



From SARS, NL29, HKU1, MERS TO SARS COV-2: a brief summary and comparison of severe acute respiratory caused by five highly pathogenic human Coronavirus

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ABSTRACT

Coronavirus is largely enveloped RNA virus which causes common cold and other gastroenteritis, the prevailing coronavirus causes severe acute respiratory syndrome[SARS-COV-2] and result in death, it was identified in December 2019, its spread is unpredictable, it contains single stranded RNA, glycoprotein, spike (s) protein which plays a major role in binding mechanism. Replication occurs in the form of budding. Since MHV (Mouse hepatitis virus) related to human strain OC43, the mouse hepatitis virus was taken to observe the replication. Because the human coronaviruses are not grown well in culture cell.

Keywords: COVID-19, Coronavirus, SARS, NL29, human Coronavirus.

I.INTRODUCTION:

The study of virus is called virology, viruses are small infectious organism which does not replicate by its own, it completely depends upon the host for replication or reproduction. It contains special protein coat called capsid. It also contains nucleic acid neither DNA or RNA. The viral nucleic acid which plays a major role in the controlling of the host's enzymatic mechanism to replicate. Capsid is the protein coat which interact with the host cell and the main function of this capsid is to protect the nucleic acid It also helps to attach and penetrate the host cell and it is made up of repeating structure of protomers. The inner genome of the capsid called nucleocapsid. Viroid cause transmissible disease in plants and lacks capsid 246 to 375 nucleotides in length. To function, viroids depends on their host as it is too small in size.

II.Coronavirus

Coronavirus was derived from the Latin word corona (crown or wreath). It was first named by June Almeida and David Tyrrel. It is a virus which causes acute respiratory syndrome, Since the spread of the virus is worldwide, it is considered to be dreadful. In 1920 the corona virus was occurred in animals. It was the earliest report of corona virus which causes acute respiratory infection in chickens. In 1933 Leland David Bushell and Carl Alfred Brandly, they isolated the virus IBV (Infectious bronchitis virus). Charles D. Hudson and Fred Robert Beaudette cultured the virus in Beaudette strain in 1937. In 1940 the animal corona virus JHM (Murine encephalitis) and MHV (Mouse hepatitis virus) was discovered and the Human corona was successfully discovered in 1960. Tyrell and Bynoe cultured novel corona virus (229E) in human kidney tissue which causes cold and then it was suppressed by ether, they also cultured B814 (virus) in human embryonic trachea. 229E, it is the human virus which contains club shaped spikes seen under electron microscope. Coronavirus was divided into three groups they are group 1, group 2 and group 3. Group 1 consist of human CoV 229E, HCoV 229E and transmissible

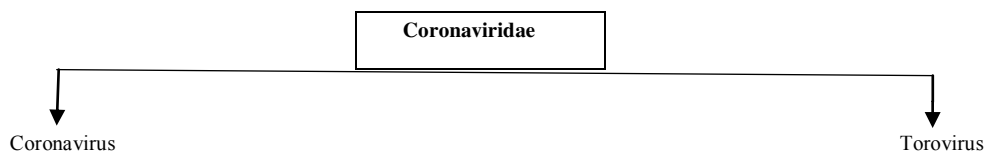
gastric enteritis virus (TGEV). Group 2 consist of HCoV-OC43, Murine hepatitis virus (MHV) and bovine CoV (BCoV). Group 3 contains avian infectious bronchitis virus (IBV), CoV (SARS-CoV).

HUMANCORONA VIRUS

- B814
- OC43
- 229E

Latter B814 lost strain, then 229E and OC43 these both are considered as the human virus.

Realm	Riboviria
Kingdom	Orthornavirae
Phylum	Pisuviricota
Class	Pisoniviricetes
Order	Nidovirales
Family	<i>Coronaviridae</i>



The genus was divided into four:

- Alphacoronavirus
- Betacoronavirus
- Deltacoronavirus
- Gammacoronavirus

Later in 2002 there was a dreadful virus called SARS-CoV, which causes atypical pneumonia, In 2003 it developed into HCoV NL63, then in 2004 it was developed into HCoV HKU1. In 2013 it was transformed into MERS-CoV and finally in 2019 there was an outbreak of SARS-CoV-2 that affects lungs and results in death too.

