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**Course : MLS 406 (virology)**

 Question

Write on the etiology, origin, structure and pathophysiology of COVID-19

Coronaviruses are a family of viruses that can cause illnesses such as the common cold, severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS). In 2019, a new coronavirus was identified as the cause of a disease outbreak that originated in China.

The virus is now known as the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The disease it causes is called coronavirus disease 2019 (COVID-19).

**ETIOLOGY**

It's unclear exactly how contagious the new coronavirus is. It appears to spread from person to person among those in close contact. It may be spread by respiratory droplets released when someone with the virus coughs or sneezes.

It may also be spread if a person touches a surface with the virus on it and then touches his or her mouth, nose or eyes.

Corona virus are zoonotic, meaning they are transmitted between animals and people, it is beloved that COVID-19 was transmitted from pangolin to humans.

**ORIGIN**

Coronaviruses belong to the Coronaviridae family in the Nidovirales order. Corona represents crown-like spikes on the outer surface of the virus; thus, it was named as a coronavirus. Coronaviruses are minute in size (65–125 nm in diameter) and contain a single-stranded RNA as a nucleic material, size ranging from 26 to 32kbs in length. The subgroups of coronaviruses family are alpha (α), beta (β), gamma (γ) and delta (δ) coronavirus. The severe acute respiratory syndrome coronavirus (SARS-CoV), H5N1 influenza A, H1N1 2009 and Middle East respiratory syndrome coronavirus (MERS-CoV) cause acute lung injury (ALI) and acute respiratory distress syndrome (ARDS) which leads to pulmonary failure and result in fatality. These viruses were thought to infect only animals until the world witnessed a severe acute respiratory syndrome (SARS) outbreak caused by SARS-CoV, 2002 in Guangdong, China ]. Only a decade later, another pathogenic coronavirus, known as Middle East respiratory syndrome coronavirus (MERS-CoV) caused an endemic in Middle Eastern countries

Recently at the end of 2019, Wuhan an emerging business hub of China experienced an outbreak of a novel coronavirus that killed more than eighteen hundred and infected over seventy thousand individuals within the first fifty days of the epidemic. This virus was reported to be a member of the β group of coronaviruses. The novel virus was named as Wuhan coronavirus or 2019 novel coronavirus (2019-nCov) by the Chinese researchers. The International Committee on Taxonomy of Viruses (ICTV) named the virus as SARS-CoV-2 and the disease as COVID-19.

**STRUCTURE**

In addition to the SARS coronavirus (treated separately elsewhere in this volume), the complete genome sequences of six species in the coronavirus genus of the coronavirus family [avian infectious bronchitis virus-Beaudette strain (IBV-Beaudette), bovine coronavirus-ENT strain (BCoV-ENT), human coronavirus-229E strain (HCoV-229E), murine hepatitis virus-A59 strain (MHV-A59), porcine transmissible gastroenteritis-Purdue 115 strain (TGEV-Purdue 115), and porcine epidemic diarrhea virus-CV777 strain (PEDV-CV777)] have now been reported. Their lengths range from 27,317 nt for HCoV-229E to 31,357 nt for the murine hepatitis virus-A59, establishing the coronavirus genome as the largest known among RNA viruses. The basic organization of the coronavirus genome is shared with other members of the Nidovirus order (the torovirus genus, also in the family Coronaviridae, and members of the family Arteriviridae) in that the nonstructural proteins involved in proteolytic processing, genome replication, and subgenomic mRNA synthesis (transcription) (an estimated 14–16 end products for coronaviruses) are encoded within the 5′-proximal two-thirds of the genome on gene 1 and the (mostly) structural proteins are encoded within the 3′-proximal one-third of the genome (8–9 genes for coronaviruses). Genes for the major structural proteins in all coronaviruses occur in the 5′ to 3′ order as S, E, M, and N. The precise strategy used by coronaviruses for genome replication is not yet known, but many features have been established.

Spherical or pleomorphic enveloped particles containing single-stranded (positive-sense) RNA associated with a nucleoprotein within a capsid comprised of matrix protein. The envelope bears club-shaped glycoprotein projections. one strain of SARSCoV-2, is 29.9 kb

Some part of virus genome encodes four essential structural proteins, including spike(S) glycoprotein, small envelope (E) protein, matrix (M) protein, and nucleocapsid (N) protein and also several accessory proteins, that interfere with the host innate immune response.

**PATHOPHYSIOLOGY**

The lungs are the organs most affected by COVID-19 because the virus accesses host cells via the enzyme ACE2, which is most abundant in the type II alveolar cells of the lungs. The virus uses a special surface glycoprotein called a "spike" (peplomer) to connect to ACE2 and enter the host cell (WHO 2020) The density of ACE2 in each tissue correlates with the severity of the disease in that tissue and some have suggested that decreasing ACE2 activity might be protective (CDC 2020), though another view is that increasing ACE2 using angiotensin II receptor blocker medications could be protective and that these hypotheses need to be tested. As the alveolar disease progresses, respiratory failure might develop and death may follow (CDC 2020). The virus also affects gastrointestinal organs as ACE2 is abundantly expressed in the glandular cells of gastric, duodenal and rectal epithelium(World Health Association. 2013), as well as endothelial cells and enterocytes of the small intestine.(Cohen J 2020).

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