**MLS 406: VIROLOGY OPEN TEST**

**THE ORIGIN , ETIOLOGY ,STRUCTURE AND THE PATHOPHYSIOLOGY OF COVID-19**

**ORIGIN OF COVID-19**

The coronavirus disease 2019 is a respiratory disease which is caused by a novel coronavirus [SARS-Cov-2].The coronavirus [covid-19] originated in wuhan china it has since then spread to other parts of the world registering as of March 1 2020 , a total of 87,137 confirmed cases globally , 79,968 recorded in china and 7169 worldwide. The covid19 virus is said to be a mutated form of the SARS (Severe acute respiratory syndrome) and the MERS virus (Middle eastern respiratory syndrome). The covid-19 marks the third introduction of a highly pathogenic and large scale epidemic coronavirus in the human populous. Several independent research groups have identified that SAR-COV-2 belongs to beta coronavirus, with an identical genome to the bat coronavirus , pointing to the bat as the natural host. The corona virus mutated to a form which can be transmitted from animal host to human and then consequently from one human to another.

**THE STRUCTURE OF COVID-19**

Coronaviruses are single-stranded positive-sense RNA viruses that possess large viral RNA genomes recent studies showed that SARS-C0v-2 has a similar genomic organization to other beta coronaviruses consisting of a 5’-untranslated region(UTR), a replicase complex encoding non-structural proteins, a spike protein (s) gene , envelope protein (E) gene , a membrane protein (M) gene ,a nucleocapsid protein (N) gene ,3’-UTR and several unidentified non-structural open reading frames. Although SARS-Cov-2 is classified into the beta coronaviruses group. It is diverse from MERS and SARS-C0v .

**SPIKE PROTEIN (S)** is heavily glycosylated, it utilizes an N-terminal signal sequence to gain access to the ER and mediate attachment to host receptors . it is the largest structure and makes the distinct spikes on the surface of the virus. For most coronaviruses, S protein is cleaved by a host cell furin-like protease into two separate polypeptides S1 and S2.

**RNA** is the genome

**Nucleocapsid protein** (N) binds to RNA invitro and is heavily phosphorylated. N protein binds the viral genome in a beads on a string type conformation. This protein likely helps tether the viral genome to replicase-transcriptase complex (RTC) , and subsequently package the encapsulated genome into viral particles.

**Envelope protein (E)** is found in small quantities in within the virus. It is most likely a transmembrane protein and with ion channel activity. The protein facilitates assembly and release of the virus and has other functions such as ion channel activity. It is not necessary for replication but it is for pathogenesis.

**Membrane protein (M)** is the most abundant structural protein . it does not contain signal sequence and exists as a dimer in the virion . it may have two different conformations to enable it to promote membrane curvature as well as bind to nucleocapsid

**Pathophysiology of covid-19**

The clinical syptoms of covid-19 patients include : fevers, cough , fatigue a small population of patients exhibited gastrointestinal infection symptoms . the elderly and the young and people with underlying diseases are susceptible to infection and are prone to serious outcomes , which may be associated with acute respiratory distress syndrome (ARDS) and cytokine storm

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