III. SARS-CoV in 2003:

SARS associated with coronavirus causes severe acute respiratory syndrome, it is an airborne disease which transmitted by saliva, droplets etc. It was first identified in February 2003 at China. The property of the SARS-CoV, they are spherical in shape about 120-160nm in diameter. It contains helical nucleocapsid which plays a major role in the protection of genetic materials, it is about 9-11 diameter. It consists of single stranded RNA; it is linear and non-segmented genome of single stranded positive sense RNA (27-32Kb). It also contains two glycoproteins and it contains large, widely spaced envelope, this envelope contains club or petal shaped spike. The replication is occurred by the budding of cytoplasm particles, these particles are matured into endoplasmic reticulum and Golgi. It causes atypical pneumonia, affects lung, liver, and immune system, it causes apoptosis (death of programmed cells) and necrosis (death of cell or tissue) to the parenchyma cells. SARS-CoV consist of non-structural protein called 3b protein (ORF4), which helps to suppress caspase activity and the nucleocapsid protein oligomerized to form a closed capsuled and contains genomic RNA, it associated with genome and packs the genome inside the cavity. In SARS-CoV, nucleocapsid contains ability to form capsid and It also another major protein coat called spike protein. Nucleocapsid is the major antigen and it is recognized by convalescent antisera. It also consists of viral structural protein called phosphorylated nucleocapsid (N) about 50-60KDa (kilodalton). The inner membrane consists of glycoprotein known as matrix protein which is embedded in the envelope liquid bilayer. The glycoprotein spikes present on the viral envelope which helps in the attachment of host target cell, at this point of time aminopeptides act as a receptor and then it is internalized by the absorptive endocytosis of the host cell membrane. The first event of the replication is the translation of viral genomic RNA, this results in the production of a virus specific RNA polymerase. The newly formed viral polymerase transcribes the full-length complementary RNA and also transcribes the templates for n used set of five to seven sub genomic mRNAs. The sub genomic mRNA is translated into a

single polypeptide. The nucleocapsid protein combines with newly synthesized genomic RNA molecules results in the formation helical nucleocapsid. The process of budding of nucleocapsid through the Golgi and endoplasmic reticulum results in replication which consist of viral glycoprotein. The matured virions are not formed by the process of budding and for the purpose of existing, it is transported in vesicles to the cell peripherals. Large number of infected cells seen in the exterior which induces fusion by S glycoprotein and requires pH of 6.5 or higher and exhibit high frequency of mutation during the process of replication. The genomic structure of SARS-CoV, RNA is organized in 13-15 ORF (open reading frames) and contains 3000 nucleotides with the similar arrangement with replicase and protease in the order of gene1a-1b and the spike (S), envelope (E), membrane (M), nucleocapsid (N) in the order of 5'-3'.

IV.HCoV NL63 IN 2003:

It is the virus which is first identified in 2003 and isolated by Amsterdam from the nasopharyngeal aspirate of a seven-month infant in 2004 at Holland. This virus is considered as the aetiological agent which causes 10% of all the respiratory diseases. It causes fever, conjunctivitis (Infection in the outer membrane of the eyeball or eyelid), coryza (Inflammation of mucous membrane in the nose). VIDISCA (Virus discovery based on cDNA-AFLP) it is the tool which was used to identify the family of the HCoV NL63. It is the single stranded RNA genome which is capped and polyadenylated and the size of the genome is 27553 bases. The order of the genome IS 5'-ORF1a-ORF1b-S-ORF3-E-M-N-PolyT-3' and 1 full length RNA and 5 sub genomic mRNAs, totally seven distinct ORFs are produced from the six distinct mRNAs. It belongs to the genus Alphacoronavirus, subgenus is Setracovirus and species is Human coronavirus NL63.

