Understanding molecular ultrastructure Coronavirus 2019 (nCoVs).

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Description

Coronaviruses (CoVs) have two main parts on their ultrastructure. First is the capsid (envelope). Second is the core part (core). These two sections are synthesized and incorporated in eukaryotic (host) cells. In this case the host cell is the epithelial cells in the respiratory system. If the molecular classification on the body of the virus, it will be obtained two major macromolecules: proteins and nucleic acids and little of carbohydrate complex [1]. The coronavirus based on the modern classification system is classified into several groups and within the group there are several types of Coronaviruses. Currently one of the very virulent types has been confirmed to be sourced in Wuhan. It is a Coronvirus 2019 (nCoVs) that belongs to group IV. This virulency activity is certainly a manifestation of changes in molecular or molecular levels and progressed to ultrastructure levels. The changes occurring in the viral genome are a serious problem. Can increase risk invasion to cells. For this it is necessary to see the characteristics of molecules at the ultrastructure level of the Coronvirus 2019.

Molecular structure on ultrastructure of capsid

Constituent domain is protein. This section functionally is the protection of genetic against external conditions as well as the role of receptors. Despite the analysis results, coronaviruses are only able to survive a few hours while outside the host. The epitop-receptor functions are produced by a specific protein on the surface. The receptors for this epitope reside in the epithelial cells of the upper and lower respiratory systems. These proteins are known as protein-S. This Protein is then the main characteristic of Coronavirus because it looks like a crown [2].

Besides protein-S there are a few more protein domains. These proteins have specific functions. This Protein is distributed almost evenly on the body part of the virus. In general, proteins in the body of the virus are structural and non-structural. These variations were coded by the genome. Many genome variations occur between the coding gene area Spike (S) and the Nucleoapsid (N). But high risk will be if strong mutation in Spike region code.

Based on the morphological analysis of Coronavirus 2019 using electron microscope researchers did not find any significant differences when compared with coronaviruses that were never found before. The Visual structure of Coronavirus is prone to. This Virus can reach a diameter of 80-160 nm with a skin thickness of around 10-12 nm. Therefore, researchers suspect that there has been a mutation in the core RNA or its genomics.

Molecular structure on ultrastructure of core

The core part is the center of the genomics information of viruses. In this structure there is RNA which is the main source of information. The RNA molecule is single strand or ssRNA. As for the molecular length RNA based analysis sequencing about 30,000 bases. Nevertheless in other studies it is mentioned about 26-32 kilo bases [3]. This RNA molecule has a resemblance to mRNA so that it can be directly transtransition. The analysis of Coronaviruses began in 1965. In the year it was discovered Human Coronavirus or hCoV-229e. To duplicate the genome and the virus device inside the host it takes a specific enzyme that is viral protease [4].

RNA molecules in the core part of the virus undergo folding and playback. This is as a small form of room compensation to be occupied by the RNA. To maintain the RNA structure in the nucleus it takes a special protein such as Histon. The end of the RNA molecule ends will contains Polyadenylation (3' Poly-A and 5' Cap A). One of the analytical techniques that become the standard of genome analysis in viruses is PCR (polymerase chain Reaction).

The genome mapping in Coronavirus is actually completed. Nevertheless, Coronavirus 2019 that spread in Wuhan, China has a high virulence. After analysis there are variations on the genomic structure. The genome of Coronavirus 2019 differs from the genome Coronavirus SARS (Sars-Covs) and the Genome Coronavirus MERS [5]. However, it has a close proximity to Corona's viral genome on Bats.

Conclusion

The coronavirus 2019 ultrastructure Virus has virtually no difference. New differences were found when analysis was performed on the sequence of DNA (sequencing Analysis). In the analysis there is a difference in the DNA arrangement between the old Coronavirus and Coronavirus 2019. The main cause is a genome-level mutation. Nevertheless, it still takes a variety of molecular analyses to see the difference in molecular level. As analysis of the sub-unit of the epitop-receptor proteins.

References

- 1. Maier HJ, Bickerton E, Britton P. Coronaviruses: Methods and protocols. Coronaviruses Methods Protoc. 2015;1–282.
- 2. Banerjee A, Kulcsar K, Misra V. Bats and coronaviruses. Viruses. 2019;11:7–9.
- 3. Coleman M, Frieman MB. Coronaviruses: Important Emerging Human Pathogens. J Virol. 2014;88:5209–12.
- Bárcena M. Cryo-electron tomography of mouse hepatitis virus: Insights into the structure of the coronavirion. Proc Natl Acad Sci. 2009;106:582–87.
- Forni D, Cagliani R, Clerici M. Molecular Evolution of Human Coronavirus Genomes. Trends Microbiol. 2017;25:35-48.

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