

Corona Virus - A Silent Slayor

Satya Rama Devi Nowpada

Assistant professor, Department of Microbiology Maharajah's Post graduate college, Vizianagaram, Andhra Pradesh, India

Abstract: Covid-19, which is famous for its spike like projections, is a novel corona virus causes serious outbreaks in Wuhan city and then becomes pandemic. Covid 19, is a well-versed modification of SARS causes respiratory infections. We anticipate that the metagenomics studies were able to control the viral attachment to host cell.

Keywords: Covid-19, Corona virus, droplets, receptors, metagenomics screening, spikes, respiratory tract infections

1. Introduction

Corona virus is renowned for its spikes on the surface, which was reminiscent of the solar corona¹. People encountered with corona shows respiratory tract infections in lethal conditions However majority of the cases results in mild symptoms that includes fever, cough and shortness of breath to viral pneumonia and multi organ failures². Loss of smell and taste is a common symptom in the early onset of infection³. SARS-COV, which is a beta lineage of corona, was controlled in 2003. In addition, encountered for second time in 2019 with new modifications and becomes pandemic. We have many serious outbreaks of corona virus because of its frequent antigenic shifts and drifts. COVID-19 was first identified in Dec 2019 in the wet markets of Wuhan city became pandemic by March 2020⁴. Corona virus is an enveloped virus of 80nm diameter with a 20nm spike length, which contains a positive sense SS RNA as a genetic material contains 30,000 ntds⁵. The genome is well organized with a 5' leader UTR transcriptase followed by structural genes spike(S) envelope(E) membrane(M) nucleocapsid (N) 3' UTR Poly A with additional haemagglutinin esterase (HE)⁶. The genome contains ORF 1a and 1b, which encodes for nonstructural proteins⁷. In addition to this it also, contains transcription regulatory sequences (TRS) before every structural gene, which is important for the expression of the genes. TRS will guide the genome to enter either into continuous or discontinuous mode of replication⁸. Important feature in corona replication is the production of multiple subgenomic mRNAs that contains sequence corresponding to both sides of RNA⁹. Corona utilize RNA dependent RNA polymerase for transcription as shown in the figure 1.

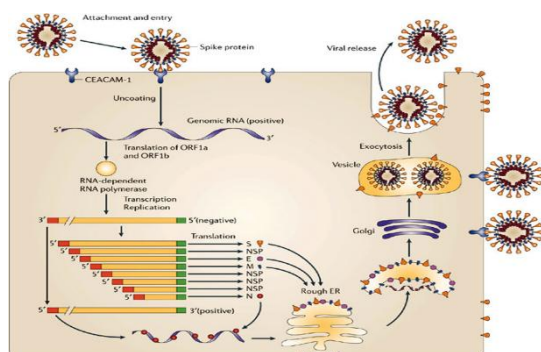


Figure 1: Summary of Replication of corona virus. Virus enters into the host cell through fusion with the surface of the host cell and the release of Viral RNA takes place in the cytoplasm. Virus utilizes the ribosomes instead of entering

into the cell nucleus and undergoes translation to form polypeptides using RNA polymerase. By utilizing RNA Pol, virus synthesizes antisense SS RNA template via continuous replication. Virus also undergoes discontinuous process to form sub genomic particles having common TRF, which leads to the synthesis of structural viral proteins. Fusion of viral progeny with structural proteins takes place in the vesicles and the phage releases out via exocytosis pathway. Credit: Cornelia C. Bergmann, *et al* / Nature Reviews Microbiology

These sub genomic mRNAs are produced by discontinuous replication are responsible for viral proteins which fuse with virion to form a complete virus. Viral progeny is produced through secretory pathway which includes RER, golgi bodies and exocytosis. Surprisingly the virus has taken a second wave in which it transmits from one to others asymptotically. Probably the virus spreads through silent carriers. So early detection of virus in asymptomatic phase is highly encourageable because most of the RNA viral infections in human have no treatment and are essentially unactionable. Intensity of viral load in the body will also depends upon the immunity and age of the individual. Therefore, the control of the spread of disease is highly essential and that is possible by controlling the virus at genome level, which is analyzed by utilizing a genomic tool. Metagenomics, a biotechnological weapon to fight against Corona, in which sequences of Covid RNA is analyzed. Many antiblockers are presently in use as an inhibitor for viral attachment to host cell, which is a primitive step of virus entry. We anticipate that by using functional genomics we can able to study the weak links on the viral genome and mutations in that areas may control the viral pathogenicity. By using different strategies of metagenomics screening we can able to develop blockers in such a way that it interferes with the transcription of genes involved in receptor synthesis leads to loss of host specificity. Meanwhile we can develop Phylochips of different sequences of viral genomes which will be maintained in the library will be helpful for further reference as the virus may cause several future outbreaks.

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