V.HCoV-HKU1 IN 2004:

It is a type of virus which causes upper respiratory disease and it was identified in 2004. It is considered as 4th human coronavirus, the symptoms are cough, nasal, fever, sputum, sore, throat, tonsillar hypertrophy. 50% of patients who affected by HCoV-HKU1 experiences febrile seizures. It is enveloped, positive sense and contains single stranded RNA virus and it also consist of Hemagglutinin esterase (HE) gene. It is similar to MHV (Mouse hepatitis virus) and its belonged to group 2a coronavirus which means not cultivatable and also consist of 32% of genomes with complete genome sequences which is considered as the lowest among all coronavirus. The genome size ranges from 29,295 – 30,097 nucleotides. It shows the gene order of 5'- replicase ORF1b, spike (S), envelope (E), membrane(M), nucleocapsid(N). It belongs to the genus Betacoronavirus, subgenus is Embecovirus and the species is Human coronavirus HKU1.

VI. MERS-CoV IN 2013:

Middle East Respiratory Syndrome Coronavirus (MERS-CoV). It is a novel coronavirus which causes acute respiratory syndrome, it was first discovered in 2012 and first isolated from Saudi Arabian patient who suffered from severe acute respiratory syndrome in June 2012. MERS-CoV is a lineage C betacoronavirus similar to bat coronavirus. Ten bat species was tested in Ghana, they found Nycteris gambiensis carry 2c betacoronavirus. Reverse transcription polymerase chain reaction is the method which is used to detect the RNA of the coronavirus. HKO4 and HKU5, these are Tylonycteris bat coronavirus which related to MERS-CoV. Human polyclonal Immunoglobulin G (IgG) was added for safety and tolerability, it is considered as the putative therapeutic agent for MERS. It contains very large genome about 30Kb with ten or more ORFs. The arrangement of ORFs 5'-ORF1a/b-S-E-M-N-poly(A)-3' similar to the C betacoronavirus. It also contains many proteins such as spike(S) protein (ORF2, which is responsible for the viral entry, receptor binding, membrane fusion), membrane (M) protein (ORF7), Nucleocapsid (N) protein (ORF8a), AP3 (ORF3), AP4a (ORF4a), AP4b (ORF4b), AP5 (ORF5). It belongs to the class is Pisonviricets, order is Nidovirales, family is Coronaviridae, genus is Betacoronavirus, subgenus is Merbecovirus and the species is Middle east respiratory syndrome.

VII.SARS-CoV-2 IN 2019:

It is a novel coronavirus which causes acute respiratory syndrome, contain spike protein which plays a major role in the receptor recognition and the cell membrane fusion process. It is a single stranded RNA and enveloped virus. The gene fragments consist of structural and non-structural protein, spike (S) protein, envelope (E) protein, membrane (M) protein, nucleocapsid (N) protein these are all considered as the structural protein, the non-structural proteins are 3-chymotrypsin like protease, papain like protease. The spike protein consists of two subunit they are S1 subunit and S2 subunit, the S1 subunit consist of receptor binding domain which is responsible for binding to the host receptor angiotensin (ACE2) converting enzyme 2. S2 subunit is responsible for viral cell membrane fusion resulting in the formation of six helical bundle via two hepted repeat domain. Spike (180-200KDa) consist of extracellular N- terminus a transmembrane (TM). Entire genome (29,881 in length) is characterized by metagenomic next generation sequences based on RNA. It contains large number of glycosylated S protein, it covers the surface of SARS-CoV-2, glycosylate is also binds to host cell receptor (ACE2) and responsible for mediation of cell viral entry. Total length of SARS-CoV-2 is about 1273aa.

VIII.COMPARISON:

PROPERTIES	SARS-CoV	HCoV NL63	HCoV-HKU1	MERS-CoV	SARS-CoV-2
Location of first detection	Guangdong, China (November 2002)	Holland (November 2002)	Hong Kong (January 2004)	Saudi Arabia (2012)	Wuhan, China (December 2019)
Incubation period	5.1 days	2-5 days	2-6 days	5 days	4-5 days
Possible intermediate host	Civet cats	Bats	Bats and Rodent	Palm civets	Pangolins
Predominant cellular receptor	ACE2	ACE2	ACE2	DPP4 or ACE2	ACE2
Mortality	10.8%	28.1 %VS 7.1%	28.1 %VS 7.1%	37%	4.6%

IX.CONCLUSION:

THEREFORE IDENTIFICATIONS OF THESE VIRUSES PAVED THE WAY FOR THE DISCOVERY OF NEW MEDICATIONS AND VACCINES.

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