genome sequences
- *Mutation hot spots in Spike protein of COVID-19:-*
  Multiple sequence alignments were done using alignment tool of NCBI virus server as well as CLUSTAL Omega. Sequence alignments from CLUSTAL Omega was viewed using MView tool. Multiple sequence Alignment of COVID-19 spike protein sequences from United States of America showed multiple mutations at few frequent locations
- *A lot of web service that we can use it to make alignment sequence as :-*
  MAFFT ---------→https://www.genome.jp/tools-bin/mafft
  PRRN----------→https://www.genome.jp/tools-bin/prrn